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THE INTERNATIONAL CONFERENCE ON BIOTECHNOLOGY 2024

15th - 19th JULY, 2024

NAF Conference Center Abuja

Theme

"BIOTECHNOLOGY AS AN ENGINE FOR ECONOMIC GROWTH"

CONFERENCE PROCEEDINGS

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NABDA Journal of Biotechnology Research (NJBR) is targeted at providing a platform for researchers and practitioners to present new research and development outputs to a global audience, in all areas of the subject of biotechnology. The areas of interest for the journal are not limited to the following topics: Agricultural Biotechnology and Bioresources, Biorisk Management, Bioethics and Biosafety, Bioinformatics, Genomics and Proteomics, Environmental Biotechnology and Bio-conservation, Food and Industrial Biotechnology and Medical Biotechnology. This is an open access journal providing immediate open access to its content on the principle that making research freely available to the public supports a greater global exchange of knowledge.

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Signed: **Prof. Abdullahi Mustapha**
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INTERNATIONAL CONFERENCE OF BIOTECHNOLOGY, 2024 (ICoB24)
CONFERENCE PROCEEDINGS

Published By

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ABUJA, NIGERIA

JULY 2024

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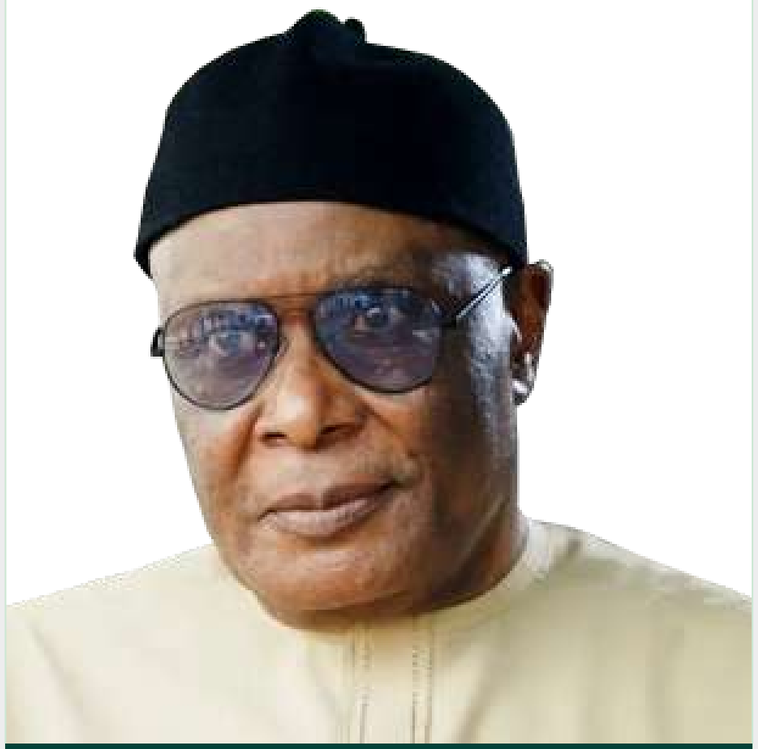

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(ICoB24)

ABOUT THE INTERNATIONAL CONFERENCE ON BIOTECHNOLOGY (ICoB24).

THEME: Biotechnology As an Engine for Economic Growth
FOCUS: Food Security, Energy, Health, And Industry

The National Biotechnology Research and Development Agency (NBRDA), under the Federal Ministry of Innovation, Science & Technology (FMIST) is proud to present the Book of proceedings of the recently held International Conference on Biotechnology (ICoB24). The influential conference brought together leading experts, researchers, and industry professionals from around the world to exchange ideas, share the latest advancements, and discuss the future of biotechnology.

CONFERENCE AIM

This conference aimed to serve as a premier platform for exchanging knowledge, exploring emerging trends, and fostering partnerships among researchers, professionals, industry experts, and policymakers.

The objectives included:

1. The highlights of advancements in biotechnology globally, discussing their potential application and benefits to the continent: The primary objective was to unite global biotechnology pioneers with the purpose of showcasing and exchanging cutting-edge advancements, emerging trends, ground-breaking research, and state-of-the-art technologies. Highlighting the advancements across multiple industries - healthcare, agriculture, industry, environment, and other sectors – demonstrates the value of biotechnology overall and – and not just agriculture.

2. The demonstration of biotechnology's potential to drive economic growth: It presented ground-breaking biotech advancements from various countries (USA, Canada, Argentina, Brazil, South Africa, Japan, Philippines, India, Sudan, Malawi etc), which have the potential to stimulate the emergence of new industries and employment opportunities in Africa and entire Global South. These innovations can play a crucial role in addressing the urgent issue of food insecurity.

3. Connecting African scientists, entrepreneurs, policymakers, and other stakeholders with international expertise: The promotion of networking, exchange of knowledge and establishment of partnerships among Nigerian stakeholders and international experts from various sectors including academia, industry, National Academies of Science, Industry, Farmer groups, government agencies, NGOs, Civil Society Organizations, and investment communities was achieved.

4. Exploration of Industry engagement which encouraged active participation and engagement of biotechnology companies and industry stakeholders who showcased their products, services and achievements.

5. Identification of opportunities and challenges for biotechnology and Biosafety: The current state of biotechnology was thoroughly examined during the conference. Priority issues, barriers to advancement, and areas of need were brought to the forefront for discussion. The focus of the discussion dwelled on formulating solutions and providing incentives to fully harness the potential of biotechnology for the betterment of economic growth and public welfare.

ICoB24 served as a platform for participants to engage in insightful discussions on a wide range of topics such as agricultural biotechnology, healthcare biotechnology, environmental biotechnology, food and industrial biotechnology, Genomics and bioinformatics. Through keynote addresses, plenary sessions, and interactive workshops, attendees had the opportunity to explore the latest research findings and technological innovations in the field of biotechnology. The conference also provided a valuable networking opportunity for participants to establish collaborations, build partnerships, and foster relationships with peers in the biotechnology community. It offered unparalleled networking opportunities, connecting like-minded individuals who shared a common passion for harnessing the power of biotechnology to tackle local challenges to improve lives; and those who may be at the consideration stage. Together, we navigated through the intricate complexities of biotechnology, exploring its potential for revolutionary breakthroughs that were once mere dreams. Additionally, the event featured poster presentations and exhibitions showcasing cutting-edge biotechnological products and services.

Thank you for being part of the ICoB2024 prestigious event.

We look forward to welcoming you again in 2026.

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SPEECHES DELIVERED

OPENING SPEECH BY HIS EXCELLENCY, THE VICE PRESIDENT, FEDERAL REPUBLIC OF NIGERIA, SENATOR KASHIM SHETTIMA, GCON, AT THE OPENING CEREMONY OF THE INTERNATIONAL CONFERENCE ON BIOTECHNOLOGY(ICoB24), MONDAY, 15th JULY 2024, NAF CONFERENCE CENTRE AND SUITES JAHI, ABUJA REPRESENTED BY SPECIAL ADVISER, SPECIAL DUTIES, DR. ALIYU MODIBBO.

Protocol

I am very delighted to be at this auspicious conference put together by the National Biotechnology Research and Development Agency (NBRDA) and for the opportunity to give this address.

I am equally delighted to note that the President, Commander-in-Chief of the Armed Forces, Federal Republic of Nigeria, Senator Bola Ahmed Tinubu, GCFR, envisions a new era of economic prosperity driven by science, technology, and innovation. We cannot achieve amazing economic transformations that will restore our pride in the comity of nations if biotechnology is on the margin of our national development agenda. To prioritise biotechnology is to accelerate and sustain inclusive economic development.

Hence, I am enthralled by the theme of this conference: "Biotechnology as an engine for economic growth." It speaks to the overriding goal of this administration. All our policies seek to foster sustainable economic growth. Our concept of growth is simple: Empowering every Nigerian to experience freedom from poverty and lead a life of dignity.

The second reason why I am enthused by the theme of this conference is because it is grounded in reality and feasibility. Biotechnology can truly reduce Nigeria's burden of food importation. It can transform the ecosystem of Nigeria's healthcare. Furthermore, it can effectively tackle issues of energy poverty. Biotechnology presents tremendous opportunities to revolutionalise industrial practices and thereby contribute to a higher rate of economic growth.

Distinguished ladies and gentlemen, it is cheering to note that the culture of accountability is well entrenched in the sciences. Accountable governance forms the bedrock for sustainable economic growth. It promotes prudent stewardship of public resources. Nigeria's economy will grow sustainably if we are steadfast in our fiduciary duties.

I am very certain that if biotechnology experts and innovators apply the principle of responsiveness in their research enterprises, food insecurity will be a thing of the past in Nigeria.

According to data from the National Bureau of Statistics trade report, Nigeria imported a total of N1.9 trillion worth of food products in 2022. These imported food products constituted 7.29 percent of the country's total imports for the year.

In previous years, Nigeria's imports of agricultural products were as follows:

N1.2 trillion in 2020; N959 billion in 2019; accounting for 5.66 percent of total imports; N857.6 billion in 2018; N886.8 billion in 2017.

Distinguished delegates and participants, conferences are marketplaces of ideas. They engender policy dialogue. Policies are the fulcrum of economic growth. Happily, the vision of the Office of the Vice President is: "To lead and serve as an effective engine room for policy formulation, harmonisation, implementation, and monitoring of the institutions of governance."

When policies are informed by empirical rigor and perspicacity, they serve as engines of economic growth. They create environments that support entrepreneurial ingenuity and safeguard against market aberrations.

This administration seeks to redress inequities. It seeks to spur socio-economic mobility through targeted policy interventions. Therefore, let me urge this noble gathering of biotech experts and innovators to leverage existing policies or engender policy dialogue aimed at ensuring that no demographic group languishes on the peripheries of opportunity. U4

We are living in an era marked by rapid technological advancements, economic disruptions, and geopolitical flux. Hence, we must keep formulating agile policies, which serve as bulwarks against volatility.

Distinguished ladies and gentlemen, this conference tacitly foregrounds the symbiotic relationship between institutional monitoring and economic growth. Institutional monitoring reinforces a culture of fiscal prudence. It also promotes the judicious allocation of resources to initiatives that yield dividends of economic growth. Furthermore, it is important to note that monitoring shapes an ecosystem wherein market actors operate on a level playing field.

In conclusion, I am hopeful that the theme of this conference will stimulate policy dialogue. Such knowledge-driven discourse would enable biotechnology to extend the confines of economic growth to all. I am also hopeful that at the end of this conference, we will all work with renewed courage to ensure no child sleeps without food in Nigeria. May your exchange of expert knowledge contribute to the formulation of instruments that will end energy poverty in Nigeria and will contribute to the creation of viable economic models for translating scientific discoveries into technologies and products. Thereby, enhancing the material condition of Africans.

I hereby declare this conference officially open and wish you very fruitful deliberations.

Thank you so much for your attention.

WELCOME ADDRESS BY THE DIRECTOR GENERAL/CEO, NATIONAL BIOTECHNOLOGY RESEARCH AND DEVELOPMENT AGENCY (NBRDA), PROF. ABDULLAHI MUSTAPHA AT THE INTERNATIONAL CONFERENCE ON BIOTECHNOLOGY HELD ON JULY 15, 2024 AT THE NIGERIAN AIR FORCE CENTRE AND SUITES, ABUJA.

PROTOCOL

I am greatly honoured to welcome you to the inaugural International Conference on Biotechnology 2024 (ICoB24) hosted by the National Biotechnology Research and Development Agency (NBRDA).

It is a great delight that ICoB24 has started in earnest and it is graced with a cream of eminent scientists, scholars, policymakers, delegates, guests, and industry leaders from around the world.

Let me seize this moment to register our profound gratitude to His Excellency, President Bola Ahmed Tinubu, GCFR, for his uncommon leadership foresight. We are inspired by his unparalleled support for the advancement of biotechnology. The positive impacts of his support are enormous on the socioeconomic wellbeing of Nigerians.

Similarly, I would like to thank the Honourable Minister of the Federal Ministry of Innovation, Science, and Technology, Chief Uche Nnaji, for providing exemplary leadership.

Esteemed delegates, it is cheering to note that the National Biotechnology Research and Development Agency (NBRDA) is driving Nigeria's sustainable economic advancement. Since its establishment in 2001, the agency's commitment to driving transformative change, unlocking new economic opportunities, and propelling Nigeria towards a prosperous future keeps intensifying.

NBRDA, as the lead promoter of biotechnology research and development, conducts novel and innovative research in priority areas of agriculture, health, industry, environment, and other strategic sectors for national development.

It is interesting to note that our articulated programmes have enhanced biotechnology utilisation in Nigeria. We have successfully laid the groundwork for sustained economic growth, job creation, and biotech startups. Our ecosystem of innovation will position Nigeria as a leading global player in the field of biotechnology.

Esteemed guests, as we exchange knowledge, collaborate, and innovate, we should bear in mind the potential of biotechnology for sustained economic growth and ethically harness it. The theme of this conference, "Biotechnology as an Engine for Economic Growth," underscores the profound impact that advancements in biotechnology can have on food security, energy production, healthcare, industrial development, and the Environment.

Very distinguished guests, it is also pertinent to restate that one of the key objectives of this conference is to highlight global advancements in biotechnology and their potential benefits for the continent. We seek to showcase biotechnology's capacity to drive economic growth. This conference will create transborder bridges that will connect African stakeholders with the rest of the world.

ICoB is designed to be one of Africa's leading platforms for collective reflection and ideation. It is an open forum for big-picture thinkers that will create more inclusive and prosperous world. Let us draw inspiration from the words of the eminent scientist, Albert Einstein. According to him: "The world as we have created it, is a process of our thinking. It cannot be changed without changing our thinking." To develop Africa, we need novel paradigms of actionable thought. We need bold thinkers who defy impossibility. It is our earnest hope that ICoB will inspire the next generation of scientists to think. Thinking scientists are torchbearers of ethical economic development.

Esteemed delegates, as this conference hopes to turn a new chapter in the history of biotechnological development in Africa, let us endeavour to think differently, challenge assumptions, embrace change, and work together. The future belongs to collaborators. The future relevance of biotechnology might be endangered if we do not join minds and hands together to turn it into an engine for economic growth.

Distinguished scientists, we live in a borderless world with vast opportunities for knowledge sharing, storing, and processing. Therefore, we should ensure the insights gained here reach a broader audience and are translated into tangible advancements in the biotechnology sector. We will ensure that the knowledge shared during this conference is properly archived, and well utilised for human development.

Very distinguished participants, we anticipate that this conference will yield significant outcomes as we seize its inherent opportunities to shape the future of biotechnology and pave the way for a brighter and more prosperous tomorrow.

In conclusion, the role of biotechnology in human development cannot be overstated. It is essential to fostering development in agriculture, medicine, environmental sustainability, and industrial innovation. Let us renew our commitment to ensuring its capabilities to further improve the quality of human life and contribute to sustainable development goals worldwide are optimally harnessed.

Thank you.

INTRODUCTORY REMARKS BY THE CHAIRMAN, LOCAL ORGANISING COMMITTEE (LOC), DR. ROSE M. GIDADO AT THE INTERNATIONAL CONFERENCE ON BIOTECHNOLOGY 2024 HELD ON JULY 15, 2024, AT THE NIGERIAN AIR FORCE CENTRE AND SUITES, ABUJA.

PROTOCOL

It is with a great sense of honour and privilege that I stand to make some introductory remarks as the Chairman of the Local Organizing Committee (LOC) for the maiden bi-annual International Conference on Biotechnology convened by the National Biotechnology Research and Development Agency (NBRDA).

I am pleased to inform you that this conference was designed on purpose and for a purpose: To advance knowledge and foster collaboration in biotechnology for the betterment of humankind. It seems pertinent for me to quickly reiterate the five core objectives of ICOB24.

1. To highlight advancements in biotechnology globally and discuss their potential applications and benefits to the African continent.
2. To demonstrate biotechnology's potential to drive economic growth.
3. To connect African scientists, entrepreneurs, policymakers, and other stakeholders with international expertise.
4. To explore Industry engagement.
5. To identify challenges and opportunities for biotechnology and Biosafety.

It seeks to become Africa's leading innovators' forum that inspires the next generation, a hub for policy dialogue, poised at the intersection of scientific enquiry and societal advancement.

The National Biotechnology Research and Development Agency is aware that the reputations of conferences are built over time. So, we are dedicated to upholding standards of excellence. The caliber of our invited speakers shows this conference aspires to exceed the global best standard. They all have well-burnished reputations for knowledge and innovation, which in part, stems from their ability to educate, impart wisdom, and inspire greatness.

Distinguished participants, we are aware that the laudable objectives of this conference cannot be realized without partnerships. We require partnerships that compress financial patronage, knowledge-sharing, and resource mobilization to translate research outcomes into solutions with market values. I therefore acknowledge and appreciate all ICoB24 partners.

Esteemed attendees, as you may have noticed, we have a well-crafted agenda that balances lectures, panels, networking, and relaxation. This is to ensure engaging interactions. Knowing that time is valuable and should be used wisely, we shall keep to the schedule. Please, let punctuality be a hallmark of your attendance. Punctuality is not merely the soul of business; it honours all participants.

We are aware that satisfied attendees are engaged participants, we also know hospitality is a recipe for success. Hence, within the limit of available funds, we shall provide the best nourishment we can to you. We urge you to cherish every moment.

The NAF Centre has made efforts to ensure that the signage and directions are clear, to enable you move to venues of sessions, exhibitions, restrooms, and so forth with ease. If you need any help, please do not hesitate to ask the ushers or any of the officials.

Before I take my seat, let me express our profound gratitude to our partners and sponsors. Your support has ensured a seamless execution of this event. They have also enhanced our capacity for impact-making collaborations. More importantly, they demonstrate and underpin a shared commitment to harnessing biotechnological solutions for human flourishing, ecological sustainability, and inclusive socioeconomic progress.

Similarly, members of the LOC would like to express their gratitude to the Director General/CEO, NBRDA, Prof. Abdullahi Mustapha, for his prudent leadership and strategic support. Your express approvals were sine qua non.

Let me also seize this medium to gratefully acknowledge the hard work of members of the organizing committee. Your dedication is unparalleled.

Lastly, we are optimistic that our deliberations will trigger transformative changes and contribute to creating a future where biotech innovation serves as an engine of eco-friendly and inclusive economic growth. Let us endeavour to catalyze innovation through dialogue and the triumph of intellect over ignorance.

REMARKS BY HIS EXCELLENCY, DR. ABDULLAHI UMAR GANDUJE,OFR, CHAIRMAN, ALL PROGRESSIVE CONGRESS (APC)PARTY, ABUJA AT THE OPENING CEREMONY OF INTERNATIONAL CONFERENCE ON BIOTECHNOLOGY OR GANIZED BY NATIONAL BIOTECHNOLOGY RESEARCH AND DEVELOPMENT AGENCY, 15-19TH JULY 22024, NAF CONFERENCE AND SUITES, JAHI.

PROTOCOL

Distinguished guests, esteemed delegates, and honored speakers,

It is an honor to address this esteemed gathering at the International Conference on Biotechnology. As the Chairman of the ruling party in Nigeria, I am proud to witness the contributions of biotechnology as an engine for economic growth in our country and around the world. Biotechnology has transformed various industries, from agriculture to healthcare, and has become a catalyst for economic development. In Nigeria, we recognize the potential of biotechnology to drive sustainable growth, create employment opportunities, and improve the quality of life for our citizens. The impact of biotechnology on agriculture cannot be overstated. Through advances in genetic engineering, crop production has become more efficient, resilient, and sustainable. This has not only increased food security inother countries that have adopted the technology but has also boosted the income of their farmers especially in USA, Brazil, Argentina, Canada, China, Japan, South Africa, Suadn etc thus contributing to economic growth in these countries.

In the healthcare sector, biotechnology has revolutionized the development of new pharmaceuticals, diagnostics, and treatment methods. The potential for biotechnology to address health challenges and improve access to healthcare is immense, and we are committed to harnessing this potential for the benefit of our people. Furthermore, the integration of biotechnology into industrial processes has the potential to drive innovation, create new business opportunities, and enhance productivity. As a government, we are committed to creating an enabling environment for biotechnology research, development, and commercialization.

We recognize the need to invest in infrastructure, education, and policy frameworks that support the growth of the biotechnology sector. By partnering with the international community and fostering collaboration between academia, industry, and government, we aim to leverage the power of biotechnology for inclusive economic growth. Nigeria, like many other nations, recognizes the transformative power of biotechnology in driving economic growth and improving lives. Our government must invest heavily in biotechnology research and development, so that we will also witness breakthroughs in agriculture, healthcare, and environmental sustainability.

The theme of this conference, "Biotechnology as an engine for economic growth," resonates deeply with our party's vision for Nigeria's future. We are committed to harnessing biotechnology's potential to diversify our economy, create jobs, and enhance the well-being of our citizens. We have established a robust regulatory framework to govern the development and deployment of biotechnology products. Our goal is to create an enabling environment that fosters innovation while protecting our citizens and the environment.As we gather at this conference, I urge all stakeholders to join hands in advancing the role of biotechnology as an engine for economic growth. Let us explore new frontiers, share knowledge, and build partnerships that will propel our nations towards prosperity.

In conclusion, I reaffirm Nigeria's dedication to biotechnology as a catalyst for economic growth and sustainable development. I urge all stakeholders to join forces in harnessing the potential of biotechnology to create a brighter future for our nations and our world.

Thank you for your attention.

Dr. Abdullahi Ganduje
Chairman of the Ruling party in Nigeria

KEYNOTE ADDRESS BY H.E CLEMENT DAVID EBRI, CON, AT THE INTERNATIONAL CONFERENCE ON BIOTECHNOLOGY ORGANIZED BY THE NATIONAL BIOTECHNOLOGY RESEARCH AND DEVELOPMENT AGENCY ON 15TH JULY, 2024 AT THE NIGERIAN AIR FORCE CENTRE AND SUITES

Protocol

I am very delighted to deliver the keynote address at this all-important international conference on Biotechnology 2024, with the theme ""Biotechnology as an Engine for Economic Growth", convened by the National Biotechnology Research and Development Agency (NRBDA).

It also gives me joy to know that this bi-annual conference, in part, stems from the strategic need for networking. In today's knowledge ecology, sustainable human capacity development cannot be achieved without networking. When experts with diverse perspectives and prowess converge, it creates avenues for generating new ideas and forming enduring partnerships.

I am optimistic that a cross-disciplinary and transborder networking platform of this status would facilitate seamless knowledge exchange, technology transfer, and capacity building. Furthermore, it will empower African scientists and entrepreneurs to thrive in the global landscape of biotech innovation. Given this, let me salute the foresight of NRBDA for creating this platform.

Distinguished ladies and gentlemen, a careful look at the theme of this conference shows its departure from "science for science's sake" to "science for societal benefits". It could be seen as an indication that the era of self-serving and ego-gratifying science is gone. We are in a new era of science for human development and economic growth. Our economic development is largely dependent on our reimagination of science. Thankfully, this conference seeks to foster such reimagination.

Esteemed scientists and policymakers, reimagining science for national development entails utilising scientific knowledge, innovation, and technology as drivers of economic growth and enhanced quality of life. It demands entrenching a scientific culture of application-oriented research that can directly benefit individuals, households, communities, and industries. We cannot truly envision and build a prosperous nation or continent without bridging the gap between the lab and life.

For science to remain the gateway to economic fortune, it demands that we do not merely seek answers but deeper questions, challenge conventions, reimagine old paradigms, and forge new ones. Delightedly, science is the art of asking critical questions. For it is driven by curiosity and enquiry. When we observe phenomena and wonder why they behave in a certain way, we formulate questions to explore them. Thereafter, we make educated guesses. So, in the spirit of scientific enquiry, let me ask seven basic questions that may serve to stimulate our collective reflection.

1. Can the tangible outcomes of our research activities be measured in terms of societal benefits?
2. Do the benefits include economic growth, food security, improved health outcomes, energy security, functional industries, and viable eco-friendly industries?
3. Do they significantly address existential challenges and promote social harmony?
4. Why are African economies growing at subnormal rates?
5. Looking at the Gross Domestic Expenditure on Research and Development (GERD) of most African nations, can we truly say that we are prepared to harness science for economic growth?
6. If we conduct quick patent counts and citations, can we truly say biotechnology is a driver of economic growth in Africa?
7. Looking at the quantitative indicators of the contributions of science to economic growth, can African scientists say they have done well?

The above questions are premised on the notion that science will not automatically fuel the engine of economic growth. This is particularly true if we do not constantly appraise the socio-economic relevance of our research efforts. Good enough, science is amenable to self-critique and a culture of validation and refutation.

I think this all-important conference would be a huge success if all we do is formulate scientific questions informed by challenges faced by African societies. Addressing the questions may spur innovative solutions, technological advancements, and improvements in the four focal areas of this conference: Food security, energy, health, and industry.

Distinguished guests, in the face of life-threatening hardship, African nations cannot afford to present science as a luxury that satisfies intellectual curiosity at the expense of taxpayers' fortune. Hence, at the risk of sounding like a reductionist, we must present science as an engine of economic growth, a contributor to social progress, ethics, and cultural enrichment. As scientists, we must ensure our research and development initiatives have significant impacts on society and that their dividends enrich generations to come.

Africa's quest for sustainable development may remain a mirage if we do not turn our laboratories into hubs of innovations that fuel eco-friendly and people-centric economic progress. Hence, as experts who put society first, our new philosophical orientation to science, technology, and innovation should have elements of utilitarianism.

Utilitarian approaches to science favour research and development that are essentially focused on producing practical benefits and applications for society. So, let me appeal to this gathering of eminent scientists, policymakers, scholars, industry leaders, and biotechnology enthusiasts that as we labour to extend the limits of human knowledge and understanding, we should also focus on immediate

practical applications that are capable of accelerating socio-economic development.

I am happy that many African leaders are firm believers in the power of science to positively transform human lives and societies. They know that national development through science begins with robust investments in research and development across various disciplines. As seen in Nigeria, key among the eight (8) priority areas encapsulated in the 2024 Budget are: "investment environment optimisation, human capital development, poverty reduction, and social security".

This demonstrates that some African governments cherish allocating resources to support scientific research that addresses national priorities such as food security, healthcare, energy, industry, and environmental sustainability. However, the present economic situation suggests that governments cannot singlehandedly undertake the development imperative of funding R&D. Therefore, they should develop viable catalogues of incentives to attract private sector investors.

Esteemed participants, I am sure you would agree with me that the research and development (R&D) intensity of most African nations does not suggest we seek to dynamize our economies by making science its backbone. The amount of resources African countries invest in R&D activities relative to their total revenue or gross domestic product (GDP) is abysmally low relative to the more industrialized economies. In the USA, for instance, the 2024 budget of President Biden set investment target for Amercan Science, Technology and Innovation (STI) to achieve America's greatest aspirations (https://www.whitehouse.gov/ostp/news-updates/2023/03/13/fy24-budget-fact-sheet-rd-innovation/), including the largest ever federal R&D of $210 billion. The 2024 US budget also provides for strenghtneing R&D enterprise, for basic and applied research that sets America apart as an innovation engine and envy of the world. According to the R&D Statistics (2022 – 2023), India's Gross Expenditure on R&D (GERD) has consistently increased over the years and more than doubled over the last decade standing at approximately USD17.2 billion in 2020 - 21; however, India's Gross Expenditure on R&D (GERD) as percentage of GDP standing at 0.65% (2020 - 2021), which is far higher than Nigeria's 0.13 % in 2022, falls behind major economies like China (2.4 %), Germany (3.1 %), South Korea (4.8 %), the United States (3.5 %) and Israel (6 %, in 2022). The increased investment in R&D has, little wonder, resultantly yielded much value to these countries. According to the India's Bioeconomy Report 2023 (December), India's bioeconomy 2020 - 2022 (revised figures) grew 37.3% from $86.0 billion in 2020 to reach $137.2 billion in 2022; and is envisioned to grow to USD300 billion by 2030 and account for 5 - 6 % of India's GDP. Therefore, to demonstrate that we are a continent that prioritises innovation and the creation of new technologies, products, or processes, for wealth and jobs creation, African countries including Nigeria must invest more in science, technology and innovation (STI) as the lever of a knowledge-based economy.

As an epistemic community that cherishes diversity of thoughts, we hope this conference will propose sector-specific investment models that would make biotechnology a veritable contributor to Africa's GDP growth.

At the moment, Africa's net exports of high-technology products paint a gloomy picture of the contribution of science, technology, and innovation to economic growth. It does not indicate we can compete in global markets. Hence, we should focus on improving the technological balance of trade by increased investments in STI.

Furthermore, as we have convened with a shared vision to connect African scientists, entrepreneurs, policymakers, and stakeholders with global experts and investors, we should endeavour to develop an actionable template that would improve the number of new products and processes introduced, improvements in productivity, and the adoption rate of new technologies by businesses and industries. In so doing, we will be enabling the continent to effectively harness its capabilities and unlock new markets.

Distinguished ladies and gentlemen, I suspect that the theme of this conference "Biotechnology as an Engine for Economic Growth" will remain a mere theoretical fact without any existential relevance to Africans, if we keep failing at the commercialization of novel scientific discoveries. We will keep playing catch-up in the comity of nations if we do not focus on translating scientific discoveries into practical applications through commercialization or technology transfer. Without any fear of contradiction, I wish to state that the existing gap between our labs and markets cannot facilitate the development of new industries, the creation of job opportunities, and sustained economic growth.

Therefore, African scientists must prioritise licensing technologies from research institutions to businesses and creating spin-off companies based on scientific research. These will greatly enhance the economic impact of scientific activities.

I think it is fair to say that it is anti-development for us to keep using our intellectual capital to conduct groundbreaking research activities without optimizing the market value of their outcomes.

Without prejudice to biomedical experts, why do we derive so much satisfaction from merely conducting excellent medical research without developing and commercialising new drugs, vaccines, and medical devices to treat diseases and improve healthcare outcomes? Is this indicative of a failure of entrepreneurial imagination? Or is it that our policy instruments are not robust enough to bridge the gap between labs and markets?

Why is food insecurity a bane of economic development when we have so many arable lands and biotech experts? A heuristic answer would suggest that it is because our knowledge of improved crop yields, development of drought-resistant crops, and sustainable farming practices is isolated from market logic.

No nation has developed without incorporating scientific knowledge with market logic. Innovation without commercialisation is a recipe for economic stagnation. It frustrates the spirit of scientific enquiry.

Distinguished ladies and gentlemen, for Africa to advance economically, we need to recalibrate the politics of funding science, technology and innovation. Our current budgetary provisions do not sufficiently support transforming scientific

advances into societal benefits compared to what obtains in the industrialized countries. Subsidising consumption is a growth retardant. However, subsidising innovation is a catalyst for economic growth.
Hence, governments of African nations should provide meaningful financial assistance to reduce the high cost of innovation activities. They should provide subsidies aimed at making new technologies more competitive in the market.
Following the above, let me propose that in the short term, commercial viability or immediate societal benefits should be a criterion for funding science-based projects. The downside of this proposal is that it might overshadow essential research that may lead to breakthroughs in the future.
Esteemed scientists, I am tempted to ask, is it naive optimism to posit that biotechnology will leapfrog Africa's economy if the politics of resource allocation is recalibrated? When I imagine a prosperous and great Africa, pictures of an Africa where biotech innovators have access to grants come to mind. For one way to measure the strength of a nation's scientific culture is to look at the amount of non-repayable funds provided by public institutions, charities, or foundations to encourage particular research, development, or innovation projects in target areas of national interest such as food security, healthcare, renewable energy, or education.
In closing, it is my considered opinion that the focus of this conference shows a commitment to making biotechnology relevant to the daily experience of people. It underscores a new mode of thinking about the overriding goal of research and development activities. Given our economic reality and global competitiveness, no African nation can afford to perpetuate ego-gratifying scientific tradition.

Thank you for your rapt attention.

SPEECH DELIVER BY HIS EXCELLENCY THE EXECUTIVE GOVERNOR OF NASSARAWA STATE, ENGR. ABDULLAHI A SULE AS DISTINGUISHED GUEST OF HONOUR ON THE OCCASION OF INTERNATIONAL CONFERENCE ON BIOTECHNOLOGY HOLDING AT NIGERIAN AIR FORCE CENTRE ABUJA, 15TH-19TH JULY 2024.

Distinguished Guests,
It is an honour to stand before you today as the Distinguished Guest of Honour at the International Conference on Biotechnology. I extend my heartfelt gratitude to the organizers for inviting me to this prestigious event, and I commend them for their dedication to advancing the field of Biotechnology.
Biotechnology has emerged as one of the most promising and transformative fields of our time. Its potential to revolutionize health care, agriculture, and environmental sustainability is unparalleled. As we gather here, experts from around the world have come together to exchange knowledge, share insights, and explore the latest advancements in Biotechnology.
The theme of this conference: "Biotechnology as an Engine for Economic Growth" resonates deeply with vision we hold for better future. Biotechnology has the power to address the most pressing challenges facing humanity, including food security, disease eradication, and environmental conservation.
In Nigeria, we recognize the immense potential of biotechnology in driving economic growth and sustainable development. Our commitment to harnessing biotechnology is reflected in our National Biotechnology Development Agency, which serves as a catalyst for innovation, research, and development in this field. We are proud of the strides we have made in biotechnology, but we also acknowledge that there is much more to be done.
As a nation, we must continue to invest in research and development, foster collaboration between academia and industry, and create an enabling environment for biotech start-ups and entrepreneurs. We must also priotize the ethical and responsible use of biotechnology to ensure that its benefits are accessible to all, without compromising safety or human dignity.
This conference provides us with an invaluable platform to share best practices, learn from each other's experiences, and forge partnerships that will drive biotechnology forward. I encourage all participants to actively engage in discussion, challenge existing paradigms, and explore innovative solutions to the global challenges we face.
I would also like to acknowledge the contributions of scientist, researchers, and industry leaders who have dedicated their lives to advancing biotechnology. Your work not only pushes boundaries but also inspires future generations to pursue careers in this exciting field. It is through your tireless efforts that we can unlock the full potential of biotechnology for the benefit of humanity.
In conclusion, I express my sincere gratitude to the organizers of this conference for their commitment to promoting biotechnology and creating a platform for meaningful dialogue. I am confident that the discussions and collaborations that will take place over the next few days will contribute to the advancement of biotechnology and pave way for a brighter and more sustainable future.
Thank you all, I wish you all a productive and inspiring conference.

GOODWILL MESSGE DELIVERED BY THE COMMISSIONER, SOKOTO MINISTRY OF INNOVATION AND DIGITAL ECONOMY, HONOURABLE BASHAR UMAR KWABO, DURING THE INTERNATIONAL CONFERENCE ON BIOTECHNOLOGY, AT THE NAF CONFERENCE CENTRE, ABUJA, BETWEEN 15-19 JULY 2024.

All Protocol duly observed.
I am indeed honored to have represented the Sokoto State Government, by extension my principal, the Governor of Sokoto State, His Excellency, Dr Ahmad Aliyu Sokoto FCNA at this very unique event.
I will start by appreciating the President, commander in chief of the Armed Forces of the Federal Republic of Nigeria, His Excellency Asiwajiu Bola Ahmed Tinubu GCFR for his countless contributions towards development of Technology, Innovation and inventions across various facets of governance in Nigeria.
This International Conference's theme 'Biotechnology as an Engine for Economic Growth' is a well thought out concept that requires us to appreciate the National Biotechnology Research and Development Agency, and indeed its supervising Ministry, the Ministry of Innovation, Science and Technology.
It is a well known fact that the ICT and Digital-economic-related contributions to the country's GDP over the past few years has been very encouraging. Recent reports shows that "about N8.4 trillion was contributed in Q4, 2023".
But little has been known on what had been tapped from the potentials of Biotechnologies in Nigeria. That is why this event is a turning point that all stakeholders needs to embrace and contribute to ensure we have adequate policies, frameworks and legislation to back the agenda of this administration, which includes harnessing all the bounties associated with Biotechnology in Nigeria.
According to the US Department of Agriculture, "there are 4 fundamental kinds of biotechnology: The four abecedarian types of biotechnology are; clinical biotechnology (red), ultramodern biotechnology (white), natural biotechnology (green), and marine biotechnology (blue)". Currently, the United States of America is the number one country in terms of development of Biotechnology worldwide. Nigeria has all it takes to be a key player in global Biotechnology development.
Be rest assured that the Government of Sokoto State is always ready to partner and collaborate with the Federal Government, multinational corporations and all other credible institutions within the organized private sector to fast track development of Biotechnology in Sokoto State for the benefit of Nigeria and Nigerians as a whole.
We thank you most sincerely for giving us the opportunity to be part of this history-in the making process, and we do hope, by the end of the week when this conference comes to a close, we would all take home, take-away a holistic communique that our respective States could use to develop Biotechnology from the grassroots, bottle top.

Thank you and wasaalamu Alaikum

GOODWILL MESSAGE DELIVERED ON BEHALF OF THE PRESIDENT OF NIGERIAN ACADEMY OF SCIENCE AT THE 2024 INTERNATIONAL CONFERENCE ON BIOTECHNOLOGY BY PROF. JOSEPH.E. AHANEKU, FAS, VICE-CHANCELLOR, NATIONAL UNIVERSITY OF SCIENCE AND TECHNOLOGY, ABUJA.

Your Excellency, the President of the Federal Republic of Nigeria, Ashiwaju Bola Ahmed Tinubu,GCFR and Grand-Patron of Science.
Your Excellency the Former President of Federal Republic of Nigeria, Dr Goodluck Ebele Jonathan,GCFR,
The Chairman of the Occasion,
The President, African Development Bank and Keynote speaker, Dr Akinwunmi Adesina, CON
The Director-General, National Biotechnology Development Agency, Prof. Abdullahi Mustapha
Your Excellencies, Invited Guest, Ladies and Gentlemen
I am pleased to be here to represent the President of Nigerian Academy of Science,Prof Eka Braide, FAS and the Academy at this important international Scientific gathering.I congratulate the Director-General of NBDA for organizing this event and for attracting the very highly distinguished speakers at this conference. I salute in a special way the keynote speaker for his Interest in advancing Science and humanity through the support from African Development Bank and advocacy which he has been championing across Africa and beyond.
2. Biotechnology has become an indispensible aspect of human development and wellbeing spanning through advancement in human and animal health to developments in pharmaceuticals, revolution and food security, and to
3.The Nigerian Academy of Science being a pre-eminent Academy had long recognized the importance of Biotechnology in the development of humanity and thus made Biotechnology a thematic area of research within the Academy's areas of specialization thereby encouraging advancement in Biotechnology research.
4.The Nigerian Academy of Science will always be ready to partner with National Biotechnology Development Agency and such other bodies or organizations for the promotion of Biotechnology research and development.
It is my earnest desire that the outcome of this conference will create palpable awareness in the area of Biotechnology research and development with the attendant economic benefits in Nigeria.
Thank you

ARow Prof.J.E. Ahaneku, FAS
Vice-Chancellor, National University of Science and Technology, Abuja

For: **President, NAS Prof. Eka Braide,** FAS.

SPEECH BY THE HONOURABLE MINISTER, FEDERAL MINISTRY OF INNOVATION, SCIENCE AND TECHNOLOGY (FMIST), CHIEF UCHE GEOFFREY NNAJI AT THE INTERNATIONAL CONFERENCE ON BIOTECHNOLOGY ORGANIZED BY THE NATIONAL BIOTECHNOLOGY RESEARCH AND DEVELOPMENT AGENCY ON JULY 15,2024, AT THE NIGERIAN AIR FORCE CENTRE AND SUITES

Protocols

It is with great pleasure that I welcome you to this significant conference organized by the National Biotechnology Research and Development Agency (NBRDA). I am delighted to acknowledge NBRDA as one of the key agencies of my Ministry that is pushing the boundaries of innovation and economic development in Nigeria.

The theme of this conference,"Biotechnology as an Engine for Economic Growth," is both apt and timely. It aligns perfectly with the Renewed Hope Agenda and the development agenda of President Ahmed Bola Tinubu GCFR and strategically advances the mission of our ministry. Which is "To facilitate the development and deployment of science and technology to enhance the pace of socio-economic development through appropriate technological inputs into productive acivities in the nation."

Distinguished guests and participants, economic growth involves the increase in the production and consumption of goods and services within an economy over a specified period. This theme is ambitious, premised on the optimistic notion that biotechnologycan significantly expand the output of our national economy.I share this optimism. Biotechnology has the potential to boost our Gross Domestic Product (GDP) by increasing the total value of all goods and services produced in Nigeria.

This optimism is grounded in the fact that science fuels production expansion.We have many patriotic and innovative biotechnologists who can ensure that more goods and services are produced and made available in our economy, thus contributing to the cconomic diversification agenda of President Bola Tinubu's administration.

I assure you that our dear President is deeply committed to ending Nigeria's overreliance on oil revenue and improving the living standards of Nigcrians.The central role of science in achieving this noble goal cannot be overstated.

FMIST has prioritized creating a supportive ecosystem for startups, providing them with necessary resources, mentorship, incubators, accelerators, co-working spaces, and networking opportunities. These support mechanisms will enable startups to grow quickly, create jobs, introduce new products and services, and stimulate competition in established industries.

Biotechnology startups are notable revenue generators. With the emerging supportive ecosystem, there is good reason to hope that Nigeria will soon experience a higher economic growth rate, driven by licensing agreements,patents,and the commercialization of products and technologies from startups.

Experts attract investors. With the high-level expertise developed in core biotechnology fields, attracting long-term investors, both domestic and foreign,should not be difficult. Investors are crucial as they stimulate efficient production and innovation.

Esteemed guests and delegates, I am strongly persuaded that food insecurity will become a thing of the past in Nigeria with the application of biotechnology for improved crop yields, drought-resistant crops, and better agricultural practices.However, this also requires attracting investors.

There are impediments to transforming Nigeria's economy through biotech innovation, such as the public's misguided aversion to biotechnology. Many misunderstand what biotechnology is and its contributions to human development. Some see it as an esoteric scientific endeavor with no tangible economic value, while others view it as advancing a dangerous agenda. To maximize biotechnology's economic benefits, as seen in the Asian Tigers, we must address these misconceptions through public education and enlightenment campaigns.

Public awareness of biotechnology's role in industrial processes, such as fermentation and enzymatic conversions leading to bio-based products like bio-plastics and bio-based chemicals, can improve the investment climate. These products are biodegradable and reduce carbon footprints, enhancing their appeal to the public and investors.

Moreover,assuring Nigerians that biotechnological practices do not occur in an ethical vacuum is essential. There are robust ethical frameworks addressing concerns related to genetic modification, privacy in genetic testing, and equitable access to biotechnological innovations.

Transforming scientific advances into societal benefits requires dispelling popular myths. For example, GM foods will not foster food security and economic growth unless we execute strategic public communication programs.Transparency and accountability in communication can counteract anti-scientific biases and phobias, ensuring our quest for a prosperous future is successful.

I am pleased that one objective of this conference is to highlight significant global biotechnology breakthroughs and underscore their applicability and potential benefits for our nation and continent. Showcasing examples of scientific research activities that have contributed to economic development can build trust and demonstrate science's practical value. This is part of why we organize the annual Science, Technology, and Innovation Expo.

In conclusion, I am confident that biotechnology will not prevail. Biotechnology will drive economic development in Nigeria and empower Nigerians to achieve their dreams.

Ladies and gentlemen, thank you for your undivided attention.

CLOSING REMARKS BY THE DIRECTOR GENERAL/CEO, NATIONAL BIOTECHNOLOGY RESEARCH AND DEVELOPMENT AGENCY (NBRDA), PROF. ABDULLAHI MUSTAPHA AT THE CLOSING CEREMONY OF THE INTERNATIONAL CONFERENCE ON BIOTECHNOLOGY HELD ON JULY 19, 2024 AT THE NIGERIAN AIR FORCE CENTRE AND SUITES, ABUJA.

Distinguished Guests,
Esteemed Delegates and participants,
Gentlemen of the Press,
Ladies and Gentlemen,

As we bring the International Conference on Biotechnology 2024 (ICoB24) to a close, it is with great honour and gratitude that I reflect on the past five days of insightful discussions, collaborations, and innovations that have transpired here.

Throughout this conference, we have witnessed the convergence of brilliant minds, the exchange of innovative ideas, enriching research presentations, engaging panel discussions, and the establishment of invaluable connections that transcend boundaries and disciplines.

The theme "Biotechnology as an Engine for Economic Growth" has resonated deeply and highlighted the crucial role of biotechnology in shaping our economic landscapes, enhancing food security, advancing healthcare, fostering industrial development, and preserving our environment.

Very distinguished guests, the seeds of transformative change have been planted here, and it is our collective duty to nurture them and allow innovation to flourish, and progress to thrive. Let us remain resolute in our commitment to harnessing biotechnology as a driver for positive change and ensure that the knowledge shared and the networks built here continue to yield benefits for years to come.

I would like to express my profound appreciation to all the distinguished speakers, scientists, scholars, policymakers, industry leaders, and delegates who have contributed their expertise, insights, and passion to make ICoB24 a resounding success. Your active participation and commitment to advancing the frontiers of biotechnology and driving sustainable economic growth through innovation are commendable.

I am also deeply grateful to our esteemed partners and sponsors, namely Agro-climatic Resilience in Semi Arid Landscapes (ACReSAL); World Bank Assisted Project, Bauchi State Government, African Seed Trade Association (AFSTA), African Agricultural Foundation (AATF), PBS, OFAB Africa, Nigerian National Petroleum Corporation (NNPC), Sheda Science and Technology Complex (SHETSCO) and Raw Materials Research and Development Council (RMRDC) whose generous contributions and support have been instrumental in making this conference a reality. Your belief in the transformative potential of biotechnology and your commitment to fostering collaboration have been invaluable.

Let me also applaud the Local Organsing Committee (LOC) led by Dr. Rose Gidado for their exceptional dedication which significantly contributed to the success of ICoB24. Your hard work and commitment are truly priceless and deeply appreciated.

Esteemed guests and participants, as we reflect on the discussions and knowledge gained at ICoB24, let us embody the spirit of innovation, collaboration, and excellence that has defined our time together. Let us ensure the insights shared reach a broader audience and are translated into tangible advancements in the biotechnology sector. It is our collective responsibility to continually push the boundaries of what is possible, challenge assumptions, and embrace change as we work together to create a prosperous future for generations to come.

Thank you once again for your participation, passion, and commitment to advancing the field of biotechnology. I look forward to the continued collaboration, inspiration, and impact that will undoubtedly emerge from our collective efforts.

I wish you all a safe journey to your various destinations and hereby officially bring ICoB24 to a close.

Thank you.

VOTE OF THANKS BY THE CHAIRMAN LOC ICoB24, DR ROSE GIDADO, FOR THE CLOSING CEREMONY OF THE INTERNATIONAL CONFERENCE ON BIOTECHNOLOGY ON JULY 19TH, 2024 AT NAF CONFERENCE CENTRE, ABUJA

Ladies and Gentlemen,
Esteemed Guests,
Distinguished Speakers, and
Dear Participants,

As we come to the close of this remarkable conference, I want to express my heartfelt gratitude to each and every one of you for making this event a resounding success.

To our keynote speaker, panelists, and presenters, your insights and expertise have inspired us and broadened our understanding of biotechnology's vast potential.

To our sponsors and partners, your support has been invaluable, and we appreciate your commitment to advancing biotechnology for the betterment of society.

To our organizers and volunteers, your tireless efforts have ensured a seamless and enjoyable experience for all attendees.

And to our participants, your engagement, questions, and discussions have enriched our conversations and fostered meaningful connections.

Thank you all for your contributions, enthusiasm, and dedication to harnessing biotechnology for a brighter future.

As we depart, let us carry with us the knowledge, inspiration, and networks forged here, and continue to work together towards a future where biotechnology improves lives and sustains our planet.

Thank you, and safe journey to all your destinations.

PROGRAMME SCHEDULE

DAY ONE - MONDAY 15, JULY 2024

TIME	ACTIVITIES AND SPEAKERS	VENUE
08:00-9:00 AM	REGISTRATION	
09:00-1:00 PM	Opening ceremony. ■ National Anthem ■ Introduction of Guests by Masters of Ceremony: **Tope Ojeme**, **Toyin Omozuwa**, *NBRDA* and **Alex Abutu**, *AATF* ■ Introductory Remarks by ICoB24 LOC Chairman **Dr. Rose Gidado** ■ Welcome Address by DG/CEO NBRDA **Prof. Abdullahi Mustapha** ■ Documentary/Spoken Word ■ Goodwill Messages – by, DG/CEOs of MDAs/Parastatals, UN/FAO Nigeria, Country Rep.; World Bank ACReSAL Project Team Lead; NUC., High Commissioners/Ambassadors, International Partners (AATF, Bill Gates, Foundation Representative, ICGEB, USAID, USDA, BAYER, Mahyco etc.), NGO's, CSO's, AFAN, SEEDAN, Banks, Captains of Industries and the President, Nigerian Academy of Science (NAS). ■ Remarks by **Mrs Esuabana Nko-Asanye**, Permanent Secretary ■ Ministers of FMA&FS, FMEnv, FMoH & SW, FMITI, FMF, FMB & EP ■ Hon Minister, Fed Min. of Innovation, Sci. & Tech, **Chief Uche G. Nnaji** ■ Remarks by **Hon. Tijjani Z. Zanna,** *Chairman House Committee on STI* ■ Remarks by **Sen. Aminu Iya Abbas,** *Senate Committee Chairman on STI* ■ Governors or their Representatives Present ■ **His Excellency, Dr Abdullahi Ganduje,** *Chairman, APC.* ■ **Senator Barau Jibrin,** *Deputy Senate President* ■ Cultural Display ■ Keynote Address 1: **Dr. Akinwunmi Adesina, CON** ■ Speech by Honourable Minister (FMIST): **Chief Uche Geoffrey Nnaji** ■ Keynote Address 2: **Dr. Ngozi Okonjo Iweala, GCON** ■ Keynote Address 3: **Chief. Clement David Ebi, CON** ■ Address by Guest of Honour: **His Excellency Dr. Goodluck Ebele Jonathan, GCFR** ■ Presentation of Awards for Special Guests ■ Address by the Vice President, Federal Republic of Nigeria, **His Excellency Senator Kashim Shettima**, **GCON**. ■ Presidential Address and opening by the Special Guest of Honour: **His**	Main Conference Hall
01:00 PM -1:30PM	**VISIT TO EXHIBITION STANDS**	
01:30PM -2:30PM	**LUNCH**	
02:30PM - 03:30PM 03:00PM- 04:30PM	**PLENARY SESSION** ***SPEAKER:*** **Prince Abdulhamid Umar,** *National Project Coordinator, World Bank ACReSAL PROJECT.* ***TOPIC:*** **Scaling Up ACReSAL's Reach and Impact: Strategies for Sustainable Agricultural Development in Northern Nigeria.** ***RAPPORTEURS:*** **Evilla Bassey Adejo, Modupe Oluwatoyin** ***SPEAKER:*** **Dr. Rufus Egbeba**, *Former DG/CEO NBMA* ***TOPIC:*** **Overview of Policy, Biosafety and Regulatory issues: Cybersecurity, Intellectual Property**	Main Conference Hall

TIME	ACTIVITIES AND SPEAKERS	VENUE
	MODERATOR: **Dr. Matthew Dore** **DISCUSSANTS** (10mins each) 1. **Agnes Asagbra**, *DG/CEO NBMA* 2. **Dr. Rufus Egbegba**, *Former DG/CEO NBMA* 3. **Prof. Emmanuel S. Dandaura**, *Director, Institute of Strategic and Development Communication ISDEVCOM, Keffi, Nasarawa State University.* 4. **Dr. Umar Bindir**, *Former DG/CEO, NOTAP* ***RAPPORTEURS*****: Evilla Bassey Adejo, Ogunremi Oluwasijibomi Charles**	Main Conference Hall
04:30PM- 05:00PM	***SPEAKER:*** **Fadi Khaizaran,** *Gen Manager, AGBL West Africa* ***TOPIC:*** **"Advanced Genomics Application & Technologies for Life Sciences Research."**	

DAY TWO - TUESDAY 16, JULY 2024

TIME	ACTIVITIES AND SPEAKERS	VENUE
09:00AM-09:45AM	***TITLE:*** **Harnessing Biotechnology for Antimicrobial Resistance (AMR) Surveillance and Control: A One Health Approach** (30-45 mins) ***SPEAKER:*** **Dr. Francisca Nwaokorie,** *Associate Professor and Medical Microbiologist College of Medicine, University of Lagos*	Main Conference Hall
09:45AM-10:30AM	***TITLE:*** **Enhancing Surveillance and Monitoring of AMR in humans, animals, and the Environment** **PANEL DISCUSSION** ***MODERATOR*****: Dr. Barth Ibeh** **DISCUSSANTS** (10mins each) 1. **Dr. Adetunji Modupeade Christianah,** *Associate. Prof. of food mycotoxicology and food safety), TRINITY UNIVERSITY, YABA, LAGOS* 2.**Dr Eugene Itua,** *Environmental Sustainability Expert/CEO Natural Eco Capital, Lagos, and Coordinator Nigeria Long term low Emissions Development Strategy (LTS).* 3. **Dr. Etinosa Ikpo,** *Federal Neuropsychiatric Hospital, Benin* ***RAPPORTEURS:*** **Dr. Joy Oladimeji-Salami and Idiongbong Asuquo**	Main Conference Hall
10:30-11:00AM	**QUESTIONS AND ANSWERS, DISCUSSION**	**MAIN CONFERENCE HALL**
11:00-11:30AM	**TEA BREAK/ POSTER PRESENTATION**	
	TECHNICAL PANEL SESSION I (ABD) ***FACILITATOR:*** **Dr. Rose M. Gidado,** *Director, Agric Biotech Dept., NBRDA*	TBS (RM. 1)
11:30-11:45 AM	***SPEAKER:*** **Dominque Koffy Kouacou**, *Country Representative, UN/FAO, Nigeria* ***TOPIC:*** **Biotechnology for Smallholder Farmers: Enhancing Productivity and Income through FAO's Interventions.**	
11:45-12:15 PM	**PANEL DISCUSSANTS** (15 mins each) ***SPEAKER 1:*** **Dr. Khalid Ishiaq,** *Ag. DG, NASC* **TOPIC: Seed Quality and Certification**	

TIME	ACTIVITIES AND SPEAKERS	VENUE
12:15-12:45PM	***SPEAKER 2*****: Dr. Okelola Sunday Folarin,** *Ag. Registrar, PVP Office, NASC* ***TOPIC:*** **Plant Varietal Protection in Nigeria: Benefits and Relevance to Food Security.**	
01:00-01:30 PM	***SPEAKER 3*****: Dr Bernard Ehirim,** *Programme Officer, Product Stewardship, AATF* ***TOPIC*****: Seed Technology and Innovation** ***RAPPORTEURS*****: Adeshina Dolapo Adetokunbo, Esther Inegbedion**	
12:15-01:30PM	**QUESTIONS AND ANSWERS, DISCUSSION**	
11:30-12:15 PM	**TECHNICAL PANEL SESSION I (EBD)** ***FACILITATOR:*** **Dr Adetunji, O. A** ***TOPIC:*** **Enhancing Environmental Sustainability Through Biotechnological Innovations: Addressing Pollution, Climate Change, and Waste Management Challenges.** ***SPEAKER*****: Prof. C.J. Ogugbue,** *University of Port Harcourt* (30-45 mins) **MODERATOR: Dr. Chizoba H. Unaeze**	TBS (RM. 2)
12:15-01:00 PM	**PANEL DISCUSSANTS** (10mins each) 1. **Prof. Magagi Joshua,** *Nasarawa State University* 2. **Prof. Sudi Ismaila Yada,** *Adamawa State University, Yola* 3. **Dr. Solomon Olayimika,** *FUT, Minna* 4. **Dr. Ibrahim Rafiu Babatunde,** *Osun State University* 5. **Dr. Bello Abdullahi,** *Bioresources Development Centre, Illorin* ***RAPPORTEURS:*** **Jacinta Osigbemhe and Victor Okoh**	
1:00-1:30 PM	**QUESTIONS AND ANSWERS, DISCUSSION**	
11:30-12:15 PM	**TECHNICAL PANEL SESSION I (MBD)** ***FACILITATOR:*** **Dr Barth Ibeh** ***TOPIC:*** **Transformative innovations: revolutionizing healthcare through Medical Biotechnology**	TBS (RM. 3)
12:15-01:00 PM	***MODERATOR:*** **Dr Barth Ibeh** **PANEL DISCUSSANTS** (10mins each) 1. **Prof. Kingsley Ubaoji** 2. **Dr. Emmanuel Balogun** **RAPPORTEURS: Ezinne Nwonu, Dr. Akinbobola Otitoju**	
01:00-01:30 PM	**QUESTIONS AND ANSWERS/INTERACTION**	
11:30-12:15 PM	**TECHNICAL PANEL SESSION I (FIB)** ***FACILITATOR:*** **Dr. G.I.B, Obioh** **TITLE: Innovations in Bioprocessing and Bio-manufacturing** **SPEAKER: Prof. Ifeoma B. Enweani-Nwokelo**, *Faculty of Medical Laboratory Science and Director, Grants Development, Nnamdi Azikiwe University, Awka, Nigeria*	TBS (RM. 4)

TIME	ACTIVITIES AND SPEAKERS	VENUE
12:15-01:00 PM	**MODERATOR: Eng. Jafar Zangina,** PhD **PANEL DISCUSSANTS (10mins each)** 1. **Prof. Olubunmi Agarry**, *University of Abuja, Abuja, Nigeria* 2. **Prof. Adeniyi A. Ogunjobi**, *University of Ibadan, Ibadan, Nigeria* 3. **Sumayya, Hamza Maishanu**, *Branch Manager, DNAlabs LTD Abuja* 4. **Miss Adejoke Lasisi**, CEO, *Planet 3R, Ibadan, Nigeria* ***RAPPORTEURS:*** **Dr. Stella Leh Togi**	
01:00-01:30PM	**QUESTIONS AND ANSWERS, DISCUSSION**	
11:30-12:15 PM	**TECHNICAL PANEL SESSION I (GBD)** ***FACILITATOR:*** **Dr. Oloruntoyin S. Ajenifujah-Solebo** ***TOPIC:*** **Prospects of Developing Indigenous Biogenome Databases through an African BioGenome Project - NBRDA Collaboration.** ***SPEAKER:*** **Prof. Julian O. Osuji,** *Director, Regional Centre for Biotechnology and Bioresources Research & NBRDA CoExcellence University of Port Harcourt, & Co-Chair, African BioGenome Project.*	TBS (RM. 5)
12:15-01:00 PM	**PANEL DISCUSSANTS** (10mins each) 1. **Frank A. Ogundolie** 2. **Dr. Effiom Ita** 3. **Dr. Victor Fadipe** 4. **Dr. Mangse George** **Rapporteurs: Ojochenemi Enejoh, Okolo Dominic**	
01:00-01:30PM	**QUESTIONS AND ANSWERS, DISCUSSION**	
01:30-02:15 PM	**LUNCH**	
02:15-02:30 PM	**TECHNICAL PANEL SESSION II (ABD)** **FACILITATOR: Dr. Rose Gidado** **MODERATOR: Prof. Chiedozie,** *ED, NRCRI, Umudike*	TBS (RM. 1)
02:30-03:30 PM	**PANEL DISCUSSANTS** (10mins each) 1. **Godwin Nana-Yaw Lemgo,** Regulatory Scientific Affairs Manager, Africa Bayer Crop Science Nairobi. Kenya: ***TOPIC:*** **Ensuring Regulatory Compliance in Biotech Crop Development: Lessons Learned from the Private Sector Experience in Africa.** 2. **Prof. Ishiyaku,** *Principal Investigator Pod Borer Resistant Cowpea (PBR), IAR, Zaria* ***TOPIC:*** **From Lab to Field: Translating Biotechnological Research into Practical Farming Solutions.**	

TIME	ACTIVITIES AND SPEAKERS	VENUE
	3. Dr. Onyekachi Francis Nwankwo, *AATF, Kenya.* ***TOPIC:*** **Beyond regulations: Post release monitoring of AgricBiotech products - case of PBR cowpea in Nigeria.** **4. Prof. Benjamin Ewa Ubi,** *Former President, Biotechnology Society of Nigeria (BSN)* ***TOPIC:*** **Biotech Crops for Climate Resilience: Adapting Agriculture to Changing Environmental Conditions.** ***RAPPORTEURS:*** **Glory Ononokpono, Osisami Olubukunola**	
02:30-03:30PM	**QUESTIONS AND ANSWERS, DISCUSSION**	
02:15-02:45 PM	**TECHNICAL PANEL SESSION II (EBD)** **FACILITATOR: Dr. Adetunji, O. A** **TITLE: Revolutionizing Energy Sustainability: Harnessing Biomass for Biotechnology Advancements in the Modern Age.** **SPEAKER: Dr. Christpeace Ezebuiro**, *NBRDA, Abuja* (30 mins) **MODERATOR: Eng. Helen Noble Okereke** **PANEL DISCUSSANTS** (10mins each) 1. **Dr. Sunday Yusuf Kpal**, *Nasarawa State University* 2. **Dr. Ozioma I Nduagu**, *Institute of Waste to Wealth (IWW), Abuja* 3. **Dr. Daniel Okoh**, *West Africa Global Aid Organization (WAGA), Abuja* 4. **Dr Olaniyi Akeem Olawale**, *Kaduna State University, Kaduna* **Rapporteurs: Chidimma Enwerem, Sochi Anaga**	TBS (RM. 2)
02:45-03:30 PM	**INTERACTION/QUESTIONS AND ANSWERS**	
02:15-02:45 PM	**TECHNICAL PANEL SESSION II (MBD)** ***FACILITATOR:*** **Dr Barth Ibeh** ***TOPIC:*** **Medical Biotechnology: Powering Health and Wealth.** ***SPEAKER:*** **Prof Mahmoud M. Bahgat,** *Head of Science & Technology Cooperation Centre, the Egyptian Academy of Scientific Research & Technology. Head of the Department of Therapeutic Chemistry, The National Research Centre, Cairo, 12311 Egypt.* ***MODERATOR:*** **Dr Barth Ibeh** **PANEL DISCUSSANTS** (10mins each 1. **Prof Kingsley Ubaoji** 2. **Dr. Emmanuel Balogun** ***RAPPORTEURS:*** **Priscilla Aondona Yahemba**	TBS (RM. 3)
02:45-03:30 PM	**QUESTIONS AND ANSWERS, DISCUSSION**	

TIME	ACTIVITIES AND SPEAKERS	VENUE
02:15-02:45 PM	**TECHNICAL PANEL SESSION II (FIB)** ***FACILITATOR:*** **Dr G.I.B Obioh** **TOPIC: Bio-catalysis and Enzyme Engineering for Industrial Applications** **SPEAKER: Dr. A.K. Lawal,** *Director, Biotechnology Department, Federal Institute of Industrial Research Oshodi (FIIRO), Nigeria.* (30 mins) **MODERATOR: Mr. Gbadebo Olukotun**	TBS (RM. 2)
02:45-03:30 PM	**PANEL DISCUSSANTS** (10mins each) 1. **Prof. E.E. Ella,** *Ahmadu Bello University, Zaria, Nigeria* 2. **Prof. N.R. Isu,** *University of Abuja, Abuja, Nigeria* 3. **Dr. Bukola Popoola,** *Ajayi Crowther University, Oyo, Nigeria* 4. **Dr. Andrew Chibuzor Iloh,** *Sheda Science and Technology Complex (SHESTCO), Sheda, Nigeria.* **RAPPORTEUR: Henry Kumba**	
02:45-03:30 PM	**QUESTIONS AND ANSWERS, DISCUSSION**	
02:15-02:45 PM	**TECHNICAL PANEL SESSION II (GBD)** ***FACILITATOR:*** **Dr. Oloruntoyin S. Ajenifujah-Solebo** **SPEAKER: Prof. Charles Adetunji,** *Dir. Research and Innovation, Dept. of Microbiology, Faculty of Science, Edo State University, Uzairue, Nigeria and President Nigerian Bioinformatics and Genomic Network.* (30-45mins) ***TOPIC:*** **Harnessing the Capabilities of Microbial Genomes for Sustainable Development.**	TBS (RM. 5)
02:45-03:30 PM	**MODERATOR: Frank A. Ogundolie** **PANEL DISCUSSANTS** (10mins each): 1. **Mr. Olayiwola Agoro,** *Deputy Director, BRTD, FMIST* 2. **Prof. Olufunke B. Shittu,** *Fed. University of Agriculture Abeokuta, Director, Biotechnology Centre.* 3. **Prof. Nnennaya Isu,** *Microbiologist, University of Abuja* 4. **Dr Andrew Chibuzo Iloh,** *Molecular Biologist, SHESTCO* ***RAPPORTEURS:*** **Olaitan Y. Falana, Rilwan Yusuf**	
02:45-03:30 PM	**QUESTIONS AND ANSWERS, DISCUSSION**	
03:30-04:30 PM	**PARALLEL TECHNICAL BREAKOUT SESSIONS (TBS)** TBS Room 1 (AGB) · TBS Room 2 (EBD) · TBS Room 3 (MBD) · TBS Room 4 (FIB) · TBS Room 5 (GBD)	TBS (RM. 1-5) **RAPPORTEURS** ■ Dr. Kalu Alfred ■ Dr. Tari Agballalah ■ Adeshina Dolapo Adetokunbo ■ Henry Kumba ■ Busari Khadija
04:30-05:00PM	**WRAP UP SESSION. REPS FROM BREAK OUT SESSION**	**MAIN CONFERENCE HALL**

DAY THREE - WEDNESDAY 17, JULY 2024

TIME	ACTIVITIES AND SPEAKERS	VENUE
09:00-09:10AM	**PLENARY SESSION 1** ***FACILITATOR:*** **DR. ROSE GIDADO** ***TOPIC:*** **Stewardship**	Main Conference Hall
09:10-09:40AM	***LEAD SPEAKER:*** **Dr. Francis Onyekachi,** *Lead Product Stewardship, AATF* ***TOPIC:*** **Stewardship for development and commercialization of Agricultural Biotechnologies in Africa: Development and implementation of viable insect resistance management strategy for Bt. products in Africa.** ***MODERATOR:*** **Dr. Ebiarede Zidafamor**, *Seed Production Coordination and Management, National Agricultural Seed Council (NASC)*	Main Conference Hall
09:40-10:25AM	**PANEL DISCUSSANTS** (10mins each) 1. **Prof. Rabiu Adamu,** *PI TELA Maize Project, IAR, Zaria* 2. **Prof. Emmanuel Kwon-Ndung,** *Federal University Lafia* 3. **Prof. Emmanuel Ikani,** *NAERLS, Zaria*	
10:25-10:45AM	***SPEAKER:*** **Prof. Terkimbi Vange** **TOPIC: Global Food Security: Role of Biotechnology in Feeding a Growing Population.**	
	PLENARY SESSION 2	
10:45-11:15AM	***SPEAKER:*** **Dr. Canisius Kanangire**, *Executive Director, AATF, Nairobi* ***TOPIC:*** **Biotech Crops and Sustainable Agriculture.** ***RAPPORTEURS:*** **Saadat Abu, Abdulkabir Adedeji**	
11:15-11:25 AM	**QUESTIONS AND ANSWERS, DISCUSSION**	**MAIN CONFERENCE HALL**
11:25-11:30 AM	**TEA BREAK/ POSTER PRESENTATION**	
11:30-12:15 PM	**TECHNICAL PANEL SESSION I (ABD)** ***FACILITATOR:*** **Dr Rose Gidado** ***SPEAKER:*** **Dr. Margaret Karembu,** *Director, ISAAA AfriCenter* **TOPIC: Is Communication Matching up with the New Agri-Innovations?** **SPEAKER** (30-45 mins)	TBS (RM. 3)
12:15-1:00 PM	***MODERATOR:*** **Dr. Patrick Aderinola** **PANEL DISCUSSANTS** 1. **Dr. Sylvester Oikeh,** *Manager, TELA MAIZE Project, AATF, Nairobi.* ***TOPIC:*** **Advancements in Genetically Modified (GM) Seeds: The case study of TELA MAIZE in Africa.**	

TIME	ACTIVITIES AND SPEAKERS	VENUE
	2. **Alhaji Yusuf Ado Kibiya, President, SEEDAN** ***TOPIC:*** **Seed Industry Collaboration and Partnerships** 3. **Daniel Aghan,** *AFSTA Nairobi Kenya* ***TOPIC:*** **Biotechnology and the Empowerment of African Farmers: Perspectives from Indigenous Seed Companies.** 4. **Prof. Florence Akaneme,** *UNN,* ***TOPIC:*** **The Future of Plant Breeding: Integrating Omics Technologies and Big Data Analytics.** ***RAPPORTEURS:*** **Roseline Joseph, Anita Oketa**	
01:00-01:30PM	**QUESTIONS AND ANSWERS, DISCUSSION**	
11:30-12:15PM	**TECHNICAL PANEL SESSION I (EBD)** ***FACILITATOR:*** **Dr Adetunji, O.A** **TOPIC: Ensuring Safe And Sustainable Practices: Biorisk Management Strategies In Biotechnology** **SPEAKER: Dr. Rufus Ebegba**, *Former DG/NBMA* ***MODERATOR:*** **Rufina Okeke** **DISCUSSANTS** (10mins each) 1. **Dr. Negbenebor Helen Ehimemen**, *Baze University, Abuja* 2. **Dr. Micheal Agbaje**, *Fed. University of Agriculture, Abeokuta* 3. **Dr. Yusuf Hajara Oyiza**, *NBRDA, Abuja* 4. **Prof. Beckley Ikahajiagbe**, *University of Benin, Edo state* ***RAPPORTEURS:*** **Elizabeth Ojo, Funmilayo Raji**	TBS (RM. 2)
01:00-1:30PM	**QUESTIONS AND ANSWERS, DISCUSSION**	
11:30-12:15 PM	**TECHNICAL PANEL SESSION I (MBD)** ***FACILITATOR:*** **Dr Barth Ibeh** ***TOPIC:*** **Biomed Breakthroughs: Driving Health and Prosperity** ***SPEAKER:*** **Prof. Kingsley Ubaoji,** *Department of Biochemistry, Nnamdi Azikiwe University, Awka*	TBS (RM. 3)
12:15-1:1:00 PM	**MODERATOR: Dr. Barth Ibeh** **DISCUSSANTS** (10mins each) 1. **Dr. Emmanuel Balogun** ***RAPPORTEURS:*** **Nkoli Emeter**	
01:00-01:30 PM	**QUESTIONS AND ANSWERS, DISCUSSION**	

TIME	ACTIVITIES AND SPEAKERS	VENUE
11:30-12:15PM	**TECHNICAL PANEL SESSION I (FIB)** ***FACILITATOR:*** **Dr. G.I.B Obioh** ***TOPIC:*** **Eco-friendly Alternatives and Bio-based Materials** ***SPEAKER:*** **Prof. Adeniyi A. Ogunjobi**, *University of Ibadan, Ibadan,* (30-45 mins) *Nigeria* 12:15-1:00PM **MODERATOR: Dr. Nosakhare P. Ajulor** **PANEL DISCUSSANTS** (10mins each) 1. **Prof. Ifeoma B. Enweani-Nwokelo**, *Nnamdi Azikiwe University, Awka, Nigeria* 2. **Prof. N.R. Isu,** *University of Abuja, Abuja, Nigeria* 3. **Dr. Comfort Tosin Olateru,** *The Polytechnic Ibadan, Nigeria* 4. **Dr. Odunlade Albert Kolawole,** *Trinity University Sabo Yaba, Lagos* ***RAPPORTEURS:*** **Kate Akubue, Binta Adamu**	TBS (RM. 4)
01:00-01:30PM	**QUESTIONS AND ANSWERS, DISCUSSION**	
11:30-12:15PM	**TECHNICAL SESSION I (GBD)** ***FACILITATOR:*** **Dr. Oloruntoyin S. Ajenifujah-Solebo** ***TOPIC:*** **Applications of genetic engineering and genome editing to improve Agriculture in Africa.** ***SPEAKER 1:*** **Dr Ntui Valentine;** *Mohamme the VI Polytechnic University (UM6P), Morocco.* **MODERATOR: Dr. Oloruntoyin S. Ajenifujah-Solebo** **DISCUSSANTS** 1. **Frank A. Ogundolie,** *Biotechnologist, Baze University* 2. **Dr. Effiom Ita,** *Lecturer, University of Calabar* 3 .**Dr. Victor Fadipe,** *Deputy Director, STP) Federal Ministry of Science, Technology and Innovation* 4. **Mrs. Nwabueze Adaora,** *ARCN, Mabushi, Abuja* ***RAPPORTEURS:*** **Okiemute Okpalefe, Rilwanu Zainab Julde**	TBS (RM. 5)
12:15-01:00PM	**TECHNICAL SESSION II** ***SPEAKER:*** **Mr Hazeez Durosomo,** *Country Manager AGBL Nigeria.* ***TOPIC:*** **Advanced Genomics Application and Technologies for Life Sciences Research** ***RAPPORTEURS:*** **Hadiza Rasheed-Jada, Rahila Jamma Yusufu**	
01:00-01:30PM	**QUESTIONS AND ANSWERS, DISCUSSION**	
01:30-02:30PM	**LUNCH**	

TIME	ACTIVITIES AND SPEAKERS	VENUE
02:30-04:30PM	**PARALLEL TECHNICAL BREAKOUT SESSIONS (TBS)** TBS Room 1 (AGB) | TBS Room 2 (EBD) | TBS Room 3 (MBD) | TBS Room 4 (FIB) | TBS Room 5 (GBD) **RAPPORTEURS** ■ Dr. Yvonne A. Onmonya ■ Frances Isegohi ■ Bamidele Iyekolo ■ Hadiza Rasheed-Jada ■ Dr. Beatrice Ojiego	TBS (RM. 1-5)
04:30-05:00 PM	**WRAP UP SESSION. REPS FROM BREAK OUT SESSION**	**MAIN CONFERENCE HALL**

DAY FOUR - THURSDAY 18, JULY 2024

TIME	ACTIVITIES AND SPEAKERS	VENUE
09:00-11:30AM	**NBRDA/USDA/OFAB/AATF SIDE EVENT**	TBS (Rm 1)
09:00-09:45AM	**PLENARY SESSION I** ***TOPIC:*** **Bioethics** ***MODERATOR:*** **Dr Mathew Dore,** *Country Coordinator, PBS Nigeria* **SPEAKER I: Dr. Chitu Princewill,** *Director/- Head of Secretariat, National Bioethics Committee, Nigeria:* ***TOPIC:*** **Nigeria's Progress in Bioethics: The Journey of the Nigerian National Bioethics Committee (NBC).**	Main Conference Hall
09:45-10:35AM	**PLENARY SESSION II** ***SPEAKER II:*** **Mr. Vitu Chinoko,** *OFAB Africa Manager, AATF, Nairobi, Kenya* ***TOPIC:*** **Addressing Societal Concerns: Ethics, Regulation, and Public Perception of Agricultural Biotechnology-** ***SPEAKER III:*** **Agnes Asagbra,** DG/CEO, NBMA ***TOPIC:*** **Regulatory Landscape for Biotech Seeds.** ***RAPPORTEUR:*** **Ola Ekundayo Temitope, Dr. Abdullahi Mohammed**	Main Conference Hall
10:35 -10:55AM	**PLENARY SESSION III** ***SPEAKER:*** **Adamu Abdullahi,** *The Ag. Executive Vice Chairman, Federal Competition and Consumer Protection Commission (FCCPC), Wuse 2, Abuja.* ***TITLE:*** **Consumer Perception About Biotechnology Seeds and Products** ***RAPPORTEUR:*** **Ola Ekundayo Temitope, Dr. Abdullahi Mohammed**	Main Conference Hall
10:55-11:05AM	**QUESTIONS AND ANSWERS, DISCUSSION**	**MAIN CONFERENCE HALL**
11:05-11:30AM	**TEA BREAK/ POSTER PRESENTATION**	
11:30-12:15 PM	**TECHNICAL PANEL SESSION I (ABD)** ***FACILITATOR:*** **Dr. Rose Gidado** ***TOPIC:*** **Socio-Economic Impact Assessment of GM Crops**	TBS (RM. 1)

TIME	ACTIVITIES AND SPEAKERS	VENUE
	SPEAKER: **Jose Falck-Zepeda** ***TOPIC:*** **Synthesis and Lessons Learned.** ***MODERATOR:*** **Dr. Jean Baptiste De La Salle Tignegre**, *Regional Director, AATF, West Africa.* **PANEL DISCUSSANTS** (10 mins each) 1. **Dr. Kwaw Andam,** *Update on the PBR cowpea evaluation* 2. **Jose Falck Zepeda,** *Update on the PBR cowpea value chain* 3. **Jose Falck Zepeda,** *Update on the Late Blight Resistant Potato* **RAPPORTEURS: Hauwa Suleiman Salith, Hauwa Kassim**	
12:15-12:45PM	**QUESTIONS AND ANSWERS, DISCUSSION**	
11:30-12:15 PM 12:15-01:00 PM	**TECHNICAL PANEL SESSION I (EBD)** **FACILITATOR: Dr Adetunji, O.A** **TOPIC: Conserving Biodiversity: Integrating Biotechnology for Sustainable Ecosystem And Genetic Resources Management.** ***SPEAKER:*** **Dr. Mekuleyi, Gabriel Olarinde**, *Lagos State University* ***MODERATOR:*** **Ebi David** **DISCUSSANTS** (10mins each) *1.* **Dr. Salsu Nura**, *ABU, Zaria* *2.* **Dr. Iloh Andrew**, *SHESTCO, Abuja* 3. **Hadiza Yaro**, *East-West Seed, Nigeria.* ***RAPPORTEURS:*** **Zainab Bello, Lucky Otuokpaikhala**	TBS (RM. 2)
01:00-01:30PM	**QUESTIONS AND ANSWERS, DISCUSSION**	
11:30-12:15 PM 12:15-1:00PM	**TECHNICAL PANEL SESSION I (MBD)** **FACILITATOR: Dr Barth Ibeh** **TOPIC: Unlocking Health Potential: Harnessing Medical Biotechnology for Global Wellness** ***SPEAKER:*** **Dr Emmanuel Balogun**, *Department of Biochemistry, Ahmadu Bello University, Zaria* ***MODERATOR:*** **Dr. Barth Ibeh** **DISCUSSANT** (10mins each) 1. **Prof. Kingsley Ubaoji** **RAPPORTEURS: Zainab Ibrahim, Doofan Bur**	TBS (RM. 3)
01:00-01:30PM	**PARTICIPANT INTERACTION/QUESTIONS AND ANSWER SESSION**	

TIME	ACTIVITIES AND SPEAKERS	VENUE
11:30-12:15PM	**TECHNICAL PANEL SESSION I (FIB)** ***FACILITATOR:*** **Dr. G.I.B Obioh** ***TOPIC:*** **Bioeconomy and Sustainable Industrial Development** ***SPEAKER:*** **Prof. Ken Ife**, *CEO/Managing Director, Bioresources and Technologies Limited, Abuja, Nigeria*	TBS (RM. 4)
12:15-1:00 PM	***MODERATOR:*** **Dr Beatrice Ojiego** **PANEL DISCUSSANTS** (10mins each) 1. **Prof. S.A. Ado**, *Ahmadu Bello University, Zaria, Nigeria* 2. **Prof Akeem Abolade Oyerinde**, *FESN - Dean, Faculty of Agriculture, University of Abuja* 3. **Dr. Agha Ukpai Agha**, *Director, National Biosafety Management Agency, Abuja, Nigeria* 4. **Dr Esther Ogunjimi**, *First Technical University, Ibadan, Nigeria* ***RAPPORTEURS:*** **Chidinma Umeakuna, Lovina Ogbu**	
01:00-01:30PM	**QUESTIONS AND ANSWERS, DISCUSSION**	
11:30-12:15 PM	**TECHNICAL PANEL SESSION I (GBD)** ***FACILITATOR:*** **Dr. Oloruntoyin S. Ajenifujah-Solebo** ***TOPIC:*** **Developing Genome Edited Products in Africa: Prospects and Challenges** ***SPEAKER*****: Prof. Muhammed Bello Yerima,** *Deputy vice Chancellor Sokoto State University.* **MODERATOR: Mr. Olayiwola Agoro**	TBS (RM. 5)
12:15-01:00 PM	**PANEL DISCUSSANTS** (10mins each). 1. **Prof. Oyerinde Akeem** 2. **Obasi Sunday,** *FMAFS* 3. **Dr. Zidafamor E.J.** 4. **Prof. Rebeccah Wusa Ndana,** *University of Abuja* **RAPPORTEURS: Jumoke Joda, Opaleye Oyetola O.**	
01:00-01:30PM	**QUESTIONS AND ANSWERS, DISCUSSION**	
01:30-02:30 PM	**LUNCH**	
02:30-04:30 PM	**NBRDA/USDA/OFAB/AATF SIDE EVENT**	TBS (RM. 1)
02:30-04:30PM	**PARALLEL TECHNICAL BREAKOUT SESSIONS** TBS Room 2 (EBD) · TBS Room 3 (MBD) · TBS Room 4 (FIB) · TBS Room 5 (GBD) **RAPPORTEURS** ■ Dr. Fatima Dantanko ■ Frances Isegoghi ■ Lovina Ogbu ■ Olaitan Falana	TBS (RM. 2-5)
04:30-05:00PM	**WRAP UP SESSION. REPS FROM BREAK OUT SESSION**	**MAIN CONFERENCE HALL**

DAY FIVE - FRIDAY 19, JULY 2024

TIME	ACTIVITIES AND SPEAKERS	VENUE
9:00-11:00 AM	**Early Career Presentations and Poster Assessment**	Main Conference Hall
11:00-11:15 AM	**TEA BREAK/RAPPORTEUR HARMONIZATION**	
11:15-12:00 PM	**Conference Closing Ceremony** ■ Presentation of award to best poster ■ Communique ■ Press Briefing ■ Vote of Thanks ■ Group Photograph	Main Conference Hall
12:00-2:30 PM	**NETWORKING/LUNCH**	
2:30-5:00 PM	**CITY TOUR/EXCURSION**	
	DEPARTURE	

*TBS: Technical Breakout Sessions

SPEAKERS' PROFILE

DR. CANASIUS KANANGIRE is the Executive Director of the African Agricultural Technology Foundation (AATF). An astute administrator, academician, and internationally recognised professional, Dr. Kanangire is an experienced technocrat with a wealth of knowledge in leadership and management of international institutions, including developing strategic partnerships and networks at regional, continental and global levels with great ability for resource mobilization. Dr Canisius Kanangire holds a doctorate degree in Aquatic Sciences and Master's degree in Freshwater Ecology from the University of Namur, Belgium.

DR. AGNES YEMISI ASAGBRA, is the Director General of the National Biosafety Management Agency (NBMA). With a Ph.D. in Food and Industrial Microbiology from the prestigious University of Ibadan, her academic prowess is complemented by a master's degree from the University of Benin and an undergraduate degree from the University of Lagos. Dr. Asagbra's career began at the Federal Institute of Industrial Research, Oshodi (FIIRO), where she excelled in fermentation technology, contributing to advancements in antibiotic and food fermentation. Her appointment as DG/CEO of the NBMA was in May 2023, marking a significant milestone in her career and that of the Agency.

PROF CHIEDOZIE NGOZI EGESI is the Executive Director of the National Root Crops Research Institute (NRCRI) Umudike, Nigeria. After successfully completed his primary and secondary education, Prof Egesi gained admission into the University of Calabar, Nigeria in 1989 session where he got his Bachelor of Science Degree, Biology in 1994. On completion of his National Youth Service Corps in 1995, he proceeded to the prestigious University of Ibadan and International Institute of Tropical Agriculture (IITA) Ibadan Nigeria where he obtained his MSc in Environmental Biology in 1997 in the Department of Crop Protection and Environmental Biology.

DR. ISHIAK OTHMAN KHALID, the Acting Director General of National Agricultural Seeds Council (NASC), is an intelligent seed expert trained both nationally and internationally in Seed Science and Seed Industry development. Dr Khalid holds a Bachelor of Agriculture (B. Ag) at the - University of Ilorin in Kwara State after which he proceeded for Masters of Science (MSc) in Agricultural Economics and later Doctor of Philosophy (PhD) in Agricultural Economics at the Abubakar Tafawa Balewa University, Bauchi. and appointed the Ag. DG, NASC in May, 2023. Started Fed. Civil Service Career as Agric. Officer II at the Fed. Dept. of Agriculture, Federal Ministry of Agriculture, Abuja in October 1990.

ENGR UMAR BUBA BINDIR (PhD), has a Masters and Doctorate Degrees in Agricultural Machinery Design and Development Engineering. Engr Bindir is a Chartered Engineer, a Fellow of both the Nigerian Academy of Engineering and the Nigerian Society of Engineers. He was the a Director General/CEO of the National Office for Technology Acquisition and Promotion (NOTAP). In 2020, he served as a Special Assistant to the President of the Federal Republic of Nigeria. Engr Bindir is the Founder and CEO of the Bindir Knowledge Centre (BKC) International, an NGO located in Yola Town Adamawa State of Nigeria.

DR. RUFUS EBEGBA is a Nigerian who has exposure with different National and international organizations and sectors spanning decades. He was awarded a Ph.D. (Environmental Biology 2016, M.Sc. (Environmental Biology), 2002 and B.Sc. (Agriculture) 1988.Ebegba had over 33 years of working experience in Government (Public sector) which covers- Administration, Policy formulation and implementation, Environmental management, Agriculture, Biosafety and Biosecurity Management, Biodiversity Conservation, Biotechnology, sustainable utilization of renewable natural resources, Enforcement of Regulations, Policies and Laws, Project Development and Implementation.

DR. SYLVESTER OIKEH is a Project Manager at AATF with more than 35 years of interdisciplinary experience in research-for-development covering project formulation, project and partnership management, natural resources management, crop improvement and deployment, and plant nutrition. He joined AATF since 2009 and coordinates the operational management and monitors implementation of WEMA Project/TELA Maize Project across ten public and private sector organizations in seven African countries. He worked in AfricaRice for five years as a Principal Scientist/Soil-Fertility Agronomist and Project Leader.

PROF. EMMANUEL HALA KWON-NDUNG, a Professor of Plant Genetics and Breeding is a versatile research and University administrator and has won national and international research grants. He is the immediate past President of the Genetics Society of Nigeria. He was a postdoctoral fellow at the Institute of Botany, Chinese Academy of Science (2004-2005). He is a Fellow of Genetics Society of Nigeria, Fellow Emergency Crisis and Risk Management Institute, Fellow African Academics Network and a Fellow Third World Academy of Science (TWAS). His current research focus is breeding Jathropha and Sugarcane for biofuel and bioethanol production.

DR. FRANCISCA OBIAGERI NWAOKORIE (Ph.D, M.Sc. MBA, FIMLSCN, FAMLSN) is an Associate Professor in the Department of Medical Laboratory Science, Faculty of Basic Medical Sciences, College of Medicine, University of Lagos. She is a Medical Microbiologist with speciality in Anaerobic bacteriology, Human microbiome, and Microbial genetics. Over the years, she has carried out research in oral microbiology focusing on genetics of *Fusobacterium nucleatum*, Clostridium Species and other anaerobes of public health importance. Her current research is on oral and gut microbiome where anaerobes play major roles in human health, immune system modulation and diseases.

DR. POPOOLA BUKOLA M. works at Faculty of Natural Sciences, Department of Microbiology and Biotechnology, Ajayi Crowther University, Oyo, Oyo State, Nigeria, as a senior lecturer. She received her Ph. D in Environment and Industrial Microbiology at the Department of Microbiology in the University of Ibadan. She has taught a variety of courses in Microbiology field at undergraduate and postgraduate level such as Microbial Genetics, Microbial Physiology, Microbial Ecology, Bacteriology, Microbial Techniques, Advanced Soil Microbiology, Advanced Environmental Microbiology, Advanced Petroleum Microbiology etc.

DR. V.O. FADIPE holds a B.Sc(Hons) Chemistry, M.Sc Chemistry, MBA(Finance), and PhD degree in Chemistry (Organic /Natural Product) from University of Zululand, South Africa. He is presently Principal Research Fellow/Deputy Director/ Head, Public Private Partnership, Federal Ministry of Innovation, Science and Technology, Abuja, Nigeria. He is an experienced multiple step organic chemistry synthesis expert, with application in drug candidate designing and discovery for infectious diseases particularly tuberculosis. He has several research publications in chemistry of natural product, management and treatment of TB.

DR. VALENTINE OTANG NTUI is an Associate Professor of Plant Genome Editing at the African Genome Center, University Mohammed VI Polytechnic, Ben Guerir, Morocco. Dr. Ntui joined UMP6 from the International Institute of Tropical Agriculture (IITA), Nairobi, Kenya, where he was a Scientist. His research centers on the improvement of agricultural crops using molecular biology, genetic engineering, and genome editing tools. In addition, Dr. Ntui teaches Plant Biotechnology courses at the University of Calabar, Nigeria. He obtained his Ph.D. degree in Plant Biotechnology, emphasizing molecular biology and plant genetic engineering, from Chiba University, Japan in 2010.

PROF. BECKLEY IKHAJIAGBE is a Faculty member at the Department of Plant Biology and Biotechnology, Faculty of Life Sciences, University of Benin, Benin City, Nigeria, where as a Professor of Ecophysiology and Environmental Biotechnology, with more than two decades of experience in research and teaching, he contributes his quota to national development through teaching, research and community service. Apart from the scores of undergraduate students he has supervised, including mentees, Prof. Ikhajiagbe has supervised over 60 postgraduate candidates, more than half of whom are Ph.D. and MPhil. candidates.

PROF. BENJAMIN UBI completed a Ph.D. in Agronomy at the University of Ibadan in 1998. His Ph.D. research was carried out at the then Biotechnology Laboratory of the International Institute of Tropical Agriculture (IITA) Ibadan where he was a Graduate research fellow and became President of the International Association of Research Scholars and Fellows (IARSAF) in 1996. Among several other research engagements, he served as Science & Technology Agency (STA) postdoc fellow under the Japan International Science & Technology Exchange Centre (JISTEC) 1999 – 2001 at the Plant Breeding Dept. (Biotech Lab) of the NARO - National Institute of Grassland and Livestock Science, Japan.

PROFESSOR CHARLES OLUWASEUN ADETUNJI is presently the director of research and innovation at Edo State University Uzairue, Nigeria. He is a fellow of Fellow of the Royal Society of Biology (UK), the Biotechnology Society of Nigeria, the Nigerian Young Academy, and the Nigerian Society of Microbiology and an affiliate member of the African Academy of Science. He was also recently listed in Stanford University's World Top 2% Scientists Rankings for 2023 and ranked 1st among the top 500 prolific authors in Nigeria between 2020 till date by SciVal/SCOPUS, not to mention he was ranked number 1 in two different fields from Biological Sciences and Agricultural science.

PROFESSOR ELIJAH EKAH ELLA is currently a Lecturer with the Ahmadu Bello University, Department of Microbiology. He obtained His PGDM, M.Sc. and PhD from University of Port Harcourt, Fed. University of Technology Minna and Ahmadu Bello University Zaria respectively. He is presently a Professor of Microbiology / Immunology. He has actively participated in teaching and research in various aspects of Molecular Biology, Immunology and Virology at undergraduate and post graduate levels. He was a member of the pioneering Staff of Centre for Biotechnology Research and Training, Ahmadu Bello University, Zaria.

PROF. FLORENCE AKANEME is a Professor of Genetics & Plant breeding at the University of Nigeria, Nsukka (UNN), where she has been teaching since 1994. She is very passionate about improving neglected & underutilized crop species. She received her BSc in Education Biology from UNN in 1988, MSc and PhD degrees in Genetics/Plant breeding also from UNN in 1992 and 1999 respectively. She co-developed a curriculum on "Ethics & World Views in Relation to Biotechnology under the EDULINK-FSBA Project which was financed by the European Union and implemented by the ACP Secretariat (2013 – 2017). She was elected the Dean, Faculty of Biological Sciences UNN from 2020 to 2022.

PROFESSOR NNENNAYA ROSEMARY ISU is a Nigerian academic who has contributed immensely to skilled man-power development. As an accomplished researcher and author, she has numerous peer-reviewed articles in national and international journals to her credit. Prof Isu is also a University accreditor and continues to contribute to improved academic curricula in educational institutions. A professor of Microbiology and Biotechnology, Prof Isu is passionate for the advancement and application of Biotechnology in Nigerian institutions.

PROFESSOR C.J. OGUGBUE is a distinguished Prof. of Environmental Microbiology in the Department of Microbiology at the Faculty of Science, University of Port Harcourt. He earned his Ph.D. in Environmental Microbiology from the University of Port Harcourt in 2005. Following his doctorate, he pursued post-doctoral training at the Aristotle University of Thessaloniki in Greece (under the Coimbra Group Europe) and at Universiti Sains Malaysia (through the TWAS-USM fellowship). His research focuses on the biodegradation and ecotoxicity of pollutants and xenobiotic compounds, wastewater treatment, the impact of microbial inoculants on tropical plants, and microbial fuel cells, among other areas.

PROFESSOR TERKIMBI VANGE (a USDA FAS Borlaug Fellow U.S.A. 201) is a Professor of Plant Breeding and Biometrics in the Department of Plant Breeding and Seed Science, Joseph Sarwuan Tarka University (formerly, Federal University of Agriculture), Makurdi, Benue State North Central Nigeria. Professor Vange is the President of Plant Breeders Association of Nigeria (pban.org.ng). He held several administrative positions in the university. He served as a member of the Governing Board of, the National Agriculture Seed Council (NASC) Abuja and a member of the Governing Council, Joseph Sarwuan Tarka University Makurdi.

PROF IFEOMA ENWEANI-NWOKELO is a Professor of Microbiology and works in Nnamdi Azikiwe University, Awka. Nigeria. She has mentored a host of Scientists through undergraduate and postgraduate programs and she is a Professor of Professors. She has enjoyed two postdoctoral fellowships tenable in Germany and Spain respectively. She has passion in promoting the use of organic indigenous plant products in addressing food security and ensuring good health especially in children under five years of age. She is also particularly interested in the exploitation of Nigerian plants bio active agents as sources of antimicrobial agents to support one health agenda.

PROF. KEN IFE is an International Development Consultant and Development Economist. He served as London Enterprise Ambassador and held various advisory roles for the UK, in her Majesty's government under Prime Ministers Tony Blair and Gordon Brown, and Mayor Ken Livingstone. This includes his position as Director at HM Home Office CDF and member of the London Food Board. He was the UK Govt DfID Trade Adviser to the Nigerian government (2011-12). Prof. Ife has been a member of the Presidential Governing Council of the Ministry of Finance Incorporated (MOFI) since January 2023.

DR. OKOH DANIEL ABANI is a distinguished expert in Waste Management/Water Sanitation & Hygiene (WASH) and Alternative Energy, specializing in waste-to-energy technologies. Dr. Abani holds a Bachelor of Science in Applied Chemistry from the Federal University of Uyo, a Master's in Material Science and Explosive Chemistry from the National Defence Academy, Kaduna, and a Ph.D. in Analytical Chemistry from the University of Abuja. He has enriched his expertise through numerous certificates from esteemed institutions worldwide, including the 6th International Training Workshop on Waste to Energy in China.

PROF. AYOKUNLE AFOLABI TOYE, Professor of Theoretical and Applied Genetics, Department of Animal Production, Faculty of Agriculture, University of Ilorin, Kwara State, Nigeria. Principal Investigator, Quantitative, Molecular and Functional Genetics Group. Associate Lecturer, Department of Biomedical Engineering, Faculty of Engineering and Technology, University of Ilorin, Kwara State, Nigeria. Chair, University of Ilorin Moringa Plantation Management Committee, University of Ilorin, Kwara State, Nigeria.

DR MODUPEADE ADETUNJI is an Associate Professor of Food Mycotoxicology and Food Safety known for her immense contribution to research related to Food Safety, specifically Mycotoxins in foods and nuts and antimicrobial resistance surveillances and control in foods and animal products. She is currently the Ag. Dean of the Faculty of Basic Medical and Applied Sciences, Trinity University, Yaba, Lagos, Nigeria. Dr Adetunji is a Post-Doctoral Fellow alumnus of the North-West University, South Africa (2017-2020), and an award recipient of "Outstanding Women in Science and Award of Excellence in Biotechnology" at the 3rd Recent Advances in Biotechnology annual conference and workshop 2023.

JOSÉ FALCK-ZEPEDA, a citizen of Honduras, is a Senior Research Fellow at the Innovation and Policy Scaling (IPS) Unit at the International Food Policy Research Institute (IFPRI). He has a Ph. D and M.Sc. in Agricultural Economics from Auburn University Alabama, a B.Sc. in Animal Science from Texas A&M University, and an Agronomist degree from Pan-American Agricultural School (Zamorano University) in Honduras. Falck-Zepeda has worked with the International Service for National Agricultural Research (ISNAR) in the Netherlands, Auburn University in Alabama, and Zamorano University in Honduras. Falck-Zepeda has authored or co-authored multiple peer-reviewed and other publications.

YUSUF ADO KIBIYA, is a graduate of Agronomy from Tuskegee University in 1983, he worked with Kano State Ministry of Agriculture and Natural Resources from Agricultural Assistant Extension and rose through various assignments up to Chief Agric Officer (Agric Services) from 1980 - 1997. In 1997, he left Government service to work as regional manager North at Dangote Group. In 1999, he was invited to serve his state as Hon. Commissioner Ministry of Agriculture and later Commissioner Ministry of Lands and Regional Planning. He was later appointed by the Fed. Govt. to serve as Executive Dir. Operations at Arable Crops Devt and Marketing plc a former subsidiary of the Fed. Min. of Agriculture and Rural Development.

MRS. SUMAYYA HAMZA MAISHANU is an exceptional Molecular Biology Professional, erudite Researcher, and passionate Teacher with fifteen years of experience. She is currently the Branch Manager at the prestigious DNAlabs Abuja, Nigeria, where she drives the organization's vision with her leadership prowess. Additionally, she serves as a member of the National Technical Committee on Biotechnology in Nigeria. Throughout her career, Mrs. Maishanu has made significant contributions to science and humanity through her excellent laboratory research, problem-solving, leadership, and teaching skills.

ALISON VAN EENENNAAM is a Distinguished Professor of Cooperative Extension in the field of Animal Genomics and Biotechnology in the Department of Animal Science at the University of California, Davis where she has been on faculty for over 20 years. She received a Bachelor of Agricultural Science from the University of Melbourne, and both an MS in Animal Science, and a PhD in Genetics from UC Davis. Her research and outreach program focuses on the use of animal genomics and biotechnology in livestock production systems. She has a multifaceted research program that has included work on the uses of DNA information and biotechnologies in beef cattle production systems.

PROFESSOR KINGSLEY UBAOJI is a distinguished academic and renowned Professor of Biochemistry in the Department of Biochemistry at Nnamdi Azikiwe University (NAU) in Awka, Anambra State, Nigeria. He is widely recognized for his significant contributions to the field of biochemistry.

PROFESSOR RABIU ADAMU. Professor Adamu is a Professor of Agricultural Entomology, with research interest in pest management , pesticides and Breeding for insect resistance in Cereals and Legumes. He is the President of the Entomological Society of Nigeria, Head of Department Crop Protection ABU Zaria and the Principal investigator TELA Maize.

DR. TAD SONSTEGARD serves as the Chief Executive Officer of Acceligen, overseeing the commercialization of their groundbreaking genetic improvement breeding platform for food animals that combines genomics, gene editing, and advanced cell culture and reproductive methods. Under Dr. Sonstegard's leadership, Acceligen has moved from making proof-of-concept animals to achieving the first commercial use approvals in multiple countries with their innovative product lines for heat tolerant beef and dairy cattle. Currently, Acceligen's focus is to develop climate-smart food animals, with additional flagship products for disease-tolerant cattle designed to reduce methane emissions.

DR. OLUWASAYO ESTHER OGUNJINMI is a Senior Lecturer in the Dept. of Industrial Chemistry and a Vice Dean of the Faculty of Natural and Applied Sciences at First Technical University in Ibadan, Oyo State, Nigeria. She holds a PhD in Organic Chemistry from the Dept. of Pure and Applied Chemistry, Ladoke Akintola University of Technology, Ogbomoso. Part of her PhD thesis is in the Chemistry Department at the University of Pretoria, South Africa. Her research interest is focused on investigating scientific bases for herbal medicines and synthesizing biocompatible materials. She has published in many prestigious national and international journals.

PROFESSOR AKEEM ABOLADE OYERINDE is the Ag. Dean, Faculty of Agriculture, University of Abuja, Nigeria. He is the National Chairman of the Standard Organization of Nigeria Technical Committee on Apiculture Products, Technical Chairman of the Food and Agriculture Organization (FAO) and Raw Materials and Research Development Council Committee on Capacity Development of Village Technicians in the Action Against Desertification (AAD) Communities in Nigeria and Council member of Entomological Society of Nigeria, Nigeria Apiculture Platform and researcher of the United Nations Framework on Climate Change (UNFCC).

DR. MEKULEYI GABRIEL OLARINDE bagged his B.Sc, M.Sc &Ph.D in Fisheries from Lagos State University in 2010, 2015 & 2023 respectively. He has taught at ESPAM Formation University (Republic of Benin) and Universite Biligua du Togo for several years. Currently, Dr Gabriel is a junior Lecturer at the Dept of Fisheries, LASU with over 35 academic publications in reputable local and international journals. He is a member of several international professional bodies. Few among them are Society of Toxicology (USA), International Society for Development & Sustainability (Japan), International society of ecological economics (USA) and Association of Science of Limnology & Oceanography (USA).

DR. MICHAEL AGBAJE is an Associate Professor of Veterinary Microbiology at the Federal University of Agriculture in Abeokuta (FUNAAB), Nigeria. He holds a PhD in Microbiology from the University of Nottingham, UK, and has extensive expertise in biorisk management. Agbaje currently serves as the Chairman of the Biosafety Committee in FUNAAB, and has received several accolades, including being named an African-Region Subject Matter Expert in Biorisk Management by the Africa CDC. He has also provided technical consultancy on biorisk management to the International Atomic Energy Agency (IAEA) in Vienna, Austria.

DR. ODUNLADE ALBERT holds PhD degree in Animal. Biotechnology from Federal University of Agriculture Abeokuta (FUNAAB), He is a lecturer and Acting Head of Dept of Biotechnology at Trinity University Sabo. He has attended both local and international conferences and published in reputable journals. He is a member of Biotechnology Society of Nig and American Society of Human Genetics. He is happily married and blessed with children Title of discussion/ presentation; Eco friendly Alternatives and Bio based materials.

DR. AGHA UKPAI AGHA is an Acting Director, Biosecurity Department in National Biosafety Management Agency. He obtained his first degree in Forestry and Environmental Management , Masters degree in Plant Biotechnology and Biosafety in Adelaide, Australia and Third degree, Ph.D in Agroforestry, University of Abuja. Dr. Agha is an expert in Biorisk Management, and has been trained in Biosafety and Biosecurity in countries like United States of America, India, South Africa ,Italy, Indonesia, Geneva, Australia etc. Dr. Agha has received many Awards on Biosafety and Biosecurity within and outside Nigeria. He also received the Prestigious Civil Service Presidential Award in 2017.

DR. ANDREW CHIBUZOR ILOH Research experience is in the fields of plant molecular biology and population genetics, focusing on applications in genetics, forensics, awareness and capacity building. His earliest research interest stems from the need to conserve threatened local plants, which play important roles in the Nutrition and Diet of Rural West Africa he is also understanding how genetics and evolutionary processes interact to influence phenotypic variation and adaptation especially in plant species in African forests. His forensic research involves the used molecular biology tools for in GM detection, providing data for regulations and risk assessment in Nigeria.

EZEBUIRO NWAGBO CHRISTPEACE attended Hamburg University of Technology (TUHH), Germany, where he obtained a Doctoral Degree in Bioprocess Engineering (specialization in Energy and Environment) with a Scholarship from the German Academic Exchange Programme (DAAD). His experiences are in technology development and deployment strategies, including water, energy, waste management, bioremediation system designs and development, and entrepreneurship promotion. He is also a Certified Project Manager. Dr. Ezebuiro NC has over 18 years of experience with government and has provided extensive support to the private sector.

DR. TOSIN COMFORT OLATERU is an academic and researcher in the field of Food Microbiology and Biotechnology, a Principal Lecturer and the present head of department, Department of Biology, The Polytechnic, Ibadan, Oyo state. She earns all her degrees including a Ph.D in Food Microbiology from the prestigious University of Ibadan. Nigeria. Her research interest include fermentation technology, antibiotic resistance, food preservation and food safety. She has published articles in notable journals and have presented papers in local and International conferences; a member of Nigerian society of Microbiology, Society for Applied Microbiology, United Kingdom, Federation of European Microbiologists.

DR. ONYEKACHI FRANCIS NWANKWO is a passionate biotechnology stewardship professional with 13 years of experience ensuring the safe and responsible development, regulation, and use of agricultural biotechnologies. Driven by a strong commitment to product safety and public education, he is dedicated to building trust in the field and harnessing the power of agricultural biotechnology for good while minimizing potential risks. Francis Onyekachi stands out in the biotechnology field, having had the unique opportunity to shepherd AgBio products from its research phase through the complex regulatory and seed systems hurdles all the way to the farmers' fields.

DR. EMMANUEL OLUWADARE BALOGUN is an esteemed biochemist, international scholar, and senior lecturer at the Department of Biochemistry and the Africa Center of Excellence for Neglected Tropical Diseases and Forensic Biotechnology at Ahmadu Bello University, Zaria, Nigeria.

DR. LAWAL, ADEKUNLE KOLAWOLE hails from Ibadan, Oyo State Nigeria and was born into the family of Mr. and Mrs. Richard Osuolale Lawal. He had his primary school education at Yaba Methodist Primary School between 1969 and 1975 and had his secondary and advanced schools at C.M.S Grammar School, Bariga, Lagos in 1980 and 1982 respectively. He proceeded to the University of Lagos where he respectively bagged his Bachelors and Masters degree in 1985 and 1987 and his doctorate degree at the University of Ibadan, Oyo State.Dr. Lawal started work at the Federal Institute of Industrial Research, Oshodi in 1988 as a Research Officer I in the Biotechnology Department.

PROF. ISMAILA YADA SUDI is a distinguished academic currently serving as a Professor of Environmental Biochemistry and Molecular Biology at Adamawa State University (ADSU) Mubi. He played a pivotal role in establishing the Department of Biochemistry at ADSU Mubi and lead it to achieve full accreditation from National University Commission (NUC). He holds a PhD (Bioscience) from Universiti Teknologi Malaysia, Malaysia, with specialization in "Insilico Studies of recalcitrant chemical degrading dehalogenase D (DehD) from Rhizobium sp. RC1". Professor Sudi served with Federal University of Technology Yola (now MAU Yola on visiting capacity in the Department of Biotechnology for seven (7) years).

DR. EFFIOM EYO ITA is a Plant Biotechnologist with interest in engineering plants for biotic and abiotic stress resistance with increased productivity and nutritional value through genome editing. As an academic and a research scientist, Dr. Effiom is committed to advancing research in plant cell engineering and plant genomics for the improvement of indigenous plant species in Africa. As a panel discussant in the International Conference on Biotechnology, Dr. Effiom brings invaluable expertise and insight into the prospect of developing indigenous Biogenome Databases through an African Biogenome Progect-NBRDA collaboration.

DR. IHUOMA CHIZARAM OKWUONU, holds B.Sc. (combined microbiology/chemistry); M.Sc (Applied microbiology); PhD (Plant Biotechnology), is an Assistant Director with the National Root Crops Research Institute (NRCRI) Umudike where she coordinates the activities of the Biotechnology Research Programme. Her research focuses on the use of modern biotechnology tools for the genetic improvement of root and tuber crops of African interest. Currently, she serves as the country PI and component lead for some biotechnology projects including the VIRCA Plus project Cassava Source-Sink Project among others. She is also an awardee of BAYER Grant4Ag in Gene Editing of Cassava.

DR. PRECIOUS ETINOSA IKPO is an expert in Immunology and Immunochemistry. She currently serves as an Assistant Director of Medical Laboratory Services and Head of Medical Laboratory services at the Federal Neuropsychiatric Hospital (FNPH) Benin City, Nigeria. She also holds an adjunct position as a Senior Lecturer in the Department of Medical Laboratory Sciences at Benson Idahosa University Benin City. Dr. Etinosa's higher academic journey began at the Ambrose Alli University Ekpoma Edo State were she obtained a Bachelor of Medical Laboratory Science (BMLS) degree in Medical Microbiology (2005).

PROFESSOR MOHAMMED BELLO YERIMA, is presently a Faculty member in the department of Microbiology at Sokoto State University, Sokoto-Nigeria. He is an expert in Microbial Biotechnology and has focus on achieving enhanced human welfare and existence using microorganisms. He is involved in research and teaching Microbiology and Biotechnology for twenty-nine years now at University level. He served the University system in different capacity and currently Deputy Vice Chancellor (Academic). Prof. Yerima is a visiting Professor to some Universities in Nigeria. He is the Immediate past President of Biotechnology Society of Nigeria.

PROF. ADENIYI ADEWALE OGUNJOBI was born to the family of High Chief Alawe of Oda Odo quarters in Omuo Ekiti, Ekiti State over five Decades ago. He started his primary education in Hospital road Primary school, Aba town in the then Imo State, now Abia State in 1975. He was later changed school to continue his education in the then Ondo State (now Ekiti State) at Saint Mary primary school, Omuo Ekiti and graduated in 1982 with excellent performance. He got admission to Omuo Ore secondary school in 1982 but got transfer to Isua High school due to movement of parent from one location to the other attending three different secondary school.

PROF. JULIAN O. OSUJI, is scheduled to speak on "Prospects of Developing Indigenous Biogenome Databases through an African BioGenome Project - NBRDA Collaboration". Being a Molecular Geneticist and Cytotaxonomist, he has functioned in various high level academic and scientific research circles nationally and internationally. Presently, he is Director, Regional Centre for Biotechnology and Bioresources Research, University of Port Harcourt & Director, NBRDA South-South Zonal Centre of Excellence as well as Principal Investigator & Team Lead, Interdisciplinary Biology Network (IB4 BioNet). He is a Co-Chair of African BioGenome Project (AfricaBP).

ADEJOKE LASISI is the founder of Planet 3R is a social enterprise dedicated to converting textile and plastic wastes into eco-friendly products using the 3R (Reduce,Reuse,Recycle) to save our planet Earth byweaving them into innovative items with the vision of creating a sustainable world without textile and plastic wastes, it became necessary for us at Planet 3R to reduce the landfill space by recycling clothes and nylons. At Planet 3R, we contribute to the circular economy by ensuring our method of conversion does not cause any other environmental hazards and use of local equipment makes our products relatively affordable.

PROF. S.A ADO, Professor of Industrial Microbiology and Microbial Biotechnology, Department of Microbiology, Ahmadu Bello University, Zaria, Nigeria

PROFESSOR OLUBUNMI AGARRY, Professor of Food Microbiology at University of Abuja with numerous peer-reviewed articles. She started her academic career as a Graduate Assistant and rose through the ranks. She has served in various leadership capacities within the University system. Currently, together with her research team harnessing bacteriocins for industrial bioprocessing

DR. YUSUF HAJARA OYIZA has a PhD in Crop Protection from the prestigious and renowned University of Abuja. She also obtained other educational degrees in Biosafety in Plant Biotechnology (Marche Polytechnic University, Ancona – Italy), Environmental Technology (Federal University of Technology Owerri), and Biochemistry (Ahmadu Bello University Zaria). Dr. Yusuf's dedication to continuous learning is evident through her international exposure and professional training received from prestigious institutions such as the University of Tromso in Norway, Michigan State University in the USA, the International Centre for Genetics Engineering and Biotechnology (ICGEB) in Italy.

the Director and Head of Department gy, his MSc degree in Biochemical & Toxicology and Ph.D in dical Biochemistry from University of lty in Immunogenomics and a Diploma in m Biosafety Training Institute, University as received several academic awards and well as published extensively in reputable peer review journals mainly in areas of immunology, pharmacology and genomics. Dr. Ibeh has University teaching and supervision experience as well as editorship of several expert opinion on HIV therapeutics.

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EXTENDED ABSTRACTS

Enhancing Natural Attenuation in Diesel-Polluted Soil by Stimulating with *Moringa Oleifera* Leaf Powder

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INTRODUCTION

Petroleum hydrocarbon pollution management typically entails a combination of physical, chemical and biological techniques aimed at ultimately eliminating the disrupting pollutant or, at least, reducing its concentration to more tolerable levels. The commonly used physical and chemical remediation techniques often become just as disruptive to the ecosystem as the pollutant; this is the reason biological approaches are now preferred and employed where feasible in remediation interventions. Bioremediation is the biological approach to pollution management. It is considered the most sustainable approach to pollutant elimination as it makes use of the natural response to the presence of pollutants in the environment (Alori *et al*., 2022). Several *in-situ* and *ex-situ* techniques exist for pollution management via biological means. *Moringa oleifera* is the most extensively studied member of the genus *Moringa*. It has several common names including the drumstick tree, the horseradish tree, the Benzolive tree and the Kelor tree. It a plant native to the tropical regions of Asia, Africa and South America. One of the important applications of this nutrient-rich plant is the production of powders from its parts – seeds, leaves, and stems (Meireles *et al*., 2020). Despite its numerous uses, there are only a few studies that assess its potential in bioremediation. This study aimed to investigate the use of *Moringa Oleifera* leaf powder (MOP) at 1% w/w and 2% w/w amendment levels to enhance the natural attenuation process during remediation of diesel-contaminated soil and to assess the impact of remediation on the soil hydrocarbon-utilising bacterial community.

MATERIALS AND METHODS

Sample Collection

The soil used for the microcosm study and the *Moringa oleifera* (MO) leaves were both collected from the agricultural farm at the University of Port Harcourt while the diesel used was purchased from the Nigerian National Petroleum Co-operation (NNPC) filling station in Alakahia, Rivers state. The MO leaves were washed thoroughly and dried in an oven before being reduced to powder

Experimental Design

The bioremediation study was carried out in replicated sets with each set consisting of 1500 g of soil and *M. oleifera* leaf powder (MOP) set up as follows: **Control 1**: Soil alone (unpolluted control); **Control II**: Soil + 5 % v/w diesel (polluted control); **Control III**: Soil + 5 % v/w diesel + 2 % w/w NPK fertiliser (standard control); **Set IV**: Soil + 5 % v/w diesel + 1 % w/w MOP and **Set V**: Soil + 5 % v/w diesel + 2 % w/w MOP.

The soil was aerated via regular tilling and moisture was maintained at 60 %. Following a 7-day acclimatisation period, the extractable total petroleum hydrocarbon (ETPH) and microbial diversity and abundance were monitored at regular intervals for 60 days.

Extractable Total Petroleum Hydrocarbon (ETPH)

The liquid-liquid extraction method was employed in determining the extractable total petroleum hydrocarbon (ETPH) content in the samples. This was done using a gas chromatograph fitted with a flame ionisation detector (Agilent 6890N, USA). The samples were extracted with dichloromethane and eluted using pentane in a capillary column. Sampling for determination of ETPH content was carried out at 15-day intervals.

Enumeration, Isolation and Characterisation of Soil Bacterial Community

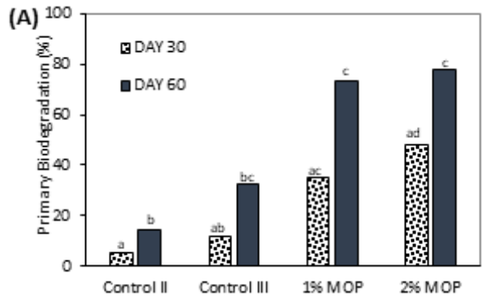
The abundance of the total cultivable heterotrophic bacteria (TCHB) and cultivable hydrocarbon-utilising bacteria (CHUB) were monitored at 15-day intervals while changes in diversity were monitored every 30 days. For TCHB, isolation was carried out on nutrient agar while plate count agar was employed for enumeration via the dilution plate technique. The plates were incubated at 30 °C ± 2 ºC for 48 h. Only plates with counts of 30 – 300 colonies were selected for enumeration. Counts were expressed as mean colony-forming units (CFU) per gram of soil. The isolates obtained were purified by streaking onto fresh nutrient media. Representative isolates were identified based on their macroscopic, microscopic and biochemical characteristics as recommended by Cheesborough (2005).

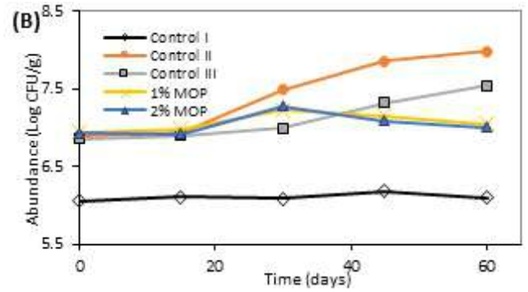
The CHUB were isolated and enumerated via the enrichment method using nystatin-amended mineral salts medium (MSM) containing 2 % diesel as the sole carbon source. Incubation was at 30°C ± 2 ºC for 48 h. Discrete colonies that developed on MSM were purified by subculturing twice via the streaking plate technique and preserved on slants for subsequent microscopic and biochemical characterisation.

RESULTS AND DISCUSSION

The TPH elimination levels of 35.08 % and 48.32 % were obtained for the 1 % and 2 % MOP amendment concentrations respectively on day 30 of the study. By the end of the study (day 60), these values had risen to 73.22% and 77.97 % respectively (Figure 1A). The TPH elimination levels obtained at the end of the study were seen to be significantly different at a 95 % confidence interval between the studies with MOP applied and the Controls; however, there were no significant differences ($p \leqslant 0.05$) between the 1 % and 2 % application concentrations for MOP. The changes in abundance of the total cultivable heterotrophic bacteria (TCHB) and (C) cultivable hydrocarbon utilising bacteria (CHUB) during the study are displayed in Figures 1B and 1C respectively. Comparisons with the control studies show that there was a general increase in the abundance of bacterial species in the soil samples in response to the presence of diesel. Growth levels seemed to reach the stationary phase by day 45, on average, after which counts began to show a decline across the board. This was not the case with the polluted control (Control II) where abundance continued to increase till the end of the study.

In tandem with the present study, Agbuon *et al*. (2016) also confirmed an increase in bacterial abundance by up to 58.0 % following the application of *M. oleifera* (MO) seed cakes in crude oil-contaminated soil. They further reported that the MO amendment resulted in a simultaneous 64.3 % reduction in crude oil concentration. The role of species of *Pseudomonas, Klebsiella, Corynebacterium, Micrococcus* and *Bacillus* amongst others in the degradation of hydrocarbon contaminants during bioremediation, as obtained in the current study, has also been confirmed in other similar studies (Agboun *et al*., 2016; Ughamba *et al*., 2019; Rahmeh *et al*., 2021).





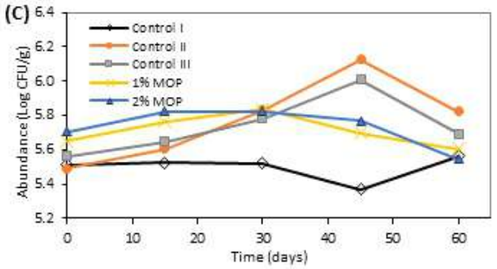


Fig. 1. (A) Extent of primary biodegradation of extractable total petroleum hydrocarbon from diesel in the contaminated soils and changes in the abundance of (B) total cultivable heterotrophic bacteria (TCHB) and (C) cultivable hydrocarbon utilising bacteria (CHUB) during the study. Different letters indicate statistically significant differences at $p \leqslant 0.05$. Control I – unpolluted control; Control II – Polluted control; Control III – Standard (NPK) control

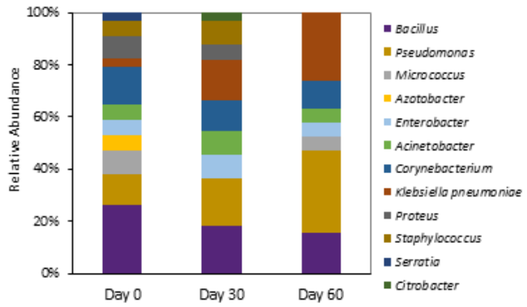


Fig. 2. Distribution of cultivable bacteria obtained during the study

CONCLUSION

The application of *M. oleifera* leaf powder was seen to enhance the abundance of soil bacteria, particularly species with the capacity to utilise diesel fractions. It also efficiently boosted the natural attenuation of diesel in contaminated soils increasing the elimination levels by up to 59.2 % and 63.9 % at 1 % w/w and 2 % w/w application levels respectively compared to the unamended control. *Pseudomonas* and *Klebsiella pneumoniae* were noted as the drivers of the remediation process at the genus taxonomic rank. The *M. oleifera* leaf powder was efficient in enhancing natural attenuation in diesel-polluted soils. Its application for bioremediation of other contaminant types should be explored further.

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Enhanced Bioremediation of Crude-Oil Polluted Soil using Saw Dust and Pig Droppings

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INTRODUCTION

The Niger Delta ecosystem is subjected to man-induced changes and is seriously threatened by increasing environmental degradation. Crude oil is a naturally occurring complex mixture of hydrocarbon and non-hydrocarbon compounds which possess measurable toxicity toward living systems (Kim, 2003). The increase in demand for crude oil as a source of energy and as a primary raw material for petroleum and allied industries has resulted in gross pollution of the environment (UNEP. 2011). Petrochemical hydrocarbons are among the environmental pollutants that affect the entire ecosystem (Ayogu *et al*., 2020). Owing to the problems associated with physical, mechanical and chemical methods of remediation of the polluted environment. Bioremediation is a means of cleaning up contaminated environments by exploiting the diverse metabolic abilities of microbes to convert contaminants to harmless products by mineralization, generation of carbon (IV) oxide and water, or by conversion into microbial biomass.

Enhanced bioremediation is a necessity in order to have a fast, safe and healthy environment that will in turn result in sustainable development. Many techniques of remediation of contaminated soil have been developed, such as physical, chemical degradation, photo-degradation. However, most of these methods have some drawbacks in completely remediating hydrocarbon contaminated soil. Some of these methods leave behind daughter compounds which are more toxic to the environment than the parent compounds (Khan *et al*., 2005). In Nigeria, no information is yet available regarding the commercial production of microbial inocula for use in bioremediation of oil polluted environments. Efforts should therefore be focused on developing indigenous fungi and bacteria for use in large scale operations in Niger Delta area of Nigeria. Scientific investigations have shown that crude oil degrading fungi (microorganisms) abound in the Niger Delta region (Yerushalmi *et al*., 2003). Bioremediation is, therefore, the answer to the removal of oil spilled in these areas and the best means of remediating such sites.

MATERIALS AND METHODS

Sources of research materials: The materials that were used for this research were pig droppings, saw dust, distilled water, Bonny light Crude oil, polluted soil, Mineral salt agar, Sabouraud Dextrose agar, Potato Dextrose Agar, Nutrient agar (Oxoid), Simmons citrate agar; 95% ethanol, normal saline. The apparatus used include electronic weighing balance (LT 502), Sieve (mesh size: 0.3 mm), Jenway 6305 UV-VIS Spectrophotometer (AAS).

Sample Collection: Surface soil (0−15 cm depth) was collected from a crude oil-contaminated site at Omoku in Rivers State using soil auger and packed into clean polythene bags and transported to the laboratory for analysis. Samples were tilled to enhance aeration and oxygen circulation in the soil samples. The sawdust or wood dust was collected from Rumuosi saw mill in Port Harcourt and transported in a clean polythene bag to the laboratory for analysis (Hussmann, 1993). Pig droppings were collected from the Faculty of Agriculture, University of Port Harcourt Demonstration Farm and transported in clean polythene bags to the laboratory (Hussmann, 1993). The sawdust and pig droppings were composted aerobically with constant tilling and watering for 4 weeks.

Description of bioremediation treatment design: The enhanced bioremediation treatment setup is composed of sets A to F. Set A contained 200 g of crude oil contaminated soil (COCS) and 100 g of saw dust (SD), set B has 200 g of crude oil contaminated soil (COCS) and 100 g of pig droppings (PD), set C has 200 g of crude oil contaminated soil (COCS) and 100 g of sawdust and pig droppings and D has only the crude oil contaminated soil (COCS) respectively. All treatments including experimental setups were constantly tilled at an interval of two days for a period of 42 days to enhance aeration and oxygen availability in the crude oil-contaminated soil undergoing bioremediation.

Spiking and tilling of soil: The soil was spiked with water uniformly to soften the soil and to allow the water to penetrate the soil matrix. The soil was tilled for a week after they were spiked, by mixing the soil and breaking the lumps using a sterile shovel. Thereafter, composite soil samples were collected and sent to the laboratory for analysis. Composted nutrient supplements were added to the soil and monitored. Samples were collected five times at two weeks intervals.

Microbiological analyses: The culturable hydrocarbon-utilizing bacteria were isolated and identified using standard recommended procedures for analyses (Obire *et al.,* 2008; Azaiki, 2009).

Physico-chemical analyses: The methods by the Association of Analytical Chemists (AOAC, 1990), were adopted for physico-chemical analysis. The analyses done were: Total Petroleum Hydrocarbon, Nitrate content, Phosphate Content, Sulphate content, Organic carbon content and Potassium content.

Statistical analysis: The data generated in the study were subjected to statistical analysis using a two-way analysis of variance (ANOVA) to determine levels of significance. If the mean difference was less than the critical ratio, the result was considered as not significant, $p>0.05$. But if the difference between means was greater than the critical ratio, the result was accepted as significant at $p<0.05$ incidence ratio.

RESULTS AND DISCUSSION

Oil-degrading bacteria in the contaminated soil environment become adaptive to the environment replicate faster and make use of the residual crude oil in the soil as a source of carbon. Chikere *et al.* (2009, 2011) reported the microbial dynamics in crude oil-contaminated soil undergoing bioremediation. The study revealed several trends including a drastic increase in hydrocarbon-utilizing bacteria with respect to nutrient supplementation and a subsequent decrease in number as nutrients were depleted. Hydrocarbon-utilizing bacteria isolated were identified to be species of *Pseudomonas*. The microorganisms must have used a special enzyme system including dehydrogenase and oxygenase to degrade the contaminants.

Physicochemical Parameter	Value obtained
TPH (mg/kg)	27640
Nitrate (mg/kg)	16.88
Phosphate (mg/kg)	23.56
Sulphate (mg/kg)	22.67
Potassium (mg/kg)	24.15
Moisture content (%)	13.16
TOC	32.39
pH	4.47

Total petroleum hydrocarbon levels decreased from 27640 to 13215 mg/kg for “A', 13961 mg/kg for “B” and 10415 mg/kg for “C”.

Physicochemical analysis of the crude oil-contaminated soil before bioremediation

There was a significant ($p<0.05$) reduction of total petroleum hydrocarbon (TPH) in all setups. The TPH levels decreased from 27640 – 13215 mg/kg for A representing a 52.7 % reduction. B had TPH reduced from 27640 – 13961 mg/kg, this corresponds to a 49.5 % reduction. C had a TPH decrease from 27640 – 10415 mg/kg indicating a 62.4 % reduction. The control, D had decreased from 27640 – 24021 mg/kg indicating a 13.1 % reduction. The hydrocarbon contaminants in the soil reduced obviously, signifying their conversion to CO_2, H_2O and biomass. Nitrate decreased by 5.3 %, 6.5 %, 7.4 % and 2.4 % respectively. Sulphate decreased by 0.6 %, 1.1 %, 4.8 % and 5.6 % respectively. Phosphate decreased by 4.4 %, 0.3 %, 4.4 % and 0.2 % respectively. Organic carbon decreased by 6.6 %, 10.3 %, 15.7 % and 18.9 % respectively. The control D decreased to zero (0) by day 42. Potassium showed a significant ($p<0.05$) decrease of 4.0 %, 1.4 %, 4.6 %, 5.7 % and 8.8 % respectively.

CONCLUSION

This study has shown that hydrocarbon-utilizing microorganisms are domiciled in crude oil-polluted environments and are capable of using residual crude oil as their sole source of carbon thereby degrading it from the environment.

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Adoption and Use Intensity of Sustainable Agricultural Practices (SAP) Among Young Rice Farmers in Ogun State, Nigeria: A Double Hurdle Approach

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INTRODUCTION

Rural young farmers contribute enormously to rice production with little access to production resources (Food and Agriculture Organization, 2018). These production resources are scarce and all strategies to maximize production through the utilization of sustainable production Technologies have not yielded their expected outcomes for optimum rice production, especially in Nigeria. Sustainable Agricultural Practices (SAP) is a collection of on-farm production techniques that ensure efficient use of resources for optimum yield without ignoring the sustainability of the entire production parameters including flora and fauna (FAO, 2020a). Several efforts in the past and present via training had been directed to farmers mostly youth to improve the productivity of rice. These include Competitive Africa Rice Initiative CARI, (2015), and the United Nations Development Programme UNDP, (2019) among others. Implying that efforts are needed in earnest to close the large gap in agricultural productivity (Tesfamicheal and Seife 2018).

Improved rice varieties have the potential to yield up to 10M tons ha^{-1} which implies that farmers can attain corresponding higher yields when appropriate practices are adopted and utilized continuously (FAO, 2020b). It is worth noting that the current state of food insecurity coupled with a high level of degradation of the agroecological system requires embracing more productive and sustainable production technologies to salvage the entire food production system (FAO, 2017). More importantly, the report of Joseph, (2021) stressed the urgent need to avert the problem of food shortage, orchestrated by climate change, pest and disease problems, and malnutrition by adopting the use of modern biotechnological tools (Abdul *et al*., 2016; Braham, 2022). Efficiency in production is not a linear process (Akinniran and Faleye, 2020). The report of Olaniran Ogunmiyi and Fanifosi (2020), asserted that adoption decision precedes that of continuity in the usage of innovation. Obviously, the determinants of these could vary. These factors span through diverse parameters including socio-economic, and participation in training, among others and had a probability of influencing both the adoption and intensity of using these practices differently. However, there is a dearth of information in relation to these factors in the study area. The objective of the study was to examine the factors influencing the adoption and intensity of utilization of SAP among young rice farmers in Ogun State.

METHODOLOGY

The study was carried out in Ogun State, southwest Nigeria based on her prominence in rice production in addition to suitable ecology (Nairaland, 2017 and National Agricultural Extension Research

Liaison Service NAERLS, (2020),). A Multi-stage sampling technique was used to select 94 young rice farmers of the age range 18-35 years (FGN, 2009).
A validated structured interview schedule was used to collect information from the respondents. Thirty-two (32) SAP items were presented and adoption of the practices was measured nominally as YES= 1 or NO=0 while the intensity of utilization was measured on a four (4) points rating scale of very often=3, often=2, sometime=1 and never=0. Prior to analysis, the data sets collected were tested for normality in the distribution pattern and homoscedasticity as suggested by (Faith, 2020). The double–hurdle regression model was used to establish the factors influencing the adoption and intensity of utilizing the practices by the respondents.

RESULT AND DISCUSSION
The mean age of the young rice farmers was 29 years while the majority (78.8%) were males. Most (73.4%) of the respondents cultivated OFADA on an average farm size of 1.1 hectares and reaped an average of 2.6 tons per hectare mostly under a rain-fed system. The major SAP utilized by the respondents at each stage of operation includes: farm planning and use of a cropping calendar (97.9%), planting at appropriate spacing of 20cm x 25cm or 30cm by 2-3 cm depth (100%) and Appropriate use of agrochemicals (100%) while the most intensively utilized SAP were on selection of sites dominated with clayey-loamy soil for planting (WMS=1.93), timely planting (WMS=2.62) and market demand/supply trend and quality improvement for rice. (WMS=2.60). The results of double-hurdle regression models revealed that years of education (β = 1.931305; 0.0144022), farm size (β= 0.0338631; 0.1444465) and output (β=0.262897; 0.00718904) jointly influenced adoption and intensity of using SAP.

CONCLUSION
It was concluded that years of education, farm size and output had an influence on both the adoption and intensity of using Sustainable Agricultural Practices.

RECOMMENDATION
This study therefore recommends that the above should be considered jointly by extension institutions in efforts to ensure sustainable rice production in Ogun State, Nigeria.

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Optimization of Growth Condition for Micropropagation of Banana (Musa spp.) in a Temporary Immersion Bioreactor System

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INTRODUCTION
Tissue culture grows plants from tissue or cells in a lab, using techniques like shoot, meristem, callus culture, somatic embryogenesis, cell suspension, and protoplast cultures for banana propagation. Banana (*Musa spp*.) is a crucial food crop and major export, grown in 130 countries, and originating from Southern Asia. (Ahmed *et al*., 2014).

In vitro propagation, especially using Temporary Immersion Bioreactor Systems (TIBs) offers advantages over conventional methods, such as higher multiplication rates, disease-free plants, and faster growth. (Ikram-Ul-Haq & Dahot, M. U. (2007). TIBs, which use intermittent immersion in liquid nutrients, enhance propagation efficiency and facilitate disease-free cultivar production. This study highlights efficient banana propagation using TIBs. (Karule *et al*., 2016; Gubbuk & Pekmezci, 2004).

MATERIALS AND METHODS
Plant Materials: Young banana suckers were collected from the National Biotechnology Development Agency (NABDA) nursery. Explants were trimmed, washed, and sterilized.
Explant Preparation: Suckers were cleaned with plant detergent (Tween 20) and water, outer leaf sheaths were removed, and shoot tips were isolated. Explants were sterilized with ethanol, and NaOCl, and rinsed with sterile water.
Culture Establishment: Explants were cultured on modified Murashige and Skoog (MS) medium with BAP and IAA, incubated at 25°C under 16h light for 8 weeks. Subculturing occurred every 4 weeks.

Temporary Immersion Bioreactor System: TIBs filled with MS medium and various BAP concentrations were used. Two treatments, 6 and 8 immersions per day, ensured nutrient exposure. Shoots were transferred to rooting media and then acclimatized in nursery bags for 4 weeks.

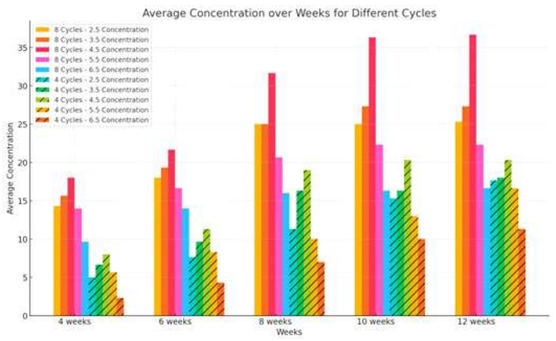
RESULTS AND DISCUSSION
ANOVA Results Interpretation:
Effect of Weeks: Significant variation in propagation (sum of squares: 3689.63) with a strong effect (F-value: 113.55) and a highly significant p-value (2.92e-52), indicating that different weeks significantly affect propagation rates.
Effect of Concentration: Substantial variation (sum of squares: 6196.85) with a very strong effect (F-value: 190.64) and a highly significant p-value (3.43e-68), showing that different concentration levels significantly influence propagation rates.
Effect of Cycles: Some variation (sum of squares: 193.03) with a strong effect (F-value: 23.75) and a significant p-value (3.45e-06), indicating that the number of cycles significantly affects propagation rates.
Effect of Replicate: Minimal variation (sum of squares: 5.02) with a weak effect (F-value: 0.31) and a non-significant p-value (0.735), meaning replication does not significantly affect propagation rates.
Residual: Represents unexplained variation within groups (sum of squares: 585.87, df: 72).

Table 1: Banana Shoot Propagation Data from TIBs: Considering BAP Concentration and Number of Cycles

WEEKS	CONCENTRATION	2.5			3.5			4.5			5.5			6.5		
	Replicate/No of Cycles	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C
4	8 CYCLES	12	14	17	13	15	19	18	17	19	15	10	17	10	10	9
	4 CYCLES	6	2	7	5	7	8	6	9	9	5	5	7	3	1	3
6	8 CYCLES	15	18	21	17	18	23	21	21	23	18	12	20	18	12	12
	4 CYCLES	8	6	9	9	9	11	10	11	13	8	8	9	5	3	5
8	8 CYCLES	20	26	29	23	23	29	28	32	35	22	17	23	18	14	16
	4 CYCLES	11	10	13	14	17	18	15	19	23	10	10	10	6	7	8
10	8 CYCLES	20	26	29	25	26	31	32	38	39	22	20	25	18	14	17
	4 CYCLES	15	13	18	14	17	18	16	20	25	12	13	14	10	8	12
12	8 CYCLES	20	27	29	25	26	31	32	38	40	22	20	25	19	14	17
	4 CYCLES	18	16	19	16	18	20	16	20	25	14	17	19	11	11	12

Table 2: ANOVA Table

Source	Sum of Squares	df	Mean Square	F-Value	P-Value
C (WEEKS)	3689.633333	4	922.408333	113.5456	2.92e-52
C (CONCENT)	6196.850000	4	1549.212500	190.6375	3.43e-68
C (CYCLES)	193.033333	1	193.033333	23.7481	3.45e-06
C (REPLICATE)	5.016667	2	2.508333	0.3086	0.735193
Residual	585.866667	72	8.137037		



This study examined the impact of concentration levels, exposure times (weeks), cycles, and replicates on banana propagation rates. ANOVA results indicated that concentration and weeks significantly affect propagation, with high F-values and negligible p-values. Longer durations (weeks) and higher concentrations resulted in increased propagation rates, suggesting their critical roles in growth, which is in agreement with Ahmed *et al*. (2014). The findings of Ikram-Ul-Haq and Dahot, M. U. (2007), also agree with our results where the number of cycles significantly influenced propagation, with more cycles yielding higher rates. Replicates did not significantly impact propagation, indicating consistency across trials. Residual variation was minimal. Overall, optimizing weeks, concentration, and cycles is essential for maximizing propagation rates. Future studies should explore the underlying mechanisms of these interactions for refined optimization strategies.

CONCLUSION

Optimizing weeks, concentration levels, and cycles significantly enhances banana propagation rates. Each factor independently affects propagation, with longer durations and higher concentrations yielding the best outcomes. Consistent results across replicates confirm reliability, emphasizing the importance of fine-tuning these parameters for efficient banana tissue culture propagation.

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Influence of Media Mixture on Egg Hatchability of African Giant Land Snail (*Archachatina marginata* (*Swainson*): Implication for a Sustainable Biodiversity Conservation and Food Security.

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INTRODUCTION

Snail is a bioresources that support the diet of both rural and urban populae. Snail is one of the bioresources that had from time immemorial been scavenged for in the bush by both old and young individuals. It is a good source of diet most especially for old men and women.

Snail production has been confirmed as a bioenterprise that yields higher returns per capital investment (Munouye and Moses, 2019). The population of snails keep decreasing due to deforestation, bush burning, use of chemicals, therefore, subjecting the ecosystem to disequilibrium, loss of biodiversity and the animal into extinction (Eboua *et al*., 2010).

In the wild, snails lay their eggs in loamy soil and this accounts for the numbers being scavenged for and exploited by humans for nutritional and other purposes. In snail farming, the common practice includes the collection of topsoil to be used as bedding material. Aside from destroying the edaphic terrains, this is not culturally acceptable. Conversely, eroded soil 'sand', and sawdust are free for usage. The report of Awohouedji *et al*. (2014) confirmed that sawdust is a good substrate for the breeding of Giant African land snails.

Several research efforts have reported on the use of media for hatching snail eggs. The use of sawdust alone has been reported to be unsuitable material for hatching eggs of snails but could be a better micro-habitat for the growth of hatchlings (Amata, 2014). Moreover, the use of absorbent cotton had been regarded as a good substrate for incubating *Achatina fulica* because of its ability to conserve (Deji, *et al*, 2011), but the occurrence of fungi contaminations cannot be ruled out in the use of these substrates (Awohouedji *at al*., 2014).

Eggs buried in loamy soil at 3 cm depth with 15% water content facilitate good hatching. However, higher hatchability is assured with increased water uptake after 15 days of incubation (Ebenso, 2006; Ugwu *et al.,* 2011). According to Ibom *et al.* (2012), the optimum incubation period of 29 ± 1.48 days is appropriate for black-skinned pure breed *A. marginata*, while Ogogo (2004), reported that the incubation period for black-skinned *A. marginata* ranged between 29 and 32 days. Topsoil and river sand as submitted by Amata,(2014) are good micro-habitual for the hatching of (*A. Marginata)* eggs But continuous scraping of topsoil may be disadvantageous and may potent ecological danger to crop production and food security.

Similarly, sustainability in the use of river sand may not be achievable due to the risk attached to the collection for commercial snail farming. Snails in their natural habitat lay eggs in soil which is composed of sand, silt, clay and organic matter in different proportions each of these components tends to perform a supportive role for snails' egg hatching. There is a dearth of information on the impact of the combination of these sharp sand, and sawdust substrates for snail egg incubation, it is against this background that this research was conceptualised and conducted to evaluate the effect of sharp sand (ShSa), fine sand (FiSa) and sawdust (SaDu) mixture on hatchability of African Giant land snail (*Archachatina marginata*).

MATERIALS AND METHOD

Pen Preparation: The snail pen used for the research was cleaned and new substrate 'wood shavings' were packed as bedding material. It was moistened before introducing to the pen. Matured snails were collected from a snail pen in the snailry unit of Bioresources Development Centre (BIODEC) Owode Yewa South. The snails were washed with clean water and introduced into the pen in even numbers with a minimum of 10 in each pen.

Constitution of Incubation Media Used: Eroded sand was collected from the roadside and sieved into sharp and fine sand while sawdust was collected from the nearest sawmill industry. Loamy soil used as a control was collected from under a cocoa farm in a village in Oke-odan, a town closer to the centre. The eroded sand and sawdust used as treatments were constituted in a definite ratio by volume, sterilised with the use of hot water and sundried for 4-5 days prior to use. In volume (v/v/v) ratio, Treatment Trt_1 consisted of 2:1:1, Trt_2 (1:2:1), treatment Trt_3 1:1:2 of sharp sand (ShSa), fine sand (FiSa) and sawdust (SaDu) mixture while treatment Trt_4 was loamy soil which served as control.

Feeding and Management: Feeding was provided *ad libitum* with pawpaw fruit and leaves, watermelon, sweet potato fruit and leaves, cassava, and riped palm fruit, the pens were routinely sprinkled with grounded bone meal. Leftovers were removed after 2-3 days and replaced with fresh feed. Water was sprinkled on the feed and the substrate at 3-day intervals. Faeces were removed and the substrate was pulverised on a routine basis.

Management of Incubator and egg collection: Each incubator was covered with a plastic net reinforced with a rubber band to avoid the escape of the young snail after hatching. The incubator was watered moderately with an equal volume of water of 40cl every 3 days to ensure that adequate moisture was provided. The pens were checked daily and the total number of eggs laid were picked with a plastic spoon and buried at 3cm depth on each treatment packed in wooden boxes used as an incubator.

Collection of Hatchlings: The number of hatchlings was counted and weighed with a sensitive balance in grams 35 days after incubation (DAI).

Water Holding Capacity of Substrate Combination as Treatment: The water holding capacity of the (WHC) of the media mixtures was carried out in the laboratory. 250ml measuring cylinders were used. Equal treatments were measured by volume and placed in the funnel stocked with cotton wool and 250ml of water was added and allowed to drain for 24 hours after which the drained water levels were taken and recorded. Thereafter, the percentage water holding capacity of each treatment was calculated.

Experimental Design: There were four (4) treatments which were replicated thrice making a total number of 12 experimental units for the whole experiment and were laid out using Completely Randomised Design (CRD).

Data Collection: Data were collected on the number of eggs hatched by counting. Percentage hatchability and water holding capacity of the treatments were calculated as:

$$\text{Percentage hatchability} = \frac{\textit{Number of Eggs hatched}}{\textit{Number of Eggs Incubated}} \times 100$$

Water holding capacity $=$ *Volume of water used - Volume of water drained*

Data Analysis: Data on the number of eggs incubated, and the number of hatchlings picked after 35 days of incubation were transformed using square root transformation while the percentage hatchability was transformed using arcsine transformation before analysis. All the original and transformed data were subjected to ANOVA using SPSS version 21 and the means were separated using (DMRT). Both the original and transformed data were reported using parallel methods on each parameter respectively.

RESULTS AND DISCUSSION

Percentage Hatchability of Incubated Eggs: As shown in Table 1 below, there was a significant ($P \leqslant 0.05$) difference in the percentage hatchability of the incubated eggs with the highest percentage (95.14 ± 4.34) recorded on treatment two on original data while the transformed data, (80.63^{a} ± 16.24) was recorded as highest on treatment three. The implication is that treatments two and three could have provided a conducive environment for the egg towards hatching.

Table 1: Percentage Hatchability of Incubated Eggs

Treatments	Original data	Transformed data
Trt_1 (2 ShSa: 1 FiSa: 1 SaDu)	50.00^{b} ± 28.87	44.53^{b} ± 17.69
Trt_2 (1 ShSa: 2 FiSa: 1 SaDu)	95.14^{a} ± 04.34	80.00^{a} ± 09.10
Trt_3 (1 ShSa: 1 FiSa: 2 SaDu)	92.59^{a} ± 12.83	80.63^{a} ± 16.24
Trt_4 (Loamy soil) control	80.30^{ab} ± 19.03	15.16^{ab} ± 13.31
Mean	79.51	67.47
C.V (%)	23.35	21.43
F-value	3.73	24.072
P-value	0.061	0.050
SEM	344.7	209.1

Means with the same superscript along the same column are not significantly different at 0.05 significant level using the Duncan Multiple Range Test Procedure (DMRT), SEM - Standard error of the Mean

Weight of Hatchlings: In Table 2, there was no significant ($P \geqslant 0.05$) difference in the weight of hatchlings picked. However, the highest weight of 2.11^{a} ± 0.41 was recorded in treatment two. This implies that treatment two provided a good ecosystem for the hatchlings probably in terms of water or sawdust for feeding.

Water Holding Capacity of the Media Mixture: Table 2 below reveals that there was a significant ($P \leqslant 0.05$) difference in the water holding capacity of the media mixtures. Treatment two recorded the highest with a mean value of 154.00^{a} ± 4.00 followed by treatment four 'loamy soil". This means that treatment two holds an optimum amount of water that perhaps facilitates the effective hatching of the eggs.

Table 2: Mean Water Holding Capacity of the Media Mixture and Mean Weight of Hatchlings Picked.

Treatments	The mean weight of hatchlings	Water holding capacity of media mixtures
Trt_1 (2 ShSa: 1 FiSa: 1 SaDu)	1.69^{a} ± 0.89	109.33^{d} ± 3.06
Trt_2 (1 ShSa: 2 FiSa: 1 SaDu)	2.11^{a} ± 0.41	154.00^{a} ± 4.00
Trt_3 (1 ShSa: 1 FiSa: 2 SaDu)	1.84^{a} ± 0.22	118.67^{c} ± 5.03
Trt_4 (Loamy soil) control	1.98^{a} ± 0.24	136.0^{b} ± 4.00
Mean	1.905	129.5
C.V (%)	27.52	3.15
F-value	0.355	69.993
P-value	0.787	0.000
SEM	0.275	16.67

Means with the same superscript along the same column are not significantly different at 0.05 significant level using the Duncan Multiple Range Test Procedure (DMRT), SEM - Standard error of the Mean.

CONCLUSION AND RECOMMENDATION

The findings concluded that treatment two showed more influence on the parameters measured as an eco-friendly protocol for snail egg incubation. It is therefore recommended that sharp sand, fine sand and sawdust mixture in a definite ratio by volume (2:1:2) could be used as incubating media for African Giant snail egg production.

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Building Trust in Biotechnology Development: Sharing Experience, Sharing Concerns

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ABSTRACT
Biotechnology development is one of the fastest and most precise, means of genetic manipulations at the cellular and molecular levels for enhanced desirable end-products. Its applications in Agriculture, Medicine, Pharmaceutical, Environmental and Marine sciences make it very useful in solving many agricultural production constraints and the development of vaccines for protection against some communicable and terminal diseases, as well as, in cleaning of marine environment for the survival of the animals, fishes and other organisms in the oceans. This paper surveyed the web for available information on how GMO crops can tame hunger that is currently ravaging many countries of the world due to the effects of climate change and its accompanying agricultural production constraints. The paper studied the ten most food sufficient nations of the world, the ten most food shortages in the globe, the ten most hunger-stricken nations of the world, the ten top countries where people are dying because of severe hunger, and how population and growth rate of some sample countries studied affect food availability for effective planning. The paper also looked into the adoption of Biotech in food production and its possible effects on food-sufficient nations, and its rejection on some hunger-stricken nations of the world. The results showed that 6 of the 10 most food-sufficient nations adopted the use of GM food, which prompted 6 of the food-shortage nations to quickly adopt GM crops. It was also observed that 4of the countries with sufficient food, are of low population and low growth rate, therefore, could afford to feed their citizens without GM food, while 4 hunger-stricken nations that do not adopt GM crops have high death rates due to hunger and thereby pushed themselves to serious avoidable wars. The paper also comparatively assessed ten countries with the most reported cancer cases and ten top countries with the lowest cancer cases to ascertain or dismiss the general speculations that cancer is positively associated with the consumption of GMO foods. The paper, based on present findings, concluded that the adoption of Biotech in food production is inevitable for many countries of the world especially Africa, India, and South America to curb famine and starvation and to be able to cope with the population growth rate. Consumption of GMO food had no direct link with cancer cases and should be ruled out until empirical study confirms such an assumption, much so that hunger kills faster than GM foods for which no evidence of adverse effects has been proven.

Keywords: Biotech, Genetically modified crop, Population growth, and Hunger-stricken Nations.

Introduction:

Biotechnology- The word Biotech was first coined and ususedn 1919 by Karoly Ereky (1878-1952), a Hungarian Agricultural Engineer. Biotech is however best described by its importance and uses than making any attempt to define it. Biotech can therefore be described as follows. Any technology that utilizes biological systems, living organisms, or part of this to develop or create different useful products for the benefit of mankind. It is a multidisciplinary field of science that involves natural sciences and engineering sciences to achieve **desired** results. It is a technology that harnesses cellular and bimolecular processes to develop **useful technologies.** It is also the use of Biology to develop new methods and organisms intended **to improve human health and society.** It can also be defined as computational Biology conceptualizing it in terms of molecules and its application (informatics) in organizing information associated with molecules on a large scale. It is the branch of applied science that uses living organisms and their derivatives to produce **products and processes**. It is a combined study, innovation and practice of natural sciences and Engineering sciences to use microorganisms and biological systems of animals and plants to **benefit society** in various sectors such as health, agriculture, food industries wastewater treatment and other fields

Building- The word building by my definition is the systematic and structural arrangement of a planned action with a trusted and accepted pattern that accomplishes a project, a task, or a policy, that will benefit the majority who care to appreciate the result. Advanced English Dictionary described the word "build" as combining materials and parts to construct something.

Trust- The Dictionary definition of trust is something held by one party (trustee) for the benefit of another (beneficiary). It went further to describe different types of trust such as active trust, blind trust, charitable trust, Clifford trust, direct trust, discretionary trust, express trust, grantor trust, implied trust, inter vivo trust, living trust, passive trust, public trust, spendthrift trust, testamentary trust, totteen trust, trust account, trustee account, voting trust.

Biotechnology innovation is an emerging science with its usefulness in Agriculture, Veterinary Medicine, pharmaceutical and fine chemical production. It is an emerging technology for the transition toward a carbon-free society and solving challenges such as health protection, energy and the environment (Donald et al, 2021.)

SHARING MY EXPERIENCES AS A PLANT BREEDER, AN AFRICAN, AN ACTIVE PRACTISING FARMER AND A SEED PRODUCER

Why should trust be built in Biotechnology Development:

- The case of organic food produced in one of the Western world countries in 2001
- The global food deficit and looming hunger in Tropical Africa
- The climate change and its attendant problem
- Insincerity of the antics
- Death and breakout of war due to hunger and starvation
- Biotech food and starvation which is the best alternative
- Should the international politics be played with food and nutritional security the most essential human need)
- Vaccine production, the product of Biotech (Covid-19, Cholera, Polio etc.) which kills faster? Exposure to Covid 19 or GMO food?
- Are huge report of empirical data in peer review journal of professionals to reject it,
- Concern for Environment vis-a-vis acceptance or rejection of Biotech, the negative impact on environment, insecticides, fungicides, chemicals, oil pollutant, insect resistance, mutations, e.t.c
- Cowless Biotech Milk production and the impact on the environment, child growth, nourishment, choice of baby sex,

Some of the Recent research in Biotechnology

1. Synthetic DNA which is used for COVID-19 and the applications
2. Development of vaccine for CoViD 19 and HPV
3. Testing and tracing COViD-19 using biotech tools such as PCR and antigen test
4. 4-D printing and tissue engineering, which can create functional and responsive biological structures
5. Stem cell research which can offer potential treatments for various diseases and injury
6. Production of milk without cow
7. Climate-smart rice genotypes (using multi-trait selection index), drought, pest.

Kind of Trust we must build on Biotech as a Nation

1. Socio-economic Trust
2. Advances and scientific development and their implications as a people, do not stay behind because of political, religious and some beliefs and opinions of some people, or stay behind.
3. The need to remove bias and speculations judging from the level of education and our enlightenment as a nation.
4. Build trust in its realistic breakthrough and benefit, and not on international trade politics and economic rivalry
5. Our economic growth as a nation and agricultural comparative advantage based on its application
6. Build trust in its development and its contribution and not because of what the antics will tell or not tell you for example (i) They all consume Biotech products such as dairy products, beef, pork and fruits. (ii) Health benefits such as vaccines, drugs vegetables and fruits that contribute to Medicare they keep pests of Biotech at home, play with them, integrate these pests into the family and write wills in favour of these pest from Biotech pests.
7. The use of Biotech processes and products (i) to clean up the pollutants in the ocean, plastic degradation and oil spillage cleaning. (ii)They consume marine and seafood that is bred and released to survive in the oceans (iii) The antics, their wives, and children work in the establishment of a Biotech business and make a fortune out of it and obtain a living on such.
8. The European Union's stand and approach should be objectively adopted by Nigeria and other tropical African countries. In August 2012, 3 maize GMOs, 2 GMO soybeans and one cotton variety have been approved for food and use. Similarly, one oil seed rape was declared safe by the European Food Safety Authority (ESAFE) which conducted an assessment on them and found them safe and authorized them suitable for use as food. Ten years later, they will re-assess its impact on society. Such should be adopted here with a sincere purpose for enhanced food and nutritional security (www.isaaa.org).
9. Building our trust on proven scientific findings and not on speculations that have no root in science. We can borrow some sense from the ESAFE approach and assess all Biotech products and not just reject or support their rejection without any proven evidence of their adverse effects on human beings.
10. Build trust in our scientists who are part of the development, evaluation, safety assessment, and toxicology and do away with the sponsor of the antics of Biotech that are enslaving us in Africa and cleverly impoverishing us to depend only on them for food, by discouraging seed of high yield potential, crops of pest resistance, high nutrition and climate-smart varieties that can cope with dynamics of weather and climates of our present generation.
11. Health benefits such as Vaccine, drugs, oils, Pets that were developed as products of Biotech are their friends, they live together, play together, feed them with products of Biotech, some give these pets kisses and exchange saliva, some write a will and give their properties to them because of the friendship and loyalty that bound them together, yet they sponsor campaign against biotechnology. You can see the deceits and insincerity of some GMO antics.
12. There is a need for Africa to borrow some sense in all efforts to produce food sustainably and stop importing the same GMO food you refuse to accept, produce and utilize here. When there is a food shortage, African leaders will be forced to import the only available GMO food for the teeming population to survive rather than dying in thousands, using FOREX and depleting their foreign reserves. Please tell me where the economic sense is. Free yourself from the economic slavery of the World giants.
13. The need to build trust in our scientists is important. The reason we have decided on the high-powered National Variety Release Committee is to accept and release only GMOs that are developed here in Nigeria, evaluated here in Nigeria, produced here in Nigeria and undergoes strict supervision and Biosafety regulations of Nigeria. Unfortunately, the one who is rich and kind enough to fund research to ensure that Africa is developed, food self-sufficient, and environmentally cleaned from hydrocarbon and other pollutants is being castigated by the ignorant who had been paid to blog about the speculation of Biotech food as being poisonous. Our Nigerian colleagues who work in Biotech Labs abroad, who have been fed GMOs for over 29 years are pitifully laughing at our ignorance.
14. Build trust in Biotechnology to enhance environmentally clean oil-producing and river-riven areas of Africa. In blue Biotech practices, oil spillage, poisonous pollutants, and plastics that are presently reducing the fishing business can be cleaned up using Biodegrading organisms to digest the plastic. Adoption of this technology will reduce Billions of Naira being spent annually to clean up the oil-extracting fields effectively, cheaply and affordably.

MY CONCERN AS A PERSON, AN AFRICAN, AND A SCIENTISTS

This paper attempted some fact findings exercises to ascertain the world food security vis-a-vis population and adoption or otherwise of Biotechnology practices in food production. The implications for the socio-economic well-being of people across the globe, and the risk of consuming GMO food or food products if any.

METHODOLOGY:

The brief study by surveying the websites looks into the ten most food-sufficient nations, ten countries with the most food shortage, their population growth, and population growth rate. The study also selected ten hunger-stricken nations and ten countries of the world where the death rate was associated with hunger. The survey also unfolds the true position of people's speculation that GMO foods were responsible for the increase in cancer diseases across the globe. It is important to declare here that information obtained in this paper is published information in the public domain that can be verified in the websites for confirmation or re-validation by people of probing minds. The data were directly from the primary sources of the organizations that reported them. My only assignment was to compile, collate and interpret them dispassionately without bias for to enlighten our minds. The countries chosen here naturally pop up by mere use of search engines, not by my volution.

RESULTS

The results of this brief search showed the following

The United States of America was the most food-secured followed by the Netherlands, Japan, Sweden, Canada, Norway, Bulgaria,

Ukraine, Russia, and Australia. The ten countries with food shortages include the Democratic Republic of Congo, Nigeria, Sudan, Afghanistan, Ethiopia, Yemen, The Syrian Arab Republic, Bangladesh, Pakistan, and Myanmar in that order. The population of the sample countries varied from 5.49 million (Norway) to 333.3 million (United States of America). The countries selected naturally fell within different regions of the globe spreading across the continents (Table 1).

The adoption of GMO crops and food products was observed in six out of the ten food-sufficient countries (United States, Japan, Canada, Norway, Russia and Australia). While four of the ten food-sufficient countries did not approve the use of GM crops or food products. These countries include the Netherlands, Sweden, Bulgaria and Ukraine. Similarly, countries with food shortages and use of GM crops and food products were six out of ten (Nigeria, Sudan, Ethiopia, Bangladesh, Pakistan and Myanmar). Democratic Republic of Congo, Afghanistan, Yemen, and The Syrian Arab Republic were yet to approve and adopt the use of GM crops (Table 1).

Other important observations are as follows:

(1) Six countries with high population density that adopted the use of GM crops and were food-sufficient examples are the USA and Russia
(2) Four of the countries (without the use of GM are food-sufficient (Netherlands, Sweden, Bulgaria and Ukraine) but with a population of less than 50 million people.
(3) Four countries with food shortages and no GM crop approval were the Democratic Republic of Congo, Afghanistan, Yemen and The Syrian Arab Republic

Table: 1 Ten Most Food sufficient and Most food Shortage Nations of the World, 2023

Rank	Country with Food sufficiency	Population (Million)	Country with a Food shortage	Population
1	United States of America*	**333.3**	Democratic Republic of Congo	105.63
2	Netherlands	**17.65**	Nigeria*	299.15
3	Japan*	122.6	Sudan*	49.36
4	Sweden	**10.64**	Afghanistan	43.37
5	Canada*	39.10	Ethiopia*	129.72
6	Norway*	5.49	Yemen	35.22
7	Bulgaria	**6.618**	The Syrian Arab Republic	23.79
8	Ukraine	**37.91**	Bangladesh*	174.70
9	Russia*	144.2	Pakistan*	245.21
10	Australia*	26.67	Myanmar*	54.96

Source: FAO 2010; https://joint-research-centre.ec.europa.eu, 2023)

Table 2 presents the ten most hunger-stricken and ten most food shortage countries in the world. The ten hunger-stricken nations of the world include Sudan, the Central Africa Republic, Niger, Chad, the Democratic Republic of Congo, Ethiopia, Yemen, Haiti, Madagascar and Afghanistan. The top nations with food shortages are Nigeria, Sudan, the Syrian Arab Republic, Bangladesh, Pakistan and Myanmar. Many of these countries of hunger-stricken by food shortages in their wisdom therefore adopted and approved the use of GM crops and food. They are Bangladesh, Ethiopia, Myanmar, Nigeria and Pakistan (Table 3). Others are still watching and trying to find solutions to food shortages in their countries. The European Union members approved GMOs in 2010 to curb hunger and used them for thirteen years and did not report an empirical study, but some members woke up and banned it in 2023, some even went organic. African countries should also use GMO food to stem starvation and death through hunger for just 10 years before reviewing whether to continue the use or otherwise instead of rejecting it and dying in thousands of ignorance.

Table 2: Ten top Hunger- Stricken and Ten Most Food shortage across the Globe

Ranking	Hunger-stricken nation	Hunger index	Ranking	Ten nations with the most food shortage
1	Sudan	28.8	9	Democratic Republic of Congo
2	Central African Republic	44.0	2	Nigeria
3	Niger	32.6	7	Sudan
4	Chad	37.2	5	Afghanistan
5	Democratic Republic of Congo	37.8	4	Ethiopia
6	Ethiopia	27.6	10	Yemen
7	Yamen	45.1	1	The Syrian Arab Republic
8	Haiti	32.7	6	Bangladesh
9	Madagascar	38.7	3	Pakistan
10	Afghanistan	29.9	8	Myanmar

From sources across the web, 2023

Table 3: Countries with GM Crop approvals on GM Approval Database

1	Argentina	25	Mexico
2	Australia	26	Myanmar
3	Bangladesh	27	New Zealand
4	Bolivia	28	Nigeria
5	Brazil	29	Norway
6	Burkina Faso	30	Pakistan
7	Canada	31	Panama
8	Chile	32	Paraguay
9	China	33	Philippines
10	Colombia	34	Russia
11	Costa Rica	35	Singapore
12	Cuba	36	South Africa
13	Egypt	37	South Korea
14	Eswatini	38	Sudan
15	Ethiopia	39	Switzerland
16	European Union	40	Taiwan
17	Ghana	41	Thailand
18	Honduras	42	Turkey
19	India	42	United States
20	Indonesia	43	Uruguay
21	Iran	44	Vietnam
22	New Zealand	45	Zambia
23	Kenya	46	Spain
24	Malaysia		

Source: ISAAA: https//www.isaaa.or

Tables 4a to 4c highlight the historical population growth of three countries (United States of America, Japan and Nigeria, to critically look at how the population growth of these countries is being managed or controlled. Nigerian population growth increased from 218,541,212 in the year 2022 to 223,804,632 in 2023 and from 223,804,632 to 229, 152,217 in 2024. Although the growth rate in 2022 and 2023 was constant at 2.41, it declined by 2024 from 2.41 to 2.39. May be for reasons of deaths due to bandits, Herdsmen attacks, Boko Haram and natural death. For Japan, it was a planned action to regularly maintain the population growth which was slightly reducing every year, with growth rates of -0.53. -0.53 and -0.54 in 2022, 2023 and 2024 respectively. The population growth and rates were slightly increasing just like Nigeria with growth rates of 0.31, 0.50 and 0.53 for 2022, 2023 and 2024 respectively. The major difference was that America had higher population growth than Nigeria and was in the table of the ten food-secured countries of the world, while Nigeria was ranked second among the ten most food shortages in the world. This calls for a big concern for the government, stakeholders in food production, Agricultural Research scientists and policymakers. Perhaps the reason for the adoption and approval of GM crops is that can boost the production of food and food items. It is also a wake-up call for nations of the world with similar situations.

Table 4a: Historical Population Growth rate for necessary Food Security Planning

Nigeria

Year	Population	Growth rate (%)
2024	229,152,217	2.39
2023	223,804,632	2.41
2022	218,541,212	2.41

Table 4b: Japan Population Growth rate

Year	Population	Growth rate (%)
2024	122,631,432	-0.54
2023	123,294,513	-0.53
2022	123,951,692	-0.53

Table 4c: United States Population Growth

Year	Population	Growth rate (%)
2024	341,814,420	0.53
2023	339,996,563	0.50
2022	338,289,857	0.31

Source: Extracted from Worldometer: Worldometer www.worldometer.info

Table 5 presents the death rate in the 10 top countries with the highest death rate associated with hunger. These figures represent number of mortalities per year in every 100,000 people. From this report, death rates of between 27.52 and 101.32 were reported confirmed. The lowest death rate from hunger and starvation was 27.52 in Eritrea while the highest was 101.32 in Angola. Others were within this range. The worrisome aspect of these situations with these countries is that they are properly located across the globe favourable agricultural ecology. There may be other factors that might be responsible for the food shortage and hunger-stricken condition of these nations, the adoption of a biotechnology system of food production would have been better than starving people to death. Many of these countries such as the Central African Republic, Sudan, the Democratic Republic of Congo, Benin, share similar latitudes with Nigeria, and Ghana where agricultural production potential is relatively high compared to many parts of the world. It is also important here to state that only three of these ten countries with the highest death rate due to hunger are not in Africa. The rest seven are located on African soils. Maybe, the reason the African Union is seriously encouraging the application of the Biotech method of food production. There was no European country or American country where people were dying of hunger yet they embraced GMOs (Table 3). Rather than rejecting GM food, they embraced it and constantly reviewed it either to retain, modify or ban it (EFSA, 2023). Whenever Africa is food-sufficient like these countries, we can then review the use of GMOs. But let us solve the problem of food shortage and starvation which is fast killing and bringing war into our domain before thinking of any side effects of GMOs that are based on speculations.

Table 5: Ten top countries with the highest rates of death due to hunger

S/N	Country	Death rate	Ranking	Policy on GM food
1	Somalia	46.27	5th	Not yet approve
2	Bangladesh	56.36	2nd	Approved
3	Mali	57.15	3rd	Not yet approve
4	Angola	101.32	1st	Not yet approve
5	Cambodia	50.19	4th	Not yet approve
6	Benin	37.71	6th	Not yet approve
7	Bolivia	31.79	7th	Approved
8	Central African Republic	29.51	8th	Not yet approve
9	Madagascar	28.32	9th	Not yet approved
10	Eritrea	27.52	10th	Not yet approved

Source: Action against hunger, 2024: https://www.actionagainsthunger

Table 6: Ten highest Cancer rates and ten lowest cancers by Country

Rank	Country with a High cancer rate	Rank	Country with the lowest cancer rate
1	Australia	1	Sudan*
2	New Zealand	2	South Sudan*
3	Ireland	3	Djibouti
4	United States	4	Timor-Leste
5	Denmark	5	Tajikistan
6	Belgium	6	Republic of Congo
7	The Netherlands	7	Bhutan
8	Canada	8	Nepal
9	France	9	The Republic of Gambia
10	Norway	10	Niger*

Do not have infrastructure to adequately identify and register cases*. **Source: Dana-Farber Cancer Institute 2022-2023

Table 6 presents the ten highest cancer-rated countries globally. From the table, some facts emerged. There is strong speculation that has not been scientifically substantiated with empirical data especially in and peer-review journal. Hence, table 6 does not directly link with cancer rate to the consumption of GMO foods. For example, five out of the ten countries captured as highest cancer-rated nations, adopted GMO food while the other five were not GMO-approved nations. Ireland, Denmark, Belgium, Netherlands, and France have not officially accepted GM foods but were placed as third, fifth, sixth, and ninth in the order of cancer top-rated nations. On the other hand, Australia, New Zealand, the United States, Canada and Norway adopted GM food but were placed first, second, fourth, eighth and tenth on the list respectively.

DISCUSSION

If GMO is the only factor responsible for cancer high rate, in Countries such as Ireland, Denmark, and Belgium. The Netherlands (which feeds mainly on organic food) and France should not have appeared on the list of the ten highest countries with cancer cases. These facts should be sufficient enough in the meantime to disabuse the speculation that GM foods are linked with cancer and to humble the antics of GM food to relax until empirical data in peer-reviewed journals affirms that. The bloggers of anti-GM should also change the narrative to support GM foods and desist from starving millions

of people in already listed countries to death for unsubstantiated information about GM foods at least for posterity.
In a similar vein, countries of the world with high rates of food shortage, or better still hunger-stricken or hunger-killing nations should rethink adopting GM food to save the lives that are wasting away for dislike of GM food.

CONCLUSION

The simple question is that if some people have been consuming GM food for more than 30 years without cancer in advanced countries like the USA, we should agree with me that hunger kills faster than GM food, (if at all) GM is inherently dangerous for human health. The present generation owes the coming generations the planet Earth and an atmosphere that is free of contaminants, where temperature and carbon imbalance is minimized, where aquatic and terrestrial animals are surviving, where vegetation is close to being natural, where genetic erosion is highly reduced, where green gas is almost non-existing, where crop yields per unit area is high, where food and nutrition is more secured, where millions of people will no longer be dying for distaste to GM food and unhealthy policy decision, where everyone is happy and where the game is win-win in nature. The solution is the adoption of GM crops which are higher yielding, disease and pest resistant, drought tolerant, well adapted to various ecologies, climate-smart, free from chemical spraying, possess good shelf life, eco-friendly and nutritionally secured.

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Targeting the HIV-1 Gag Protein with Bioactive Small Compounds from Indigenous Edible and Medicinal Plants: An *in-silico* Approach.

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Introduction

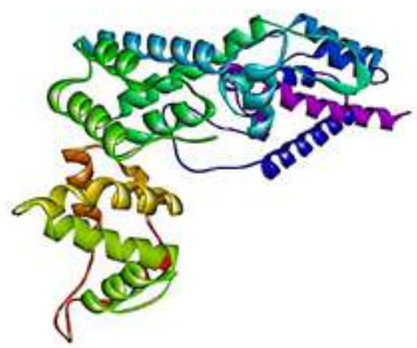
Human Immunodeficiency Virus (HIV) remains a global health concern, with millions infected and many dying from HIV-related causes (UNAIDS, 2023; WHO, 2023). The HIV-1 Gag protein is pivotal in the virus's lifecycle, facilitating viral particle assembly and release. Specifically, the Gag p6 domain plays a vital role in viral budding, replication, and infectivity. Targeting Gag p6 is a promising approach for developing new antiretroviral drugs (Chen & Wang, 2024). Maturation inhibitors like Bevirimat offer a novel approach to inhibit HIV-1 maturation, rendering viral particles non-infectious. However, challenges such as resistance, side effects, and limited clinical data must be addressed through ongoing research and development (Dick & Cocklin, 2020). Plant bioactive compounds, or phytochemicals, have garnered attention for their diverse chemical compositions, therapeutic potential, and safety. These compounds are increasingly being increasingly being explored in modern drug discovery and development for HIV treatment (Chaachouay & Zidane, 2024).

Methodology

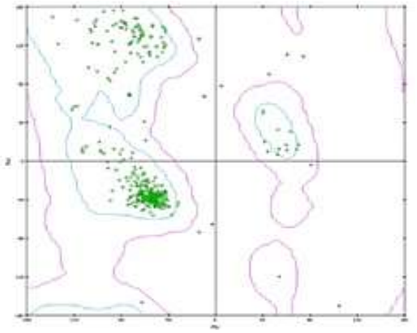
The crystal structure of HIV-1 Gag protein (PDB ID: 2GOL) was retrieved from the Protein Data Bank (Fig. 1). The visualization tool, PyMol was used to remove water molecules and ligands from the protein structure (DeLano, 2020). The online server, Chiron was used for energy minimization to reduce the steric clashes of the protein. The Ramachandran and hydrophobicity plots of the protein were used to validate the protein structure and were generated using the DiscoveryStudio visualization tool. The 3D conformers of 1,040 natural compounds found in indigenous edible and medicinal plants along with the reference compound were downloaded from the PubChem database in their structure-data file (SDF) format. All the compounds were earlier screened for compliance with the Lipinski Rule of 5 (Lipinski *et al.,* 2001) and Veber's rule (Veber *et al.,* 2002). Through the Open Babel plug-in tool on the Virtual Screening Molecular Docking Software, PyRx (version 0.8), all the ligands along with the reference compound were uploaded and molecularly docked against the HIV-1 Gag protein (Dallakyan and Olson, 2015). The reference compound had a score of -8.3 kcal/mol which was used as the cut-off score. Further screening for bioavailability (Ghose *et al.,* 1999), ADMET (absorption, distribution, metabolism, excretion and toxicity), and bioactivity were performed using the SWISSADME, pkCSM, and SWISSTargetPrediction webservers respectively (Pires *et al.,* 2015; Daina *et al.,* 2017)

Results and discussion

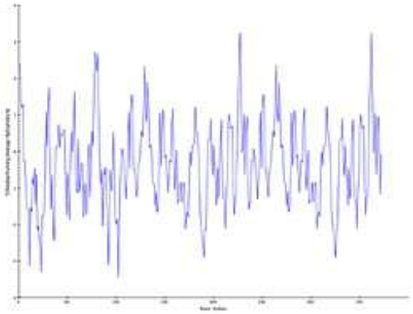
The results of the molecular docking, bioavailability and ADMET screenings revealed Strophanthidin as the lead compound (Table 1; Fig. 2). The reference compound, Bevirimat, was shown to violate two critical Lipinki rules (Molecular weight of more than 500 and Octanol-water partition coefficient of more than 5) (Lipinski *et al.,* 2001) and also the Ghose filter rule of Molar refractivity; and these are critical in drug bioavailability and absorption (Ghose *et al.,* 1999).



A



B



C

Fig. 1. A. The 3D structure of the HIV-1 Gag protein Structure. **B.** The Ramachandran plot of the HIV-1 Gag protein shows the amino acid residue conformation. **C.** The Hydrophobicity plot of the HIV-1 Gag protein shows the regions of high and low hydrophobicity.

Strophanthidin, however, had no violations. The ADMET analysis predicted that even though Bevirimat was non-toxic and had good metabolism and excretion, it had poor absorption and distribution properties. Strophanthidin on the other hand was predicted to have overall good properties except for relatively poor blood-brain barrier and central nervous system permeability (Pires *et al*., 2015).

Conclusion

Strophanthidin has been predicted to have better pharmacokinetic properties than the reference compound Bevirimat. Further studies are however needed to confirm and validate its potential as a maturation inhibitor.

Table 1. Molecular docking score of the reference and lead compounds against HIV-1 Gag protein.

Ligand/Compound	Binding Affinity (kcal/mol)
Bevirimat (Reference compound)	-8.3
Strophanthidin	-8.4

ADMET PARAMETERS	Bevirimat (Reference)	Strophanthidin
ABSORPTION		
Water Solubility (log mol/L)	-2.911	-4.473
CaCO2 Permeability (log Papp in 10^{-6} cm/s)	0.462	0.813
Intestinal Absorption (Human)(% absorbed)	57.1	73.21
Skin Permeability (log Kp)	-2.735	-3.909
P-glycoprotein Substrate (Yes/No)	No	Yes
P-glycoprotein Inhibitor I (Yes/No)	No	No
P-glycoprotein Inhibitor II (Yes/No)	Yes	No
DISTRIBUTION		
VDss (Human) (log L/kg)	-1.663	0.143
Fraction Unbound (Human) (Fu)	0.065	0.38
BB Permeability (log BB)	-0.413	-0.602
CNS Permeability (log PS)	-2.458	-3.098
METABOLISM		
CYP2D6 Substrate (Yes/No)	No	No
CYP3A4 Substrate (Yes/No)	Yes	Yes
CYP1A2 Substrate (Yes/No)	No	No
CYP2C19 Inhibitor (Yes/No)	No	No
CYP2C9 Inhibitor (Yes/No)	No	No
CYP2D6 Inhibitor (Yes/No)	No	No
CYP3A4 Inhibitor (Yes/No)	No	No
EXCRETION		
Total Clearance (log ml/min/kg)	-0.276	0.624
Renal OCT2 Substrate (Yes/No)	No	No
TOXICITY		
AMES toxicity	No	No
Max. Tolerated Dose (Human) (log mg/kg/day)	0.371	-0.487
hERG I Inhibitor (Yes/No)	No	No
hERG II Inhibitor (Yes/No)	No	No
Oral Rat Acute Toxicity (LD50) (mol/kg)	2.391	2.357
Oral Rat Chronic (LOAEL) (log mg/kg_bw/day)	1.022	1.833
Hepatotoxicity (Yes/No)	No	No
Skin Sensitisation (Yes/No)	No	No
T. pyriformis Toxicity (log ug/L)	0.285	0.306
Minnow Toxicity (log mM)	2.387	2.387

Fig. 2. The ADMET profile of the reference and lead compounds.

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Peptide Composition and Enzyme Activities of Selected Freshwater Fish Mucus from Taqwai Lake in Niger State.

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INTRODUCTION

Fish are a diverse group of animals with specialized aquatic existence that are generally accepted all over the world as a cheap source of animal protein. These Fish were farmed at different water sources such as; seas, lakes, lagoons, swamps, rivers, streams, creeks, ponds, and tanks (Lee *et al.,* 2020). Life in the aquatic environment is usually controlled by a complex interplay between aquatic animals and their surrounding environment, although fish require a physiological adaptation to thrive in the environment. This interaction has the capability of exposing the aquatic species to injurious substances which can be both pathogenic or saprophytic, with the ability of digesting and degrading the fish tissues (Shabir *et al.,* 2018). Fish on the other hand normally maintain a healthy state by protecting themselves against invaders using a complex system of innate and adaptive defence mechanisms (Lee *et al.,* 2020).

Fish mucus is a biological interface between fish and its surrounding environment and is predominantly produced by epidermal goblet cells which comprise water and gel-forming macromolecules known as mucin and other glycoproteins (Al-Rasheed *et al.,* 2018). Mucus acts as a store of immune exciting cells like immunoglobulins and complement proteins. Proteolytic enzymes as well as antimicrobial proteins and peptides are secreted by the mucus when produced and act as immediate protection for the fish against pathogenic microorganisms (Uyan *et al.,* 2020). Antimicrobial peptides (AMPs) secreted by the fish mucus function as a first-line defence against microbial attacks. They protect the fish against a wide variety of bacterial, fungal, viral, and other pathogenic infections by disruptive or pore-forming actions (Rajini *et al.,* 2020). Proteins or peptides present in the fish mucus form pores on the bacterial membrane that cause the oozing out of cellular contents which alters the ionic gradients of the membrane leading to the death of bacteria. The mucus secreted protects their skin from dehydration and pathogenic invasion. The rate of mucus composition and secretion are in response to microbial exposure and environmental perturbations such as hyperosmolarity, temperature change, pH and acidity which varies by species (Kumari *et al.,* 2019).

Antibiotic resistance from infectious pathogens has become a serious therapeutic issue that has been attributed to the recent increase in mortality Marta *et al*., (2023). Similarly, the indiscriminate use of antibiotics in the treatment of infections, necessitates the development and dissemination of drug-resistant microorganisms that nullify the effect of active drug components (Tastan & Sonmez, 2020), resulting in increased dosage of antibiotics which poses a higher risk of hepatoxicity, neurotoxicity, and other adverse effect both in fish and human. Nevertheless, the resistance caused by these microorganisms is highly efficient by modifying the genes that code for the mechanism of multidrug resistance Marta *et al*., (2023). However, the various approaches to prevent or combat these infections have compounded the problem of multidrug resistance which poses a greater risk to the health of fish and its surrounding environment (Bilen *et al.,* 2020). Moreover, since the demand for animal protein has intensified aquaculture practices (Tastan and Sonmez 2020) since Fish are grown under intense aquaculture systems, they are susceptible to diseases due to constant interaction with pathogenic microorganisms in the environment and environmental pollution of the natural water bodies (Bilen *et al.,* 2020).

Studies by various researchers have shown the antibacterial effect of mucus from different fish on both human and fish pathogenic microorganisms (Marta *et al*., 2023; Lee *et al.,* 2020; Rocío *et al*., (2023); Momoh *et al.,* (2014); Nwabueze, (2014); Olayemi *et al.,* (2015); and Akunne *et al.,* (2016). Despite the relevance of fish mucus, there is a scarcity of information on the chemical constituents, antibacterial capabilities, and enzyme activities of fish mucus from Taqwai Lake Niger state. Thus, this study was conducted to explore the potential of fish mucus as a valuable source of antimicrobials and to provide a better understanding of the component molecules in fish mucus that enhance its survival in a microbial-rich environment. However, proteins and peptides from fish mucus could be a potential source of natural antibiotics for pharmaceutical applications

Methodology

Eighty live fish from three different fish species of tilapia fish, giraffe-head catfish, and catfish, were obtained from local fishermen at Taqwai Lake Minna, Chanchaga local government area of Niger State. Farmed catfish were purchased from a nearby farm by the lake. The different Fish were collected separately in a well-ventilated aquarium box and were also authenticated by Dr (Mrs.) Chukwuemeka of the Animal Biology Department Federal University of Technology Minna.

The Mucus of the different Fish were collected following the method of Subramanian *et al.,* (2008). The proximate composition of the crude mucus extract was determined using the method described by AOAC (2003). Amino acid analysis was done by ion exchange HPLC chromatography using the Applied PTH Amino Acid Analyzer using methods described by Benitez (1989).

Assay of Enzyme Activities: Prior to the assay, the freeze-dried samples were reconstituted in 2 mL of the respective enzyme assay buffers and centrifuged at 9300 g for 2 minutes at 4°C. 50 µL of the supernatant was then used for each of the enzyme assays described below. The protease activity of the crude mucus was determined using the azocasein hydrolysis assay (Firth *et al.,* 2000). Lysozyme activity was determined using a turbidimetric assay (Ross *et al.,* 2000), while the Alkaline phosphatase activity was determined experimentally using Palaksha *et al.,* 2008 method.

Free radical Scavenging using 2, 2-Diphenyl-1-Picrylhydrazyl (DPPH): The antioxidant activity of the plant extracts was estimated using the DPPH radical scavenging assay as reported by Garcia *et al.,* 2014.

Data Analysis: Data were analyzed using SPSS statistics version 23 and Microsoft office Excel Professional Plus 2010 (Redmond, WA, USA). Mean, standard error of the mean (SEM), range, tables and charts were used to present the results using One-way analysis of variance (ANOVA), followed by Turkey and Duncan's multiple range tests. Data were considered statistically significant at $p < 0.05$.

RESULTS AND DISCUSSION

This study provides brief documentation on the peptide composition and enzymatic activities of mucus from the selected freshwater Fish collected from Taqwai Lake in Niger state. It confirms the presence of macromolecules such as; protein, carbohydrate, and lipids in the mucus of giraffe head catfish, tilapia fish and African mud catfish. The investigation also reveals the presence of antioxidant activity, enzyme activity and total protein composition of the freshwater fish mucus. The high amount of protein recorded in the mucus of farmed catfish may be a result of nutrient-rich feed or poor supply of water in the pond resulting in microbial contamination of the pond. The high-fat content recorded in wild catfish when compared to the farmed catfish may be a result of diet inclusion with phytoplankton Reverter *et al*. (2018) which helps to protect against bacterial and fungal attacks. The total protein composition is shown in the table below.

Sample	Concentration (mg/mL)
Giraffe head catfish	1.41 ± 0.05^{b}
Tilapia fish	1.93 ± 0.04^{c}
Catfish farmed	1.87 ± 0.02^{c}
Catfish wild	0.71 ± 0.02^{a}

All values are presented in Mean ± Standard error of triplicate experiments. Values with different superscript alphabets down the column are significantly different at $p<0.05$

Enzymes such as Lysozyme, alkaline phosphatase, and protease are important innate immune enzymes that protect the fish against invading microbes (Sridhar *et al*., 2020). The result of the free radical scavenging activities in the mucus also protects the Fish from their environment.

CONCLUSION:

Based on the research findings, it was observed that fish mucus of African catfish, Tilapia fish, and Giraffe-head catfish contain essential and non-essential amino acids which are the building blocks of the protein macromolecules. The mucus of fish exhibits enzymatic activities such as; proteases, lysozymes, and alkaline phosphatase which act as both antimicrobial and antiproliferative properties that have the capability of inhibiting the growth of pathogenic and non-pathogenic microorganisms.

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Prevalence of Malaria Parasitaemia amongst Asymptomatic Pregnant Women Attending Antenatal Clinic within Jos, North Central, Nigeria: A Biotechnological Tool for Control of Malaria.

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INTRODUCTION

Malaria is considered one of the most important of all tropical diseases in terms of morbidity and mortality on a global scale. It is estimated that some 2 billion individuals are at risk with over 100 million developing overt clinical diseases and more than 1.5-2.7 million deaths every year. Malaria infection is caused by a human parasitic disease generally characterized by frequent bouts of high fever, headache and body pains that affect people of all ages. It is caused by the presence of a parasite of the genus *Plasmodium (*commonly *Plasmodium falciparum, Plasmodium vivax, Plasmodium malariae, or Plasmodium ovale Plasmodium knowlesi)* within red blood cells. The disease is transmitted by the female *Anopheles* mosquito and is most common in Tropical and subtropical Countries of the world. The concept of malaria has been synonymous with its most obvious symptoms of recurrent cycles of fevers and chills (Chedraui*et al*., 2016). The infection is transmitted from one person to the other through the bite of infected Anopheles mosquitoes (Igwe*, et al.,* 2014). The *Plasmodium* is a single-cell microscopic organism that invades the red blood cells of the human body after a bite by an infected female *Anopheles* mosquito during a blood meal (Webberly, 2016; Azikwe *et al.,* 2012). Pregnant women and children are particularly vulnerable to complications of malaria if untreated. It is estimated that malaria potentially affects about 50% of the World's population majority of whom are in sub-Saharan Africa and that almost 30 million women are threatened by malaria infection during pregnancy. It has been reported as a major cause of at least 10,000 maternal deaths and about 200,000 newborn deaths annually (Okpere *et al*., 2010). It is an important public health parasitic infestation in the tropics and tropical Africa bears the greatest of the world's burden of the disease (Nwaneri *et al*., 2015; Ogbu *et al.,* 2015). Even though Intermittent Preventive Treatment in pregnancy (IPTp) is administered to pregnant women after the first trimester to prevent maternal death from malaria-associated anaemia and low birth weight, coverage levels remain below National targets (WHO, 2017). In pregnancy, malaria is a major Public Health problem with serious consequences to both the expectant mother and the foetus. Malaria increases susceptibility to other infections (Nwaneri *et al.,* 2015). The risk of infants dying during the post neonatal period has also been identified to rise higher in children born with placental malaria especially complicated by Human Immunodeficiency Virus (HIV) infection (Bawa *et al*., 2014). Pregnant women and children under the age of five years are at risk of severe disease and mortality from malaria (Nwaneri *et al*., 2015). Ogbu *et al*., (2015) also noted that the importance of malaria in pregnant women and the general population in Nigeria and indeed the entire Sub-Saharan Africa cannot be over-emphasized because pregnant women have been shown to have an increased susceptibility to infestation by malaria parasites.

MATERIALS AND METHODS

The research was carried out within two Primary Health Care clinics in Jos in the LGA; PHC clinic Dogon Agogo situated right inside the council headquarters and PHC Clinic Jos Township located about 1.5 kilometers, west of the Council headquarters.

Study Design/Inclusion Criteria

A total of 240 Healthy pregnant women (with no history of fever, no fever, and no symptoms suggestive of malaria) attending ANC for the first time in their current pregnancy, who had not been treated with antimalarial medicine in the preceding two weeks, were recruited for the research at the two Primary Health Care Centers. All women with a body temperature > 37.5oC were excluded. Asymptomatic malaria parasitaemia was defined as the presence of asexual parasites in the blood without symptoms of illness and a temperature of < 37.5oC.

Sample Collections

Blood samples from the subjects were collected weekly from each of the two healthcare facilities. A total of sixty (60) samples were collected weekly over a period of four weeks

Preparation and Staining of Thick Blood Film

Slides preparation was based on the WHO Malaria Microscopy Standard Operating Procedure (MM-SOP-08) (2006)). Thick blood films from finger-prick blood were immediately prepared on the slides assisted by two qualified Laboratory Technicians. Thick blood films were prepared from finger-prick blood samples.

RESULT AND DISCUSSION:

Table 1: Age Distribution of symptomatic pregnant women

Age Group	No (%)	No Infected (%)
15 – 24	121 (50.4)	17 (7.08)
25 – 34	92 (38.3)	13 (5.41)
35 - 44	27 (11.3)	3 (1.25)
Total	240 (100)	33 (13.8)

Table 1 shows the level of malaria infection among asymptomatic pregnant women of varying age brackets with 15-24 years having a total prevalence of 7.8%, next is the age bracket 25-34 with 5.41% while age group 35-44 years had a prevalence level of 1.25% implying malaria infection is high among younger asymptomatic pregnant women. This agrees with the findings of Igwe *et al*., (2014) that malaria parasitaemia at first booking is significantly higher in primigravidae and young women who had not taken anti-malaria treatment before. This could be a result of the exposure of the multigravidae women to intermittent preventive treatment (IPTp) for pregnant women and health education tips on malaria prevention at previous antenatal clinics.

Table 2: Frequency of Parasitaemia Density among Asymptomatic pregnant women.

Group	Age Group (% infection)		
	15 – 24 (%)	25 – 34 (%)	35 – 44 (%)
Mild	4 (23.50)	4 (30.76)	3 (100)
Moderate	8 (47.06)	6 (46.15)	0 (0)
Severe	5 (29.40)	3 (23.07)	0 (0)
TOTAL	17 (100)	13 (100)	3 (100)

Table 2 shows the frequency of distribution of malaria parasitaemia as mild, moderate and severe cases of parasitaemia occurred more in age groups 15–24 years at 8 (47.06%) and 5 (29.40%). While ages 25 – 34 years recorded a slight percentage in infection rates it was however recorded at ages 35–44 years with no case of either moderate or severe parasitaemia among asymptomatic women under the study.

Table 3: Density of malaria parasitaemia amongst pregnant women.

Age groups	No (%)	No Infected (%)	Density (%)
15 -24	121 (50.4)	17 (7.08)	17 (51.52)
25 - 34	92 (38.3)	15 (5.41)	13 (39.39)
35 - 44	27 (11.3)	3 (1.25)	3 (9.09)
Total	**240 (100)**	**33 (13.8)**	**33 (100)**

Table 3 shows the age distribution of asymptomatic pregnant women examined and the percentage of infection in each age group. The level of malaria infection among asymptomatic pregnant women of the age bracket of 15 -24 years is high with a total prevalence of 7.8%, followed by the age bracket of 25 - 34 with a prevalence of 5.41% while the age group of 35 - 44 years had a prevalence level of 1.25%. This implies that malaria infection is high among younger asymptomatic pregnant women. This could be a result of the exposure of the multigravidae women to intermittent preventive treatment (IPTp) for pregnant women and health education tips on malaria prevention at previous antenatal clinics.

Table 4. Prevalence of Malaria Parasite in Asymptomatic pregnant women

Malaria Parasite	No infected	% infected
Positive (+)	33	13.8
Negative (-)	207	86.2
Total	**240**	**100**

Table 4 shows the overall prevalence of malaria parasitaemia amongst asymptomatic pregnant women. The result reveals that 33 out of the 240 asymptomatic pregnant women representing 13.8% tested positive for the malaria parasite, while the remaining 207 tested negative representing 86.2%. This implies that the prevalence level of malaria parasite infection amongst asymptomatic pregnant women is high. The result is in line with the findings of Omalu *et al*., (2012) who reported a prevalence rate of 13.82% after screening for congenital malaria among pregnant women in Minna, Niger state, North Central Nigeria. This is however lower than the 77.6% prevalence reported by Igwe *et al*., *(*2017) among un-booked parturients at Abakaliki, Nigeria and it is higher than the prevalence reported by Agomo *et al*., (2009), one of the lowest malaria prevalence of 7.7% among pregnant women in Lagos, South-West Nigeria. Ogbu *et al.,* (2015) who had reported a 38.8% prevalence of malaria parasitaemia among asymptomatic women at booking visits in a tertiary hospital (Garki Hospital, Abuja), North Central Nigeria.

Table 5: Density of Multigravidae women (≥ three times (3)) aged 25 – 44 years.

Density	No (%)
Mild	6 (66.7)
Moderate	3 (33.3)
Severe	0 (0)
Total	**9 (100)**

Table 5 shows malaria density distribution within multigravidae women was mildly high at 66.6% (6) while moderate parasitaemia was shown to be 33.3% (3).

Asymptomatic malaria parasite infection was found to be common among pregnant women on their first antenatal visit to the health care facilities, however, the severe form of the infection was mostly among primigravidae women while the multigravidae women recorded the moderate and mild forms of the infection. Out of the 13.8% prevalence of asymptomatic malaria parasite infection observed in this research, pregnant women of the age group of 15 - 24 years recorded the highest prevalence of 50.4% followed by the age bracket of 25 - 34 with a prevalence of 38.3%. Age groups of 35-44 years have a prevalence level of 11.3% implying that malaria infection is high among younger asymptomatic pregnant women. This shows that there is no significant difference in the density of malaria infection between asymptomatic primigravidae and multigravidae women.

CONCLUSION AND RECOMMENDATIONS

The overall prevalence of malaria parasitaemia amongst asymptomatic pregnant women in parts of Jos North LGA, Plateau state is 13.8%, therefore asymptomatic malaria parasitaemia is common among pregnant women at their first antenatal care in Jos North. This also implies that pregnant women may not exhibit apparent signs and symptoms of malaria but may carry the parasites in their blood and so may be sources of further transmission of the infection. The study has also shown that the prevalence and severity of malaria parasitaemia is higher in primigravidae than in multigravidae women likely due to the exposure of the latter to malaria prevention strategies. It has also shown that the malaria parasite density level is higher among younger (15 - 24) pregnant women than in the older ones. The study further supports the position of Okpere *et al.,* (2010) that many cases of malaria infection in pregnancy are asymptomatic. Non-governmental organisations and government agencies involved in malaria control and interventions should extend survey activities to include periodic diagnosis of asymptomatic persons especially pregnant women to identify and treat them thereby reducing malaria transmission. Standard malaria testing kits and facilities should be made available in all healthcare facilities to screen pregnant women even if they are in the facilities for a different health need.

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Isolation, Screening and Molecular Characterization of Polyhydroxyalkanoates Producing Bacteria from Olususun Landfill Soil and Sludge in Lagos State Nigeria.

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INTRODUCTION

Environmental and health problems associated with the use of synthetic plastics are major factors driving the embrace of bioplastics made from biopolymers that are ecologically friendly and biodegradable (Obebe and Adamu 2020). Polyhydroxyalkanoates (PHAs) are biopolymers made by bacteria growing under limited nutrients and abundant carbon sources (Kumar *et al.,* 2020). They have similar chemical, thermal and mechanical properties as synthetic polymers and can serve as suitable alternatives in plastic production (Ali and Jamil 2016, Vicente *et al.,* 2023). They are easily degraded by indigenous soil microbes when introduced into the environment (Kung *et al.,* 2007). Polyhydroxyalkanoates have been the subject of in-depth research and as of 2010 have been commercially produced by some companies in the United States (Procter and Gamble), Germany (Biomer Inc.), China (Lianyi Biotech), Brazil (PHB Industrial Company) (Naheed and Jamil 2014). The objective of this work was to identify and characterize novel PHA-producing bacteria from Olususun landfill soil and sludge in Lagos, Nigeria.

MATERIALS AND METHODS

Bacteria were isolated from soil and sludge samples collected from Olususun landfill, Lagos, Nigeria on nutrient and PHA detection agars (NA and PDA). Pure isolates were subsequently screened for PHA accumulation using the viable colony staining method with Nile Red and Nile Blue A (Spiekermann *et al.,* 1999). Sudan Black B staining was also done for intracellular detection of PHA (Fadipe *et al.,* 2020). Colonial and cellular morphologies, Grams and catalase reactions of selected PHA-positive isolates were observed. Selected PHA positive isolates were characterized by 16SrRNA sequencing and sequences deposited in the NCBI-GenBank. Phylogenetic analysis was performed using the p-distance method of the neighbor joining algorithm in MEGA 11.

RESULTS AND DISCUSSION

A total of three hundred and thirty-six isolates were obtained from which fifty-one colonially distinct isolates were screened. Thirty-two isolates were positive for PHA production showing bright orange, blue, and yellow fluorescence with Nile Red and Nile Blue A indicating the presence of PHA (Figures 1a-c). Sudan Black B staining revealed the presence of blue-black intracellular bodies. The two selected PHA positive isolates were D1 (DTO1) and G2 (DTO2). Both isolates are Gram-positive rods, D1 was catalase-negative while G2 was catalase-positive (Table 1). Amplification of the 16SrRNA hypervariable region in extracted bacterial genomic DNA of isolates D1 and G2 produced PCR amplicons of approximately 1500bp (Figure 2a). Isolate D1 (PP916594) was identified as *Priestia megaterium* sharing 99.91% homology with *Priestia megaterium* ANA29. Isolate G2 (PP916595) was identified as *Priestia flexa* sharing 99.91% homology with *Priestia flexa* NBRINE3.2. The phylogenetic tree shows isolates D1 (DTO1) and G2 (DTO2) clustering with *Priestia megaterium* and *Priestia flexa (*formerly *Bacillus flexus)* strains respectively (Figure 2b) thus confirming their identities.

Table 1: Morphological Characterization, Gram's and Catalase Reactions of Selected PHA Positive Isolates.

S/no	Isolate Code	Colonial Morphology: Shape	Colour	Margin	Elevation	Gram's Reaction	Cellular Morphology	Catalase
1	A_1	Circular	Cream	Entire	Flat	Positive	Rods in singles	Positive
2	A_2	Circular	Cream	Entire	Flat	Positive	Cocci in clusters	Positive
3	B	Circular	Cream	Entire	Flat	Positive	Rods in singles	Positive
4	C	Punchiform	Cream	Entire	Flat	Positive	Cocci in singles and chains	Positive
5	***D_1**	**Circular**	**Cream**	**Entire**	**Flat**	**Positive**	**Fat Short Rods in singles and chains**	**Negative**
6	D_2	Circular	Cream	Entire	Flat	Positive	Fat Short Rods in singles and chains	Negative
7	E	Circular	Cream	Entire	Flat	Positive	Cocci in clusters and singles	Positive
8	F	Circular	Cream	Entire	Flat	Positive	Rods in singles	Positive
9	***G_2**	**Circular**	**Cream**	**Serrated**	**Flat**	**Positive**	**Rods in two**	**Positive**
10	H_1	Circular	Cream	Entire	Raised	Positive	Very short coccoid rods	Positive
11	I	Circular	Cream	Entire	Flat	Positive	Coccoid rods	Positive
12	J	Circular	Cream	Entire	Flat	Positive	Rods in singles	Negative
13	K	Circular	Cream	Entire	Flat	Positive	Rods in singles	Positive
14	L	Circular	Cream	Entire	Flat	Positive	Short rods	Negative
15	M	Circular	Cream	Entire	Flat	Positive	Cocci in singles	Negative
16	N	Punchiform	Cream	Entire	Flat	Positive	Cocci in chains	Positive

*Selected PHA Producers are in **bold**.

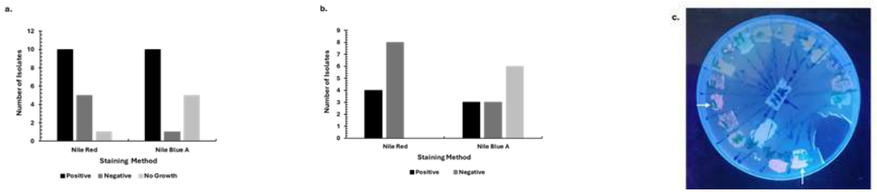

Figure 1 a - c: a – Screening Summary of Soil PDA Isolates on Nile Red and Nile Blue A (24 hours). **b –** Screening Summary of Sludge PDA Isolates on Nile Red and Nile Blue A (24 hours). **c -** Screening of Selected Isolates on Nile Red PDA Plates (white arrows indicate selected PHA-positive isolates).

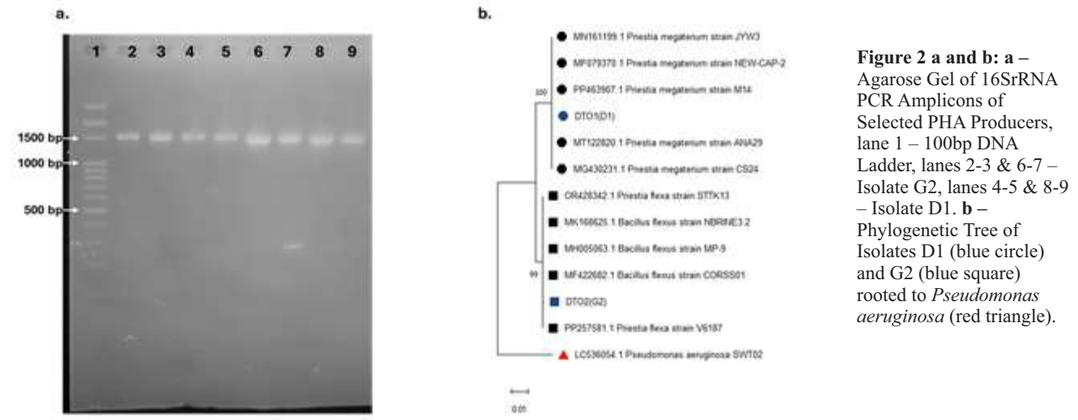

Figure 2 a and b: a – Agarose Gel of 16SrRNA PCR Amplicons of Selected PHA Producers, lane 1 – 100bp DNA Ladder, lanes 2-3 & 6-7 – Isolate G2, lanes 4-5 & 8-9 – Isolate D1. **b –** Phylogenetic Tree of Isolates D1 (blue circle) and G2 (blue square) rooted to *Pseudomonas aeruginosa* (red triangle).

CONCLUSION

The bacteria isolated from Olususun landfill soil and sludge have the potential for PHA accumulation and thus application in bioplastic production.

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Sterilization Protocol for *In-vitro* Propagation of Date Palm (*Phoenix dactylifera*) Using Seed: Optimizing Dormancy Breaking and Sterilization Protocols

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INTRODUCTION

Date palm (*Phoenix dactylifera* L.) is highly valued for its nutritional, medicinal, cultural, and religious significance. However, its propagation faces challenges due to its perennial and dioecious nature, limiting effective vegetative methods. (Jain, 2012). *In-vitro* propagation offers a promising solution but is hindered by seed dormancy and contamination issues. (Al-Khayri and Naik, 2017). This study aims to optimize protocols for breaking seed dormancy and ensuring sterile conditions in in-vitro propagation. By testing various dormancy-breaking treatments and sterilization protocols, we seek to enhance germination rates and reduce contamination, thereby improving the efficiency and reliability of date palm propagation. (Al-Khayri and Naik, 2017).

Materials Methods

Date palm (*Phoenix dactylifera* L.) seeds were treated with four dormancy-breaking methods: overnight soaking in distilled water, Hydrochloric acid immersion, hot water treatment, and a control. Three sterilization protocols using different concentrations of Sodium Hypochlorite (NaOCl) were tested to ensure sterile conditions. Sterilized seeds were cultured on Murashige and Skoog (MS) medium under light and dark conditions to assess germination. Germination and contamination rates were recorded over 27 days. Data were analyzed using ANOVA and Tukey's HSD test, with experiments conducted in triplicate and at least 10 seeds per treatment.

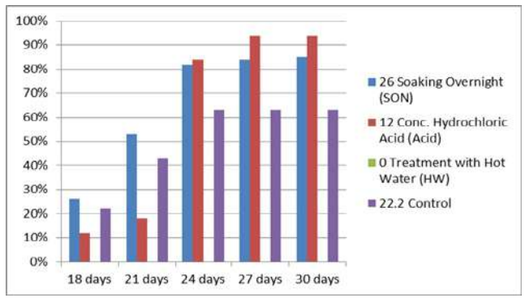
RESULT AND DISCUSSION

The analysis shows that the treatments (Soaking Overnight, Concentrated Hydrochloric Acid, and Hot Water) have a statistically significant impact on the germination rates of date palm seeds. The finding shows significant treatment differences

(ANOVA: F = 29.099, p = 0.0000). Acid treatment proved most effective, yielding up to 94% germination at 27 and 30 days. Soaking Overnight was also high, attaining rates up to 85% at 30 days, albeit less than Acid. Hot Water treatment, however, showed no germination, implying ineffectiveness for date palm seed dormancy breaking.

The ANOVA results showed a very high F-value (29.099) and an extremely low p-value (0.0000), indicating that the differences in germination rates among the treatments were statistically significant. This suggests that the dormancy-breaking treatments had a considerable effect on the germination success of date palm seeds this is in agreement with (Al-Khayri and Naik, 2017). The study successfully identified effective dormancy-breaking and sterilization protocols for the in-vitro propagation of date palm seeds. Concentrated Hydrochloric Acid emerged as the best dormancy-breaking treatment, while Protocol A was the most effective sterilization method, this sterilization falls in line with (Jain, 2012) findings.

Source of Variation	DF	SS	MS	F-Value	P-value
Between Treatments	2	40,177.6	20,088.8	29.098539	0.0000
Within Treatments	42	28,995.6	690.371429		
Total	44	69,173.2			



CONCLUSION

The study successfully identified effective dormancy-breaking and sterilization protocols for the in-vitro propagation of date palm seeds. Concentrated Hydrochloric Acid emerged as the best dormancy-breaking treatment, while Protocol A was the most effective sterilization method. These findings offer practical solutions to enhance the germination and propagation of date palms, contributing to agricultural practices and the conservation of this valuable species.

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Characterization of Some Selected Nigerian Indigenous Tomato Accessions (Morphology, Molecular and Yield).

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INTRODUCTION

Tomato (*Solanum lycopersicum Linn.*), a member of the Solanaceae family, is an economically significant vegetable cultivated globally for both fresh consumption and processing. Originating from the Andean region, the domestication of tomatoes has resulted in a variety of cultivated forms with significant genetic diversity (Albrecht *et al.,* 2010). In Nigeria, tomatoes are a staple, accounting for about 48% of daily vegetable consumption (Olajide and Oladiran, 2014).

The improvement of tomato varieties through breeding programs has traditionally relied on morphological, biochemical, and molecular markers. Among these, molecular markers such as Randomly-Amplified Polymorphic DNA (RAPD) have proven invaluable for evaluating genetic relationships and identifying superior genotypes (Bai and Lindhout, 2007). Despite challenges with reproducibility (Samia *et al.,* 2015), RAPD remains a cost-effective and time-efficient tool in the absence of more advanced techniques.

This study aims to develop a morpho-molecular and yield screening system to identify the best tomato accessions in Nigeria, addressing the need to trace phenotypic, yield and genotypic relationships using characters from locally available tomato fruits. By combining morphological, yield and molecular analyses, this research seeks to enhance the selection process for improved tomato genotypes, ultimately contributing to higher yield and better quality in tomato production.

METHOD

Sample Collection: Twelve accessions of Indigenous tomato samples were collected from the National Centre for Genetic Resources and Biotechnology (NACGRAB), with detailed information documented:|NGB 01232 - NC1 - North Central, NGB 01301 - NC2- North Central, |NG/RM/01/01/01- NW1- North West, NGB 01237 - NW2 -North West, NGB 01302 -NE1 - North East, NG/SA/07/10/002- NE2 - North East, NGB 01207 - SE1- South East, NGB 01209 - SE2-South East, NG/MR/01/005 - SW1 - South West, NG/AA/09/037 - SW2- South West, NHGB/09/113 - SS1- South South, NHGB/09/114 - SS2 - South South (Source: NACGRAB).

Viability Test: Seeds from each accession were tested for viability using the floating technique (Falusi et al., 2012). Viable seeds (those that settled at the bottom) were selected for planting.

Experimental Design: The experiment was conducted in a screen house facility at the National Biotechnology Development Agency (NABDA), Abuja, using a Randomized Complete Block Design (RCBD) with five replicates per accession (Nwosu et al., 2014). Five seeds of each accession were sown in pots filled with rich loamy soil and irrigated twice daily.

Evaluation: Growth Monitoring: Emergence days and plant heights were recorded every two weeks. The number of leaves, leaflets, and branches was also noted.

Yield Parameters: Data on flower set (days to flower emergence, days to flower opening), fruit set (number of buds, aborted buds, fruits per plant), and fruit characteristics (size, shape, color, weight of 10 fruits) were collected (Falusi et al., 2012).

Molecular Characterization: DNA Extraction: DNA was extracted using the Sarkosyl Nitrogen Method from 0.5g of fresh apical leaves. The extracted DNA was quantified using a NanoDrop spectrophotometer. Primers Screening: Twelve arbitrary decamer primers were screened, with those showing high polymorphism used for RAPD-PCR analysis.

PCR Amplification: DNA was amplified using standard PCR conditions with a set of RAPD primers. The PCR products were analyzed using agarose gel electrophoresis, visualized with ethidium bromide, and documented (Samia et al., 2015).

Data Analysis: Data were analyzed using ANOVA and DMRT at P < 0.05 with SPSS 16.0. Molecular data were processed using RAPDistance Package Software and NTSYS-pc to construct dendrograms using UPGMA.

RESULTS AND DISCUSSION

Morphological Parameters.

Table 1: Analysis of variance for the mean of morphological parameters in tomato accessions.

Accession Symbol	No. of Days to emergence	No. of Leaflets/plant	No. of leaves/ plant	No. of branches/ plant	Plant height (cm)
NC1	9.00±0.40^{ab}	29.4±18.9^{b}	7.87±4.90^{a}	4.25±1.11^{a}	8.10±5.12^{b}
NC2	10.00±0.40^{b}	20.2±10.1^{a}	6.47±2.86^{a}	4.25±1.11^{a}	6.93±3.46^{a}
NW1	8.00±0.20^{ab}	64.4±40.5^{c}	12.7±6.81^{d}	5.65±1.38^{b}	11.2±6.22^{d}
NW2	8.00±0.75^{ab}	47.9±27.8^{b}	10.3±5.09^{b}	4.35±1.10^{a}	10.8±5.00^{c}
NE1	7.00±0.55^{a}	48.4±30.4^{b}	9.00±4.08^{ab}	4.40±1.16^{a}	10.4±4.67^{c}
NE2	6.00±0.60^{a}	33.4±14.2^{ab}	9.93±4.02^{ab}	4.30±1.14^{a}	16.1±5.36^{f}
SE1	9.00±0.25^{ab}	31.5±16.0^{ab}	8.13±3.51^{ab}	4.35±1.20^{a}	9.65±4.57^{bc}
SE2	6.00±0.40^{a}	36.3±18.1^{ab}	7.73±2.70^{a}	4.05±1.11^{a}	8.92±3.78^{b}
SW1	6.00±0.0^{a}	38.9±19.7^{ab}	8.80±3.80^{ab}	4.15±1.24^{a}	14.6±6.89^{e}
SW2	7.00±0.25^{a}	48.5±24.6^{b}	11.1±5.09^{c}	5.15±1.38^{b}	9.38±4.10^{bc}
SS1	8.00±0.63^{ab}	49.1±29.1^{b}	10.4±4.80^{b}	4.25±1.11^{a}	11.6±5.44^{d}
SS2	7.00±0.20^{a}	65.5±35.9^{c}	10.9±5.15^{b}	5.00±1.29^{b}	12.3±5.05^{e}

Values are means ±SE, values followed by different superscript (s) across the column are significantly different at p<0.05.

Yield parameters

Flower Set and Fruit Set Analysis

Table 2: Analysis of variance for the mean of the flower set and Fruit set

Acces. fruit formed symbols	No. of days to flower emergence	No. of days to opening flower/plant.	No. of flower Buds formed.	No. of flowers Buds	No. of aborted.
NC1	63.0±0.40c	67.0±0.40c	17.0±0.70b	4.00±0.32ab	13.0±0.95b
NC2	63.0±0.37c	66.0±0.37c	12.0±1.56a	4.00±0.60ab	9.0±1.03a
NW1	58.0±1.32ab	64.0±1.56b	61.0±15.4e	18.00±4.98d	43.0±10.4e
NW2	60.0±1.16b	64.0±1.80b	22.0±2.98c	4.00±1.03ab	17.0±2.13c
NE1	61.0±0.74b	64.0±00b	12.0±1.58a	3.00±0.75a	9.0±1.21a
NE2	61.0±0.63b	66.0±0.68c	11.0±2.91a	3.00±0.86a	8.0±2.28a
SE1	60.0±1.08b 10.0±0.68ab	63.0±1.11b	12.0±0.84a	2.00±0.25a	
SE2	60.0±0.45b	63.0±0.89b	23.0±2.65c	6.00±0.80b	17.0±2.18c
SW1	54.0±2.10a 15.0±1.46bc	58.0±1.90b	19.0±1.66b	4.00±0.60ab	
SW2	59.0±1.02ab	63.0±0.89b	24.0±2.92cd	5.00±0.81ab	18.0±2.25c
SS1	58.0±1.32ab 20.0±2.69cd	61.0±1.29ab	28.0±3.98d	8.00±1.56c	
SS2	54.0±1.67a	55.0±1.10a	28.0±4.63d	6.00±1.28b	22.0±3.41d

Values are means ± SE, values followed by different superscript (s) across the column are significantly different at p<0.05.

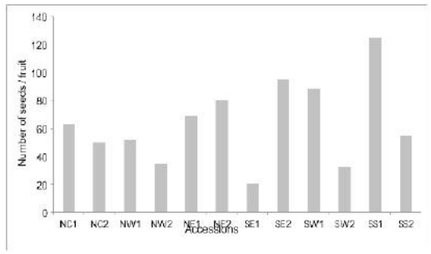
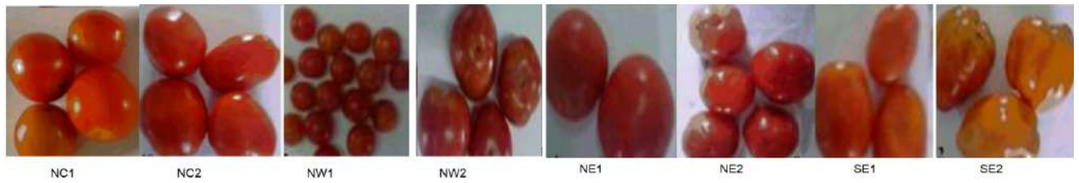


Figure 1: Number of seeds per fruit of each accession

Fruit Phenotypic Variance: The fruits obtained from the different accessions were phenotypically different from one another.



DNA Quantification: The result shows that the entire DNA extracted was of good quality because their purity was up to 1.5 and above, with concentration(ng) and purity(µl) ranging from SS1 112.1 / 1.53 to NW2- - 412.4 / 1.63.

Table 3: DNA Quantification

Accessions	concentration / ng/µl	purity
NC1	185.9	1.51
NC2	175.6	1.54
NW1	382.7	1.72
NW2	412.4	1.63
NE1	341.9	1.72
NE2	132.5	1.55
SE1	398.7	1.76
SE2	287.7	1.52
SW1	121.1	1.61
SW2	222.4	1.66
SS1	112.1	1.53
SS2	289.8	1.53

DNA fingerprinting of the Tomato Accessions

The primers that were used in this have been useful for assessing variabilities among the tomato accessions. The number of amplification products obtained was in the range of 2-8, and the primer OPA-18 produced the highest (83%) polymorphic information content (PIC), followed by OPA-02 with (80%) PIC. This is an indication that these primers are the best for determining variability in tomatoes. The polymorphic band range from 1 to 5 bands and the polymorphic percentage range from 25 to 85%.

CONCLUSION

Determining the variability of yield and yield-related components will enable the plant breeders to infer the extent of environmental influence on yield; since yield and its components are quantitative characters that are affected by the environment. This research is useful for the selection of improved tomato genotypes for maximum yield production. Conclusively traits like; fruit weight, number of flowers per plant and number of fruits per plant showed a positive relation with yield as well and they have a direct effect on yield. These can be used as selection indices in tomatoes to bring about an improvement in fruit yield. The fruit and flower set parameters are yield characters too. These characters could be used as selection indices in Nigerian tomatoes to bring about an improvement in fruit quality and quantity.

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Heavy Metal Accumulation in Selected Plants around Obajana Cement Factory and Mount Patti Lokoja, Kogi State

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Introduction

The increasing industrialization and anthropogenic activities have led to the release of heavy metals into the environment, posing a threat to ecosystems and human health. Understanding the mechanisms of heavy metal accumulation in plants is crucial for developing effective strategies to mitigate environmental pollution (Okoye *et al*., 2017).

It has been established that the soil accumulates significant concentrations of hazardous metals resulting from human activities (Chen Z *et al*., 2015). Heavy metals, such as lead (Pb), cadmium (Cd), and mercury (Hg), originate from natural sources and human activities.

Industrial discharges, agricultural practices, and urbanization contribute significantly to heavy metal pollution in soil and water being metal ions, heavy metals cannot be degraded or destroyed, therefore their stability makes them persistent toxic substances in the environment. Heavy metals as environmental contaminants can be found in the air, soil, and water, which pose health hazards to the public (Rahman, & Singh, 2019). The contribution of heavy metals to environmental pollution from different processes including industrial, agricultural, and mining has been the subject of much research in recent years (Akoto *et al*., 2008).

Aim

This study aims to determine the heavy metal accumulation capacity of selected plants growing around Obajana Cement Company and Mount Patti Lokoja, Kogi State.

Objectives

I. To investigate the concentration of selected heavy metals in the leaves of selected plants at the two sites.
II. To compare the amount of heavy metals between the plants and sites.
III. To compare the amount of heavy metals in these plants with the World Health Organization (WHO) permissible level.

Heavy metals are metals and metalloids having atomic densities greater than 5g/cm3. The presence of heavy metals in the environment is of great ecological significance due to their toxicity at certain concentrations, translocation through food chains and non-biodegradability which is responsible for their accumulation in the biosphere (Opaluwa *et al.,* 2012). The dilemma is that heavy metals, compared with organic pollutants, are more harmful because they are persistent contaminants that can pose a wide range of chronic toxic effects (Ma *et al*., 2016).

In dumpsites, heavy metals such as Cadmium (Cd) Copper (Cu, Chromium (Cr), Lead (Pb), Zinc (Zn) and Nickel (Ni) are also usually found due to remains from metals and other products (Shayley *et al*., 2009). However, despite the existence of governmental policies and regulations, the proper disposal, handling and management of municipal solid waste (MSW) has become one of the critical environmental challenges in the Country (Essien *et al*., 2019). After the processes of oxidation and corrosion, these metals will dissolve in rainwater and leach into the soil from where they are picked up by growing plants thereby entering the food chain (Ukpong *et al.,* 2013). Improper waste management methods also pilot the contamination of underground water, while most of the metals are being washed away by runoff into streams and rivers thereby contaminating the marine environment (Onwuka *et al.,* 2014).

Method

- Collection of Plant Samples: Five plant species, i.e., Banana, Pawpaw, Coconut, Guava and Mango were selected for the current study.
- Preparation of the Leaf samples: the method outlined by (Altaf *et al.,* 2021) was adopted for this study, where 6ml of nitric acid (HNO_3) was added to 0.1g of dried plant leaves and kept overnight at 25 degrees.
  The filtered solution was used to measure the eight heavy metals (Pb, Zn, Ni, Mn, Cu, Co, As and Fe). Determination of Heavy Metals in the leaf samples Heavy metals determination in all the plant samples was done using atomic absorption spectroscopy.
- Data were subjected to One-Way ANOVA to determine any significant differences in the concentration of metals extracted by treatments of leaves sampled from two sites

Result

SAMPLE IDENTITIES	Cd	Cu	Fe	As	Mn	Pb	Ni	Zn
COCONUT CONTROL	<0.01	0.086	0.13	<0.01	0.110	<0.01	0.070	0.896
	<0.01	0.088	0.128	<0.01	0.110	<0.01	0.072	0.895
BANANA CONTROL	0.02	0.110	0.174	0.040	1.096	0.010	0.064	1.384
	0.010	0.110	0.175	0.040	1.092	0.010	0.065	1.382
MANGO CONTROL	0.010	0.100	0.185	<0.01	0.785	<0.01	0.100	1.024
	0.010	0.100	0.187	<0.01	0.783	<0.01	0.100	1.026
PAWPAW CONTROL	<0.01	0.068	0.120	0.020	0.957	0.020	0.095	0.786
	<0.01	0.071	0.120	0.010	0.953	0.010	0.093	0.784
GUAVA CONTROL	<0.01	0.075	0.139	<0.01	1.025	<0.01	0.056	0.635
	<0.01	0.073	0.136	<0.01	1.100	<0.01	0.058	0.636
COCONUT	0.020	0.100	0.110	<0.01	0.228	0.020	0.089	0.679
	0.020	0.098	0.110	<0.01	0.225	0.020	0.091	0.675
BANANA	0.010	0.115	0.215	0.060	1.171	0.020	0.043	1.523
	0.010	0.113	0.217	0.058	1.17	0.020	0.050	1.525
MANGO	0.010	0.113	0.220	0.020	0.894	0.010	0.120	1.510
	0.010	0.112	0.221	0.020	0.896	0.010	0.120	1.510
PAWPAW	<0.01	0.081	0.173	0.010	0.574	0.020	0.075	1.025
	<0.01	0.080	0.174	0.010	0.576	0.010	0.078	1.022
GUAVA	0.030	0.092	0.26	0.020	0.845	0.010	0.081	0.679
	0.020	0.090	0.262	0.020	0.842	0.010	0.080	0.676

Conclusion

In Conclusion, heavy metals such as lead, cadmium, mercury, zinc,

nickel, chromium, cobalt, and iron all have various toxic effects on plants when present in excess amounts. They can inhibit plant growth, disrupt photosynthesis, damage cell structures, and interfere with nutrient uptake, leading to chlorosis, stunted growth, and even plant death. Understanding the mechanisms of heavy metal toxicity in plants is crucial for mitigating their harmful effects and developing strategies to remediate contaminated soils.

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The Ribulose-1,5-Bisphosphate Carboxylase/Oxygenase Gene (*rbcL*) Sequence Reveals the Genetic Architecture of the African Yam Bean (*Sphenostylis stenocarpa,* Hochst Ex. A. Rich Harms)

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INTRODUCTION

African yam bean (*Sphenotylis stenocarpa)* is threatened by genetic erosion of its landraces due to a lack of proper conservation and breeding strategies. To date, the genetic variations present in *Sphenotylis stenocarpa* have not been fully elucidated. Consequently, an understanding of the genetic variations and their relationships will provide the needed information for efficient breeding schemes. However, limited efforts have been made in genetic variation studies in the genus *Stenocarpa*. There is little or no information on ribulose bisphosphate Carboxylase large gene marker analysis of *Sphenostylis stenocarpa*. This research was designed to provide information on the genetic diversity and relatedness of 47 AYB accessions of *Sphenostylis stenocarpa* using *rbc*L markers.

MATERIALS AND METHODS

Sample collection

Forty-seven seeds of AYB accessions were obtained from the Cross River, Ebonyi and Plateau States, as well as the International Institute of Tropical Agriculture (IITA), for the study.

Genomic DNA extraction and PCR amplification

The genomic (gDNA) extraction of 47 AYB accessions was carried out at the Bio Science Centre, International Institute of Tropical Agriculture (IITA) using the ZR Quick-DNA Plant/Seed Miniprep™ Kit (Zymo Research, California, USA) according to the manufacturer's instructions. Polymerase chain reaction (PCR) was performed for the ribulose-bisphosphate carboxylase gene (*rbcl*) with the primers *rbc*L-F535 (5' CTTTCCAAGGCCCGCCTCA 3') and *rbc*L-R705 (3' CATCATCTTTGGTAAAATCAAGTCCA 5'). The PCR products were stained with GelRed nucleic acid stain (Thermo Fisher Scientific) and examined via 2% agarose gel electrophoresis via visualization under the UV light "Gel Doc EZ Gel Documentation System" (Bio-Rad). The PCR products were purified using the Zymo DNA Clean & Concentrator Kit (Zymo Research).

DNA sequencing

The purified PCR amplicons of the respective samples were sequenced in both primer directions using the BigDye Terminator v3.1 Kit (Applied Biosystems, California, USA) according to the manufacturer's instructions.

Data analysis

The data were analyzed using MEGA and Gene Alex software.

RESULTS AND DISCUSSION

The phylogenetic tree for the *rbc*L gene of AYB presented in this study showed that the accessions were not grouped based on origin, as there was an intermixing of accessions between different locations within each subcluster. The clustering pattern of accessions revealed by the *rbc*L gene was different from the pattern observed in the SSR analysis of Shitta *et al*. (2015) and the AFLP analysis of Ojuderie *et al*. (2014). Moreover, the clustering of accessions in the present research was not based on geographical origin, which corroborated the findings of previous reports (Moyib *et al*., (2008;) Adewale *et al*., (2014). The PCoA revealed that AYBs from different locations were clustered into five main groups (clusters I, II, III, IV and V). These results are consistent with the findings of Udensi *et al*. (2022), whose PCoA revealed five major clusters. The results of the principal coordinate analysis (PCoA) did not reveal any traceable pattern of clustering. However, the local AYB accessions, especially those obtained from Ekoli-Edda, Obubra Idomi, Abakaliki and Jos, seemed to be clustered or grouped with the same accessions from the IITA germplasm (TSs 61, TSs 224, TSs 130, TSs 58, TSs 84, TSs 67, TSs 91, TSs 98, TSs 625 and TSs 571). The above results confirmed the reliability of the PCoA and phylogenetic evolutionary tree analysis and suggested that there was obvious gene flow between different AYB accessions at the genomic level. The PCoA revealed a total genetic variation of 26.38% in this study. Our findings contrast with the findings of Olomitutu *et al*. (2022) in AYB using SNP data. SSR primer analysis revealed greater (36%) genetic variation. Our findings are in accordance with those of Adewale *et al*. (2014), who reported a total genetic variation of 26%.

The linear genetic distance within and among the gene sequences of the AYB plants in our study was 3.0000 ⩾ LGD ⩾9.0000. The narrower the linear genetic distance (LGD), the closer the AYB accessions were to each other (the origin and/or location) in Nigeria, and the lower the genetic diversity was. We observed that the linear genetic distance (LGD) among the AYB accessions investigated was 4.582576 between Nigeria-TSs561 and Nigeria-TSs69, which was the narrowest. A greater linear genetic distance of ⩽5.591 was documented in legumes (Udensi *et al*., 2022). Teyioué *et al.* (2018) reported an LGD⩽0.29 in cowpea lines, implying a narrow genetic base in the cowpea germplasm. These findings are consistent with our present study and imply that the clustering of *rbc*L gene sequences is a function of the LGD. Analysis of molecular variance (AMOVA) revealed 1% variance among populations and 99% within populations, suggesting very low genetic diversity among the AYB accessions in the IITA germplasm and local populations. The genetic variation in the *rbc*L gene revealed that the total number of haplotypes was 45. These findings imply that the investigated AYB accessions share more conserved genes and therefore are more related to each other. These findings are in tandem with the findings of Udensi *et al*. (2022), who reported relatively low numbers of haplotypes for Pigeon pea and cowpea (26 and 22, respectively), using *rbc*L gene markers. This is an indication that haplotype number is specific to the species and the population that they inhabit.

Our results revealed a haplotype diversity of 0.998±0.005 which implies that AYB shares more conserved *rbc*L genes than other genes. These findings contrast with the findings of Popoola *et al.* (2023), who reported a haplotype diversity of 0.594 in the *rbc*L gene of AYB. Udensi *et al*. (2022) reported a haplotype diversity of 1 for both pigeon pea and cowpea. The results of nucleotide diversity was 0.22741±0.0003. Similarly, Popoola *et al*. (2023) reported a very low value of 0.00382 for nucleotide diversity in AYB accessions. Our finding is in line with the findings of Udensi *et al*. (2022), who reported relatively low nucleotide diversity values of 0.02455 for cowpeas. However, a greater nucleotide diversity of 0.73019 was observed in pigeon peas (Udensi *et al*., 2022) than in this study (0.22741). A total of 0.22741 AYB accessions for the *rbc*L gene exhibited low heterozygosity in the AYB population. Analysis of the selection pressure on the *rbc*L sequences revealed nine sites under positive selection pressure, which was greater than the negative site index of six. In our study, 13.342 nonsynonymous to synonymous substitutions (d_N-ds) were selected for positive selection, while -8.299 d_N-ds were selected for negative selection. This indicates that many alleles of DNA in AYB accessions are under positive selection due to continuity, which may eventually result in population structuring and speciation over time. Negative selection pressure was also recorded among accessions of AYB, but the d_N-ds substitution rate and negative site index were lower. This is an indication that the rate of negative/purifying selection among AYB was low. Among 47 AYB accessions, 47 single-nucleotide polymorphisms in the *rbc*L gene had more nonsynonymous mutations than synonymous mutations and greater nucleotide changes, resulting in more transversion mutations than transition mutations. It is apparent that the variation that was observed in the *rbc*L gene among accessions of AYB was mostly from nonsynonymous and transversion mutations.

CONCLUSION

The use of *rbc*L gene marker approaches proved to be a viable tool for determining the genetic relatedness and diversity of AYB accessions, which is critical for the genetic improvement of this crop. Taken together, these results revealed very narrow genetic and SNP variations in the 50 AYB accessions investigated. Selection from non-closely related accessions, such as TSs111 and TSs19, should be adopted and critically screened for introgression to enhance effective breeding and genetic improvement schemes.

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Effect of *Mimosa pudica* Seeds in Cell Lines and Wistar Rats: Toxicity Studies

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1. INTRODUCTION: *Mimosa pudica* L. (Fabaceae) is commonly known as Humble plant, Sensitive plant, Touch-me-not, Sleepy plant and Laajvanti. The plant is found in both tropical and sub-tropical regions including Europe, Africa and Asia. It is used traditionally for the treatment of diabetes, urinary infections, hemorrhoids, dysentery and fever. In this study, the toxic effect of *Mimosa pudica* seeds ethanolic extract was investigated in cell lines (RIN-5F pancreatic cells and HepG2 liver cells) and Wistar rats.

2. MATERIAL AND METHODS: *Mimosa pudica* seeds were a kind gift from AMSAR Private Limited, Indore, India. The plant extract was prepared using 70% ethanol. RIN-5F pancreatic cells and HepG2 liver cells were purchased from National Centre for Cell Science, Pune-411007, Maharashtra, India. Wistar rats of both sexes (200-220 g) were used in this study. All the reagents used are of analytical grade. This study was carried out using *in vitro* and *in vivo* models. In the *in vitro* model, cytotoxic effect (cell viability) of the extract was determined in cell lines (RIN-5F pancreatic cells and HepG2 liver cells) where as in the *in vivo* model, acute and sub-chronic toxicity of the extract was investigated in Wistar rats via oral route of administration. The effect of the ethanolic extract on cell viability was determined according to the method described by Thakkar et al., 2014 with slight modifications. In the cell viability assay, increasing concentrations (0.625, 1.25, 2.5, 5.0 and 10.0 μg) of the plant extract was used in the treatment groups and distilled water was used in the untreated group (control). Acute and sub-chronic toxicity studies of the extract were investigated using the method of Lorke, 1983 and Sunday et al., 2016 respectively. The extract was administered to Wistar rats once in acute toxicity study and daily for 21 days in sub-chronic toxicity studies. The food intake, water intake and body weight of Wistar rats were measured during the sub-chronic toxicity study. At the end of the toxicity study, relative organ (liver) weight and serum concentration of biochemical parameters (aspartate aminotransferase, alanine aminotransferase and creatinine) were measured. The results were analyzed using one-way analysis of variance (ANOVA) followed by Dunnett *post hoc* multiple comparisons tests at 95 % ($P < 0.05$) level of significance.

3. RESULTS AND DISCUSSION

3.1. Acute toxicity of *Mimosa pudica* seeds ethanolic extract in Wistar rats: The ethanolic extract of *Mimosa pudica* seeds caused no mortality in Wistar rats after acute oral administration of the sample. The median lethal dose (LD_{50}) was ⩾ 5000 mg/kg body weight.

3.2. Effect of *Mimosa pudica* seeds ethanolic extract on the viability of RIN-5F and HepG2 cells: The plant extract exerted a significant ($P < 0.05$) concentration dependent decrease in the viability of RIN-5F and HepG2 cells (Fig. 1 and Fig. 2). The extract at 0.625, 1.25 and 2.5 μg caused no significant change in the percentage of viable RIN-5F and HepG2 cells when compared with the control (untreated cells) [Fig. 1 and Fig. 2]. However, at higher concentrations (5.0 and 10 μg), there was a significant ($P < 0.05$) decrease in the viable cells when compared with the control and also with the lower concentrations of the plant extract (Fig. 1 and Fig. 2). RIN-5F pancreatic cells and HepG2 liver cells have 50% inhibition concentration of 9.48 and 9.09 µg respectively.

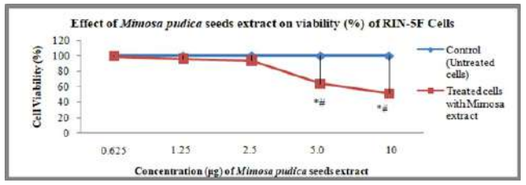

Fig. 1. Effect of *Mimosa pudica* seeds ethanolic extract on the viability (%) of RIN-5F pancreatic cells. The results are presented as the mean ± SEM, n = 3. * $P < 0.05$ compared to the control (untreated cells); # $P < 0.05$ compared to lower concentrations of the plant extract (0.625, 1.25 and 2.5 μg).

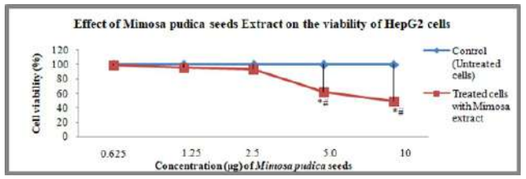

Fig. 2. Effect of Mimosa pudica seeds ethanolic extract on the viability (%) of HepG2 liver cells. The results are presented as the mean ± SEM, n = 3. * P < 0.05 compared to the control (untreated cells); # P < 0.05 compared to lower concentrations of the plant extract (0.625, 1.25 and 2.5 µg).

3.3 Effect of *Mimosa pudica* Seeds Extract on body weight, food intake, water intake and relative organ weight: *Mimosa pudica* seeds ethanolic extract exerted no significant ($P < 0.05$) change in body weight, food intake, water intake and relative organ (liver) weight of Wistar rats when compared with the control (Fig. 3, 4, 5 and 6).

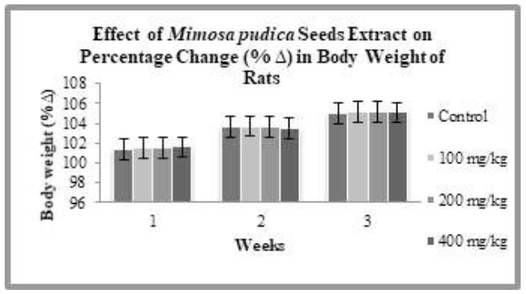

Fig 3. Effect of *Mimosa pudica* Seeds on Body Weight of Rats.

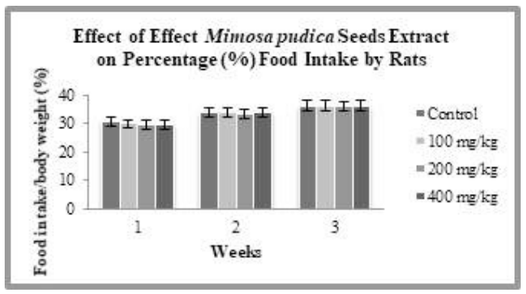

Fig. 4. Effect of *Mimosa pudica* Seeds on Food intake by Rats

Control: 10 mL/kg distilled water; 100, 200 and 400 mg/kg *M. pudica* seeds ethanolic extract; Values are mean ± SEM; n = 7.

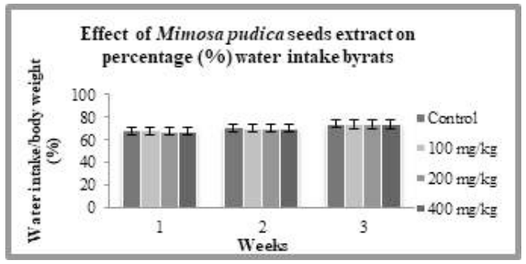

Fig. 5. Effect of *Mimosa pudica* Seeds on Water intake by Rats; n=7.

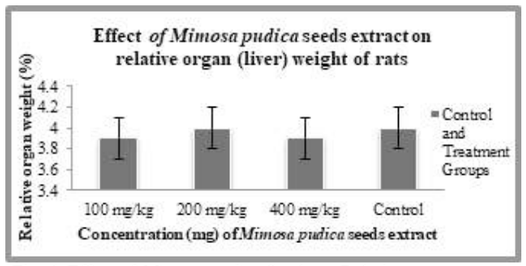

Fig. 6. Effect of *Mimosa pudica* Seeds on Relative organ weight; n=5.

Control: 10 mL/kg distilled water; 100, 200 and 400 mg/kg *M. pudica* seeds ethanolic extract; Values are mean ± SEM.

3.4 Effect of *Mimosa pudica* seeds ethanolic extract on biochemical parameters: The plant extract exerted no significant ($P < 0.05$) change in serum concentration of biochemical parameters (aspartate aminotransferase, alanine aminotransferase and creatinine) when compared with the control (Fig. 7).

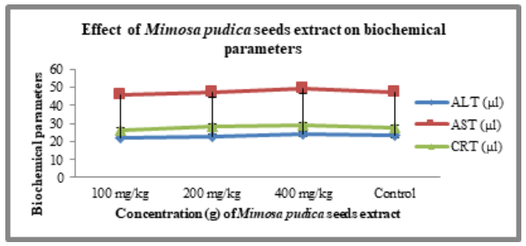

Fig. 7. Effect of *Mimosa pudica* hydro-ethanolic seeds extract on serum alanine transaminase (ALT), aspartate transaminase (AST) and creatinine (CRT) levels.

Control: 10 mL/kg distilled water; 100, 200 and 400 mg/kg *M. pudica* seeds ethanolic extract; AST (aspartate aminotransferase); ALT (alanine aminotransferase); CRT (creatinine); Values are mean ± SEM; n = 5.

4. CONCLUSION: *Mimosa pudica* seeds at low doses might have no cytotoxic effect on pancreatic (RIN-5F cells) and hepatic cells (HepG2 cells). The seeds of *M. pudica* might be safe when administered acutely via oral route (p.o.) and it might have no toxic effect on some liver enzymes when administered (p.o.) daily for twenty-one days in Wistar rats.

5. ACKNOWLEDGEMENT: Sunday Rita M. acknowledges the post-doctoral fellowship award from The World Academy of Sciences, Italy (TWAS) and Department of Biotechnology, Ministry of Science and Technology, Government of India, New Delhi (DBT). She also acknowledges National Biotechnology Research and Development Agency, Abuja, Nigeria for granting her the opportunity to undertake the fellowship programme. Authors acknowledge the School of Biotechnology (SBT), Devi Ahilya University, Indore, India and DBT for their facilities that were used in this study. Authors also acknowledge the Ayurvedic Medicine Company; AMSAR Private Limited, Indore, India for providing the pulverized seeds of *Mimosa pudica* as a gift and the help rendered by Dr. H.S. Parmar of SBT, Devi Ahilya University, Indore, India for creating the link with AMSAR Private Limited for the supply of the pulverized plant seeds.

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Comparative Study of Four Conventional DNA Extraction Protocols for Fall Armyworm

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INTRODUCTION

Fall armyworm (FAW) *Spodoptera frugiperda*, is a polyphagous and ravenous pest, destroying maize plants the world over. Many other species with very similar destructive patterns have been reported recently and these necessitate more objective molecular characterization and genomic research works towards their containment. Many studies have proposed different DNA extraction methods that could provide quality DNA for their molecular downstream analysis. This study objectively compared and modified four conventional protocols, which are cost-effective, rapid and yield good-quality DNA.

METHODS

The detergent concentrations were varied to dissolve the phospholipid bilayers of the cell membrane and organelles, and the salt concentration was also varied to break up protein chains that bind around the nucleic acids and ethanol was used to precipitate the

DNA. The CTAB (Cetyl Trimethyl Ammonium Bromide - 100mM Tris, 1.4M NaCl, 0.02M EDTA, 2% CTAB, 0.2% β-mercapto ethanol); CTAB-PVP (CTAB-Polyvinyl pyrolidone - 20mM EDTA, 100mM Tris-HCl, 1.5M NaCl, 2% CTAB, 4% w/v PVP, 2% v/v β-mercaptoethanol; SDS (Sodium Dodecyl Sulfate – 10mM NaCl, 10mM Tris-HCl, 50mM EDTA, 0.5% SDS, 0.2% β-mercapto-ethanol and Urea (Urea added to SDS as the detergent).

RESULT AND DISCUSSION

The result of the Analysis revealed significant variation in DNA purity at 1% ($p<0.01$) level with values ranging from 1.83 ± 0.2154 (Urea) to 2.05 ± 0.2123 (SDS). Also, DNA yield or concentration among the protocols at 1% ($p<0.01$) level with values ranging from 784.77 ± 388.80 (PVP) to 2854.08 ± 1274.87 (CTAB). This indicates that CTAB has the best yield while PVP has the least yield. This was due to the high ionic strength of CTAB in the solution which gets bound to the polysaccharides, and forms complexes that are removed during chloroform application. Cytochrome oxidase 1 (mtCO1) gene was sequenced. CTAB protocol has the highest DNA yield as the most potent detergent used. Tissues are rich in complex polysaccharides and secondary metabolites (plants). These interfere and co-precipitate with DNA; CTAB and other chemicals are used to minimize the effect of these metabolites. Hence, the lysate is very important where DNA is practically released from the cell before purification. Here are the functions of the DNA extraction buffer ingredients (1) The detergent dissolves the phospholipid bilayers of the cell membrane and organelles, (2) the salt breaks up protein chains that bind around the nucleic acids, and (3) the ethanol precipitates the DNA. However, the varying concentrations largely affect what each component is capable of handling (Shepherd and McLay, 2011; Heikrujam *et al*., 2020). A low concentration of CTAB will not be able to do the job because, at low ionic strength, it would precipitate nucleic acid and other polysaccharides, leaving protein and neutral polysaccharides in the solution but higher concentration as reported by Sambrook *et al.* (2001). However, the high ionic strength of CTAB in the solution gets bound to the polysaccharides to form complexes and then precipitate and washes away.

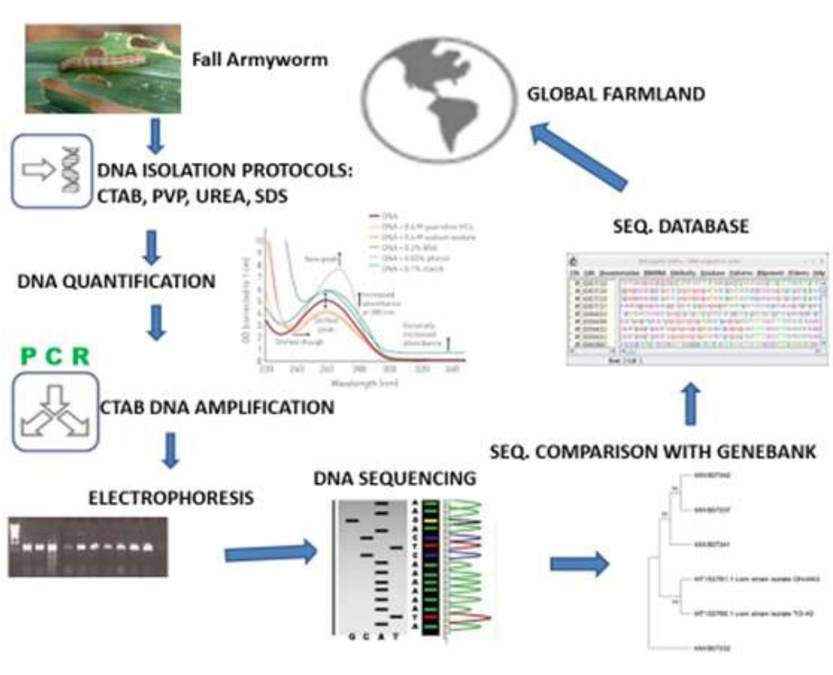

Figure 1.0: Schematic representation of procedure of molecular characterization of Fall Armyworm.

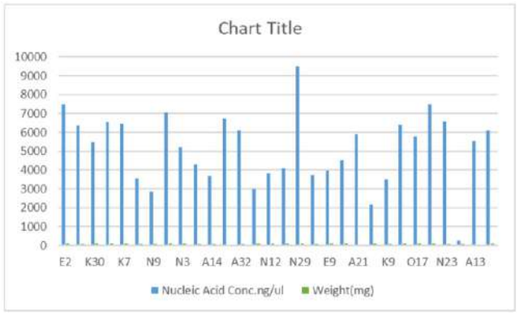

Figure 2.0: Barchat of CTAB Nucleic Acid concentration against the weight of larva used.

Figure 2.0: Bar chart of the weight of larva used against the quality of DNA recovered from CTAB

CONCLUSION

The CTAB conventional method can be used in lieu of kits when there are little or no funds for extraction kits.

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Assessing the Socio-Economic Implications of Biotechnology-Enhanced Food Accessibility and Affordability

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INTRODUCTION

Biotechnology has emerged as a pivotal tool in addressing global food security challenges driven by population growth, environmental constraints, and socio-economic disparities '(Okonko et al., 2006). This review explores how biotechnology enhances food accessibility and affordability through innovations like genetically modified organisms (GMOs) and biofortified crops. These advancements have significantly boosted agricultural productivity by introducing traits such as pest resistance, drought tolerance, and improved nutritional profiles (Qaim, 2016). Examples like Bt cotton and Bt maize highlight their potential to increase yields, reduce pesticide use, and lower production costs, thereby contributing to food security and environmental sustainability(Ziberman & Marra, 2010; Okonko et al., 2006).

The economic feasibility of biotechnology-enhanced foods is critical, particularly for vulnerable populations. While biotech crops can reduce costs for farmers and consumers, initial adoption expenses pose challenges, especially for smallholder farmers '(Mekonnen et al., 2023). Policy frameworks play a crucial role in shaping regional disparities in food affordability, influenced by varying regulatory environments and market dynamics (Bessems et al., 2020; Lewis et al., 2023). However, ensuring equitable access and managing potential socio-economic inequalities remain imperative considerations in the implementation of biotechnological advancements (Okonko et al., 2006). Biotechnology also holds promise in addressing nutritional deficiencies through biofortification initiatives like Golden Rice, enriching staple crops with essential nutrients to improve public health outcomes in developing regions (Qaim, 2016; Anyanwu et al., 2024).

METHODOLOGY

This research utilized a cross-sectional design to evaluate how biotechnology impacts food affordability in Nigeria, focusing on variations in the Cost of a Healthy Diet (CoHD) and the influence of rising food costs on accessibility to nutritious diets. Data from the National Bureau of Statistics provided insights into CoHD, household income levels, and food expenditure patterns across regions. Secondary data analysis compared CoHD between regions with differing biotechnology adoption levels, using government reports and international food price databases. National household surveys contributed demographic data to examine disparities in diet affordability across age, gender, income, and location. Statistical analyses, including descriptive statistics and time series analysis of CPI and Food CPI from April 2023 to April 2024, revealed trends and impacts of food cost increases on diet affordability.

RESULTS AND DISCUSSION

The results section of this research paper presents the findings derived from the data collected during the study. This section aims to objectively report the key outcomes and observations, emphasizing the most significant data that support the research hypotheses. In Nigeria, CoHD is the lowest price of food items required to satisfy global norms as outlined in the Healthy Diet Basket (HDB), a globally applicable collection of standards that incorporates commonalities among the majority of national food-based dietary guidelines (FBDG) (Table 1). The HDB was developed as a baseline by which nations might compare and assess the affordability and expense of healthy diets; nations without a national FBDG that has been measured, such as Nigeria, are best served by using the HDB.

Table 1: Description of Health Diets Basket (HDB)

Food Group	Number of food items selected	Energy content (kilocalories)	Share of total calories (%)	Typical weights of example foods (g)
Starchy Staples	2	1,160	50	322 g dry rice
Oils and Fats	1	300	13	34 g oil
Fruits	2	160	7	230-300 g
Vegetables	3	110	5	270-400 g
Legumes Nuts and Seeds	1	300	13	85 g dry bean
Animal Source Foods	2	130	13	210 g egg
Total	11	2,330	100	

The table shows that the daily calorie intake is 2,330 kilocalories, distributed across 11 food items. Starchy staples provide the most energy at 1,160 kilocalories (50%), followed by oils and fats, legumes, nuts, seeds, and animal-source foods, each contributing 300 kilocalories (13%). Fruits and vegetables add 160 kilocalories (7%) and 110 kilocalories (5%) respectively. This highlights a diet predominantly reliant on starchy staples, with significant contributions from fats, proteins, and smaller contributions from fruits and vegetables.

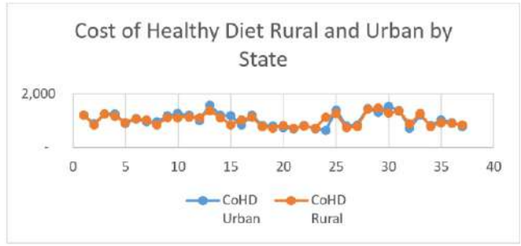

Figure 1: Cost of Healthy Diet in Rural and Urban States

The cost of a healthy diet (CoHD) varies widely across Nigerian states, with southern states generally having higher CoHDs due to factors like higher food prices and urbanization. For example, Ekiti's CoHD is N1483, while Kogi's is N706. Northern states, closer to agricultural areas, tend to have lower CoHDs. Intra-regional differences also exist, such as Ekiti being more expensive than Lagos, and Gombe having a lower CoHD than its neighbours. These variations suggest the need for region-specific strategies to improve food access and affordability.

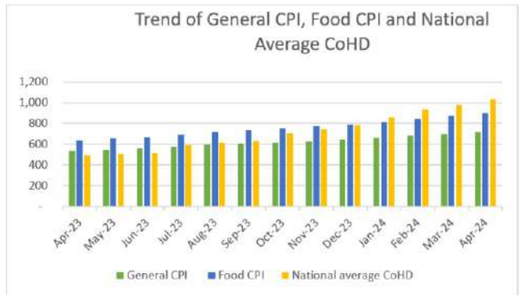

Figure 2: Trend of General CPI, Food CPI and National Average CoHD

Nigerians are increasingly struggling to afford healthy food as inflation rises. From April 2023 to April 2024, the Consumer Price Index (CPI), Food CPI, and National Average Cost of a Healthy Diet (CoHD) all showed significant increases, with food prices rising faster than the overall cost of living. This trend is driven by global supply chain issues, seasonal agricultural changes, and local demand and supply shifts. As a result, many Nigerians may face food insecurity. Further analysis is needed to pinpoint specific price drivers and inform policies to ensure access to affordable, nutritious food.

DISCUSSION

Food environments significantly influence household access to nutritious food, with global initiatives like the Cost and Affordability of a Healthy Diet (CoAHD) helping assess food security by identifying the cheapest combination of retail food items meeting nutritional needs (Nations, 2024.). In Nigeria, the Cost of a Healthy Diet (CoHD) varies across zones due to differences in food prices, income levels, and dietary patterns. The South West region faces higher CoHDs due to urbanization and transport costs, while the North West benefits from proximity to agricultural areas, resulting in lower costs (Skindilias et al., 2014). State-level variations also exist, with Ekiti having the highest CoHD and Katsina the lowest, highlighting regional economic pressures. Intra-regional differences are also notable, such as Ekiti being more costly than Lagos in the South West, and Gombe having a lower CoHD than its northern neighbours. Rising inflation exacerbates food affordability challenges, with food-specific inflation outpacing general inflation due to global supply chain disruptions and local demand shifts.

CONCLUSION

The assessment of the Cost of a Healthy Diet in Nigeria highlights significant regional and socioeconomic disparities, with higher costs predominantly in southern states and urban areas. These disparities necessitate targeted interventions to enhance the affordability and accessibility of nutritious food, especially for vulnerable populations. Strategies such as boosting local food production, improving transportation and distribution infrastructure, and implementing policies to stabilize food prices are essential. Additionally, as biotechnology solutions evolve, their potential to reduce food costs and increase the availability of affordable, healthy options must be analyzed.

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Biotechnology and Bioplastics: Current Trends and Future Perspectives

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INTRODUCTION

Fossil-based plastics have become a huge challenge in the 21st century as their indiscriminate disposal has been associated with various health and environmental hazards. Various approaches have been proposed to tackle the menace of plastic pollution, and the use of bioplastics as viable alternatives to conventional plastic materials has increasingly gained attention. Bioplastics can be described as plastic materials derived from renewable biopolymer resources, such as plants, algae, and bacteria. The most common biopolymers include Polylactic acid (PLA), Polyhydroxyalkanoates (PHAs), Starch-Based Bioplastics (SBP) and Poly Ethylene Terephthalate (PET) (Kourmentza *et al.,* 2017). The global bioplastics market is predicted to reach USD 45.2 billion by 2029 and this has been attributed to the growing awareness of environmental issues associated with conventional plastics as well as regulatory policies by different national and international bodies (Markets and Markets, 2022). Several challenges continue to limit the widespread adoption of bioplastics, including production costs, availability of feedstock and property deficiencies (Shahzad *et al.,* 2021).

Enhancement of Microbial Production of Biopolymer Precursor through Metabolic Engineering

The production of some biopolymer precursors involves microbial fermentation suggesting that metabolic engineering can be used to build cellular systems which are efficient for the production of bioplastics through different routes. This includes manipulation of biosynthetic pathways, introduction of heterologous genes, enhancement of enzyme efficiency and optimization of substrate utilization, to improve the yield and the quality of biopolymer precursors. For instance, techniques such as the CRISPR-Cas systems can be used to enhance biopolymer precursor production in some microorganisms by redirecting metabolic flux towards desired pathways. There are also reports of the enhancement of PLA production through the engineering of *E.coli* and *Bacillus subtilis* strains to overexpress the key enzymes involved in the lactic acid biosynthesis pathway (Kourmentza *et al.,* 2017). Similarly, the production of PHAs has been improved by engineering bacterial strains, such as *Cupriavidus necator* and *Pseudomonas putida*, to redirect carbon flux towards the accumulation of desired PHA monomers. There are also reports of the use of *E. coli* to produce bioplastics referred to as "aquaplastics" and the production of cellulose film from extracts of *Cladophora* algae (Shahzad *et al.,* 2021). Also, the rewiring of metabolic networks in industrial microorganisms like *Corynebacterium glutamicum* has led to a substantial increase in PHA production. These studies therefore indicate that genetic engineering of microorganisms specifically for industrial-scale production of biopolymer precursors is a promising approach in the development of bioplastics.

Enzymatic Optimization for Bioplastic Synthesis

Another approach focuses on the optimization of enzymatic catalysis for bioplastic production. This could be in the form of optimization of enzymatic systems for the production of bioplastic precursors as well as the direct enzymatic polymerization of these monomers. For instance, genetic modification of lactate dehydrogenase enzymes of some microbes such as *Lactobacillus* and *Bacillus* species has been used to enhance their catalytic efficiency for lactic acid production (Kourmentza *et al.,* 2017). Similarly, modification of PHA synthase enzyme activity to improve its activity, substrate specificity, and polymerization kinetics has been reported (Shahzad et al., 2021). Also, enzyme modification of starch and other biopolymers have been explored, hence optimization of the bioprocesses of enzymatic activity could yield products with desired properties.

Bioplastic development from waste materials and future perspectives

Various types of waste materials have been explored as potential sources for the bioprocessing of bioplastics in addition to waste management (Kuchlyan *et al*., 2021). For instance, researchers have investigated the conversion of lignocellulosic waste such as corn stover, wheat straw, and sugarcane bagasse into bioplastic precursors like lactic acid and PHAs through microbial fermentation and enzymatic hydrolysis. Also, the use of waste cooking oil, glycerol (a byproduct of biodiesel production) and even food waste have been explored for the synthesis of bio-based polyesters and polyurethanes (Naranjo *et al*., 2021). There are reports of a cellulose-based bioplastic film developed from oil palm empty fruit wastes in Indonesia. The study also demonstrated that the cellulose had a high purity with a 30% yield (Isroi *et al*, 2017). Sodium alginate has also been obtained from brown seaweeds (Sargassum) which are characterized by uncontrollable growth. This indicates that developing bioplastics from these sources ensures that there is not a threat to food security. Although alginate-based bioplastics are usually brittle, various modifications can be applied to improve them. While most bio-based plastics such as alginate-based and starch-based are brittle, several modifications can be made to enhance their properties and attributes (Kim & Manjula-Basavann, 2024) Modification using biotechnology has been applied to enhance the properties of other bioplastics including chitosan, keratin, pectin and cellulose.

CONCLUSION

The development and property enhancement of bioplastics through biotechnology holds interesting prospects for the future. Advancements in metabolic engineering and enzymatic optimization have contributed to the enhancement of microbial production of bioplastic precursors as well as the utilization of waste materials as feedstock for the development of novel bioplastic materials. Property performance and cost are still the major limitations, hence collaborative efforts among researchers, policymakers and other stakeholders are crucial to accelerating the adoption of bioplastics materials for various packaging applications.

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Determination of the best Sterilization Method in the Tissue Culture of Neem Tree (*Azadirachta indica*)

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INTRODUCTION

Neem is a tree that is native to India and widespread to many African countries, including Nigeria that is of economic importance and can be used for multiple purposes (such as medicinal, plantation, and fertilizer) (Gupta et al., 2017). Despite all the above benefits, the noble tree was propagated traditionally by seeds, although it shows heterozygosity due to meiosis. To obtain the seed you must wait for the tree to attain maturity, which is almost 5 years. And even after getting the seed, it has a short viability period. Therefore, the only way is to regenerate the Tree through Tissue culture, which makes it necessary to establish the explant *in vitro* by sterilizing it. This will allow one to select the vigorous growing tree with the desired trait to be cultivated and multiplied in *in-vitro* conditions all year round. The most difficult step in the establishment of a Neem tree in the plant tissue culture is the sterilization stage(Singh, 2018). Balaji *et al*., (2003) recorded the best result by using 0.1% $HgCl_2$ for 5 minutes by utilizing flower petals as explant. Chaturvedi et al. (2004) Achieved the best sterilization with 2cm stem cutting from 50 old trees by treating with 0.15% $HgCl_2$ for 13 minutes. As can be seen, many researchers archived the sterilization stage of the tree without protocol, and they mostly used seeds that still cause variation due to meiosis. The main aim of the paper was to determine the best sterilization method for the micropropagation of the Neem tree.

MATERIALS AND METHOD

The current research was carried out at the biotechnology and plant tissue culture laboratory at Yazd University, Yazd Province, Islamic Republic of Iran. The neem plant was obtained from a greenhouse located at Bandar Abbas city. Obtaining sterilized explants is difficult because, in the process of sterilizing living material, care should be taken to eliminate only the bacterial and fungal contaminants while maintaining the biological activity of the explant. For this matter, right from the arrival of the plant "Mancozeb" was applied to the plants at a dose of 1.5kg/L. The plant parts containing 2 to 3 nodes were collected and used as explants. Subsequently, the explants were washed carefully under tap water for twenty minutes. The explants were again washed with running tap water to remove any trace of detergent for 5 minutes. Then the explants were sterilized by one-time washing with five different concentrations of $HgCl_2$ regarded as the treatments (0% (control), 0.5%, 1.0%, 1.5% and 2%) at different durations of time (10minutes,11minutes,12minutes and 13minutes), followed by washing with double distilled water 3 times. Each treatment consisted of 12 replications. The sterilized explants were carefully transferred to the large sterile glass Petri plates with the help of sterile forceps under strict aseptic conditions in the lamina hood and put on the MS medium supplemented with 0.1mg/L BAP. The cultivated culture vials were transferred for incubation in the growth room at a controlled temperature and under light conditions. The temperature of 25±2^{0}C was maintained in the growth room with 2000-3000lux light for a 16:8 light and darkness ratio. The cleanness is maintained in this room to keep it from any contamination. The relative humidity was also maintained at 50%. The Data obtained were subjected to a one-way analysis of variance (ANOVA) using a full factorial experiment based on a completely randomized design (CRD). If ANOVA indicated statistically significant differences, the means were separated using Duncan's multiple range test (DMRT) at $p<0.05$. SPSS software version 26 was used for all data analysis.

RESULT AND DISCUSSION

The result showed a significant difference in terms of $HgCl_2$ concentration for both browning, fungal contamination and survival percentage of the explant. The means after being separated by the Duncan multiple range test (DMRT) depicted, the explant sterilized with 0.15% of $HgCl_2$ showed the lowest browning percentage of 10.42% (Figure 1(a) and 2(a)) while the highest browning percentage was observed in treatment sterilized with 0.2% $HgCl_2$ (39.58%). The lowest fungal contamination was also recorded in the treatment with 0.15% $HgCl_2$ concentration having only 18.75% while the treatment with the highest fungal contamination was 0.05% $HgCl_2$ having 77.08% contamination (Figure 1(b) and 2(b)). The highest survival percentage of 70.83% was observed in treatment sterilized with 0.15% $HgCl_2$ while 0.05% has the lowest survival percentage of 8.33% (Figure 1(c) and Figure 2(c)).

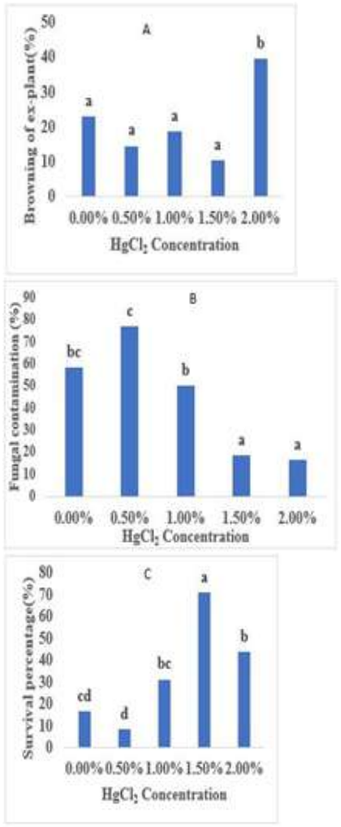

Figure 1 Effect of varying HgCl2 concentration on (a). Browning percentage (b). Fungal Contamination (c). Survival percentage, of Neem tree explants. Columns with different letters are significantly different from each other at $p< 0.05$.

Table 1 The effect of different concentrations of $HgCl_2$ and time on sterilization of explants for the survival of the Neem tree.

Traits	S.O.V	Df	MS
Browning	$HgCl_2$	4	0.152***
	Time	3	0.012ns
	$HgCl_2$×Time	12	0.24ns
	Error	40	0.039
Fungal contamination	$HgCl_2$	4	0.816***
	Time	3	0.024ns
	$HgCl_2$×Time	12	0.084ns
	Error	40	0.061
Survival	$HgCl_2$	4	0.726***
	Time	3	0.013ns
	$HgCl_2$×Time	12	0.095ns
	Error	40	0.067

Values with ***, *, ns means differ significantly at ($p < 0.01$), ($p <0.05$), No significant difference at ($p < 0.05$) respectively.

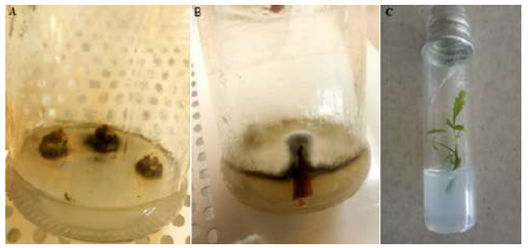

Figure 2 (a). Browning of explants (b) Explants contaminated by fungi (c). Healthy Neem explants

Likewise, time and the interaction between time and $HgCl_2$ showed no significant difference in browning, fungal contamination, and survival percentage of the explant (Table 1). To conclude, the explants were not at all contaminated by bacteria. The most difficult problem is obtaining survived explants of neem in its tissue culture. The explants were mainly contaminated by fungus and rarely by bacteria, as stated by(Chaturvedi et al., 2004) and confirmed in the present study. This result shows less browning in all the treatments, except 0.2% $HgCl_2$ which shows the highest browning percentage due to the accumulation and activity of the phenolic compound, and also a high concentration of $HgCl_2$ may be toxic to the explants as obtained by(Hashim et al., 2021).

Furthermore, the fungal attack was also lesser at the 0.15% and 0.2% $HgCl_2$concentration, indicating the effectiveness of the HgCl2 in sterilizing the neem tree. This result is in agreement with the findings of(Chaturvedi et al., 2004) and(Bello et al., 2022) for direct somatic embryogenesis. The studies of(Rafiq and Dahot, 2010) and (Houllou et al., 2015) were all contrary to the present findings because of the different parts of the plants they used, usually immature fruits, leaflets, and flower petals, or due to the genetic content of the plant used, most of them also carried out indirect somatic embryogenesis, which is also contrary to our research.

CONCLUSION

Based on the result obtained, it can be concluded that the neem tree can be established for plant tissue culture by using $HgCl_2$ as a sterilizing agent for 10 to 13 minutes at a 0.15% concentration. A higher concentration of 0.2% causes a lot of browning. It can also be deduced that Neem is rarely contaminated by bacteria and mostly by fungi at all concentrations of $HgCl_2$.

Recommendations

Different sterilization times should also be investigated to find the exact sterilization time for the establishment of the plant.

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Germination Performance of Cowpea (*Vigna unguiculata*) Seeds Treated with Entomopathogenic Isolates

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INTRODUCTION

Pesticide treatment of stored seed against pests should not come at the expense of seed quality including the seed germination viability ((Dan *et al.* 2012). Pesticide treatments may have the potential to affect seed germination and overall viability depending on the type of pesticide used, the concentration applied, and the specific characteristics of the seeds themselves (Araújo *et al.,* 2023). Synthetic chemicals have been persistently used in agriculture for field and stored pests, especially in developing countries which negatively affects the growth and physiological parameters of the

crop including the germination performance of the seed (Maldani *et al*. 2021). These synthetic chemical pesticides not only affect crop growth and physiology but also have shortcomings, especially in the food safety of crops when used as storage pesticides, as the produce usually contains high levels of chemical pesticides considered dangerous to human health (Nwosu and John, 2022). Several studies have also shown that it pollutes the environment, contributes to climate change, and affects non-target organisms when also applied in fields.

The use of biological control measures as an alternative to synthetic chemical pesticides is increasingly encouraged owing to the problem of toxicity the synthetic chemicals impact on crops. Among the most globally considered biological control measures for agricultural pests is the use of entomopathogenic microorganisms. These entomopathogens are naturally occurring microorganisms with insecticidal properties against several agricultural pests including Lepidoptera, Diptera, Coleoptera, and Hymenoptera among others. However, limited attention is paid to the impact of these entomopathogens used as pesticides on the germination performance of seeds. In this study, the germination viability of stored cowpea seeds treated with isolates of entomopathogens (*Beauveria bassiana, Metarhizium anisopliae, Verticillium lecanii* and *Bacillus thuringensis*) usually considered suitable candidates in research efforts towards developing microbial-based options for agricultural pest control was investigated.

METHODOLOGY

The pure microbial isolates were subjected to liquid fermentation technology using sucrose water as a substrate to maximize the microbial load. The isolates of *Beauveria bassiana*, *Verticillium lecani*, *Metarhizium anisopliae* and *Bacillus thuringensis* obtained through liquid fermentation with a microbial load of 2.56 x 10^4 CFU/ml, 4.44 x 10^6 CFU/ml, 2.15 x 10^5 CFU/ml and 3.66 x 10^6 CFU/ml were also at 20ml inoculated each into 50gms of sterilized talc powder, sealed appropriately and stored at room temperature as solid media for one month and microbial load determined. The germination performance of cowpea seeds treated with microbial isolates was performed as described by Behluli *et al.* (2016). Five (5) ml of the liquid-fermented isolates of *Beauveria bassiana*, *Verticillium lecani*, *Metarhizium anisopliae* and *Bacillus thuringensis* respectively were separately sprayed in air-tight containers containing 100gms of cowpea seeds. Also, 5g of solid media of the isolates of *Beauveria bassiana*, *Verticillium lecani*, *Metarhizium anisopliae* and *Bacillus thuringensis* respectively were applied in air-tight containers containing 100gms of the cowpea seeds.

The germination viability of the cowpea seeds treated with the liquid and solid media of the microbial isolates and stored for ten (10) weeks was determined using the standard germination test adopting the seed germination vigour (SGV) and the seed germination ability (SGA) as key parameters. The SGV was calculated based on the germination percentage on half of the complete days of the experiment while the SGA was calculated based on the percentage of seed germination on the final day of the testing. Germination counts were taken from 1 to 6 days after sowing. Seeds were considered germinated when the tip of the radicle had grown free from the seed coat, otherwise known as radical emergence (El Balla *et al.,* 2011).

RESULTS

The study revealed that the cowpea seed treatment with the microbial isolates in their liquid and solid media showed no significant impact when compared with control on both SGV and SGA at the end of 1st and 5th-week storage post-treatment. However, a significant effect was seen at the end of 10th-week storage post-treatment with the liquid medium of *Verticillium lecanii* showing better germination performance (SGV = 58.33±1.67 and SGA = 71.67±3.33) among other isolates in a liquid medium when compared with the control (SGV= 68.33±1.67 and SGA = 80.00±2.89) and the isolate of *Bacillus thuringensis* in its solid medium revealing better germination performance (SGV= 58.33±3.33 and SGA= 71.67±1.67) among other isolates in a solid medium when compared with the control (SGV= 68.33±1.67 and SGA= 80.00±2.89). The comparative analysis of the treatment with the microbial isolates in its liquid and solid media for SGV and SGA showed no significant difference with the control except at the 10^{th} week storage post-treatment where all the microbial isolates showed slight significant differences in reduced germination performance when compared with the control.

CONCLUSION

This study concludes that isolates of *Beauveria bassiana, Metarhizium anisopliae, Verticillium lecanii* and *Bacillus thuringensis* do not reduce germination performance of cowpea seeds when used as microbial pesticides against cowpea storage pests. However, at longer storage post-treatment of cowpea seeds with these entomopathogenic isolates, the germination performance may be reduced.

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A Metagenomic Approach to the Characterization of Lignolytic and Gas-Producing Anaerobic Microbiota and their Effects on Cow Dung Substrate.

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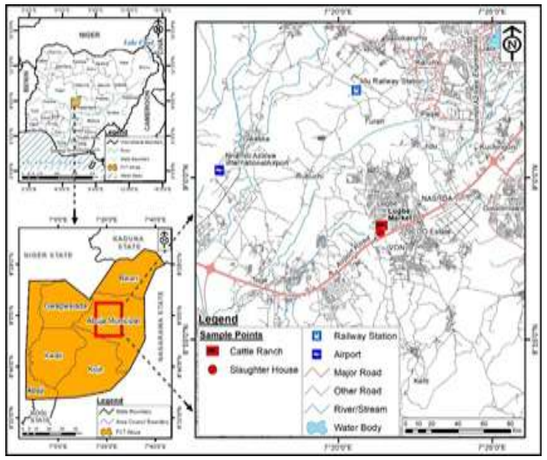
INTRODUCTION

One of the most efficient systems for harnessing the unreached energy found in lignocellulosic substrate is found in the rumen of animals such as cattle and sheep. The fermentation process which includes hydrolysis, acidification, cytogenesis and methanogenesis that occurs during anaerobic digestion is crudely similar to the digestive process that occurs in the rumen as earlier described, it is far less efficient. One reason for the reduced efficiency of anaerobic digestion compared to the rumen likely lies in differences in the microbial populations between these two environments, therefore the need for microbial seeding cannot be jettisoned. Microbial seeding is the introduction of specific microorganisms into a system or process in order to improve its inherent ability. Agriculture on average produces 23.7 million tons of food daily and 21% of the world's greenhouse gas emissions (Duque-Acevedo *et al.,* 2020). This has led to the rising need for the elimination of the waste.

METHODOLOGY

Biochemical Test and Cultural Characterization: This was carried out using the methods of Sagar *et al*. (2022) and Archary *et al*. (2022).

Screening of isolate for lignolytic ability; Isolates were screened for lignolytic property (mineral solution, 2.5g\L, KH2PO41 g\L, $Nacl_2$, 2.5g\L.MgS0.7H200.2g\L, $CaCl_2$ 0.1 g\L (clear zone target).
Molecular characterization and metagenomics were carried out using the method of Katharina *et al*. (2022).



Map showing one of the sample Locations

Phylogenetic tree for methanogens used in biogas production

RESULTS

Conversion of cow dung waste using molecularly identified anaerobes from mixed waste which include *Uncultured Methanobacteriaceae archaeon clone KR-H07A06, Candidatus Methanoperedenaceae archaeon GB37, Candidatus Methanoperedenaceae archaeon* GB37, *Methanothermobacter thermautotrophicus* strain CCSD, *Pseudomonas sp.* strain NPK*, Candidatus Methanoperedenaceae archaeon* GB50 was achieved. Metagenomics revealed the presence of the genera *Bacteroidota* (26.91%), *Firmicutes* (25.87%), *Chloroflexi* (12.35%), *Proteobacteria*(7.24%), *Planctomycetota* (6.31%). *Firmicute*(29.8%) were the second most abundant genera. Within the phylum *Firmicute,* the genera *Clostridium* (19.94%), *Bacillus* (3.11%), *Anaerolineae* (12.32%) were identified. Clones were predominantly *Actinobacteriota* (50%). *Planctomycetota* (13.73%), *Chloroflexi* (7.96%), *Firmicutes* (5.56%), *Proteobacteria* (4.48%), *Bacteroidota* (4.48%), *Chloroflexi* (7.96%). Members of the class *Actinobacteria* (46.31%), *Planctomycetes* (12.34%), *Anaerolineae* (6.45%), *Clostridia* (4.40%), *Bacteroidia* (4.24%), *Alphaproteobacteria* (3.34%), *Acidimicrobiia* (1.38%) were identified. All the species identified are strict, obligate or facultative anaerobes.

CONCLUSION

From all the findings in this work, it can be concluded that the presence of these anaerobic bacterial communities led to the increase in gas yield because they were able to degrade cellulose and other fibre components more rapidly during microbial metabolism (anaerobic digestion).

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Disparities in Proximate Analysis and Screening of Saw Dust Substrate for Biogas Production using Isolates from Mixed Fruit and Vegetable Residue, Cow Dung from Lugbe F.C.T Abuja and Saw Dust from Odi Sawmill, Bayelsa State.

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INTRODUCTION

Sawdust or wood dust could be referred to as the by-product of cutting, grinding, drilling, sanding or otherwise pulverizing wood with a saw or other tool. It is composed of fine particles of wood. Sawdust is made up of three major components; Lignin, Hemicellulose and cellulose (Alexander, 1997; Erikson *et al*., 1990). India is found as 4th largest petroleum-consuming country with the USA preceding (N. Sonnichsen 2021), China and Japan, with a high impact on the growth economy of 6–8% per year which can create further strong dependency on various types of petroleum products (petrol, kerosene or natural gases) with more environmental causing health problems, risks and challenges like global warming and climate change. Biogas and biomass-based energy (bioethanol and biohydrogen) production can be provided as good options for replacing fossil fuel energy via developing and enhancing the cost-effectiveness of bioprocess for bioenergy opportunities in rural communities worldwide. Third-generation biofuels from microalgae and wood sawdust species can be suitably synthesized with environmental, economic and social benefits for the worldwide population with the reflection of high energy efficiency for road map of individual to industry level consumption (R.K Srivastava 2019).

Methodology

Source of Sample
Sawdust, samples were collected from the Sawmill located at Tipper garage, federal Housing, Airport Road, Ahmadu Bello Way, Lugbe, Abuja.

Sample collection
Sterile polyethylene bags were used to collect the sample (50kg) and was transported to the International Institute of Tropical Agriculture, Ibadan, Ibadan, Oyo state, Nigeria.

Study Design
For each of the three substrates which include cow dung, mixed fruit and vegetable residue, proximate analysis was carried out. The parameters analysed include Nitrogen, Moisture content, Ash, Organic matter, Carbon, Carbon nitrogen ratio, Calcium, Potassium, Magnesium, Sodium, Manganese, Ion, and Copper.

MC	ASH	OM	©LOI	CN	SAW DUST PROXIMATE ANALYSIS
%	%	%	%	%	
0.2	2,8	88.10	51.0	0.2:51.1	

Proximate Analysis of Saw Dust from Tipper Garage, Abuja.

KEY: N = Nitrogen; MC = Moisture content; OM = Organic matter; C (loi) = Carbon (by loss of ignition)

RESULTS AND DISCUSSION

The results depict a high concentration of organic matter and carbon in sawdust from Bayelsa as shown in Table 4.1 and Figure 4.1, the carbon-nitrogen ratio was not balanced and did not meet the requirement for a stress-free methanation process. The required [C: N] ratio for optimum biogas production in organic matter ranges from 20:1 and 30:1. The [C: N] ratio obtained in this work is 50:0.1 which implies that the substrate or wood has a very high concentration of carbon and is deficient in Nitrogen. Therefore, if this wood substrate must be used for bio methanation, nitrogen should be augmented by using supplements rich in nitrogen such as tannery effluent, corn, soya bean milk, ground nut cake, gram flour, ammonium sulfate and urea during pretreatment of substrates, and also, the concentration of carbon must be regulated to meet up with the biomethane potential (BMP) requirement for this substrate. Optimum concentrations of organic matter increase the speed and rate of biomethanation. Cow dung on the other hand had higher concentrations of Sodium (70.8), Manganese (194.56) and Ion (198.86) compared to other parameters while potassium, magnesium, nitrogen, Calcium, Fats and ash were very low in both cow dung and mixed fruits. Potassium triggers the activation of important biochemical enzymes for the activation of Adenosine triphosphate (ATP), therefore the need for potassium-rich supplements while using this substrate cannot be over-emphasized. The effects of different potassium and nitrogen pretreatment strategies on the anaerobic digestion (AD) performance of rice straw were investigated by Juan Luo *et al,* 2020. The result showed that potassium hydroxide, ammonia and water combined pretreatment achieved the highest biomethane production. Manganese is a metal essential cofactor for the oxygen-evolving complex (OEC) of the polysynthetic machinery, catalyzing the water-splitting reaction in photosystem ii (PSII) of the electron transport chain. Since cow dung recorded a high concentration of manganeses, this depicts its suitability in biomethanation on its ability to facilitate the systems of energy pathways in microbial metabolysis. On the same note, Cow dung should be supplemented during methanation with substrate rich in potassium, magnesium, nitrogen, calcium and fats since it has them in low concentrations. A high concentration of manganese and ion was also recorded in cow dung as shown in figure 4.3. This information is very crucial and must be checked for supplementing and optimum performance during biomethanation (Biomethanepottensial) (BMP).

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Prevalence of Direct Acting Antiviral Resistant Variants among HCV Infected Individuals in Kaduna State, Nigeria

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Keywords: Hepatitis C Virus, resistant, variants, DAA, substitution

INTRODUCTION

Despite the paradigm shifts in the treatment of hepatitis (alpha interferon to Direct direct-acting antivirals (DAAs) therapy), there is an increase in resistance to these antiviral agents (Bhatia and Gupta, 2020). Direct-acting antivirals (DAAs) act by inhibiting enzymes which are crucial in the replication of HCV in the hepatocytes. This results in > 90% sustained virological response (Bhatia and Gupta, 2020).

Multiple variants of HCV (quasispecies) have emerged as a result of a lack of proof-reading ability of the viral polymerase, the high rate of HCV replication and selective pressures (Bhatia and Gupta, 2020). These variants are genetically distinct and some might harbour baseline resistance-associated substitutions (RASs), which can result in DAA resistance at varying degrees (Lontok *et al*., 2015).

MATERIALS AND METHODS

Collection of samples
Blood samples (5 mL) were aseptically collected from HCV-positive blood donors who are DAA naïve. After clotting, the samples were centrifuged for 2 mins at 2000 rpm and the sera were stored at a refrigerating temperature (-4°C) for further analysis.

NA extraction and cDNA Synthesis
Hepatitis C virus RNA was extracted from the ELISA seropositive serum samples using the Quick-RNA Viral Kit as per the manufacturer's instruction. The extracted RNA was used to synthesize complementary DNA (cDNA) using the ProtoScript II First Strand cDNA Synthesis Kit.

PCR amplification conditions and sequencing of HCV *NS3*, *NS5A*, and *NS5B* genes
Amplification of HCV *NS3*, *NS5A*, and *NS5B* genes was achieved by nested PCR using primers designed in this study and amplification conditions described by Li *et al*. (2017).
NS3, NS5A, and NS5B Sequence analysis for detection of RAVs
Resistance Associated Substitution (RAS) analysis to detect RAVs was carried out using the Geno2pheno HCV tool (https://hcv.geno2pheno.org/index.php).

RESULTS

Four (4) RASs were identified in HCV belonging to subtype 1b (T54S, Y56F, V170T and L159F) while two (2) RASs were identified in HCV belonging to subtype 1a (N174S and M28V) (Table 1). Frequency and Prevalence of Resistance Associated Variants (RAVs) are shown in Table 2. The frequency and prevalence of NS3 RAV were 4 and 36.36% respectively. While the frequency and prevalence of NS5A RAV and NS5B RAV were 1 and 9.09% each. Overall, four of the blood donors were infected with RAV strains of HCV, giving a prevalence rate of 36.36% (4/11).

Table 1: Distribution of Resistance Associated Substitution (RAS) based on HCV subtypes

Genes	Resistance Associated Substitution (RAS) GT1a	GT1b
NS3	N174S	T54S, Y56F, V170T
NS5A	M28V	None
NS5B	None	L159F

Table 2: Frequency and Prevalence of Resistance Associated Variants (RAVs)

Region	n = 11	Frequency of RAV	Prevalence (%) of RAV
NS3		4	36.36
NS5A		1	9.09
NS5B		1	9.09

DISCUSSION

In this study, numerous amino acid substitutions were identified, some of which were associated with resistance (namely V170T and T54S) or reduced susceptibility (namely M28V, Y56F, N174S and L159F) to one or more DAAs. However, most of the substitutions were not associated with DAA resistance. This observation is in line with the report of Malandris *et al.* (2021).

RASs were observed to be more common in subtype 1b (4) compared to subtype 1a (2) in this study. This might be because only one (1) subtype 1a was identified in this study compared to subtype 1b that were ten (10). Similarly, Sayana *et al.* (2020) reported that the prevalence of RAS was higher in HCV subtype 1b compared to HCV subtype 1a.

In this study, 36.36% of blood donors with PCR-positive samples were found to be infected with HCV RAVs i.e. strains that harbour at least one RAS in one of the three DAA targeted regions namely NS3, NS5A and NS5B. NS3 RASs were identified as the most frequent RASs in this study. This is contrary to the findings of Li *et al.* (2017) and Bertoli *et al.* (2018) where NS5B RASs were the most frequent and the report by Chen *et al.* (2016) that RASs to NS5A inhibitors are frequently detected in HCV genotype 1.

CONCLUSION

In conclusion, the prevalence of Resistant Associated Variants of HCV among blood donors in Kaduna state was 36.36%.

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Stakeholder Participatory Approach to Explore Enablers and Barriers for Upscaling Bioenergy Technologies Towards a Sustainable Biogas Adoption in Nigeria

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INTRODUCTION

Bioenergy refers to energy uses of biomass, whether for heating, power generation or transport. Burning pure biomass for heating and cooking purposes among rural Nigerian households has gained significance, however, this approach of generating bioenergy has a detrimental impact on the vulnerable population of the communities (Ugwu et al., 2022). Despite the enormous benefits of waste-to-fuel conversion, many developing nations are still heavily dependent on inefficient wood-based biomass to meet their daily energy needs. For instance, nearly half of the world's population and about 81% of households in Sub-Saharan Africa rely on wood-based fuel as their dominant source of energy (International Energy Agency, 2023). In 2021, over 83 % of Nigerians lacked access to clean cooking technologies and fuels as about 175 million Nigerians depend on solid fuel as a source of fuel for cooking (World Health Organization, 2024). Heavy reliance on dirty cook-fuel has caused about 128 million deaths in 2019 –(Murray et al., 2020). Of these, 84,000 were children under 5.

Nationally, over one in ten deaths of children under the age of 5 is caused by household air pollution. In addition, the high demand for wood fuel has largely contributed to an estimated 100 million cubic meters of firewood being consumed annually, making Nigeria one of the highest rates of deforestation in the world, at over 3.3% per year (Yusuf & Razaq, 2023). As a result, the country lost over 1.33 Mha (9.3%) of tree cover translating to around 724 $MtCO_2e$ emissions between 2001 and 2023 (Watch, 2024). With the abundant biomass energy resources such as around 43.1 billion tons/year of wood fuel, 61 million tons/year of animal waste, 83 million tons/year of crop residue and Solar radiation of about 3.5 - 7.0 kWh/m^2/day (Gatugel *et al*., 2015) Nigeria can achieve universal energy access. Evidence shows Nigeria can harness its vast biomass potential to provide sustainable clean cooking and power its homes. On this note, the current study aims to use a stakeholder participatory approach to explore sustainable biogas adoption and penetration and strategies to upscale biogas technology in Nigeria, by identifying relevant stakeholders that facilitate the adoption and penetration of biogas technology; and analyze the strengths, weaknesses, Opportunities and Threats to biogas technology; strategic recommendations to upscale biogas/renewable natural gas in Nigeria will be developed.

METHODOLOGY

The identified stakeholders were drawn from about 14 institutions with affiliates ranging from state and national ministries, rural women leaders, farmers associations, energy investors, financial institutions and energy regulators. They were then invited to a workshop organized in a participatory setup. In a mixed method approach, Secondary and primary data was obtained from literature, through focused group interactive sessions comprising stakeholders in the energy sectors. Around 50 stakeholders were selected and dissected into groups of 5 for a more participatory interaction, according to Figure 1. Implementing the participatory technique enabled stakeholders to share their opinions about biogas adoption irrespective of their experience and educational background. Materials used for the stakeholders' participatory technique included clipboards, sticker notes, pens, pencils, erasers, sharpeners, temporary and permanent markers and cardboard and breadboards. Qualitative data were collected from a focused group discussion that engaged the stakeholders using the materials and method discussed in the section.

Furthermore, a stakeholders' participatory (SP) approach and

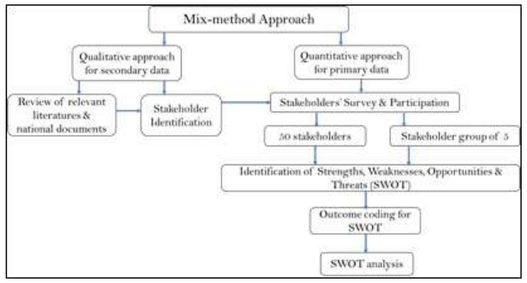

Figure 1. Methodological framework to the study
(Source: Current Study, 2024).

insights obtained were subjected to Strengths, Weaknesses, Opportunities and Threats analysis, thus a SWOT analysis. The SWOT analysis explored what stakeholders considered the best and worst options and provided successful strategies for future policy development. Insights obtained from the participatory discussions were used to design a comprehensive SWOT analysis (Onyekaozuoro et al., 2023).

RESULTS AND DISCUSSION

Stakeholders' participation according to SWOT analysis

Using the obtained information from the participatory survey, the stakeholder landscape revealed diverse affiliations and mandates of the participating respondents, irrespective of educational background. The variables that could serve as Strengths, Weaknesses, Opportunities and Threats (SWOT) are coded from the information received from the participatory discussion among the stakeholders. A summary of the SWOT analysis obtained during the participatory survey is presented in Figure 2. According to Figure 2, in the case of strength, over 70% of stakeholders have identified that the abundant availability of feedstocks as plants and animal waste can be leveraged to enhance biogas adoption. Also, over 71% of respondents have claimed that the adoption of biogas will address the energy gap, especially in rural areas as an opportunity for the Nigerian state, thus enhancing energy access deployed in a decentralized manner.

Also, weak policy and legislation were identified by over 80% of the stakeholders as significant weaknesses in achieving the adoption and penetration of biogas in Nigeria. Also, major threats identified among the stakeholders included inadequate integrated sewage system, unconscious orientation, lack of integrated public sewage buildings and public defecation. More so, farmers' education, guaranteed availability of feedstock at a reasonable price and secure supply of biomass of appropriate heterogeneity are reliable approaches to ensuring the sustainability of the strengths.

CONCLUSION AND STRATEGIC ACTION PLAN

Results from the study revealed that with the abundance of

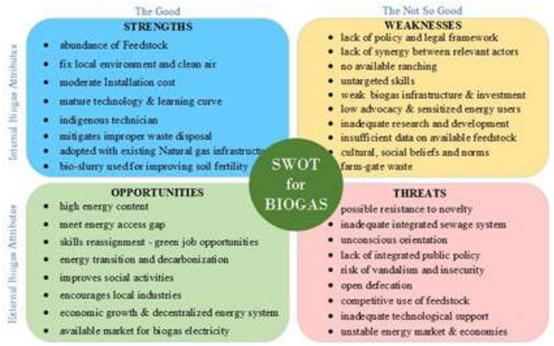

Figure 2. Outcome from SWOT analysis
(Source: Current study, 2024).

feedstock across the country and the high tendency of curbing indiscriminate waste disposal upscaling of biogas technology as an alternative clean energy solution in Nigeria is possible. In addition, with huge national benefits, appropriate trade-offs and synergy among the identified barriers and enablers were considered a reliable measure that would further enhance the sustainable adoption of the clean solution. Also, achieving an equilibrium point for a robust strategic action plan is important. The study has identified SWOT analysis as a reliable modelling tool for modelling participatory theories that deliver reliable policy recommendations.

The following action plans were obtained from a biogas-SWOT analysis.

i. Legislate integrated buildings: such as hotels, government/public buildings, student hostels, dormitories, etc., with large numbers of occupants have an integrated sewage system compatible with generating renewable natural gas;
ii. Provide incentivize and motivate ranching system: keeping domestic animals like cattle in a large space of land would enhance generating feedstocks for biogas;
iii. Ensure deliberate awareness and biogas technologies advocacy among farmers;
iv. Provide attractive incentives for bioenergy investors;
v. Ensure adequate synergy between relevant actors;
vi. Empower research institutes on research and development of renewable biogas.

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Energy and Economic Analysis of an Integrated Bioethanol-Biogas Production System

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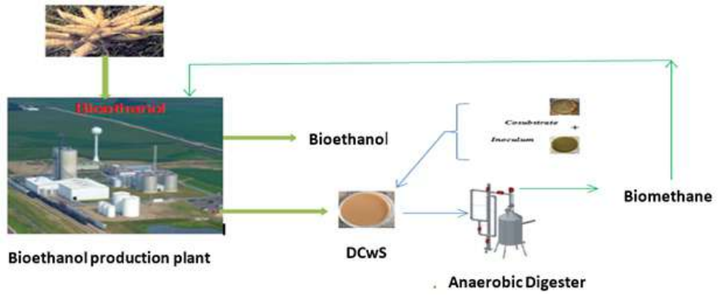
INTRODUCTION

The sustainability of ethanol production is threatened by the large volume of Distilled Cassava with Soluble (DCwS) generated as process waste and the high primary energy consumption in its production process. This study was carried out to evaluate the energy and economic performances of a 1000 l/d cassava-based bioethanol plant sited at the Bioresources Development Centre Ogbomosho (O-EMD) when operated in both stand-alone mode and when integrated with an anaerobic digester, for onsite treatment and conversion of DCwS to biogas. The plant's boiler consumes 192 tons/year of firewood to raise steam and generates 13500 l/d of DCwS wastewater.



METHODS

Data for the study were gathered from the results of laboratory analysis of DCwS samples (Ibrahim *et al*., 2022), O-EMD operations, open literature, and information from third-party organizations such as the Ibadan Electricity Distribution Company and the Central Bank of Nigeria. Having estimated the size of the anaerobic digester required to treat DCwS at its daily generation rate, its construction, installation and total capital costs were all estimated and adjusted for inflation by applying the capacity-based cost estimation method, some economic factors, and engineering rules of thumb (Amin Salehi *et al*., 2010; Towler and Sinnott, 2008), to the known construction cost of a digester of similar design (Amigun and Von Blottnitz, 2010). Based on these cost values, economic indices such as the annual profit (P), payback time (PBT), net present value (NPV), and the internal rate of return (IRR) were calculated as the basis for comparing the economic performances of the O-EMD plant when operated in stand-alone mode and as an integrated bioethanol-biogas production system.

Similarly, their performances were compared in terms of energy output-to-input ratio. Energy input was mainly thermal energy to raise steam for distillation (E_{dis}), electric energy (Ec) for running motors, pumps, etc., and the transportation energy (E_T) required to move DCwS for offsite disposal, whereas, energy output was the energy contents of the produced bioethanol and biogas, based on their lower heating values (LHV).

RESULTS AND DISCUSSION

The results showed that DCwS has good potential for biogas production with a biomethane yield of 247 Nml/gVS. Economic analysis revealed that integrating a 598 m^3/d capacity biogas unit with the O-EMD brings in an extra profit of nearly ₦61 million per annum above the stand-alone operation, with the total investment cost recouped within 4 years. Over the assumed 10-year lifespan of the digester, the discounted value of the initial investment would have grown by nearly ₦ 55 million, at an average rate of 21.3% per year. Additionally, the integrated system is nearly twice more energy efficient as the stand-alone bioethanol plant and can replace 192 tons of burnt firewood every year with biogas.

High methane yield from DCwS serves as an incentive for choosing anaerobic digestion as a viable treatment technology for distillery wastewater. Also, a highly positive NPV with an IRR value (21.3%) that is well above the prime interest rate of 15.54% invested in the digester installation (integrated system) a very worthwhile and profitable venture. The PBT of 4 years and IRR of 21.3% are respectively lower than 7 years and higher than the 16.2% values reported by Kemausaur *et al*. (2015), although for a smaller capacity (500 m^3) digester with 15 years of plant life. The difference could be due to the economies of scale.

CONCLUSION

Results from this study showed that when a bioethanol plant is integrated with an anaerobic digester, its operation is economically profitable and environmentally friendly. It is recommended that further research considering different digester configurations and operational modes should be explored. Effluent, known as digestate, from the digester, is neutral, rich in nutrients, and has been established as a viable organic fertilizer (Ola *et al*., 2022). The economic implication of this should be investigated.

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Optimized Enzyme Production in Mono and Co-Culture Fermentations of *Aspergillus niger* and *Trichoderma harzianum* Using Pretreated *Indigofera arrecta* Seeds

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Keywords: *Aspergillus niger, Trichoderma harzianum, Indigofera arrecta* seeds, Alkaline pretreatment, Biological pretreatment, Tannase activity, Phytase production

INTRODUCTION

Solid-state fermentation (SSF) is a microbial fermentation process where selected microorganisms such as bacteria, fungi, and yeasts grow on a moist, solid, non-soluble organic substrate, which serves as both a support and nutrient source in conditions with minimal free-flowing water (Manan and Webb, 2017). This process is particularly effective in breaking down anti-nutritional factors (ANFs) present in cereals and legumes, which can inhibit protein bioavailability (Horlacher *et al*., 2023). Common heat-stable ANFs include phytates and tannins (Joye, 2019), with tannins being prevalent in the bran of sorghum, millet, and legumes like peas and faba beans (Sarwar *et al*., 2012). These compounds form insoluble complexes with minerals, carbohydrates, and proteins, reducing their bioavailability (Horlacher *et al*., 2023). While heating does not affect tannins or their complexes, microbial tannase activity can rapidly break them down (Pontonio *et al*., 2020).

Phytic acid acts as a potent chelating agent due to its reactive phosphate groups, binding with minerals (e.g., Ca, Mg, Fe, Zn) and amino acids, thus decreasing the bioavailability of proteins and micronutrients (Grupta *et al*., 2015). Microbial and endogenous phytase activity can remove up to 90% of phytic acid. Various food sources such as bread nut, cashew nut, and fluted pumpkin contain tannins, phytic acid, and trypsin inhibitors, which lower protein digestibility. Fermentation significantly reduces the activity of these ANFs, enhancing protein digestibility and nutrient availability (Fagbemi *et al*., 2005). Enzymatic hydrolysis during fermentation plays a crucial role by reducing levels of ANFs and increasing the bioavailability of proteins, free fatty acids, iron, and sugars through the action of amylases, proteases, and lipases (Sharma *et al*., 2020).

Mixed cultures are more effective than monocultures in producing bioactive peptides in fermented foods (Martinez-Villaluenga *et al*., 2017). For example, co-cultures with yeasts significantly enhance mineral availability in soymilk by degrading phytic acid, achieving substantial increases compared to mono-cultures (Rekha and Vijayalakshmi, 2010). Similarly, co-cultures of L. acidophilus and Lp. plantarum in cowpea fermentation is more effective at reducing ANFs and producing vitamins, leading to significant reductions in phytic acid and trypsin inhibitors (Sanni *et al*., 1999).

Indigofera arrecta seeds, rich in natural tannins and phytates, represent a promising substrate for enzyme production. Pretreatment of these seeds through alkaline or biological methods can enhance their suitability as substrates by making nutrients more accessible to microorganisms (Ahmadu *et al*., 2017; Ahmadu *et al*., 2020). This study aims to investigate the time course of tannase and phytase production in both mono-culture and co-culture fermentations using *Aspergillus niger* and *Trichoderma harzianum* on pretreated *Indigofera arrecta* seeds.

MATERIAL AND METHODS

Collection and preparation of samples

Indigofera arrecta fruits were collected from the Zaria metropolis with identification done at the Herbarium of the Department of Biological Science, Ahmadu Bello University, Zaria, Nigeria where voucher number 663 had already been assigned to *Indigofera arrecta*. The fruits were sun-dried for 3-4 days, threshed and winnowed. Dust and other foreign materials were removed to obtain clean seeds which were ground in a bench mill. The ground seeds were then stored in plastic containers for subsequent analysis (Ahmadu *et al*., 2020; Ahmadu *et al*., 2017).

The following pretreatments were carried out on the ground sample of *Indigofera arrecta*:

1. Alkaline pretreatment: Two hundred grams of the ground sample was mixed with 1L of 0.25M NaOH solutions for 1 hour after which the mixture was neutralized with 0.1M HCl. The residue was washed with distilled water and dried to constant weight at 800C in the oven (Ahmadu *et al*., 2020; Ahmadu *et al*., 2017; Shipnei *et al*., 1995).
2. Biological pretreatment: Forty grams of the sample was moistened with 200ml of distilled water to obtain 70% w/v of moisture in a 1L Erlenmeyer conical flask. The mixture was autoclaved for 30min at 121°C. After cooling, it was inoculated with spore suspension of *Ustilago maydis* and incubated at 28°C for 21 days (Ahmadu *et al*., 2020; Ahmadu *et al*., 2017).

Microbial Culture

Isolation of *Aspergillus niger*: Isolation of *Aspergillus niger* from soil samples was performed by the soil dilution method (Johnson *et al*., 1959). Ten grams of soil sample was added to 90 ml distilled water in a shaker for one hour. Then, 10 mL aliquot from this suspension was transferred aseptically to 90 ml distilled water. This dilution process was repeated to get dilutions up to 10-5. From the dilution suspension, one millilitre of aliquot from the soil sample was spread on Petri dishes containing Potato Dextrose Agar (PDA). The identification of *Aspergillus niger* was made by the simple microscopic method of Ellis (Ellis, 2006). Pure isolates of *Aspergillus niger* were subcultured on slants and stored at 4°C.

Isolation of *Trichoderma harzianum*: Rice stems and leaves were cut into 5 mm pieces and added to 150 mL distilled water in a shaker for 30 minutes. Then, 10 mL aliquot from this suspension was transferred aseptically to 90 mL distilled water. This dilution process was repeated to get dilutions up to 10-5. From the dilution suspension, one millilitre of aliquot from the phyllosphere sample was spread on an RB-S-F selective medium (Davet and Rouxel, 2000) in Petri dishes. The dishes were incubated at 26±1°C in the dark for 4 days. Individual isolates were identified at the species level using morphological keys and fungal species descriptions (Bisset, 1991; Gams and Bisset, 1998; Zafari *et al*., 2004). Pure isolates of *Trichoderma harzianum* were subcultured on slants and stored at 4°C.

Fermentation Process

Preparation of inoculum: The *Aspergillus niger* and *Trichoderma harzianum* spore inoculum were separately prepared by adding 10 ml of sterile distilled water containing 0.2% Tween 80 to a fully sporulated slant culture. The spores were dislodged by vigorous shaking and the spore number was estimated by direct microscopic enumeration using a cell-counting hemocytometer. (Neubauer chamber; Merck, S.A., Madrid, Spain). The volume of spores suspension was adjusted to 2.75 x 107 spores/ml and the harvested *Aspergillus niger* and *Trichoderma harzianum* spores were used as inoculums in the fermentation of the pretreated *Indigofera arrecta* seeds.

Fermentation of Sample: Each flask containing 10g of pretreated *Indigofera arrecta* seeds was mixed with mineral salt solution (g/l; KH_2PO_4, 2.5; KNO_3, 5.0; $MgSO_4$. $7H_2O$, 1.0; Na_2SO_4, 1.0; $FeCl_2$, 0.02; $ZnSO_4$. $7H_2O$, 0.0015; CuSO4. $5H_2O$, 0.003 and $MnSO_4$, 0.001) in distilled water in the ratio 1:2 autoclaved and inoculated

with 2.75x 10^7 per ml spores suspension from each microbe separately and the volume halved in co-culture combination. The samples were then incubated and allowed to ferment for 7 days.

Enzyme Activity Assays

Tannase Activity: Tannase activity was estimated by colorimetric method (Mondal *et al.,* 2001). The reaction mixture contained 0.3 ml of substrate tannic acid (0.5% w/v in 0.2 M sodium acetate buffer, pH 5.5) and 0.1 ml of the enzyme. This reaction mixture was incubated at 30°C for one hour. The enzymatic reaction was terminated by the addition of 3 ml of BSA (Bovine Serum Albumin) solution (1mg/ml) which also precipitated the residual tannic acid. A control was prepared side by side using the heat-denatured enzyme. The tubes were then centrifuged (5, 000 x g, 10 min) and the precipitate was dissolved in 3 ml SDS-triethanolamine (1% w/v, SDS in 5% v/v, Triethanolamine) solution. One ml of $FeCl_3$ reagent (0.01 M $FeCl_3$ in 0.01N HCl) was added to the tube and was kept for 15 min at room temperature for stabilization of the color. Absorbance was read at 530 nm against the blank (i.e. without tannic acid). The specific extinction coefficient of tannic acid at 530 nm was found to be 0.577 (Mondal *et al.,* 2001). Using this coefficient, one unit of tannase activity is defined as the amount of enzyme required to hydrolyze 1Mm of the substrate (tannic acid) in 1 min under assay conditions.

Phytase Activity: The phytase activity was determined by the incubation of 1 ml of the culture sample at 37°C for 30 min in a 0.2M sodium acetate buffer (pH 5.5) containing 0.5% sodium phytate (dodecasodium salt of phytic acid [$C_6H_6O_{24}P_6Na_{12}$]; Sigma, St. Louis, Mo. USA). The reaction was terminated by the addition of 1 ml of trichloroacetic acid (15% [w/w]). After the addition of 2 ml of a coloring reagent (3.66 g of $FeSO_4 \cdot 7H_2O$, 0.5 g of $(NH_4)_6Mo_7O_{24} \cdot 4H_2O$, and 1.6 ml of concentrated H_2SO_4 in 50 ml of distilled water), the chilled sample in ice water was followed by incubation for 10 min at 30°C. The released phosphate was determined at 750 nm using a UV-VIS spectrophotometer (JASCO International Co. Ltd., Tokyo, Japan). A standard curve for sodium phosphate was made for each independent experiment. One unit was defined as 1m mole of phosphate produced per minute.

RESULTS AND DISCUSSION

The time course of tannase and phytase production was examined to identify the optimal incubation period for maximum tannase production. Table 1 and Table 2 presents the changes in tannase activities in both mono-culture and co-culture combinations of *Aspergillus niger* and *Trichoderma harzianum* on alkaline and biologically pretreated *Indigofera arrecta* seeds, monitored over a 7-day incubation period. Maximum tannase activity was observed in the simultaneous co-culture of *Aspergillus niger* and *Trichoderma harzianum* on the pretreated seeds after 3 days of incubation, with enzyme activities of 13.68 µmol/min and 11.55 µmol/min, respectively. Enzyme activity was first observed at 24 hours and steadily increased over time. The organism reached optimal production of phytase and tannase at different times. A decline in enzyme yield with prolonged incubation could be attributed to the reduced nutrient levels in the medium. By treating tannin-rich plants with tannase, the tannin content is reduced, making them suitable as a supplement in animal diets (de Sena *et al*., 2014). Studies by Mohan *et al*. (2014) identified an incubation period of 96 hours as optimal for maximizing tannase production from *Aspergillus foetidus* MTCC 3557. Studies by Peña-Lucio *et al*. (2023) demonstrated that during the final hours of fermentation (from 96 to 120 hours), tannase activity increased with a novel strain of *A. niger* TBG 28A in tea (*Camellia sinensis*) residues.

Maximum phytase production during co-culture fermentation (Tables 3 and 4 below) was observed at 72 hours (3 days) of incubation, with enzyme activities of 3.26 µmol/min for the alkaline pretreated sample and 5.97 µmol/min for the biologically pretreated sample. The maximum phytase yield for the monocultures of the alkaline pretreated sample and the biologically pretreated sample was observed on day 3 and day 4 respectively. Further increase in incubation time also resulted in a decline in enzyme yields. Isoenzymes produced by different fungi can influence the efficiency of phytic acid hydrolysis per unit of enzyme (Dhariwal and Tarafdar, 2023). The elevated phytase and tannase activity observed in the co-culture incubation of both pretreated samples could be attributed to the synergistic interaction between the two compatible strains of microorganisms, leading to an increased rate and quantity of enzyme production. The substantial reduction in enzyme activity in the alkaline pretreated sample, compared to the biologically pretreated sample, could be due to the incorporation of salts into the biomass during pretreatment. This may result in the formation of degradation products (Kucharska *et al*., 2018) and the release of natural biomass fermentation inhibitors.

CONCLUSION

The study underscores the significant impact of substrate pretreatment and fermentation methods on enzyme yields, demonstrating how these processes enhance enzyme production rates and quantities. The decline in enzyme activity beyond the optimal incubation times suggests nutrient depletion as a limiting factor for prolonged enzyme production. These findings underscore the potential of co-culture fermentation strategies in optimizing enzyme production for industrial applications. Utilizing pretreated *Indigofera arrecta* seeds as a substrate, this approach offers a promising avenue for improving the efficiency and cost-effectiveness of enzyme production processes. Further research could focus on refining co-culture conditions and exploring additional pretreatment methods to maximize enzyme yields.

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A Review of Current Biotechnological Solutions to Land Degradation, Desertification and Drought.

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INTRODUCTION

The major environmental challenges of the 21st century have been attributed to a combination of natural factors and human activities over time, hence the need for increased global awareness of the impact of these challenges and the deliberate actions required to safeguard the future of the ecosystem. The United Nations Environmental Programme (UNEP) since its establishment in 1972, has been at the forefront of creating awareness on environmental issues and promoting various intervention programmes in this regard. The theme for the 2024 World Environment Day draws attention to the enormous challenges faced due to land degradation, desertification and drought in many areas of the world. Land degradation describes the deterioration or loss of the productive capacity of land which decreases its potential to support life. Desertification describes the process of gradual land degradation of fertile land into arid or semi-arid areas due to a combination of natural processes and human activities while drought describes abnormal deficiencies in surface and subsurface water supplies over time (https://www.unccd.int/resources/publications/land-numbers-2019-risks-and-opportunities accessed 25th June 2024; https://www.unep.org/events/un-day/world-environment-day-2024 accessed 27th June 2024).

Various intervention programmes have targeted global land restoration including those initiated by the United Nations Convention to Combat Desertification (UNCCD), Global Environment Fund (GEF), United Nations Office for Outer Space Affairs (UNOOSA), the Global Land Degradation Information System (GLADIS), G20 Global Land Initiative, Great Green Wall/Action against Desertification (GGW/AAD), Ecological Fund Office (EFO) and Geneva Environment Network. Understanding the driving factors surrounding land degradation, desertification and drought is key for strategic restoration, hence, most of these programmes highlight the need for a scientific approach to solving environmental challenges. This study therefore focuses on the potential application of biotechnological tools to address land degradation, desertification and drought.

BIOTECHNOLOGICAL APPROACHES TO LAND RESTORATION

Current advances in biotechnology can be applied for environmental restoration and conservation of bioresources, particularly the application of genetically modified trees to enhance resilience to desertification and carbon sequestration as well as microbial biotechnology for soil restoration. Generally, genetic improvement of trees has specifically targeted modification of lignin content, enhancement of performance and growth rate, herbicide and pathogen resistance as well as stress tolerance. Some of the notable modified trees include American chestnut, English elm, Chinese polar trees and Eucalyptus. Most of the genomic approaches used to induce drought and stress tolerance in trees have focused on genes for signal perception and transduction rather than the overexpression of structural genes. Some of the reports available on modified genes include SmCP (Cysteine protease), HbDHN1 and HbDHN2 (Dehyrdin), APX (Ascorbate Peroxidase), (codA) Choline oxidase, MaSTS 1-4 (Stilbene synthase), Glactinol synthase (GolS2) (Polle *et al.,* 2019). Modification of the Eucalyptus tree to withstand extreme temperature was reportedly developed by Arborgen, Inc. although deregulated in the USA as of 2010. The tree was reported to contain a cold-inducible promoter driving a C-repeat binding protein from *Arabidopis thaliana*. Genetic transformation of trees is however a bit more complicated compared to microbial gene modification. Figure 1 describes the process of tree transformation.

With the development of international carbon markets, the United Nations and different national bodies have developed various incentives which encourage the planting of trees with high carbon sequestration potential. To this effect, biotechnology has been applied to improve the carbon sequestration potential of some trees to mitigate the looming climate crisis in some countries. For instance, Living Carbon, a US-based company developed a genetically modified poplar tree which was a hybrid product of common aspen (*Populus tremula*) and white poplar (*P. alba*) to enhance its carbon absorption ability. Synthetic biology can therefore be a useful tool to improve climate adaptation and recovery through enhanced carbon removal through targeted modification of tree genomes. There have always been regulatory restrictions on the commercialization of genetically modified trees in several countries however with better understanding and wider acceptance, some GM tree products might be available for deployment in the near future.

Another approach involves the application of genetically engineered microorganisms for land restoration activities through the enhancement of soil structure, nutrient availability, plant growth and resistance to stress. Maestre *et al.* (2017) reported the application of biocrust-forming microorganisms such as mosses, lichens, and cyanobacteria to enhance resilience to land

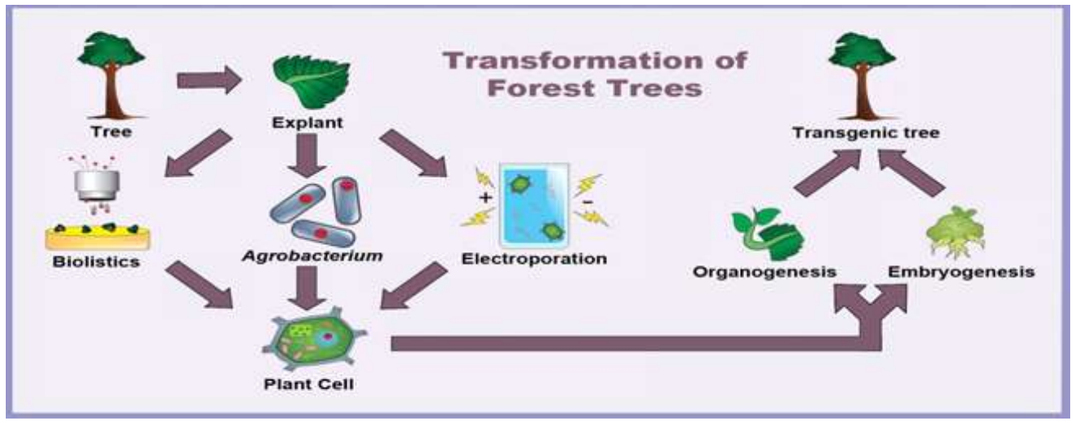

Figure 1: Schematic description of tree transformation (Castellanos-Hernández 2011)

degradation. The biocrust system has been demonstrated to influence a number of activities that affect soil integrity and has been applied for the restoration of dry lands in the USA, Israel and China. *Bacillus subtilis* has been genetically modified to enhance organic acid production and increased phosphate availability which leads to improved plant growth and soil structure, thereby aiding the recovery of degraded soils. Similarly, there are reports of genetic modification of *Trichoderma spp.* for expression of chitinase and glucanase enzymes, which break down the cell walls of soil-borne pathogens hence promoting land restoration through healthier better soil structure. Genetic modification of *Halomonas elongata*, a salt-tolerant bacterium has been reported to enhance the production of an osmo-protectant ectoine which increases salt tolerance in plants ensures the reclaiming of salt-affected lands and prevents further desertification. The introduction of biochar for land restoration has currently gained attention. Through its action, biochar enhances soil structure and water retention which can be used to achieve strategic land revitalization (Ghosh and Maiti, 2021)

Several reports highlight the application of genetically modified microorganisms for the utilization of toxic compounds, hence achieving some form of land restoration through bioremediation. CRISPR-Cas9 technology has been used to engineer microbes with enhanced abilities for bioremediation and nutrient cycling (Sheth *et al.,* 2016). *Pseudomonas putida* has also been engineered to express additional alkane hydroxylase genes, enhancing its ability to degrade a wider range of hydrocarbons in the recovery of oil-contaminated soils. Overall microbial biotechnology, can be deployed for small- and large-scale land restoration

CONCLUSION AND RECOMMENDATION

As the world explores different solutions to environmental challenges, biotechnology can be incorporated into various land restoration programmes. To this effect, a schematic plan for the application of biotechnology for land restoration in Nigeria is hereby proposed which includes land degradation mapping of Nigeria, determination of the nature of degradation or underlying factors, identification of plants or micro-organisms of interest, Bioengineering design, regulatory compliance and then field trials. Further consultations with all stakeholders including policymakers are suggested to ensure all regulatory frameworks are in place for Nigeria to achieve its land restoration target of 4 million hectares within its borders by 2030.

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Development of Bioanalytical Test Kits for Rapid Monitoring of Lead and Arsenic Contamination in Water (A Review)

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INTRODUCTION

Bioanalytical kits or biosensors can be described as devices that utilize the activity of a biological receptor element to generate signals that can be translated into quantitative information about an analyte in a specific medium (Thevenot *et al.,* 2001). With respect to heavy metals, they can be designed to determine their presence and concentration current in different media; currently, lead and arsenic are reported to be among the most prevalent and toxic heavy metals available (Balali-Mood *et al.,* 2021). Most of the techniques for determining heavy metals utilize complex instrumentation, which usually involves sample pretreatment as well as well-trained operators. (Odobašić *et al.,* 2019). With full details of contamination levels in a given environment, the use of biosensors presents a simple, cost and time-effective approach for onsite monitoring of lead and arsenic in water.

GENERAL STRUCTURE AND OPERATION PRINCIPLE OF BIOSENSORS

A biosensor construct is composed of three distinct sections; a recognition bioreceptor element, a signal transducing system (electrical, optical, or thermal) and an amplification/processing system. (Velusamy *et al.,* 2022). Biosensors have been classified based on their detection approaches mainly the type of transduction system or type of biorecognition element (the bioreceptor or other biocomponents). Based on the transduction system, biosensors could be electrochemical, optical or thermometric while based on the bioreceptor, biosensors could be immunosensor-based, enzyme-based or whole cell-based, although the use of other biomolecules has been reported (Mohanty and Kougianos 2006). A biosensor construct is described in Figure 1.

CURRENT TRENDS IN THE DETECTION OF LEAD AND

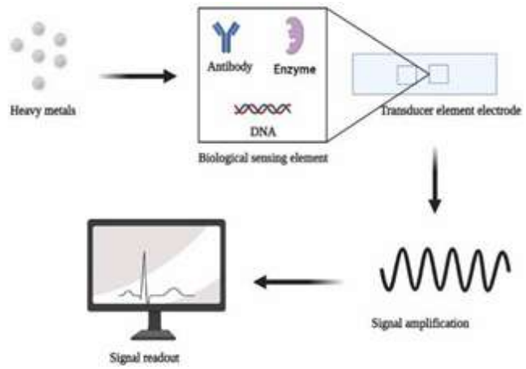

Figure 1. Schematic illustration of the principle of biosensors (Velusamy, *et al.,* 2022).

ARSENIC USING BIOSENSORS.

The immobilization of enzymes on different platforms particularly nanoparticles has been reported for the detection of lead in contaminated water. This includes the immobilization of DNAzyme on magnetic beads or magnetite-based nanoparticles (Xu *et al.,* 2020), and gold-based nanoparticles (Wu *et al.,* 2020). Immobilization of other enzymes such as urease, alkaline phosphatase and acetylcholine esterase have also been reported as well as non-enzymes such as a tripeptide glutathione linked to gold nanoparticles (GNPs). Generally, the use of gold-based nanoparticles as an enzyme immobilization platform has been highlighted in several reports, suggesting its suitability in the development of signal pathways for lead detection.

For arsenic detection, enzymes particularly acetylcholinesterase and DNAzyme, have been reported however, some studies also report the use of whole-cell bacteria (WCB) as bioreceptors for arsenic detection. A good number of reports indicate the use of *E. coli*-based reporter proteins in the biosensor construct and there are suggestions that reporter proteins obtained from genetically modified strains of *B. subtilis, S.aureus,* and *pseudomonas p.,* could also be viable for arsenic detection (Diesel *et al.,* 2009). Other bacteria-based biosensor constructs have been reported including *Salmonella typhimurium* flagellin while a simple chromogenic endospore-based biosensor was designed utilizing the change in pH for the detection of arsenic in drinking water. Overall, there are more reports of the use of WCB-based biosensors for arsenic detection.

Designing a kit that can detect both lead and arsenic in a single device can be recommended for onsite heavy metal monitoring. Eom *et al.* (2020) reported the use of a spore-forming fermentative bacterium, *Clostridium guangxiense* for the screening of water contaminated with lead and arsenic alongside other heavy metals. The reports therefore suggest the suitability of enzyme-based biosensors for lead detection and bacteria-based receptors or arsenic detection as seen in Table 1; however, the choice of the appropriate signal pathway for the sensor design will depend on available information on the state and levels of heavy metal contamination within a chosen environment

CHALLENGES AND LIMITATIONS OF LEAD AND

Table 1: Some Biosensor Kits for lead and arsenic detection

Heavy metal	Bio-receptor design	Detection Limit
Lead	DNAzyme-based/Magnetic beads sensor.	37 pM.
	DNAzyme/gold based	2pM, 38 fg mL^{-1}, 80 pM
	Glutathione/gold nanoparticles (GNPs)	47.6 nM
	Urease/CeO2 nanoparticles.	0.019 ± 0.001 μM
	DNA/ Fe3O4	5−10 ppm
	fluorescence resonance energy transfer (FRET) / biochip (Met-lead 1.44 M1)	24 nM.
Arsenic	DNAzyme	2 ppM
	WCB/ genetically modified strains of *E.coli*, *B.subtilis*, *S.aureus*, and *pseudomonas p.*	Not stated
	WCB/ Salmonella typhimurium flagellin	Not stated
	WCB/ *Escherichia coli* DH5α	5 -100 ppb
	Detectable drop in pH and a chromogenic system using endospores	less than 10 ppb arsenate
	Acetylcholinesterase enzyme activity.	1.1 × 10−8 M
Lead and arsenic	*Clostridium guangxiense*; inhibition of fermentative gas	101.33 mg/L for As and 243.45 mg/L for Pb

ARSENIC DETECTION IN WATER USING BIOANALYTIC TEST KITS

The limitations of the detection of lead and arsenic using rapid test kits have been highlighted in several reports. Inaccurate results in the form of overestimation of lead concentrations have been attributed to the varying levels of sensitivity for dissolved and particulate lead in water during on-site monitoring (Kriss *et al.* (2021). Similarly, the presence of arsenic as either the arsenite (Ars^{III}) or arsenate (Ars^{V}), could influence the sensitivity of detection with arsenite reported to be more toxic than arsenate.

CONCLUSION

To this effect, it can be suggested that the design of a biosensor kit for onsite monitoring should begin with a detailed mapping of lead and arsenic contamination. This would suggest suitable designs for a cost-effective biosensor kit, before the pilot design, field trials and subsequent deployment.

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Precision Weed Management in *Sorghum bicolor* [L.] Moench Cultivation using AI and Allelopathic Biocontrol

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INTRODUCTION

The objective of the study is to create a Support Vector Machine (SVM) model, analyze the efficacy of *Aloe vera* extract (AVE) and determine the economic viability of using *Aloe vera* extract as a weed control strategy for *Sorghum bicolor* [L.] Moench production. By focusing on these aspects, this research aimed to contribute a more sustainable and economically viable solution for weed management in sorghum cultivation.

MATERIALS AND METHODS

The field experiments were conducted at the Research and Training Farm, Faculty of Agriculture, Bayero University, Kano and the Research and Training Farm, Faculty of Agriculture, Kano State University of Science and Technology (KSUT), Gaya during the 2023 rainy season. The twelve weed management strategies were replicated three times in a randomized complete block design and applied to sorghum.

RESULTS

The findings discovered that all treatments except the weedy check significantly reduced weed biomass and density ($p < 0.0001$) compared to the weedy check at both locations. Sequential application of Pendimethalin at 3.0 kg active ingredient (a.i) ha^{-1} applied as pre-emergence (PE) followed by (*fb*) Halosulfuron at 0.25 kg a.i ha^{-1} applied as post-emergence (POE) generally achieved the best weed control, followed by hoe weeding at 3 and 6 weeks after sowing (WAS) and some *AVE* combinations at the two locations. Pendimethalin + Halosulfuron produced the highest sorghum yields (2892.48 kg ha^{-1} at BUK and 3147.25 kg ha^{-1} at Gaya), followed by hoe weeding (2805.00 kg ha^{-1} at BUK and 2913.92 kg ha^{-1} at Gaya) for both locations. All *AVE* treatments showed yields higher than the weedy check. At both locations, the weedy check had the lowest Benefit Cost Ratio (BCR) (0.26 at BUK and 0.39 at Gaya), indicating lower profitability relative to the Total Variable Cost (TVC), *AVE* 50% (w/v) integrated with hand weeding at 6 WAS had the highest BCR (1.02 at BUK and 2.18 at Gaya), indicating relatively higher profitability compared to the TVC. In general, satisfactory values of the analyzed metrics, which indicate good classifier performance for the differentiation of the study class were achieved using the algorithm. However, it should be emphasized that the values obtained from the precision was 50%.

RESEARCH HIGHLIGHTS

This study suggests the potential of AVE as a sustainable weed control strategy for sorghum production, particularly when integrated with hoe weeding and halosulfuron. The use of machine learning algorithms particularly the SVM for weed detection in agriculture offers a promising approach for optimizing weed management practices.

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Sustainable Aquaculture Innovations in Nigeria: Leveraging Maggots *(Hermetia illucens*) for Advanced Fish Feed Solutions

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INTRODUCTION:

The need for sustainable aquaculture is becoming increasingly urgent due to rising global food demand and environmental concerns. Insect-based feeds have emerged as a promising innovative solution, with black soldier fly (*Hermetia illucens*) larvae, or maggots, standing out due to their high nutritional value and ability to convert organic waste into protein-rich biomass.

It has been determined that using insects to produce aqua feeds is an environmentally friendly, renewable, and sustainable alternative source of protein with an attractive amount, quality, and suitable nutritional content (Adeoye, 2020). This study examines the potential of maggot-based fish feeds to tackle the challenges of high feed costs and environmental sustainability in aquaculture, particularly in Nigeria.

BACKGROUND OF STUDY:

Traditional fish feeds, heavily reliant on fishmeal and soybean, contribute to overfishing and environmental degradation. *Hermetia illucens* larvae are notable for their high protein, lipid, and mineral content, closely matching the nutritional profile of fish meal. These larvae thrive on organic waste, such as agricultural by-products and household food scraps, making them an environmentally friendly option. Their ability to compost waste materials and flexibility in cultivation size further enhance their suitability as a sustainable feed source (Oonincx *et al*., 2012). This makes them a nutritional, economical and environmentally viable option for fish feed formulation.

DISCUSSION:

The economic and environmental benefits of maggot-based fish feeds are multifaceted. Economically, they reduce production costs by utilizing low-cost organic waste as feedstock, thereby lowering the overall cost of fish production. Environmentally, they alleviate pressure on overfished marine resources and improve waste management practices by recycling organic waste into valuable protein biomass. Shelomi (2020) reported that black soldier fly farms and composting facilities were being established worldwide to convert waste into animal feed while providing economic and environmental benefits.

In recent years, the cultivation of Maggot Black Soldier Fly (BSF) has become an alternative for processing organic waste because it has no adverse side effects on the environment. BSF larvae can be an alternative to conventional feed. Feed formulations have been widely used, but the price is relatively high. BSF larvae can be fed with various foods such as kitchen waste, fruits, vegetables, liver, fish waste, urban waste, human waste, and animal waste. Maggot BSF can decompose organic waste containing 60% to 90% water content. In addition, maggot black soldier fly food is high in protein and carbohydrates, suitable for larvae for nutritional needs (Sealey *et al*., 2021). The practical use of maggots in fish diets has demonstrated positive impacts on fish growth rates and overall health. Studies indicate that fish fed with maggot-based diets show comparable, if not superior, growth performance to those fed with conventional feeds. Additionally, the larvae's rich nutrient profile supports robust fish health, reducing the need for supplementary feeds (Barrangan *et al*., 2017).

The effects of replacing fish feed with black soldier fly larvae on the development of catfish fingerlings were investigated in a 60-day experiment by Fawole *et al*. (2020). According to the research, fish fed a 50% HP (*Hermetia illucens*) diet had the largest final body weight. The results of the study showed that black soldier fly larvae could replace fishmeal by up to 50% without having an impact on the growth of the fingerlings. Similarly, Hammed *et al* (2023) concluded that fishmeal could completely be replaced with black soldier fly in the diet of the African catfish, although they recommended a 40% replacement. Research shows that nutrition is very important in fish farming because 50-60% of the production cost is spent on feed. Black soldier flies have a protein and amino acid composition comparable to fish meal. The high fat and protein content of black soldier fly larvae encourages their use in feed and food processing and production. Despite these advantages, challenges remain. Scalability of maggot production, consumer acceptance, and regulatory frameworks are key areas that need to be addressed to fully integrate maggot-based feeds into mainstream aquaculture. Furthermore, optimizing cultivation techniques and ensuring consistent feed quality are critical for widespread adoption.

CONCLUSION:

Hermetia illucens larvae represent a viable and innovative solution for sustainable aquaculture. Their use not only reduces feed costs and enhances fish growth rates but also offers significant environmental benefits by mitigating waste and conserving marine resources. As the aquaculture industry in Nigeria seeks sustainable growth, maggot-based feeds provide a promising path forward. Future research and development efforts should focus on overcoming current challenges to fully realize the potential of this eco-friendly feed alternative.

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Exploring the Ethnopharmacological Potential of *Guiera senegalensis*: A Multidisciplinary Investigation into its Antibacterial Efficacy and Molecular Basis of Action

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INTRODUCTION
Background: Ethnomedicinal tapestry in traditional African medicine is interwoven with indigenous knowledge, botanical wealth, and spiritual connections. The study is aimed at exploring the ethnopharmacological potential of *Guiera senegalensis* and its reported antibacterial effect against clinical pathogens like *Staphylococcus aureus* and *Escherichia coli*.

Methods: The study was carried out beginning with an investigation of the phytochemical composition of *Guiera senegalensis* through LC/MS-MS. Subsequently, the predicted bioactive compounds from LC/MS were subjected to molecular docking studies using Maestro-schrodinger to assess their interactions with dihydrofolate reductase (DHFR), a key enzyme in folic acid metabolism. This was followed by experimental validation through microbiological assays, including determination of the zone of inhibition, minimum inhibitory concentration (MIC), and minimum bactericidal concentration (MBC) assays.

Results: Results: *Guiera senegalensis* exhibited efficacy against both *S. aureus* and *E. coli*, as evidenced by the substantial zones of inhibition. *Staphylococcus aureus* and *Streptococcus pneumoniae* were highly sensitive, showing a significant response at all tested concentrations. On the other hand, *Escherichia coli* and *Salmonella typhi* only responded at 1000 µg/ml and higher, proving to be ineffective at 500 µg/ml. Similarly, *Pseudomonas aeruginosa* and *Aspergillus flavus* required 2000 µg/ml and above to show any effect, with no effectiveness observed at 1000 µg/ml and below. Mucor species, unfortunately, did not show any response at any concentration. Lastly, *Candida albicans* exhibited a response at 1000 µg/ml and higher but proved to be ineffective at 500 µg/ml. Molecular docking studies revealed binding interactions between the bioactive compounds from LC/MS-MS, particularly kaempferol, and crucial bacterial enzymes. Furthermore, *in silico* predictions suggested favourable pharmacokinetic and pharmacodynamic properties, reinforcing the potential therapeutic efficacy of these compounds.

Conclusion: This study supports the antimicrobial effect of *G. senegalensis*, which substantiates the ethnomedicinal claims associated with *the plant* but also shows its potential as a plant containing bioactive compounds with significant antibacterial properties. The identification of kaempferol as a key antimicrobial agent in *G. senegalensis provides the* molecular foundation for future drug development. *Therefore, it* is a promising candidate for further pharmaceutical exploration, bridging the realm of cultural heritage and contemporary biomedical research.

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Advancements in Management Strategies for Tropical Fruits and Vegetables Based on Post-Harvest Physiology and Biochemistry: A Case Study of Oranges and Pumpkin Leaves

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INTRODUCTION
Tropical fruits and vegetables are an essential part of a healthy diet, providing vital nutrients, vitamins, and minerals. They are also a significant source of income for many small-scale farmers and rural communities in tropical regions. However, the production and distribution of these crops face numerous challenges, including post-harvest losses, disease and pest management, and marketing and logistics issues. In recent years, there have been significant advancements in management strategies for tropical fruits and vegetables, aimed at improving productivity, reducing losses and enhancing sustainability. These advancements include the adoption of innovative technologies, sustainable practices and market-driven approaches. The post-harvest handling of tropical fruits and vegetables is a critical stage in ensuring their quality and long shelf life. Understanding the post-harvest physiology and biochemistry of these crops is essential for implementing effective management strategies. This review is to explore recent advancements in management applications based on the post-harvest physiology and biochemistry of tropical fruits, with a specific focus on oranges and pumpkin leaves. This paper reviews the recent developments in management strategies for tropical fruits and vegetables. It also explored the current trends, challenges, and opportunities in the production, processing, and marketing of these crops, and discussed the implications for future research and development, which is a target of the Sustainable Development Goal (SDG) 12.3 (United Nations 2015) as well as discussed current knowledge of physiological, biochemical, and metabolic mechanisms that can contribute to the realization of these goals.

Post-harvest physiology and Biochemistry: Post-harvest physiology and biochemistry are important aspects of understanding the changes that occur in fruits and vegetables after they are harvested. These changes can impact the quality, nutritional content, and shelf-life of the produce, which are:

- ***Respiration and gas exchange***: Respiration is a crucial physiological process in post-harvest fruits and vegetables, involving the exchange of gases such as oxygen and carbon dioxide. Respiration rates impact the metabolic processes, heat production, and ripening of produce. It is important to manage and control respiration rates to prevent excessive fruit softening, loss of nutritional quality, and accumulation of undesirable by-products (Saltveit, 2019).
- ***Ethylene production and action*:** Ethylene is a gaseous plant hormone that plays a significant role in the ripening of many fruits. After harvest, some fruits continue to produce ethylene, which can influence other physiological processes and lead to ripening and senescence. Understanding the ethylene production and action in harvested fruits and vegetables helps in determining the optimal storage conditions, post-harvest treatments, and management practices to control quality and shelf-life (Lelièvre *et al*., 2017).
- ***Enzymatic and non-enzymatic reactions*:** Post-harvest fruits and vegetables undergo various enzymatic and non-enzymatic reactions that can impact their quality and nutritional composition. Enzymes such as pectinase, cellulase, and protease can cause textural changes, softening, and loss of firmness. Non-enzymatic browning reactions, such as Maillard and enzymatic browning, can result in undesirable color changes. Understanding these reactions helps in developing strategies to minimize quality losses and preserve nutritional integrity (Brecht, 2020; Zhang *et al*., 2019).
- ***Changes in phytochemicals and antioxidants*:** Phytochemicals and antioxidants present in fruits and vegetables contribute to their health-promoting properties. Post-harvest handling and storage conditions can affect the levels of these compounds. Factors such as temperature, light exposure, and oxygen levels can influence the degradation or synthesis of phytochemicals, impacting the antioxidant capacity and nutritional value of the produce (García-Pastor *et al*., 2020; Wu *et al*., 2014).

Importance of Post-harvest Handling in Tropical Fruits and Vegetables. Post-harvest handling plays a crucial role in maintaining the quality, shelf-life, and market value of tropical fruits and vegetables. Proper handling practices can minimize losses due to spoilage, improve nutritional quality, and ensure food safety. Here are some key reasons why post-harvest handling is important in tropical fruits and vegetables: Minimizing spoilage and extending shelf life Wills *et al*., (2017) and Rahman *et al*., (2018), preserving nutritional quality Ebrahimzadeh *et al*., (2021), ensuring food safety FAO, (2017) and enhancing market value and economic returns (Zhou *et al*., 2017). Adhering to proper handling techniques is essential for sustaining the quality and marketability of these valuable agricultural commodities.

Factors Influencing Post-harvest Quality and Shelf Life
Post-harvest quality and shelf-life of oranges and pumpkin leaves are critical factors in determining the value and marketability of fresh produce. Several factors influence the post-harvest quality and shelf life of agricultural produce, including oranges and pumpkin leaves;

- **Temperature management:** Controlling temperature is crucial as it affects the rate of biochemical reactions in fruits and vegetables. Maintaining optimal temperature conditions can help slow down physiological processes, reduce respiration, and delay ripening and senescence.
- **Humidity control**: Appropriate humidity levels during storage can help prevent excessive water loss or moisture buildup, which can lead to spoilage or the growth of molds and bacteria.
- **Ethylene sensitivity**: Ethylene is a natural plant hormone that accelerates fruit ripening and senescence. Some fruits and vegetables, like oranges, are sensitive to ethylene and can deteriorate quickly when exposed to it. It is essential to store ethylene-sensitive produce away from ethylene-producing fruits or in ethylene-controlled environments.
- **Packaging:** Proper packaging can protect produce from physical damage, minimize moisture loss, and prevent contamination by microorganisms. Packaging materials with specific gas permeability can also modify the fruit's internal atmosphere, slowing down ripening and extending shelf life.
- **Handling and storage conditions:** Rough handling during harvesting, packing, and transportation can cause bruising, cuts, or other physical injuries, accelerating decay. Proper handling practices, gentle transportation, and suitable storage conditions like adequate ventilation, cleanliness, and protection against pests can help maintain quality.
- **Post-harvest treatments:** Various post-harvest treatments, including washing, disinfection, and the application of coatings or post-harvest fungicides, can help control microbial growth, reduce decay, and extend shelf life.
- **Maturity stage at harvest**: Harvesting fruits and vegetables at the appropriate maturity stage is crucial. Under-ripe or over-ripe produce may have a shorter shelf-life or inferior quality. Harvesting at the right stage of maturity ensures maximum flavor, nutritional content, and longer post-harvest life.
- **Pre-harvest factors:** Pre-harvest factors like agricultural practices, crop management, pest and disease control, and nutrient management can impact post-harvest quality. Good agricultural practices can contribute to healthier, less damaged produce with better post-harvest characteristics.

Recent Evolutions in Management Applications:
***Precision agriculture*:** The use of advanced technologies, such as global positioning systems (GPS), remote sensing, and data analytics, has transformed the way farmers manage their operations. These technologies enable farmers to monitor various aspects of their crops, including soil conditions, water availability, and pest infestations, leading to more optimized and efficient management practices. (Kaur, B., Sidhu, G.S., and Singh, V. 2021). Blockchain technology is being explored to improve traceability in the post-harvest supply chain. This can enhance transparency, reduce fraud, and provide consumers with detailed information about the origin and journey of agricultural produce. Mobile applications are being developed to empower farmers with tools for managing post-harvest activities. These apps may provide information on optimal harvest times, storage guidelines, and market prices.

***Internet of Things (IoT) in Agriculture*:** IoT solutions are being employed to enhance management practices in agriculture.

Through connectivity and data exchange among devices and systems, IoT helps in real-time monitoring and decision-making. For example, IoT-enabled sensors can measure soil moisture levels, temperature, and humidity, providing insights to optimize irrigation schedules. (Arslan, S., and Ghorbel, A. 2021). IoT sensors are increasingly used to monitor and manage conditions during post-harvest handling, transportation, and storage. These sensors can track factors such as temperature, humidity, and storage conditions, helping to prevent spoilage and maintain quality. Integration with e-commerce platforms enables seamless transitions from post-harvest processes to online marketplaces, enhancing accessibility for both producers and consumers.

***Farm management software*:** There have been advancements in farm management software that integrate various functions like crop planning, inventory management, finance, and analytics. These applications provide farmers with comprehensive tools to streamline their operations and make data-driven decisions (Ursin, T.B., Bakkegard, R.I., Bleken, M.A., and Forbord, M.S. 2021). Integrated cold chain management systems utilize technology to monitor and control the temperature of storage and transportation facilities. This is crucial for preserving the quality of perishable produce during transit. Advanced data analytics and predictive modelling are applied to post-harvest management, enabling better decision-making. Machine learning algorithms analyze historical data to predict optimal storage conditions, shelf-life, and potential quality issues. Automation and robotics are finding applications in post-harvest processes, such as sorting, packing, and quality control. This reduces labour-intensive tasks and improves efficiency.

***Sustainability tracking and reporting*:** Management applications are incorporating features to track and report on sustainability metrics related to post-harvest practices. This aligns with the growing emphasis on sustainable and responsible agricultural practices. Digital quality management systems help in standardizing and ensuring the quality of agricultural produce during the post-harvest phase. This includes features for inspection, grading, and certification. Platforms offering end-to-end visibility in the supply chain are emerging. These platforms enable stakeholders to track the movement of produce, anticipate delays, and optimize logistics for efficient post-harvest management.

***Collaborative platforms for stakeholders*:** Platforms that facilitate collaboration among various stakeholders in the post-harvest supply chain are gaining prominence. These platforms may include farmers, processors, distributors, and retailers, fostering better communication and coordination. Remote monitoring systems allow stakeholders to remotely oversee post-harvest facilities. This is particularly beneficial for large-scale operations, enabling timely interventions in case of issues.

***Advanced technologies and innovations*:** Advanced technologies and innovations include; Non-destructive techniques for assessing quality and ripeness, modified atmosphere packaging, controlled atmosphere storage, and Integration of nanotechnology and biotechnology in post-harvest management.

CONCLUSION:
This review discusses recent advancements in the management of tropical fruits and vegetables, focusing on the post-harvest physiology and biochemistry of oranges and pumpkin leaves. We have also discussed current innovative strategies, technologies, and practices that can enhance post-harvest quality, extend shelf-life, and reduce post-harvest losses. Ultimately, the paper aims to contribute to sustainable tropical agriculture practices by maximizing the economic value of these essential crops.

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Huanglongbing: A Threat to Citrus Production in Nigeria

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INTRODUCTION
Citrus represents one of the most significant tree crops grown for nutritional and industrial benefits. Nigeria is Africa's largest citrus producer and the ninth in the world (IITA, 2001). However, Huanglongbing (HLB), often known as citrus greening disease, threatens this thriving sector. The pathogenic uncultivated phloem-inhabiting bacteria, *Candidatus* Liberibacter spp., is responsible for HLB (Bove, 2006). The fastidious gram-negative bacteria belong to the Rhizobeaceae family with three species affecting citrus crops- *C. Liberibacter africanus* (CLaf), *C. Liberibacter asiaticus* (CLas) and *C. Liberibacter americanus* (CLam). HLB is transmitted by the African citrus psyllid (*Trioza erytreae*) and the Asian citrus psyllid (*Diaphorina citri*). The disease gives rise to symptoms such as yellow mottling of leaves, asymmetrical fruit development, lateral root damage causing the death of citrus trees, and undesirable flavours in citrus products, rendering them unmarketable. HLB was first detected in sweet oranges (*Citrus sinensis*) from four citrus sites in Benue state, Nigeria, in a survey of twenty sites in Benue and Nasarawa states (Ajene *et al*., 2020). To date, it is the only case of HLB reported in Nigeria. *Diaphorina citri* of Asian origin, a vector of *Candidatus Liberibacter asiaticus* (CLas), has been identified in citrus trees in Oyo State, Nigeria (Oke *et al*., 2020). The deficiency of research data to ascertain the spread of the disease and its socioeconomic effects indicates a lack of adequate preparedness and management strategy to mitigate the disease in Nigeria. The emergence and spread of HLB raises concerns because citrus crops are vital for the Nigerian economy and nutrition. Hence, we highlight the relevance of applying genomics and genetics as a cutting-edge strategy to manage and mitigate the impact of HLB on Nigeria and global citrus production.

IMPACT OF HLB ON GLOBAL CITRUS PRODUCTION
Major citrus-growing regions have experienced a significant reduction in citrus production, with over forty countries infected by HLB in Africa, and Asia, including the US. Over a hundred million HLB-infected citrus trees have been destroyed across Asia. HLB has resulted in over seventy per cent reduction in Florida's citrus production (NASS, 2019). The extent of HLB damage to citrus production in Nigeria is unknown due to insufficient survey data.

HLB MANAGEMENT STRATEGIES AND CHALLENGES
Currently, there is no established cure for HLB. Understanding of *C. Liberibacter* species has been hindered by its uncultivability which prevents their full characterization. However, significant progress has been made to culture CLas *in vitro* and successfully reintroduced back to psyllids and citrus plants (Zheng *et al*., 2024). There are environmental concerns about the use of antibiotics for HLB treatment. A truck injection system for direct delivery of therapeutic compounds to citrus trees to prevent direct environmental and human exposure is being studied (Ojo *et al*., 2024). Removal and replacement of HLB-infected trees with healthy nursery stock and pesticide control of psyllid vectors are traditional approaches for HLB management. Molecular diagnostic techniques have been developed, such as 16S rRNA polymerase chain reaction (PCR), quantitative PCR (qPCR), and Loop-mediated isothermal amplification (LAMP) methods for HLB detection. Studies have reported using nanotherapeutics, plant immunity inducers, and foliar micronutrient applications to combat HLB.

RELEVANCE OF GENETICS AND GENOMICS APPLICATION IN HLB MANAGEMENT
Genomics possesses potent tools such as genome sequencing for elucidating the complexities of HLB. Sequencing data provides an insight into the pathogenic and metabolic pathways of *C.* Liberibacter spp., critical for developing local anti-HLB compounds and innovative diagnostic tools in Nigeria. There are no HLB-resistant citrus varieties. Gene editing technologies, such as CRISPR/Cas9 systems, could provide precision in gene modification to develop HLB-resistant citrus varieties (Alquézar *et al*., 2021). The genomics-genetics nexus has paved the way for the discovery of efficient diagnostic techniques, and it is crucial for developing a comprehensive genomic database of local citrus varieties and HLB strains to expedite breeding efforts in Nigeria.

GOVERNMENT INTERVENTION IN HLB MANAGEMENT
The government can create an enabling environment through effective policies to foster local and international collaborations between Nigerian research institutions and relevant private sectors. The regulatory framework would enable HLB surveillance systems, training, and capacity-building programs for farmers, essential for HLB management in Nigeria.

CONCLUSION
HLB poses a significant threat to global citrus production, necessitating innovative management strategies. In addition to adequate government support, applying genomics and genetics tools would provide a concrete understanding of the biology of HLB to develop effective long-term management strategies, ensuring economic viability and food security in Nigeria.

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Expression of Mutant Inactive Form of Cysteine Protease (Berghepain-1) from Blood Stream *Plasmodium Berghei* using Prokaryotic System

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INTRODUCTION
Malaria remains a deadly disease, particularly in sub-Saharan Africa (WHO, 2023). In 2022, the World Health Organisation reported about 250 million cases of the disease in 85 malaria-endemic countries, over 1 million of the cases were reported from Nigeria. Antimalarial drug resistance is a major deterrent to the

elimination of malaria globally–, therefore new chemotherapeutic and vaccine candidates are being sought (Ippolito *et al*., 2021). Potential targets for new malaria therapy include falcipain cysteine proteases. Cysteine proteases of the papain family have been characterised in *Plasmodium falciparum* (falcipains), *Plasmodium berghei* (berghepains) and *Plasmodium vivax* (vinckepains). Falcipain-1 is involved in the invasion of red blood cells by merozoites while falcipain-2 and falcipain-3 are implicated in haemoglobin hydrolysis to supply the parasite's amino acid needs particularly in the trophozoite stage. Several cysteine protease inhibitors such as Cystatin and Chagasin are documented to exhibit *in vitro* and *in vivo* antimalarial activity. Studies on falcipain 2 showed that the substitution of any of the active site residues (Glutamine Q36, Cysteine C42, Histidine H174 and Asparagine N204) resulted in a complete loss of activity of the enzyme (Na *et al*., 2024). The mutation would make for safer vaccine candidates. The mounting evidence that cysteine proteases play a major role in the survival of the malaria parasite indicates that methods of inhibiting the enzymes will cure malaria. We report the cloning, expression and purification of recombinant berghepain-1 (BP1) protein.

METHOD

Construction of *Plasmodium berghei* cysteine protease BP1 mutants

In vitro PCR site-directed mutagenesis was carried out on pVAX plasmid vectors containing C-terminal strep-tagged wild-type BP1 gene as the template (pVAX-*BP1*Strep). Following temperature cycling, a *DpnI* reaction mixture was set up to digest the parental DNA template and select for synthesised DNA containing the mutation (pVAX-*BP1*mutStrep). The inactive mutant form of the BP1 contained an alanine residue instead of the active-site cysteine residue (pBP1c300a). The plasmid constructs were transformed into chemically competent XL1-Blue *E. coli.* Positive clones were identified via colony PCR amplification and sequenced commercially in both directions at the Max Plank Institute (Bremen, Germany).

Cloning and Expression of BP1 Recombinant Protein

Plasmids for the expression of catalytically inactive BP1 were constructed by amplifying the entire DNA sequence encoding strep-tagged mutant BP1 gene from pVAX-*BP1*mutStrep plasmid. The PCR product was purified and ligated with pET28a plasmid containing N-terminal his-tagged Maltase Binding Protein (MBP) fusion protein digested with *SpeI* (10 U/µl) and *XhoI* (10 U/µl); giving rise to the construct- pET28a-*HisMBPBP1*mut*Strep*. After *E.coli* Rosetta transformation, positive clones were selected via colony PCR and tested for expression in 20 ml culture.

Large-Scale Expression, Purification and Solubilisation of BP1 Recombinant Protein

Protein expression was induced in 1 L bulk culture of bacteria containing pET28a-*HisMBPBP1*mut*Strep* with 1 mM isopropyl β-D-thiogalactopyranoside (IPTG) at 37°C for 60 min and harvested by centrifugation. The recombinant protein, HisMBPBP1mutStrep was expressed in Rosetta *E. coli* expression system as inclusion bodies and purified under denatured conditions using Ni-NTA and Strep-Tactin affinity columns according to the manufacturer's instructions.

RESULTS AND DISCUSSION

Papain-family berghepain-1 is a homolog of falcipain-1, in *P. berghei*. It was amplified based on sequence homology with other cysteine proteases and reported in 1992 (Rosenthal & Nelson, 1868). The expression and characterisation of recombinant falcipain-1 has been challenging, making our knowledge of its functions limited (Rosenthal, 1868). Berghepain-1 (PlasmoDB ID: PBANKA_1321700), an orthologue of falcipain-1 (FP1), has an open reading frame (ORF) of 1560 bp that encodes a 60kDa protein. The alignment of the sequences using Geneious Software (pro v5.5.9) showed that site-directed mutagenesis converted the active-site cysteine residue to alanine in the mutant BP1 gene (pBP1c300a). Full-length recombinant protein HisMBPBP1mutStrep was expressed. The majority of the protein was expressed as shorter chain proteins which may have been as a result of protein degradation. Also, the codon usage bias of the *E. coli* Rosetta may have been exhausted by the corresponding transfer RNA (tRNA). The A-T component of malaria genes is about 80%, with long clusters of rare *E. coli* codons frequently occurring. This often leads to "premature translational termination, frameshift events and mistranslational amino acid substitutions" as a result of the codon usage bias which makes the expression of recombinant malaria proteins in *E. coli* complicated (Ahuja et al., 2006).

CONCLUSION

The present study shows that the mutant forms of the BP1 gene leading to catalytically inactive recombinant mutant BP1 protein were expressed in an *E.coli* expression vector. The result suggests that recombinant BP1 protein can be expressed for utilisation as a malaria vaccine candidate.

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Computational Allergenicity Assessment of *Escherichia coli* Protein Toxins Found in Food

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INTRODUCTION

Food allergy is a mystery problem in numerous ways. This condition has the potential to be life-threatening and affects millions of individuals(). The ability of a substance to trigger sensitization and allergic reactions is known as allergenicity, and it is frequently connected with the IgE antibody (). Substances that can cause allergic reactions through the immune system are broadly referred to as allergens. Numerous substances including foods react with specific IgE antibodies, leading to the patient's allergy symptoms. Their ability to travel to cells and release chemicals can cause symptoms, particularly on the nose and throat., lungs, ears, lining of the stomach and skin().

Public health worldwide is constantly concerned about food poisoning (). The main causes of food poisoning are bacteria, parasites and viruses. It has been reported that Asia and the sub-Saharan have the utmost cases of ailment which can be traced back to food poisoning with about 200,000 cases of death due to food poisoning in Nigerians. Food allergies are also contributing factors to food poisoning (). Foodborne diseases can be caused by a significant number of pathogenic microorganisms such as *Escherichia coli* 0157:H7, *Bacillus cereus, Clostridium* sp., *Staphylococcus aureus*, *Salmonella sp*, *Shigella sp*, etc. (Ozabor et al., 2024). It has been reported that an allergy may be triggered or exacerbated by infection with certain bacterial species (). Furthermore, new evidence suggests that *S. aureus* plays an unanticipated role in allergic conditions. —(). Allergic airway inflammation is one of the consequences of *S. aureus ()*. The increase in food allergies due to various substances in both adults and children is one of the primary concerns for mankind, as food allergies through food and feed are one of primary concerns (). Many reliable software and tools can predict the allergenicity of a given protein without any uncertainty –(;).

MATERIALS AND METHODS

Protein toxin sequence retrieval: Six Protein sequences of toxin proteins of the foodborne pathogenic bacteria (*Escherichia coli*) were obtained from the National Center for Biotechnology Information database (https://www.ncbi.nlm.nih.gov/protein/?term=bacterial+toxin+food+protein)

Allergenicity assessment of the protein toxin sequences: The sequences were analyzed for Allergenicity using the AllerTop server https://www.ddg-pharmfac.net/AllerTOP/. AllerTOP is the first alignment-free server for *in silico* prediction of allergens based on the main physicochemical properties of proteins().

RESULTS AND DISCUSSION

Table 1 shows the five protein toxins retrieved from the NCBI database with their accession number, their probable `allergenicity scores as well as their nearest protein determined computationally. *In silico* analysis of the five protein toxins of the *Escherichia coli* species analyzed revealed that toxins [Escherichia coli O104:H21 str. CFSAN002237] 111 amino acids toxin [Escherichia coli] 39 amino acids protein found to be probable allergens and their respective nearest proteins from other databases as UniProtKB accession number Q8N0N0 and NCBI gi number 1362656. It has been reported that bacteria possess the general mechanisms that promote allergies (Nordengrün et al., 2018). The data generated by using in silico methods can be utilized to decide if more in vitro and in vivo testing is needed, which includes serum screening. as recommended by Codex Alimentarius Commission (2009) and Goodman, 2008 (Ladics, 2008).

CONCLUSION

Table 1: *Escherichia coli* toxin proteins and their probable allergen scores

Toxin Protein	Accession number	Probable allergen score	The nearest protein
Toxin [*Escherichia coli* O104:H21 str. CFSAN002237] 111aa protein	ERF95362.1	Defined as allergen	UniProtKB accession number Q8N0N0
Toxin [*Escherichia coli* O104:H21 str. CFSAN002237] 125aa	ERF92839.1	Defined as non-allergen	UniProtKB accession number P36894
Toxin [Escherichia coli] 124 aa protein	KLH92944.1	Defined as non-allergen	UniProtKB accession number P14655
Toxin [toxin [*Escherichia coli*] 81 aa protein	KLH19480.1	Defined as non-allergen	NCBI gi number 1362656
Toxin [*Escherichia coli*] 39 aa protein	KLG62026.1	Defined as allergen	

It is possible to gain more significant benefits by integrating omics approaches with bioinformatics tools, which provide understanding related to the assessment of the quality of food and its safety in the near future. These predictive results can be used as a guide to comprehend how bacterial toxin is the driver of food allergy processes.

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Biopharmaceutical Drug Discovery and the Role of Biochromatographic Techniques for Biotherapeutics in Modern Biotechnology

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INTRODUCTION

Drug discovery is finding possible new therapeutic entities by applying computational, experimental, translational, and clinical models. Even with the breakthroughs in biotechnology and our understanding of biological systems, finding novel therapeutics is still exceedingly time-consuming, expensive, challenging, and inefficient, resulting in few new therapeutic discoveries (Zhou & Zhong, 2017). Biopharmaceuticals are essentially biological drug products derived from contemporary molecular biology techniques; they are sourced through biotechnological procedures from genetically modified organisms, organs, tissues, microbes, animal fluid cells, and organs (Tartaglia *et al*., 2018). Apart from small molecules, biopharmaceuticals, particularly therapeutic antibodies, are becoming a significant class of medications. Significant progress has been made in computational methods for enhancing these protein-based treatments' stability, selectivity, and affinity. Preclinical research on animal and cell models, as well as human clinical trials, are all part of the process of developing and discovering new drugs. Afterwards, the drug must receive regulatory approval before being put on the market (Qureshi *et al*., 2022). Since the release of recombinant human insulin onto the market over thirty years ago, biopharmaceuticals have fundamentally transformed the biotechnology sector, and the primary goal of biopharmaceutical development is to maximize therapeutic benefit while minimizing the risk of treatment-related toxicity (Cauvin *et al*., 2015; Szkodny & Lee, 2022). As protein and peptide biopharmaceuticals are complex, they require a wide range of analytical methods for characterization and analysis (Song *et al*., 2023). The separation and purification of proteins (including enzymes), peptides, polysaccharides, oligonucleotides, and nucleic acids is the primary emphasis of biochromatography, which is the chromatography of biological molecules or macromolecules. Conceptually, biochromatography can be seen as the separation (analysis and purification) of biomolecules (Maier-Rosenkranz, 2016).

This review will discuss several recent developments in liquid chromatography stationary phase technology for separating macromolecule compounds, including the development of column material and separation interactions. This development aims to demonstrate the use of liquid chromatography across length scales of target molecules, which are larger biomolecules, particularly proteins, as biotherapeutics during biopharmaceutical processing.

METHODOLOGY

The available information on the terms Biopharmaceuticals, Biochromatography, biotherapeutics, proteomics, Macromolecules, Biological molecules, Proteins, Biopurification, Protein Chromatography, Liquid Chromatography, Biopharmaceutical drug discovery, and Separation Science was collected via a library and electronic searches in PubMed, ScienceDirect, Google Scholar, and Google Browser.

MAIN FINDINGS

Chromatography is essential to manufacturing biotech medicines because of its unparalleled resolution, resilience, and scalability, making it the foundation of the purifying process (Rathore *et al*., 2015). As a result, more work has gone into creating innovative, reliable, and efficient purification instruments; liquid chromatography is one such instrument that is frequently used to purify biomolecules (Dupree *et al*., 2020). The physicochemical properties of the proteins—such as size, charge, Hydrophobicity, and affinity—and the kind of support being utilized are the basis for separation. Multidimensional orthogonal (alternative selectivity) separation can increase overall resolution, enabling deeper mining of the proteome, as demonstrated in many of the applications mentioned subsequently (Nice, 2020). However, advances were recorded in Biopharmaceutical processing in the following sections of Biopurification;

- Operational Mode (Batch (fixed bed/Single column) and Continuous (moving bed/multicolumn),
- Dimension (1-D (1-Dimensional) and 2-D (2-Dimensional)
- Stationary Phase/adsorbent or adsorption mode (Column (Resin)- based and Membrane-based)
- Workflow methods (Medium-pressure technique and High-pressure technique)
- Physico-chemical Parameters (Size, shape, Charge, and hydrophobicity)

It is well known that chromatography is the basis for the traditional methods used to purify proteins, including affinity, size exclusion, and ion exchange chromatography (Aslam *et al*., 2016). Diverse adsorbents have been developed that use different aspects of the protein to facilitate separation. These qualities, which are more significant and influence the separation process, are as follows, along with the chromatographic technique: Size and shape (gel filtration/size exclusion chromatography, SEC), Net charge and distribution of charged groups (ion exchange chromatography, IEC), Isoelectric point (chromatofocusing, CF), Hydrophobicity (hydrophobic interaction chromatography, HIC; reversed-phase chromatography, RPC), Metal-binding (immobilized metal ion affinity chromatography, IMAC), Content of exposed thiol groups (covalent chromatography, CC), Biospecific affinities for ligands, inhibitors, receptors, antibodies, and so on (affinity chromatography, AC) (Freitag, 2013; Rusli *et al*., 2022).

DISCUSSION

Ideally, Chromatographic stages make up one or more of the downstream procedures used for therapeutic proteins. Though most of these processes are still done in batch mode, traditional methods also involve packed column and batch mode operation. In the biopharmaceutical sector, however, continuous production has drawn attention (Angarita Velasquez, 2014). Due to the high adsorption capacity and protein separation accuracy of traditional column chromatography, biological agents' downstream processing has thus far been primarily dependent on the use of packed bed resin columns (Singh & Herzer, 2017). The continuous mode of operation mitigates the drawbacks of the batch mode of operation. Additionally, it can function in four modes: concurrent, carrousel, countercurrent, and annular. Annular continuous chromatography is a technique in which the chromatography bed is packed into a rotating annulus (Mehta, 2019).

However, several cutting-edge stationary phases have been developed as potential substitutes for resins, such as membrane chromatography, mixed-matrix membrane chromatography, and monolithic columns (Orr *et al*., 2013; Nath *et al*., 2022). The rapid growth of high-resolution techniques (high-performance liquid chromatography, HPLC; fast protein liquid chromatography, FPLC) on an analytical and laboratory preparative scale as well as for industrial chromatography in columns with bed volumes of several hundred litres has been made possible by the development of new porous resin supports, new bonded porous silicas, and new crosslinked beaded agaroses (Lacki & Brekkan, 2011). Most macromolecules, in synthetic and natural forms, display property distributions simultaneously in multiple parameters but the multidimensional distributions of such complex materials cannot be fully resolved by one-dimensional separation techniques like size-exclusion chromatography (SEC). As a result, the characterization of macromolecules is increasingly being done using two-dimensional separation techniques (Kilz & Radke, 2015).

CONCLUSION

The use of biopharmaceuticals has increased significantly over the past two decades. Many original biological drugs were registered, mainly protein-based products, produced by a biotechnological method. Separation is based on the physicochemical characteristics of the proteins (e.g., size, charge, Hydrophobicity, affinity) and the nature of the support used. Benefiting from the technical breakthroughs in recombinant genetic engineering and manufacturing, the development of biotherapeutics for disease treatments has thrived in the last decades; the importance of bioanalysis in the initial discovery and preclinical/clinical developments of biotherapeutics has been well-recognized. Accurate, sensitive, selective, robust, and high throughput quantification is essential to obtain fundamental temporal data for pharmacokinetic (PK), pharmacodynamic (PD), and toxicokinetic (TK) analyses.

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No Evaluation of Hybrid and Open-Pollinated Tomato Varieties for Growth and Fruit Yield in Nigeria

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INTRODUCTION

Tomato (*Solanum lycopersicum* L.) is a major fruit vegetable worldwide. Tomato fruits contain many essential vitamins and minerals. It is a main component of Nigerian dishes thus improving its nutritional quality. Tomato has high moisture content and water activity, making it susceptible to microbial growth, resulting in massive post-harvest losses (Fagbemi et al., 2021) Genetic resources of crops and vegetable diversity are declining all over the world at a rate of 1–2% annually(Ficiciyan et al., 2021).

In recent years, locally adapted tomato varieties have been replaced with high-yielding hybrid varieties, resulting in the bulk of commercially available tomato seeds being hybrid. Hybrids are produced by crossing two different specific parents selected for desirable traits that result in preferred traits from each parent and tend to show superior performance in controlled environments in terms of high yield, disease resistance, uniformity, and early maturity. However, open-pollinated seeds are old unchanged cultivars for generations that result from natural pollination and contain useful genes, are adapted to environmental stresses, have good nutritional quality with exceptional flavor, and are genetically more diverse.

Tomato productivity highly depends on the potential of the genotype used, its yield and quality have been reported to be under genetic control and hence do vary widely with cultivars "(Lemma et al., 2024). There are numerous tomato varieties available to farmers therefore choosing the right one to plant can be challenging especially with variation in Nigeria's climate from region to region. The performance of open-pollinated in comparison to hybrid varieties, under different environmental conditions has not been intensively researched. Considering the agroecological importance of enlarging and securing variety diversity in light of changing environmental conditions and the increase in population as well as the need to promote tomato production **(Ficiciyan et al., 2021).** This review aims to offer insights that can guide farmers in making informed decisions on selecting the most suitable varieties to plant to optimize resources, improve livelihoods, and contribute to broader food security goals. The study compares findings from several tomato evaluation experiments conducted through on-farm trials at various agro-ecological zones of Nigeria, focusing on key agronomic traits like plant height, number of leaves per plant, days to flowering, and other yield parameters like number of fruits per plant, and fruit weight.

SOME TOMATO EVALUATION EXPERIMENTS CONDUCTED THROUGH ON-FARM TRIALS AT DIFFERENT AGRO-ECOLOGICAL ZONES

Six vegetative and four fruit-related traits were measured in an experiment that compared the performance of seven tomato landraces to an improved variety (Cal-J) at Ibadan, Oyo state. The study revealed that certain landraces, particularly USI/2/15, exhibited consistent and significant outperformances over other genotypes, including the improved variety. Two other landraces (USI/3/15 and USI/7/15) consistently maintained equal performances with Cal-J. This indicates that the landraces possess useful genes that should be explored and could be valuable for breeding programs(Adewale and Adebo, 2018).

Field experiments were conducted at Makurdi, Benue state on two tomato hybrid varieties (F1 Lindo and F1 Jaguar) a local variety (Local check), and an improved variety (Roma Savanna VF), where the highest values for fruit length, fruit diameter, number of fruits/plant, weight of fruits/plant and fruit yield was observed for Roma Savanna. The same variety was earlier than all the other varieties and took the least number of days to flower, followed by F1 Jaguar and F1 Lindo. The local variety took longer days to flower compared to the other varieties, an indication that the development of hybrid varieties for the southern Guinea savanna of Nigeria may not be of any economic advantage(Ojo et al., 2013).

Experiments were conducted at Ogbomoso, Oyo state to evaluate the growth, fruit yield, and quality of seven varieties of tomato in the Guinea Savannah zone of South West Nigeria. The tomato varieties used included five hybrid varieties (DT97162A(R), DT97/215A, Tropical, Roma VF, UC82B) and two local varieties (Ibadan Local and Ogbomoso Local). The results showed that higher fruit yield was recorded from UC82B, closely followed by Ibadan and Ogbomoso local. DT97/162A(R) gave the highest plant height whereas Ogbomoso local recorded the highest number of leaves at 6 weeks after transplanting. Although there was inconsistency in the results of the nutritional compositions of tomato fruits, the local varieties (Ogbomoso and Ibadan Local) recorded higher nutritional values followed by UC82B (Olaniyi et al., 2009). In Akungba-Akoko, Ondo State, ten quantitative traits were assessed among forty tomato accessions. The performance comparison between hybrid varieties and landraces showed that certain hybrid varieties exhibited exceptional performance in specific key traits compared to landraces. For example, hybrid accession T33 (UC82B) demonstrated outstanding performance in terms of fruit yield and average fruit weight, indicating superior productivity compared to some landrace accessions. Additionally, other hybrid varieties like T24 (DERICA), T26 (NADIRA), T27 (KIARA), T28 (PANTHER17), and T29 (COBRA26) also displayed unique characteristics in traits such as fruit yield, average fruit weight, and pericarp thickness. The study highlighted the diversity and performance differences between hybrid and landraces, providing valuable insights into the genetic variability and potential for improvement within each group(Gbadamosi et al., 2020).

In another study, nineteen tomato samples from seven states (Kano, Kaduna, Bauchi, Katsina, Nassarawa, Niger, and Plateau) in Northern Nigeria were collected for a comprehensive study of the morphological characteristics of tomato varieties grown in the region. From the results, Kaduna Tangino was recommended for fruit width, Dan India for fruit length, UTC 1 for thickness of the fruit wall, Derica sweet for single fruit weight per plant, and UTC 02 was recommended for total fruit weight per plant. The study highlighted the genetic potential and diversity of tomato varieties in Northern Nigeria, providing valuable insights for targeted breeding programs and the conservation of genetic resources for future utilization(Fagbemi et al., 2021).

In Benin, Edo state, four tomato cultivars, comprising two local cultivars (BNL and EKL) and two improved cultivars (IMPA and IMPB) were evaluated based on thirty-two qualitative and quantitative characters. It was observed that the local accession, BNL gave the highest fruit yield though it had small fruits. The accession also had a fine fruit shape and texture. BNL therefore represents a valuable genetic resource to breeders for increased fruit yield, good shape, and fine-textured fruits, which will be of better market value. The local accession, EKL gave the largest fruit size though its fruit shape is not attractive. Furthermore, the biochemical properties of the two local cultivars are comparable to those of the two improved cultivars(Ogwu et al., 2017).

CONCLUSION

The choice between hybrid and open-pollinated tomato varieties is based on the specific needs and circumstances of the farmer as it is evident that both hybrid and open-pollinated tomato varieties have distinct advantages. Hybrid varieties often excel in terms of yield, uniformity, and disease resistance. While open-pollinated varieties demonstrate resilience and adaptability and can perform equally or better than hybrids in stressful environments. Therefore, the open-pollinated varieties are important reservoirs of useful genes. This flexibility in choice ensures that all farmers can select the most appropriate variety to maximize productivity and ultimately contribute to food security in Nigeria.

RECOMMENDATION

To better leverage the strengths of both hybrid and open-pollinated tomato varieties, it is recommended that farmers should consider climate and location among other factors, as important in selecting tomato varieties based on their specific farming conditions and goals. By adopting Integrated Variety Selection, developing locally adapted hybrids, and implementing improved agronomic practices for enhanced tomato fruit yield. Similarly, the involvement of various stakeholders (researchers, extension officers, farmers, consumers and traders) at the beginning of the breeding process is necessary.

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Morphological, Biochemical and Molecular Characterization of Yam in Response to Anthracnose Disease

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INTRODUCTION

Yams (*Dioscorea* spp.) are important for food security. There are significant biotic stresses negatively impacting its production and therefore, affecting its yield potential (Bassey, 2017; Ntui *et al*., 2021; Okon *et al*., 2022). Yam anthracnose Disease (YAD) caused by *Colletotrichum alatae* has been described as the most devastating fungal pathogen of yam in West Africa, accounting for about 50 – 90 % of yield losses in extreme conditions (Ntui *et al.,* 2021; Koima *et al.,* 2023). The biochemical and molecular mechanism of YAD has not been fully understood. So, anthracnose isolates were collected from YAD-infected leaves, isolated and characterized by cultural and molecular methods, 42 yam collections were screened for resistance to YAD and metabolite profiling to identify those associated with YAD resistance. A total of 20 putative biochemicals linked to anthracnose resistance were identified. Further, the expression profile of some susceptibility genes confirmed the YAD screening results.

MATERIALS AND METHODS

Collection of yam-infected leaves

Infected white guinea yam (*D. rotundata*), bitter yam (*D. dumetorum*), and water yam (*D. alata*) leaf samples were collected for fungal isolation.

Culture and isolation of fungal pathogens

Fragmented tissues (1cm) from the sterilized leaves showing symptoms of anthracnose were inoculated on the PDA supplemented with chloramphenicol (1000 mg/L) and incubated at ambient temperature (28 ± 2^{0}C) for 7 days and observed every 24 hours.

Identification of fungal isolates using morphological and cultural characteristics

Identification of the isolates was done based on the method described by Sutton (1992). The isolates were identified by comparing their morphological and cultural characteristics with published photographs and descriptions documented by Barnett and Hunter (2006).

Molecular characterization of fungal isolates

Extraction of fungal Genomic DNA

DNA was extracted from the different fungal isolates by CTAB method and as modified by Okon *et al.* (2022).

Amplification of fungal genomic DNA by PCR

PCR was performed using primers for the Internal Transcribed Spacer (ITS) gene of *C. alatae* as described by Okon *et al.* (2022) with the primers YamCgITS2 (5' CCTGCGGAGGGATCATTACT 3') and (3'AAGTTCAGCGGGTATTCCTACC 5')

Sequencing of the PCR product

The purified products were sequenced using Big Dye Terminator in ABI 3130 DNA sequencer (Applied Biosystems, California, USA)

in both primer directions. The sequences were assembled, edited, and analyzed using SnapGene software (www.snapgene.com).

Phylogenetic analyses

The assembled sequences were used in BLASTn searches against the GenBank database (http://www.ncbi.nlm.nih.gov/BLAST) to identify the most similar sequences available in the database. The sequences in the GenBank that showed the highest similarity to the isolates were aligned using the ClustalW program and used in phylogenetic analysis with 1000 bootstrapping. Phylogenetic and molecular evolutionary analyses were done using MEGA version 7.

Data analysis

A completely randomized experimental design was used. Data collected were subjected to descriptive statistics using GenStat Discovery Edition 12.

Collection of yam landraces and establishment in the field: Forty-two (42) yam collections were collected and screened for resistance to YAD.

Morphological characterization of 42 yam collections: Yam minisetts were planted in Randomized Complete Block Design (RCBD) with three replications. Morphological data was collected based on the methods of the International Plant Genetic Resources Institute's (IPGRI) descriptors of yam (*Dioscorea* species) (International Plant Genetic Resources Institution, 1997).

Screening of yam collections for YAD resistance: The screening was conducted on the field and the plants were freely exposed to the prevailing natural infestation level of YAD. Symptoms were recorded 24 Weeks after planting when over 80 % of the plants presented symptoms. Data were collected on the Number of leaves per plant and the number of infected leaves per plant; Disease incidence (DI %) and Disease severity (DS %) were calculated according to the modified method of Manadhar *et al.* (2016) This was done using the five-point scale range of Aduramigba – Modupe *et al.* (2014).

Biochemical characterization of yam collections using GC–MS: The leaves of eight landraces selected based on their resistance were collected and subjected to GC-MS. The –GCMS analysis of biochemical compounds from the different extracts of the leaves was done using Agilent Technologies GC systems with GC-7890A/MS-5975C model (Agilent Technologies, Santa Clara, CA, USA).

Relative expression of susceptibility genes: RT-qPCR analysis was performed to determine the expression levels of the two anthracnose susceptibility genes *Downey Mildew Resistance 6* (DMR6) and *Sugars Will Eventually be Exported Transporters* (SWEET14). The E.Z.N.A®. A total RNA kit (Omega Bio-tek) was used to extract RNA from the young leaves of these samples and cDNA was synthesized using the LunaScript™ RT SuperMix kit (New ENGLAND BioLabsInc.). The Ubiquitin gene was used as an internal control to check the quality of the cDNA. RT-qPCR was performed with the primers DrDMR6_F and DrDMR6_R, DrSWEET14_F and DrSWEET14_R, and DrUBQ_F and DrUBQ_R. The $2^{-\Delta Ct}$ method was used to calculate the relative gene expression levels (Livak and Schmittgen, 2001).

RESULTS AND DISCUSSION

24 isolates were obtained and classified into Slow Growing Grey (SGG), Slow Growing Olive (SGO) and Fast Growing Grey (FGG). The 24 isolates were described based on morphological characteristics including Mycelia growth rate which ranged from slow to moderate and fast. SGG form has been observed to cause 100 % leaf defoliation and premature death of up to 76 % inoculated plants (Abang 1997). Mycelia's colour varied showing brownish-grey, white with a purple centre and white turning brown with age, light pink colour, purple and grey-velvety. Spore colour was observed to be brown, blue, and gold across the different isolates. The morphology of the mycelia was cottony and velvety across the isolates. The hyphae were mostly aseptate and septate; and fruiting bodies were globose, obovate, elliptical, cylindrical and Fusoid. Pathogens causing anthracnose were reported in previous studies to show variability in morphology, colony colour and growth rate (Kwodaga *et al.,* 2020; Abang *et al.,* 2002). ITS2 gene, Primer YamCgITS2-F&R for *Colletotrichum alatae* amplified 21 isolates when the 24 isolates were subjected to PCR analysis with PCR fragments of approximately 500 bp obtained. The PCR products obtained using primer YamCgITS2-F&R were purified and sequenced. The identity of the nucleotide sequences among the 24 isolates was determined using MultAlin. Alignment of the nucleotide sequences of the isolates showed nucleotide sequence identities ranging from 73.36 to 97.82 % among the isolates. *Daldinia eschscholtzii* had the highest blast similarity of 97.82 % closely followed by the duo of *Diaporthe* spp. and *Pestalotiopsis* spp. with 95.49 %. The nucleotide sequences were compared with those of published ITS sequences of *Daldinia eschscholtzi, Colletotrichum alatae* and *Fusarium* spp. respectively. The evolutionary relationship was decoded using the UPGMA method.

Variation was observed in leaf shape, leaf colour, tuber and tuber flesh characteristics. Tuber

shapes observed included cylindrical, oval, irregular and round. One distinct variety was snake-like.

Yam landraces with disease severity index (DSI) ranging from 0.03 – 1 were classified as Highly Resistant (HR) and these included *Uho*, *Ugedie*, *Oshahe*, *Kinim*, *Amaragbo*, *Ugaku*, *Igbode ogede*, *Achikpe*, *Ukolokilu*, *Lekuleku* and *Ogede*. Similarly, landraces *Agba, Agbam, Ajijro, Ajaba, Anem, Amola, Efala onere, Egbeja, Ehinkpe, Esange, Ichacha, Paper, Udanyi, Ugge* and *Yeibo* with DSI ranging from 1.18 – 9.63 were identified as Resistant (R). *Gbakwasi, Ijibo, and Punch* ranged from 11.38 to 19.89 and were classified as Moderately Resistant (MR). *Usughu* was Susceptible (S) with 30.67. Highly Susceptible varieties with DSI from 38 to 91.9 included *Obangha, Aloshi, Obuna onglor, Okpolukata, Ndiseme, Obulaa, Ochokpa, Ntaniko, Uhimoka, Obuna otayi kabor* and *America*. This grouping is in congruence with Kauakou *et al.* (2007) where 3 response groups – Resistant (R), Susceptible (S) and Highly Susceptible (HS) were identified.

Based on the PCA analysis of the biochemical compounds in the yam leaves, the compounds accounting for the difference in resistance were identified in resistant varieties. They included Cis – vaccenic acid, octadecene, cyclohexadecane, docosene, Z – ethylhexyl phthalate, dodecatrien-1-ol, oleic acid, trimethylsiloxane, hexadecanoic acid, octadecenoic acid, dodecanoic acid, octadecanoic acid, 1-docosene, Trans-13, octadecenoic acid, butyl – 9- hexadecenoate, 9 octadecenoic acid, tetrasilocane, benezene, n-hexadecane and 6, 11 – dimethyl 1-2, 6, 10 – dodecatrien – 1 – ol. Carlson *et al.* (2019) reported significant upregulation of octadecanoic acid activity in several tissues in sorghum when infected with *Fusarium pseudograminearum* thus, stamping its authority as a biochemical resistance marker. A study by Amrullah *et al.* (2023) reported that octadecanoic acid was associated with the resistance mechanism of shallots against anthracnose.

The expression of anthracnose susceptibility genes SWEET14 and DMR6 was tested in 5 out of the 42 yam landraces using qPCR. The 5 landraces were selected based on the result of the field screening for anthracnose. The expression profiles of the two genes showed their highest expression in susceptible varieties and downregulation in resistant varieties. According to Singh *et al.* (2022), the downregulation of SWEETs may play positive roles in plant defence response affecting biochemical processes linked with defence and production of secondary metabolites.

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Crossability Between Two Accessions of Cowpea

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INTRODUCTION

Cowpea (*Vigna unguiculata* L. Walp), commonly known as "black-eyed pea," is a warm-season legume crop originating in Africa and cultivated for over 5,000 years, making it one of the world's oldest crops (Wiersema and León, 2013). Known for its resilience and drought tolerance, cowpea thrives in diverse agroecological zones, particularly arid and semi-arid climates (Sanginga *et al.,* 2003). Culturally and nutritionally significant, cowpea serves as a staple food in many African countries, providing essential protein, fibre, vitamins (such as folate), and minerals (including iron and potassium) (Ndiaye *et al.,* 2017). In agriculture, cowpea plays a crucial role as a cover crop and in intercropping systems, enhancing soil fertility through nitrogen fixation. Its ability to withstand challenging conditions, such as drought and soil degradation, underscores its importance in sustainable farming practices (Ehlers and Hall, 1997). The crop's limited genetic variability, primarily due to its self-pollinating nature, and the lack of improved varieties capable of withstanding environmental conditions exacerbate these vulnerabilities, resulting in yields often below their potential and economic losses for farmers (Ajayi *et al.*, 2014; Ajetomobi and Abiodun, 2010). Enhancing the genetic base of cowpea is crucial for improving its productivity and resilience.

Genetic techniques are essential for developing crop varieties with desirable traits such as higher yields, pest resistance, and environmental adaptability (Tester and Langridge, 2010). GMOs like PBR cowpea or BT cowpea offer a source of desirable genes to revolutionize agriculture by allowing precise manipulation of an organism's genetic makeup, leading to increased yields and reduced chemical inputs (Brookes & Barfoot, 2018). Genetic variation provides the raw material for developing improved crop traits (Lopes-Caitar *et al.,* 2013). By selecting parent plants with desirable traits and compatible genetic backgrounds, breeders can achieve successful hybridization (Doebley *et al.,* 2006). Crossability, the ability of different genotypes to interbreed and produce fertile offspring, is fundamental for introducing genetic diversity and developing hybrid varieties with enhanced traits (Acquaah, 2012). This process increases adaptability to changing conditions, pests, and diseases (Gur and Zamir, 2004) and allows for the creation of hybrids that exhibit superior yield and quality (Hochholdinger and Hoecker, 2007). Moreover, crossability accelerates breeding programs by combining desired traits from different sources, reducing the development time for new varieties (Melchinger *et al.,* 2018), and harnessing plant genetic diversity for agricultural improvement. Therefore, the present study was aimed at investigating the magnitude of crossability between a pod borer resistant and a susceptible accession of cowpea, to assess direct and reciprocal crossability between two accessions of cowpea and to determine the extent of the influence of morphological traits on the crossability of two accessions of cowpea.

MATERIALS AND METHODS

Two accessions of cowpea used for the study SAMPEA 20T and TVu-17327 which is an improved variety with brown seed coat color were obtained from National Biotechnology Development Agency, NABDA. Abuja and from the International Institute of Tropical Agriculture (IITA), Ibadan, respectively. The experiment was conducted at a screen house in the Department of Plant Science Biotechnology, Adekunle Ajasin University, Akungba-Akoko, Nigeria. Polythene pots were utilized for planting, and daily watering was implemented to maintain optimal growing conditions. The pollination process involved meticulous procedures, including emasculation and precise anther transfer for the crosses. Data collection encompassed various growth parameters and crossability-related traits. Data were analyzed using one-way ANOVA with the cross as a fixed factor in SPSS version 20. Pearson's correlation was used to assess relationships between morphological characters and crossability, the interrelations among morphological characters, and the influence of parental traits on crossability.

RESULTS AND DISCUSSION

Plants displayed high variability in crossability traits, with coefficients of variation ranging from 31.40 in the number of flowers crossed (NFC) to 77.43% in the percentage of pod set. Reciprocal crosses showed a mean of 6.13 flowers crossed/plant, 0.87 pod set, 12.43% pod set, and 9.71 cm average pod length, with high variability similar to direct crosses (CV = 37.42; 85.76%). (Tables 1 and 2). The correlation analyses (Tables 3 to 6) revealed significant positive correlations between various crossability traits. Similar positive correlations were observed for the reciprocal crosses. The findings revealed considerable variability in crossability traits, particularly in the number of pods set, percentage of pod set, and average seed weight. These results are similar to the findings of Ajayi *et al.* (2020) in cowpeas and Gbadamosi *et al.* (2023) in tomatoes.

CONCLUSION AND RECOMMENDATION

The findings highlight the significance of emergence percentage,

Table 1. Crossability traits for the direct cross (SAMPEA-20T×TVu-17327)

Trait	NFC	NPS	PPS (%)	APL (cm)	ASPP	ASW (g)	NDM
Number	15	15	15	15	15	15	15
Min	4.00	1.00	11.10	10.30	7.00	0.10	37.00
Max	10.00	3.00	50.00	19.20	17.00	0.40	46.00
Sum	97	21	366.90	171.50	147.00	2.36	487.00
Mean	6.47	1.4	24.46	11.43	9.80	0.16	32.47
Standard error	0.52	0.25	4.89	1.65	1.47	0.03	4.37
Coefficient of variation (%)	31.40	70.40	77.43	56.02	58.26	69.89	52.17

NFC: Number of flowers crossed; Number of pods set; Percentage of pods set; Average pod length; Average seeds per pod; Average seed weight; Number of days to pod maturity

Table 2. Crossability traits for the reciprocal crosses (TVu-17327×SAMPEA-20T) for accessions of cowpea

Trait	NFC	NPS	PPS (%)	APL (cm)	ASPP	ASW (g)	NDM
Number	15	15	15	15	15	15	15
Min	4.00	1.00	12.50	10.00	8.00	0.10	38.00
Max	9.00	2.00	25.00	18.20	16.00	0.20	44.00
Sum	92.00	13.00	186.50	145.70	121.00	1.40	405.00
Mean	6.13	0.87	12.43	9.71	8.07	0.09	27.00
Standard error	0.59	0.19	2.55	1.94	1.64	0.02	5.12
Coefficient of variation (%)	37.41	85.76	79.43	77.37	78.61	83.16	73.45

NFC: Number of flowers crossed; Number of pods set; Percentage of pods set; Average pod length; Average seeds per pod; Average seed weight; Number of days to pod maturity

Table 3. Pearson's correlation analyses among crossability traits of accessions of cowpea for SAMPEA-20T × TVu-17327

Trait	NFC	NPS	PPS	APL	ASPP	ASW	NDM
NFC	1	-0.06	-0.51	-0.13	-0.14	0.25	-0.5
NPS		1	0.85**	0.67**	0.76**	0.43	0.73
PPS			1	0.63*	0.72**	0.43	0.66**
APL				1	0.88**	0.74**	0.94**
ASPP					1	0.59*	0.89**
ASW						1	0.77**
NDM							1

*: Significant at P ⩽0.05; **: Significant at P ⩽0.01. NFC: Number of flowers crossed; Number of pods set; Percentage of pods set; Average pod length; Average seeds per pod; Average seed weight; Number of days to pod maturity

Table 4. Pearson's correlation analyses among crossability traits of accessions of cowpea for TVu-17327 × SAMPEA-20T

Trait	NFC	NPS	PPS	APL	ASPP	ASW	NDM
NFC	1	0.68	0.49	0.54*	0.55*	0.31	0.54*
NPS		1	0.92**	0.87**	0.87**	0.60*	0.84**
PPS			1	0.93**	0.90**	0.79**	0.92**
APL				1	0.85**	0.85**	0.95**
ASPP					1	0.72**	0.93**
ASW						1	0.90**
NDM							1

*: Significant at P ⩽0.05; **: Significant at P ⩽0.01. NFC: Number of flowers crossed; Number of pods set; Percentage of pods set; Average pod length; Average seeds per pod; Average seed weight; Number of days to pod maturity

Table 5. Pearson's correlation analysis for the influence of SAMPEA-T20 on the crossability traits of accessions of cowpea for the crosses SAMPEA-20T × TVu-17327

Trait	NFC	NPS	PPS	APL	ASPP	ASW	NDM
EM	0.92**	0.87**	0.79**	0.46	0.76**	0.39	0.8
PH	0.36	0.41	0.76**	0.51*	0.25	0.01	0.33
NL	0.42	0.85**	0.67**	0.47	0.99**	0.1	0.41
NMB	0.73**	0.02	0.08	0.19	0.01	0.86**	0.25
TLL	0.07	0.11	0.04	0.24	0.05	0.77	0.16
TLW	0.57*	0.42	0.36	0.54*	0.18	0.6	0.6
DFF	0.53*	0.89**	0.57*	0.99**	0.39	0.55*	0.98**
TNF	0.39	0.27	0.76**	0.19	0.68**	0.24	0.42

*: Significant at P ⩽0.05; **: Significant at P ⩽0.01. EM: Emergence percentage; PH: Plant height; NL: Number leaves; NMB: Number of main branches; TLL: Terminal leaflet length; TLW: Terminal leaflet width; DFF: Days to first flowering; TNF: Total number of flowers; NFC: Number of flowers crossed; Number of pods set; Percentage of pods set; Average pod length; Average seeds per pod; Average seed weight; Number of days to pod maturity

Table 6. Pearson's correlation analysis for the influence of SAMPEA-T20 on the crossability traits of accessions of cowpea for the crosses TVu-17327 × SAMPEA-20T

Trait	NFC	NPS	PPS	APL	ASPP	ASW	NDM
EM	0.43	0.13	0.05	0.03	0.4	0.06	0.12
PH	0.05	0.17	0.23	0.49	0.15	0.89**	0.37
NL	0.68**	0.73**	0.46	0.41	0.96	0.87**	0.85**
NMB	0.59*	0.82**	0.77**	0.71**	0.85**	0.65**	0.67**
TLL	0.06	0.04	0.06	0.02	0.02	0.13	0.04
TLW	0.35	0.93**	0.97**	0.72**	0.86**	0.97**	0.76**
DFF	0.3	0.72**	0.42	0.64*	0.32	0.75**	0.57*
TNF	0.16	0.27	0.41	0.14	0.61	0.5	0.37

*: Significant at P ⩽0.05; **: Significant at P ⩽0.01. EM: Emergence percentage; PH: Plant height; NL: Number leaves; NMB: Number of main branches; TLL: Terminal leaflet length; TLW: Terminal leaflet width; DFF: Days to first flowering; TNF: Total number of flowers; NFC: Number of flowers crossed; Number of pods set; Percentage of pods set; Average pod length; Average seeds per pod; Average seed weight; Number of days to pod maturity

plant height, leaf-related traits, terminal leaflet characteristics, flowering timing, and floral abundance in determining the success of hybridization in cowpeas. The positive correlations observed indicate that optimizing germination conditions, enhancing plant architecture, and fine-tuning flowering characteristics can collectively contribute to improved pod set, seed development, and overall maturity. These insights are instrumental for cowpea breeding programs, offering a nuanced understanding of the factors that influence successful hybridization. Breeding efforts can be tailored to prioritize traits such as germination efficiency, specific plant morphologies, and flowering characteristics to enhance overall crop productivity. It is crucial to acknowledge the context-specific nature of these correlations; as different genetic backgrounds or environmental conditions may influence trait interactions. Therefore, a targeted and context-aware approach is essential for harnessing these correlations effectively in breeding programs. This study advances our understanding of the intricate relationships between quantitative and crossability traits in cowpea, providing a foundation for future research and breeding strategies aimed at developing resilient and high-yielding cowpea varieties. It is important to consider both genetic and morphological factors in breeding programs to enhance cowpea productivity and resilience to biotic stresses, contributing to sustainable agricultural practices in Nigeria. The hybrids derived from the crosses are recommended for their performance assessment in the F1, F2, and subsequent generations focusing on identifying specific traits associated with pod borer resistance and susceptibility, as well as their influence on overall cowpea productivity.

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Molecular Docking Analysis of *Hyptis Suaveolens* Constituents as Inhibitors of Aflatoxin O-Methyltransferase (OMTA)

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INTRODUCTION

A significant number of aflatoxin-contaminated foods are abandoned due to strict regulations in several countries, this necessitates a pressing need to explore new options and strategies to mitigate aflatoxin contamination to avert global food shortage issues, coupled with the emergence of new fungal strains. As fungi such as *Aspergillus* sp. which produces aflatoxins, continue to grow and spread like wildfire, specific inhibitors that target aflatoxin synthesis are important biological probes for the investigation of aflatoxin synthesis mechanism in these fungal species. Inhibitors' roles are vital in the development of novel aflatoxin control strategies (Sakuda *et al.,* 2024). Despite the progress being recorded in the control of fungal pathogens and diseases, certain issues such as resistance to drugs, as a result of incessant usage and overdependence, are posing severe side effects and threats to the public healthcare systems globally. *Hyptis suaveolens is* a member of the highly medicinally and phytochemically rich family referred to as Lamiaceae. The medicinally essential phytochemicals such as tannin, phenols, flavonoids, alkaloids, terpenoids, saponins, and essential oils. These compounds possess diverse attributes such as antifungal, antibacterial, antiseptic, and antiviral activities. In recent years, *in silico* tools have been utilized in predicting the anti-microbial efficacy of probiotics efficiently. Therefore, target identification for specific polyphenols should be geared towards the development of plant-based drugs. The anti-aflatoxigenic impact of applied extracts was assessed with a simulated media to evaluate mycelial growth inhibition and aflatoxins reduction with an in-silico study via molecular docking against cytochrome P450 monooxygenase and polyketide synthase (Sabry *et al.,* 2024).

MATERIALS AND METHODS

The study investigated the inhibitory potentials of compounds sourced from *Hyptis suaveolens* against aflatoxin production using *in silico* methodologies. Molecular docking analysis was employed to predict the molecular interactions and binding energies of these compounds against a crucial protein, namely O-methyltransferase, associated with aflatoxin production in Aspergillus spp.

Plant Sample Collection: The plant material, *Hyptis suaveolens* was collected around the bushes in Gusau, Zamfara State Nigeria, and identified at the National Institute for Pharmaceutical Research and Development (NIPRD/H/7387). The leaves were then harvested for further experiments.

Extraction of *Hyptis* essential oil and Chemical analysis: Extraction of essential oil from leaves of *Hyptis suaveolens* and analysis of chemical composition was achieved using the method described by Aguele *et al.* (2023). The essential oil was extracted from the leaves of *Hyptis suaveolens* by steam distillation method as described by Lubis *et al.* (2023). The essential oil was stored in a suitable container for further use. Gas chromatography-mass spectrometry (GC-MS) analysis, as outlined by Johnson *et al.,* 2020, was utilized to identify the constituents of *Hyptis suaveolens* essential oil. Shimadzu GC-MS - QP2010 PLUS was used for the analysis.

Homology Modelling of *Aspergillus flavus* O-methyltransferase: The amino acid sequence (in Fasta format) of Aspergillus flavus O-methyltransferase, with Accession No: KAJ1715386, version KAJ1715386.1, was retrieved from the National Center for Biotechnology Information database (https://www.ncbi.nlm.nih.gov/). Subsequently, the sequence was utilized to search for a suitable template from the SWISS-MODEL template library. The AlphaFold DB model of *Aspergillus parasiticus* sterigmatocystin 8-O methyltransferase (Q12120.1.A) was chosen as the template for performing homology modelling to establish the lacking 3D structure of Aspergillus flavus O-methyltransferase. This modelling process was conducted using the SWISS-MODEL web server (http://swissmodel.expasy.org/), and the Global Model Quality Estimation (GMQE) was employed to assess the model's quality.

Preparation of proteins for molecular docking: The homology model of O-methyltransferase was prepared for docking using the

protein preparation wizard panel on Glide (Johnson *et al.*, 2022b; Schrodinger Suite 2023-1).

Receptor Grid Generation: To define the size and position of the binding site of the proteins for ligand docking, the receptor grid was generated using the receptor grid generation tool of Schrödinger Maestro 13.5. (Johnson *et al.,* 2022a).

Preparation of Ligands for molecular docking: The structure data files (SDF) of 50 bioactive compounds from *Hyptis suaveolens*, identified through GCMS analysis, as well as the reference compounds, were sourced from the PubChem database (https://pubchem.ncbi.nlm.nih.gov/). The referenced compound included S-adenosyl-L-methionine (standard ligand of O-methyltransferase). To achieve low-energy 3D structures with suitable chiralities, the compounds were prepared using the Ligprep panel of Maestro 13.5 (Schrödinger Suite 2023-1) (Johnson *et al.*, 2022b).

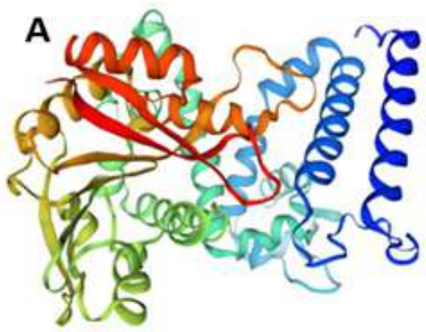
Protein-ligand docking: Molecular docking analysis was conducted using the Glide Ligand Docking panel of Maestro 13.5 on Schrödinger Suite 2023-1. The prepared ligands and the receptor grid file were imported into the workspace of Maestro. Docking of the compounds into the binding pocket of the target protein was performed using extra precision. The van der Waals radius scaling factor was set at 0.80 with a partial charge cut-off of 0.15 for ligand atoms, and the ligand sampling method was configured to be flexible (Johnson *et al.*, 2022b)

RESULTS AND DISCUSSION

Homology model of *Aspergillus flavus* O-methyltransferase A: The results of the quality assessment of the homology model of *Aspergillus flavus* O-methyltransferase A are shown in Table 1. The model has a sequence identity of 96.41 % with the template, a coverage of 0.98, and a GMQE of 0.90. Figure 1 shows the 3D structures of the template and model. The two structures appear similar to a large extent.

Table 1: Model evaluation scores for *Aspergillus flavus* O-methyltransferase A

Template	Model	Sequence Identity	Coverage	GMQE
Q12120.1.A Sterigmatocystin 8-O-methyltransferase. AlphaFold DB model of AFLP_ASPPU (gene: aflP, organism: *Aspergillus parasiticus* (strain ATCC 56775 / NRRL 5862 / SRRC 143 / SU-1))	Aspergillus flavus O-methyltransferase A	96.41 %	0.98	0.90



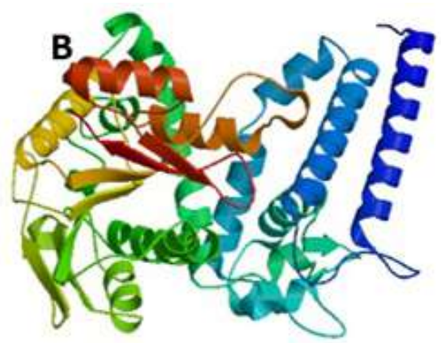


Table 1: 3D structure of A: *Aspergillus parasiticus* O-methyltransferase; B: *Aspergillus flavus* O-methyltransferase homology model

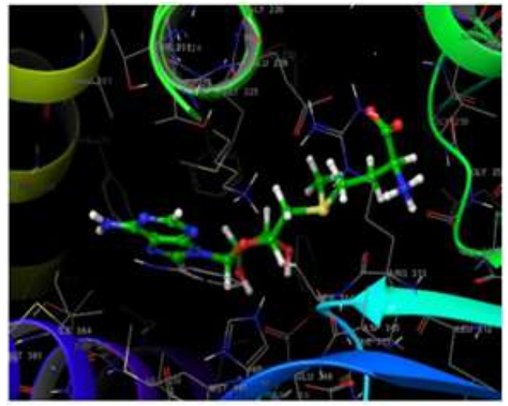
Molecular docking with O-methyltransferase: Table 2 presents the binding energies of ten top-scoring compounds from *Hyptis suaveolens* leaf extracts against O-methyltransferase. Notably, the reference compound, S-adenosyl-L-methionine, achieved the lowest binding energy, scoring -7.835 kcal/mol. Among the compounds derived from *Hyptis suaveolens*, the membrane exhibited the best docking at -6.569 kcal/mol. Figures 3 illustrates the 3D and 2D depictions of the molecular interactions between amino acid residues of O-methyltransferase and S-adenosyl-L-methionine, along with the top five compounds from both plant sources. A detailed breakdown of the hydrogen bonds and hydrophobic contacts established by the compounds with O-methyltransferase showed that S-adenosyl-L-methionine engaged in two hydrogen bonds with ASP 318 and one each with LYS 232, ARG 313, and GLY 254 within a hydrophobic pocket formed by residues MET 225, LEU 260, HE 315, PHE 207, PHE 221, LEU 372, VAL 368, PHE 164, ILE 364, and TRP 409. The test compounds occupied the same binding pocket as the reference compound and interacted with most of these amino acid residues, among others. The compound (3S,3aR,3bR,4S,7R,7aR) - 4 - Isopropyl-3,7-dimethyloctahydro - 1H -cyclopenta[1,3] cyclopropa[1,2]benzen-3-ol from Hyptis suaveolens, formed hydrogen bonds with LYS 232.

Homology model of Aspergillus flavus O-methyltransferase A: A homology model for *Aspergillus flavus* O-methyltransferase A was developed using the AlphaFold DB model of Aspergillus parasiticus sterigmatocystin 8-O methyltransferase (Q12120.1.A) as a template, due to the unavailability of the 3D structure of *Aspergillus flavus* O-methyltransferase A in the PDB database. The assessment of the model's quality indicated its suitability for subsequent molecular docking studies. The model closely resembled the 3D structure of the template, as illustrated in Figure 1 (A and B), aligning well with a sequence identity of 96.41%. Additionally, the assessment considered the coverage value and GMQE score. The GMQE score, which is coverage dependent, provides an overall model quality assessment comprising of values ranging between 0 and 1, with values close to 1 indicating higher expected quality. A coverage value of 0.98 signified that the model covered 98% of the target sequence, while the GMQE score of 0.90, indicating a high expected quality, affirmed the adequacy of the structure for molecular docking analyses with compounds from *Hyptis suaveolens*.

Molecular docking with O-methyltransferase: The results from molecular docking analyses reveal varying levels of binding affinity of specific compounds from *Hyptis suaveolens* towards O-methyltransferase. However, the reference compound, S-adenosyl-L-methionine, demonstrated the lowest binding energy, signifying its superior binding affinity for the enzyme. As a cofactor, S-adenosyl-methionine assumes a pivotal role in the catalytic process of O-methyltransferase by acting as a methyl group donor during the methylation of sterigmatocystin to O-methylsterigmatocystin. This reaction represents a key step in the aflatoxin biosynthesis pathway of filamentous fungi like *Aspergillus flavus* and *A. parasiticus*. Compounds that can bind and interact at the S-adenosyl-methionine binding site of O-methyltransferase are likely to inhibit the enzyme's activity.

Table 2: Binding energies (docking scores) of ten top-scoring compounds of *Hyptis suaveolens* leaf extract against O-methyltransferase a

Compound	PubChem CID	Docking score: ΔG Energy (Kcal/mol)
Reference Compound		
S-adenosyl-L-methionine	34755	-7.835
***Hyptis suaveolens* compounds**		
Cembrene	6436662	-6.569
Sandaracopimaradiene	443469	-5.494
Beta-Bisabolen-12-ol	5352901	-5.278
5,15-Rosadiene	519329	-5.197
(3S,3aR,3bR,4S,7R,7aR)-4-Isopropyl-3,7-dimethyloctahydro-1H-cyclopenta [1,3] cyclopropa[1,2]benzen-3-ol	11976203	-4.980
Bicyclo[5.3.0]decane, 2-methylene-5-(1-methylvinyl)-8-methyl-	564533	-4.866
Alpha.-Selinene	6432455	-4.802
Ledene oxide-(I)	534497	-4.672
Isocaryophyllene	5281522	-4.643
Cholest-14-en-3-ol, (3beta,5alpha)-	22295611	-4.524



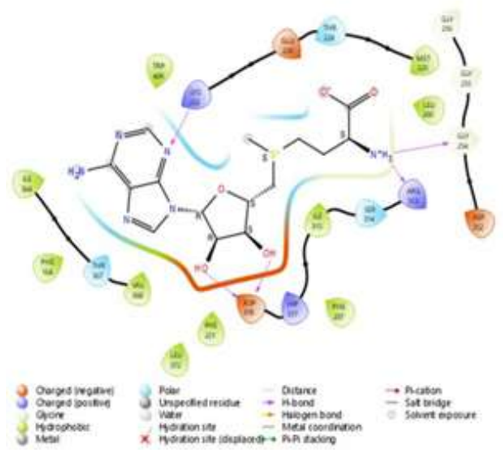


Figure 3: The 3D and 2D representations of the molecular interactions of amino acid residues of O-methyltransferase with S-adenosyl-L-methionine

In the compounds derived from *Hyptis suaveolens*, cembrene showed the most favourable docking, followed by sandaracopimaradiene, beta-Bisabolen-12-ol, 5,15-Rosadiene, and (3S,3aR,3bR,4S,7R,7aR)-4-Isopropyl-3,7-dimethyloctahydro-1H-cyclopenta [1,3] cyclopropa [1,2] benzen-3-ol. These compounds occupied the same binding pocket as O-methyltransferase and interacted with some of the binding site amino acid residues, suggesting them as possible inhibitors of the enzyme. The hydrogen bond interactions exhibited by (3S,3aR,3bR,4S,7R,7aR)-4-Isopropyl-3,7-dimethyloctahydro-1H-cyclopenta [1,3] cyclopropa[1,2]benzen-3-ol from *Hyptis suaveolens*, with LYS 232 in the S-adenosyl-methionine binding site of the enzyme, suggests their potential to compete with this enzyme cofactor, thereby impeding the aflatoxin biosynthetic pathway. Additionally, the hydrogen bond interaction of l-(+)-Ascorbic acid 2, 6-dihexadecanoate and ethyl linolenate with HIP 317 is noteworthy. HIP 317 acts as a proton acceptor in the enzyme's active site, and their interaction with the compounds could hinder the catalytic activity of the enzyme and the overall aflatoxin biosynthesis.

CONCLUSION

In this study, computational techniques were employed to perform a virtual screening of compounds extracted from *Hyptis suaveolens* for their inhibitory potential on aflatoxin synthesis. A database of phytochemicals present in *Hyptis suaveolens* was gathered from literature sources and public databases. The selected compounds

were docked into the active sites of key enzymes involved in aflatoxin production, such as cytochrome P450 enzymes and aflatoxin polyketide synthase (AFS). The binding affinities between the compounds and target enzymes were calculated using scoring functions to predict the interaction strength. Absorption, distribution, metabolism, excretion, and toxicity (ADME/T) properties of the top-ranked compounds were predicted to evaluate their drug-likeness and safety profiles. The *in silico* analysis identified several compounds from *Hyptis suaveolens* that exhibited significant inhibitory potentials against aflatoxin synthesis. Additionally, ADME/T analysis indicated favorable pharmacokinetic properties for these compounds, indicating that they are suited to take active roles in their development as aflatoxin inhibitors. The result of this study revealed the potential of *H. suaveolens* compounds as natural inhibitors of aflatoxin production. By targeting key enzymes involved in aflatoxin biosynthesis, these compounds offer a mechanism for mitigating fungal contamination in food and feed sources. *In silico* analysis suggests that compounds derived from *Hyptis suaveolens* possess inhibitory effects on aflatoxin production by targeting O-methyltransferase. Further experimental studies, including *in vitro* and *in vivo* assays, are needed to validate the safety and efficacy of these compounds as aflatoxin inhibitors. Additionally, efforts should be geared towards expounding the underlying mechanisms of aflatoxin inhibition by constituents of *Hyptis suaveolens* to optimize their application in agriculture, food and other industries.

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Luffa cylindrica: Potential for Research and Commercialization

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INTRODUCTION

Luffa cylindrica is an important edible and medicinal plant that belongs to the Cucurbitaceae family. It has many common names including smooth luffa, sponge luffa, vegetable sponge gourd, climbing okra, dishcloth gourd, and Chinese okra (Akinyinka *et al.,* 2022). Locally in Nigeria, it is commonly referred to as kankan or kankan Oyibo in Yoruba, while the Hausas call it Soosoo. The Igbos named it Asisa. The plant is widely distributed in humid tropics and Asia and can grow up to a length of 30 feet with fleshy egg-shaped dehiscent fruit with a green papillary dermis, transversely characterized with black crevasses with 7–20 cm three lobes leaves and oval-shaped fruits which can reach up to 60cm in length (Akinwumi *et al.,* 2021).

DISTRIBUTION

Luffa cylindrica is widely distributed in the humid tropics and Asia, with its origin debated between Africa and Asia. In West Africa, it grows naturally and is known locally as 'white people's sponge. The plant grows extensively as a weed in Nigeria and other African countries.

TRADITIONAL AND MEDICINAL USES

Luffa cylindrica has diverse ethnomedicinal uses across Africa and

Plate 1: Matured dry fruit of *Luffa cylindrica* (Source: BIODEC, Ogbomoso)

Asia. In Ghana, its fibre is used to filter water and palm wine (Al-Snafi, 2019). In Togo, leaf formulations are used in treating oedemas and malaria. Zulu people use leaf decoction for stomach pain, In Tanzania, root and leaf formulation reduce the risk of pregnancy termination. The leaves stimulate wound healing and stomach upset in Rwanda even facilitates childbirth in Uganda. In Congo-Brazzaville, leaf decoctions are effective against whooping cough. Root formulation is used for nose cancer in Gabon while in the Democratic Republic of the Congo, root and leaf extract is used as an aborticide. *Luffa cylindrica* has diverse ethnomedicinal uses. The young fruit and leaves can be consumed or cooked as vegetables. The charred seeds contain edible oil while the seed cake can be used as compost due to its nitrogen and phosphorus content (Al-Snafi, 2019).

PHARMACOLOGICAL ACTIVITIES

Luffa cylindrica leaf extract exhibited antioxidant properties. Methanol extract of *Luffa cylindrica* thermally processed by different methods was found to show varying degrees of antioxidant properties as measured by thiobarbituric acid, DPPH, ferric thiocyanate and ferric reducing antioxidant power radicals scavenging assays (Yadav *et al.,* 2017) The aqueous-ethanol extract of *Luffa cylindrica*_leaves displayed anticancer effects against MCF-7, BT-474, and MDA-MB-231 cell lines which epitomize three sub-types of breast cancer: luminal A, luminal B, and triple-negative, attributed to the presence of phytochemicals such as apigenin and luteolin (Abdel-Salam *et al.,* 2019). The ethyl acetate extract of *Luffa cylindrica* leaves displayed antifungal activity. Some compounds isolated from the benzene and petroleum ether *of Luffa cylindrica* seeds also displayed anti-fungal properties against *Candida albicans*. Similarly, the petroleum ether extract obtained from fruit showed potent antibacterial activity (Hossain *et al.,* 2010). The chloroform and n-hexane extract of *Luffa cylindrica* leaves showed potent antibacterial activity against gram-positive and gram-negative bacteria. The chloroform extract of the whole plant showed wound healing activity in a rat model by reducing the wound area and time of epithelization.

CHEMICAL COMPOSITION

The plant is rich in nutrients and phytochemicals, several studies have revealed that leaves, fruits, and seeds are a rich source of carbohydrates, protein, fibre, fats, amino acids and minerals (Onigemo *et al.,* 2020). The minerals found in the seeds of the *Luffa cylindrica* plant include sodium, iron, phosphorus, calcium, zinc, potassium, manganese, copper, chromium, and magnesium (Ogunyemi *et al.,* 2020). Phytochemical screening tests carried out on the plant showed that leaf exract contained saponin, alkaloids and cardiac glycosides while the seed extracts contained steroidal rings. Quantitative analysis of the sponge revealed that it contains ascorbic acid, anthocyanins, flavonoids and phenolics respectively (Reddy *et al.,* 2010).

Plate 2: *Extraction of Luffa cylindrica* seeds for further seed multiplication

Plate 3: Packaged *Luffa cylindrica* seeds

CONCLUSION AND RECOMMENDATION

This review provides an up-to-date and comprehensive summary of the traditional uses, pharmacology and phytochemical composition of Luffa cylindrica. It has been eaten as food and used in folk medicine and the treatment of many diseases such as syphilis, bronchitis, and amenorrhea for several years, especially in Africa and Asia. In the last few decades, the plant has attracted attention due to its potential pharmacological actions including anti-inflammatory, anticancer, antioxidant, antiviral, antimicrobial, anti-diabetic, hepatoprotective, sedative, anthelmintic, antipyretic, anti-epileptic, hypoglycemic, skin protection. However, like many other medicinal plants, efforts should be made to standardize its usage in different disease models through activity-guided bioassays and isolation of active principle(s), as well as, more mechanistic and comprehensive safety studies as well as more clinical studies on *Luffa cylindrica* are needed to enhance its pharmaceutical potentials. *Luffa cylindrica* holds great potential as a repository of beneficial phytochemicals that can be leveraged for the betterment of human health. Research efforts should therefore be directed at optimizing the bioactive extracts and phytochemicals for improving quality of life.

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Characterization of Fungi Associated with Barbing Tools in Lugbe, FCT, Abuja, Nigeria

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INTRODUCTION

Barbing which is the act of removing by cutting, shaving or trimming human hair has been on for a long term. However, this *Latin-derived* activity became an act of professional occupation in modern times (Ryan and Ray, 2014). There are differences in styles and choice of barbing style and coupled with high demands, there has been an ever-increasing need for this activity both at local and urban levels. The demand is on the one hand due to the ever-growing hairs on the human body naturally. It is estimated that an average human being has approximately 300, 000 hairs on their scalp with a growth rate of approximately half an inch per month (Elewski, 2000). This has therefore led to the establishment of several barbing industries all over towns and cities in Nigeria. It is an important professional in many modern communities around the world being owned and managed by individuals in such communities. Reports indicated that an estimated 25% of the world's population suffers from dermatomycosis, a barbing-related skin disease. Though these infections are regarded as non-lethal, they compromise the quality of life of infected patients.

Problem Statement

In many cities and even villages, the establishment of barbing salons has been on the increase, thereby the tendency of fungal-associated infections (mycosis) to increase morbidity and mortality in the individual becomes obvious. Barbing shops which are classified as personal service establishments, may pose potential health concerns to their clients including the risk of infection and sometimes injury (Mbajiuka *et al*., 2014). Most of the spores of these fungi are transmitted through barbing tools either as blood-borne or other infestations.

Justification

Transmission of fungal infection can be by direct person-to-person contact, or indirectly by shared fomites or instruments (Enemour *et al*., 2012). Fungal infections can be prevented with adequate knowledge of the mode of transmission and an understanding of basic hygiene.

Aim

This study was carried out to isolate and characterize fungi of barbing tools origin in some shops within Lugbe, Federal Housing Estate, FCT, Abuja, Nigeria.

METHODS

A total of 400 samples were collected from tools (comb, towel, brush) and surfaces of 20 barber shops in the study areas and were examined for the presence and kinds of fungi using some mycological techniques which included serial dilution of the samples and surface-swapped materials from the respective shops in sterile peptone water. An aliquot of 0.1ml of 10^{-2} and 10^{-4} dilutions was respectively pour-plated in sterile Potato Dextrose Agar (PDA) supplemented with Streptomycin and then incubated at 28^{0}C for five days (Cheesbrough, 2000). The resulting discrete colonies were sub-cultured, purified, and viewed under lactophenol cotton blue stained preparations under the microscope and their respective fungal features were compared with standard literature.

RESULTS AND DISCUSSION

Yeast and moulds are responsible for dermatomycosis which are mycotic diseases of skin. They have recently become important fungal infections due to their ability to spread by various inanimate objects from person to person who share objects such as hats, combs, brushes, towels, linens and slippers, which are contaminated by hair, and detached skin of infected persons. After the findings in this study, out of the five tools studied, lubricating oil was the most contaminated. *Aspergillus niger*, *Rhizopus stolonifera*, *Alternaria chlamydospore*, *Microsporum audouinii* and *Trichophyton equinum* were the predominant fungi isolated from the samples. Based on the percentage occurrence, lubricating oil had the highest percentage occurrence of fungi, (43.6%), followed by towel, 23.5%, brush, 11.4%, clipper, 10.4% and surfaces the lowest, being 11.1%. The findings of this work align with that of Eribo *et al*. (2017). The presence and inclusion of dermatophytic fungi from the samples are worrisome because most of the materials and tools used on the head routinely after the clipper must have been heat/chemical-sterilized.

CONCLUSION AND RECOMMENDATIONS

These tools were found to be the potential vehicles for the transmission of superficial fungal infections such as ringworm of the scalp (*Tinea capitis*), caused by fungi of genera Trichophyton, Microsporum and Epidermorphyton. It is hereby highly recommended that the common lubricating oil be prepared by incorporating antifungal agents in the formulations to reduce the possibility of customers returning home with one infection or the other despite the aesthetic uses.

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Bioprospection of *Azanza garckeana* Botanicals for Diabetes Management *in vivo*

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INTRODUCTION

Diabetes is a chronic metabolic disorder affecting people of all age groups, associated with chronic hyperglycemia, long-term damage, dysfunction, and organ failure. It is a metabolic disorder characterized by high blood glucose, high insulin production, high insulin resistance, or insulin intolerance, due to the destruction of carbohydrates, protein, and lipid metabolism (Nambirajan *et al.,* 2018). Several symptoms such as polyuria, blurred vision, polyphagia, polydipsia, and weight loss also accompany diabetes. Out of the various types of diabetes, the development of Type 2 Diabetes Mellitus (T2DM) is very high and common with the detection of about 90% of all cases (Lawal *et al.,* 2022). Currently, there are approximately 600 million people with diabetes and an increased prevalence of 783 million people has been estimated to occur by 2045 (International Diabetes Federation [IDF], 2021). Sub-Saharan Africa is estimated to have 20 million people with diabetes, and Nigeria has the highest number with an estimated 3.9 million people (or an extrapolated prevalence of 4.99%) of the adult population aged 20-79 years old (World Health Organization, 2013). Approximately 50% of diabetics lack proper diagnosis and treatment, with a significant economic burden. The IDF Atlas 2021 predicts diabetes-related health expenditures to reach USD 1.03 trillion by 2030. Despite synthetic drug advancements, side effects limit their use. Traditional practices and studies show medicinal plants' therapeutic potential (Nanman *et al*., 2023). The rising prevalence and complications of diabetes necessitate effective management strategies and novel antidiabetic agents from plants (Japhet *et al*., 2024). *Azanza garckeana*, a Malvaceae family plant used in Africa, treats various diseases including diabetes (Blessing *et al*., 2022). This study explores *A. garckeana*'s bioprospection for diabetes management *in vivo*.

METHODS

The plant parts (leaf, fruit, stem, and root bark) of *Azanza garckeana* were collected from Tula village, Kaltungo Local Government Area of Gombe State. The plant was identified and authenticated at Forest Herbarium, College of Forestry, Jos, and assigned Voucher specimen no.FHJ82022. The plant parts (Leaf, Root bark, Stem, and Fruit) were extracted by cold maceration, the extracts were then stored in desiccators. All other chemicals were of analytical grade. A total of twenty-eight male white Albino rats (Wistar Strain) weighing between 150–250g were distributed into seven (7) groups of four (4) rats each obtained from the animal house University of Jos, Plateau state, Nigeria. Animal handling and experimentation were approved by the ethical committee of the University of Jos, Plateau State, Nigeria. In compliance with internationally accepted principles for human handling and use of laboratory animals in the Canadian Council on Animal Care Guidelines and Protocol Review. The method of Etuk (2010) was employed. The rats were treated with aqueous extract of *Azanza garckeana* parts at 100 mg/kg bw and the standard (100 mg/kg b.w. metformin). All treatments were administered daily for 28 days through the oral route with the aid of an oesophagal cannula. Animals were sacrificed following animal Care Guidelines and Protocol Review and blood samples were collected for biochemical analysis. The data collected were presented as Mean ± SEM of 4 replicates and were analyzed using the Duncan multiple range test following one-way Analysis of Variance (ANOVA) using IBM SPSS 23.0 computer software package (SPSS Inc., Chicago U.S.A). Differences at P< 0.05 were considered significant.

RESULTS AND DISCUSSION

The phytochemical analysis of the aqueous extracts of the stem bark, root bark, leaves and fruit extracts of *Azanza garckeana* indicates the presence of flavonoids, saponin, carbohydrates, alkaloids, tannins, terpenes, steroids, phenols, anthraquinones, and cardiac glycoside. The leaf extract presented a high number of phytochemicals. Table 1 shows significant ($p < 0.05$) increases in serum glucose and decreases in protein and albumin levels in diabetic controls compared to normal controls. Treatment with leaf, fruit, and root extracts significantly ($p < 0.05$) reduced glucose levels, comparable to standard drug effects, while stem extract showed no improvement. Albumin and total protein levels normalized after treatment with different plant parts, suggesting protective effects against diabetes-induced changes. These measurements reflect metabolic status and are used to evaluate kidney and liver function.

The results present the effects of *Azanza garckeana* plant part extracts (all at 100 mg/kg) on lipid profiles in streptozotocin-induced diabetic rats. Compared to normal controls, diabetic controls show significantly ($p < 0.05$) elevated total cholesterol, triglycerides, and LDL, with significantly ($p < 0.05$) reduced HDL. The standard drug treatment improves all parameters. Among the 100 mg/kg plant extracts, root and leaf show the most promise, normalizing total cholesterol and reducing triglycerides, though HDL remains low and leaf extract raises LDL slightly. The stem extract (100 mg/kg) unexpectedly increases all lipid parameters, while the fruit extract (100 mg/kg) lowers triglycerides but elevates LDL. Therefore, these showed varying effects of *Azanza garckeana* parts on diabetic rat lipid profiles, with root and leaf extracts showing potential therapeutic benefits, while stem extract effects warrant further investigation.

Table 1: Effects of Aqueous Extract of Different Parts of *Azanza garckeana* Botanicals on Glucose, Protein and Albumin Levels in Streptozotocin-Induced Diabetic Rats.

GROUPS	GLUCOSE (mmol/l)	TOTAL PROTEIN (g/l)	ALBUMIN (mg/dl)
Normal Control	5.00 ± 0.25	75.00 ± 2.52	38.00 ± 0.58
Diabetic Control	30.16 ± 32.52	67.00 ± 0.58	30.00 ± 1.53
Diabetic Treated STD Drug	5.85 ± 0.29	74.53 ± 0.86	39.54 ± 0.29
Diabetic Treated Leaf 100 mg/kg	5.20 ± 0.06	75.00 ± 0.58	39.50 ± 0.29
Diabetic Treated Root 100 mg/kg	10.10 ± 0.06	68.00 ± 0.59	35.60 ± 0.31
Diabetic Treated Stem 100 mg/kg	31.50 ± 0.29	79.00 ± 0.58	32.53 ± 0.29
Diabetic Treated Fruit 100 mg/.kg	6.90 ± 0.06	82.50 ± 0.29	44.00 ± 0.58

If p-value is greater than 0.05, mean values are not statistically significant ($p < 0.05$) Values are expressed as mean ± SEM, n=4.

TABLE 2: Effects of Aqueous Extract of Different Parts of *Azanza garckeana Botanicals* on Lipid Profiles in Streptozotocin-Induced Diabetic Rats

Treatment Groups		Total cholesterol (mmol/L)	HDL (mmol/L)	Triglyceride (mmol/L)	LDL (mmol/L)
Normal Control		2.40 ± 0.06	1.06 ± 0.04	0.86 ± 0.04	0.88 ± 0.04
Diabetic Control		3.10 ± 0.06	1.73 ± 0.05	2.00 ± 0.06	0.76 ± 0.16
Diabetic-treated drug	STD	2.12 ± 0.17	1.58±0.139	1.61 ± 0.29	1.11 ± 0.05
Diabetic-treated 100 mg/kg	Leaf	2.26 ± 0.09	0.96 ± 0.09	0.65 ± 0.03	1.25 ± 0.08
Diabetic-treated 100 mg/kg	Root	2.00 ± 0.06	0.92 ± 0.04	0.53 ± 0.04	0.99 ± 0.01
Diabetic-treated 100 mg/kg	Stem	3.63±0.145	1.99 ± 0.01	2.13 ± 0.09	1.36 ± 0.04
Diabetic-treated 100 mg/kg	Fruit	2.70 ± 0.12	1.24 ± 0.03	0.96 ± 0.03	1.65 ± 0.04

If p-value is greater than 0.05, mean values are not statistically significant ($p < 0.05$) Values are expressed as mean ± SEM, n=4

Effects of Aqueous Extract of Different Parts of *Azanza garckeana* Botanicals on Serum Enzymes in Streptozotocin-Induced Diabetic Rats

The study examined the impact of *Azanza garckeana* plant component extracts (leaf, roots and fruits at 100 mg/kg on serum enzyme levels in streptozotocin-induced diabetic rats.

Compared to normal controls, diabetic controls show significantly ($p < 0.05$) elevated levels of ALT, AST, and ALP, indicating liver impairment. The standard drug treatment improves all parameters, reducing enzyme levels below normal control values. Among the 100 mg/kg plant extracts, the leaf shows the most potential, bringing ALT, AST, and ALP levels close to normal control values. Root and fruit extracts also demonstrate positive effects, significantly reducing enzyme levels compared to diabetic controls. The stem extract (100 mg/kg) unexpectedly shows little beneficial effect, with enzyme levels remaining similar to or slightly higher than diabetic controls. The "all part" extract (100 mg/kg) shows

moderate improvement in enzyme levels. Therefore, these results demonstrate varying effects of *Azanza garckeana* parts on diabetic rat liver enzyme profiles, with leaf extract showing the most potential for hepatoprotective benefits, while stem extract effects warrant further investigation.

Table 3: **Enzymes in Streptozotocin-Induced Diabetic Rats**

Normal Control	92.66 ± 6.69	129.33 ± 8.35	80.00±9.018
Diabetic Control	256.67 ± 67.33	326.67 ± 33.23	256.67 ± 59.83
Diabetic Treated Standard Drugs	63.57 ± 2.62	79.52 ± 5.47	50.03 ± 2.32
Diabetic Treated Leaf 100 mg/kg	93.37 ± 0.88	138.00 ± 4.04	81.67 ± 1.20
Diabetic Treated Root 100 mg/kg	71.16 ± 0.60	154.00 ± 2.31	71.16 ± 0.60
Diabetic Treated Stem 100 mg/kg	245.00 ±1.16	385.6 ± 2.85	266.43 ± 1.27
Diabetic Treated Fruit 100 mg/kg	71.33±0.881	152.00 ± 0.58	63.33 ± 0.88
Diabetic Treated All part 100 mg/kg	91.23 ± 0.79	194.67 ± 24.78	89.33 ± 1.45

If p-value is greater than 0.05, mean values are not statistically significant ($p < 0.05$) Values are expressed as mean ± SEM, n=4.

CONCLUSION

The aqueous leaf extract of *A. garckeana* possesses the most significant antidiabetic activity, this might be as a result of the various phytochemical components present in the leaf extract.

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Seroprevalence of Dengue Virus in Patients Attending Some Selected Hospitals in Zaria, Kaduna State; Nigeria

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INTRODUCTION

Dengue is a disease caused by dengue virus. The disease is primarily transmitted through the bite of an infected Aedes mosquito. It can be classified as either asymptomatic/symptomatic or severe dengue. Four serotypes of the virus which are in circulation have distinct interactions with the host immune response, but they share about 65% genome similarity (Tizhe *et al.,* 2023). Primary infection with any of the serotypes provides lifelong immunity against the same serotype and temporal immunity against other serotypes. Severe forms of infection are usually due to secondary infection with other serotypes. Current control and management of dengue depend primarily on vector control measures. Data on dengue remains key in addressing the threat posed by the disease.

METHODOLOGY

Malaria Detection

Blood samples collected from suspected patients across three hospitals were tested for malaria and antibodies against dengue. Malaria parasitemia was determined by microscopic technique. Thick and thin blood films were prepared on grease-free and clean glass slides. Thin blood films were fixed with 100% methanol prior to staining. The films were air-dried and stained with 10% freshly prepared Giemsa stain maintained at pH 7.2. Stained blood films were viewed under a light microscope at x1000 magnification (WHO, 2010). The detection of malaria was based on the observation and identification of asexual stages of *Plasmodium* on thick blood films, while thin blood films were used in the observation and identification of *Plasmodium* species. In the absence of a parasite, the films were declared negative (WHO, 2010).

Dengue Antibody Detection

Sera samples obtained from the patients were used to screen for the presence of dengue IgM antibody using an Enzyme-Linked Immunosorbent assay-specific kit according to the manufacturer's instructions (RD-Diagnostics, Dengue IgM ELISA, C-DIM-K23). A positive ELISA result was defined as having an antibody index value >1.1.

RESULTS

Out of the 190 patients recruited across the three hospitals, 156 (82.1%) tested positive for malaria parasites, while 85 (44.7%) tested positive for dengue IgM detection assay. Dengue seroprevalence of 44.7% was recorded across the three facilities. Fifty-eight (58) or 30.5% of patients were found to be co-infected with dengue and malaria in these areas.

CONCLUSION

The study established the occurrence of dengue infection with an overall prevalence of 44.7%. The study also established the possibility of dengue and malaria co-infection, hence febrile illnesses should not be limited to malaria only. Other aetiologies of febrile illnesses should be considered to prevent misdiagnosis and consequent untold hardships. With an overall seroprevalence of 44.7%, dengue may be endemic in this area but has remained undetected.

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Phytochemical Composition and LCMS/MS Analysis of *Guiera senegalensis* Aqueous and Methanolic Leaf Extracts: A Potential Source for Traditional African Medicine

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ABSTRACT

BACKGROUND

Guiera senegalensis is a significant medicinal plant widely utilized in traditional African medicine, this plant has been traditionally employed to treat a variety of ailments. However, comprehensive phytochemical profiling is essential to elucidate the compounds responsible for its pharmacological effects.

MATERIALS AND METHODS

A detailed phytochemical investigation of *Guiera senegalensis* leaves using LC-MS/MS analysis was conducted in this study. The leaves were subjected to both aqueous and methanolic extraction processes. The choice of methanol as a solvent was driven by its effectiveness in extracting a broad range of phytochemicals, including steroids, flavonoids, phenolic compounds, and terpenoids.

RESULTS AND DISCUSSION

The LC-MS/MS analysis revealed a complex phytochemical profile, identifying 46 unique compounds across the extracts. Among the identified compounds, galloylquinic acid derivatives, phenolic acids, and flavonoids were prominent. The study also highlighted the presence of tannins, beta-carboline alkaloids, naphthopyrans, flavonoids, and alkaloids in varying quantities. Relevant bioactive compounds such as mucilage, apigenin, rutin, gallic acid, kaempferol, myricitrin, rutin, and quercetin were identified, showcasing the plant's rich pharmacological potential that is associated with diverse pharmacological effects, including anti-inflammatory, antibacterial, anticancer, cardioprotective, neuroprotective, and antiallergic properties.

Table 1: Phytochemical constituents of the extracts and quantity

PHYTOCHEMICALS EXTRACTS	MEOH	AQUEOUS
Saponins	**+ 15%**	**+ 20%**
Tannins	**+ 1.6%**	**+ 2.72%**
Phenolic compounds	**+ 2.13%**	**+ 1.82%**
Alkaloids	**+ 7%**	**+ 8%**
Flavonoids	**+ 23%**	**+ 17.6%**
Terpenoids	**+ 30%**	**+ 10%**
Cardiac glycosides	**+ 0.88%**	**+ 0.01%**
Anthraquinones	-	-
Steroids	**+ 4.5%**	**+ 3.42%**
Carbohydrates	+	+

Key: Present: +; Not present: -

CONCLUSION

This study showcases the potential health benefits of *Guiera senegalensis*, presenting it as a valuable resource in traditional African medicine. The comprehensive identification of bioactive compounds opens new avenues for research and development, aiming to harness the plant's full therapeutic potential. These findings contribute significantly to the understanding of the phytochemical complexities of *Guiera senegalensis* and its application in modern medicine.

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Amplification of 16S rRNA and Cry 1Ab Genes Of Indigenous *Bacillus thuringiensis* Strains Isolated from Selected Soils in the Federal Capital Territory (FCT), Nigeria

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ABSTRACT
Background
Bacillus thuringiensis (Bt) is a gram-positive, facultative anaerobe and spore-forming bacterium known for producing insecticidal proteins (Rajashekhar, 2015; Paddock *et al.,* 2024). The bacterium has the ability to produce some insecticidal proteins during sporulation, which are deposited as crystalline aggregates parasporal crystals known as δ-endotoxins.These δ-endotoxins are toxic to a great number of insects thereby making the bacterium a very useful microorganism as source of material for the control and management of various insect pests on the farm, specifically the orders *lepidoptera, Diptera* and *Coleoptera* and some *Hemiptereta* (Sanahuja, *et al.,* 2011; Rajashekhar, 2015). *Bt* has been widely and successfully used as a plant-incorporated protectant (PIP) in various transgenic crops due to its high specificity, cost-effectiveness, and environmental friendliness. Most strains currently utilized for commercial and research purposes originate from foreign isolates (Mehlo et al., 2005). This study aims to conduct molecular characterization of indigenous Bt strains isolated from soils in the Federal Capital Territory (FCT), Nigeria. Isolating indigenous variants of this bacterium as broad-spectrum agricultural bio-insecticides in Nigeria will reduce reliance on exotic and costly microbial variants and provide proprietary rights for future applications.

Methodology
Bacillus strains isolated from soils in selected locations within the FCT, previously identified as *Bt* through microbiological and biochemical analyses (Ajenifujah-Solebo et al., unpublished data, 2023), were subjected to molecular characterization using 16S rRNA and Cry 1Ab gene primers. DNA was extracted from bacterial cells harvested from overnight cultures of pure isolates incubated at 30 ± 2°C in nutrient broth, following the Norgen Biotek crop kit protocol. PCR amplification of the 16S rRNA and Cry 1Ab gene primers (sequences provided in Table 1) was performed under specific thermal cycling conditions (Table 1) (Saleem and Shakoori, 2013). For gel electrophoresis, the PCR products were run on a 1% agarose gel at 90V for 30 minutes and visualized under UV light using a Gel Doc (Transilluminator).

Results
The DNA concentration of the nine isolates ranged from the lowest value of 50.4ng/µl in sample 4 to the highest value of 145.8ng/µl in sample 7. The DNA concentrations obtained are acceptable range for molecular analysis, with the minimum recommended DNA concentration of 50ng/µl.
The expected band size for 16S rRNA amplification is 1400 kb. The lane for the respective isolates and the DNA ladder marker is as shown.
Figure 1 and 2 shows the band sizes of the extracted DNA on gel. The band sizes of 1400bp on amplification of 16S rRNA gene and 1000bp on amplification of Cry 1Ab gene suggest the presence of *Bt* strains in the soil samples.

Table 1: 16S rRNA and Cry1Ab primer sequences and thermal cycling conditions

S/N	NAME	SEQUENCE	TM	MW
1	16S rRNA ABNL-27F	5'-AGAGTTTGATCMTGGCTCAG-3'	59.4°C	6160.1
	ABNL-1492R	5'-TACGGYTACCTTACGCTT-3'	56.9°C	5746.3
2	Cry1Ab ABINL-Cry1Ab-1 F	5'ACCATCAACAGCCGCTACAACGACC3'	67.9°C	7533.9
	ABINL-Cry1Ab-2 R	5'TGGGGAACAGGCTCACGATGTCCAG3'	69.5°C	7732.1

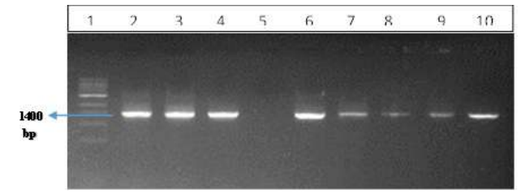

Figure 1. Amplification of 16S rRNA gene in isolated *Bacillus thuringiensis* strains at 1400 bp

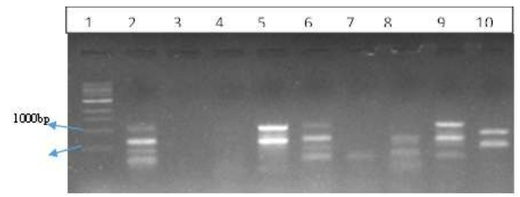

Figure 2. Amplification of Cry 1Ab gene in isolated *Bacillus thuringiensis* strains at 120 - 1000bp

KEY: Legend for figure 1 and 2

Well No.	Samples ID (16S rRNA)		Samples ID (Cry 1Ab gene)	
1	1 kb DNA Ladder		1 kb DNA Ladder	
2	1	+	1	+
3	2	+	2	
4	3	+	3	
5	4		4	+
6	5	+	5	+
7	6	+	6	
8	7	+	7	+
9	8	+	8	+
10	9	+	9	+

+ amplification observed in sample

Conclusion
The amplification of the 16S rRNA and Cry 1Ab genes at the expected base pair (bp) sizes of 1400 bp and between 120-1000 bp respectively confirms that the isolated strains are bacteria and specifically *Bacillus thuringiensis.* Therefore, indigenous *Bt* strains were successfully isolated from soils in the selected locations within the FCT.
Wide applications with success have been recorded due to their high specificity and cost-effectiveness aside from their being environmentally friendly, the bacterium can be isolated from native soil as indigenous, wide-spectrum bio-insecticides against many agricultural crop pests in Nigeria.

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Prospecting for Natural Compounds with Therapeutic Potential Against HIV-1 Tat Protein Using Computational Tools

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INTRODUCTION
Human Immunodeficiency virus (HIV) remains one of the world's most serious health challenges, with over 38 million infected (Forezi *et al.,* 2020). The virus primarily infects and depletes $CD4^+$ T helper cells, increasing the risk of infections and progression to Acquired Immune Deficiency Syndrome (AIDS) (Crisan & Bora, 2021). While antiretroviral therapies (ART) have been effective, concerns remain about multidrug resistance, poor compliance with treatment regimens, and side effects (Wan & Chen, 2014; Panel on Antiretroviral Guidelines for Adults and Adolescents, 2024). HIV-1 Tat, the first protein released upon virus entry, promotes viral replication and dissemination, even with effective ART (Ajasin & Eugenin, 2020). Both the virus and various host cells involved in HIV pathogenesis are susceptible to Tat (Cafaro *et al.,* 2024). Tat has also been associated with HIV-1 latency and comorbidities like neurocognitive disorders and cardiovascular impairment (Ajasin & Eugenin, 2020). These roles make Tat an attractive drug target, yet no clinically approved Tat inhibitors exist (Puhl *et al.,* 2019). Traditional herbal plants are a rich source of bioactive compounds with therapeutic potential (Sreeram *et al.,* 2023). Therefore, this study was to identify natural compounds with inhibitory activity on HIV-1 Tat using computational tools.

METHODS
The 3D crystal structure of the drug target, HIV-1 Tat Protein (PDB ID: 8CCW) was downloaded from the Protein Data Bank (Figure 1). The protein structure was visualized and cleaned up using Pymol Software. The webserver, Chiron was used to reduce steric clashes within the protein structure. The 3D structures of a pre-screened library of 1,040 compounds derived from Indigenous and edible African plants were downloaded in sdf format from the PubChem database, along with the reference compound, Roscovitine (PubChem ID: 160355). The PubChem ID, chemical and physical properties of all compounds were retrieved from PubChem. All ligands including Roscovitine were uploaded to PyRx Software 0.8 version and docked against the HIV-1 Tat protein target. Docking results were screened using the binding affinity score of Roscovitine, i.e., -8.1 kcal/mol as a cut-off score to identify the compounds with the best binding affinity to HIV-1 Tat. The bioavailability and ADMET (absorption, distribution, metabolism, excretion and toxicity) profiles of the compounds with the best binding affinity were assessed using SwissADME and pkCSM webservers, respectively.

RESULTS AND DISCUSSION

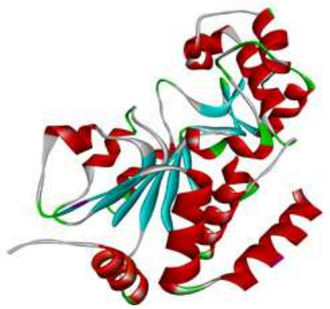

Figure 1. 3D crystal structure of HIV-1 Tat Protein.

The bioavailability of compounds is determined by a set of variables known as Lipinski's Rule of Five, Veber's rule and Ghose filter as shown in Table 1. These rules collectively state that hydrogen bond acceptor, hydrogen bond donor, Log P (octanol-water partition coefficient), molecular weight, topological surface area, rotatable bonds and molar refractivity should be ⩽ 10, ⩽ 5, ⩽ 5, 500 g/mol and ⩽ 140 A^2, respectively. Also, the number of rotatable bonds should be ⩽ 10 and the molar refractivity should be within the range of 40 – 130 cm^2 (Rowaiye *et al.,* 2021).
The reference and lead compounds did not violate any of these rules

Table 1. PubChem ID, chemical and physical properties of the reference and lead compounds.

	Roscovitine (Reference)	Gibberellin A20	Gibberellin A44	Gomeric Acid	Andrographolide
PubChem ID	160355	5280481	5460372	101286255	6436016
Molecular Weight (g/mol)	354.45	332.39	346.42	322.48	350.45
XLogP3	3.16	1.2	1.62	4.81	2.16
Hydrogen Bond Donor Count	3	2	2	1	3
Hydrogen Bond Acceptor Count	4	5	5	3	5
Rotatable Bond count	8	1	1	2	3
Topological Polar Surface Area (TPSA) Å²	87.89	83.83	83.83	46.53	86.99
Heavy Atom Count	26	24	25	23	25
Saturation (Fraction Csp3)	0.42	0.79	0.80	0.95	0.75
Molar Refractivity	104.88	86.18	90.69	94.32	95.21
PAINS alert	0	0	0	0	0

Variables	Roscovitine (Reference)	Gibberellin A20	Gibberellin A44	Gomeric Acid	Andrographolide
ABSORPTION					
Water solubility (log mol/L)	-3	-2.636	-2.839	-3.795	-3.494
Caco-2 Permeability (log Papp in 10–6 cm.s-1)	1.293	1.186	1.182	1.417	1.07
Human Intestinal absorption (% absorbed).	89.24	98.911	99.298	92.332	95.357
Skin Permeability (log Kp)	-2.735	-2.735	-2.735	-2.735	-3.794
P-glycoprotein substrate (Yes/No)	Yes	No	No	No	No
P-glycoprotein I inhibitor (Yes/No)	Yes	No	No	No	No
P-glycoprotein II inhibitor (Yes/No)	No	No	No	No	No
DISTRIBUTION					
VDss (human) (log L/kg)	0.418	-0.829	-1.111	-0.14	-0.286
Fraction unbound (human) (Fu)_	0.349	0.418	0.3	0.247	0.281
BBB Permeability (log BB)	-1.199	-0.209	-0.178	0.615	-0.598
CNS Permeability (log PS)	-2.846	-2.998	-2.289	-2.69	-2.691
METABOLISM					
CYP2D6 substrate (Yes/No)	No	No	No	No	No
CYP3A4 substrate (Yes/No)	No	Yes	Yes	Yes	Yes
CYP1A2 inhibitor (Yes/No)	Yes	No	No	No	No
CYP2C19 inhibitor (Yes/No)	No	No	No	No	No
CYP2C9 inhibitor (Yes/No)	No	No	No	No	No
CYP2D6 inhibitor (Yes/No)	No	No	No	No	No
CYP3A4 inhibitor (Yes/No)	No	No	No	No	No
EXCRETION					
Total Clearance (log ml/min/kg)	0.95	0.417	0.36	0.539	1.183
Renal OCT2 substrate (Yes/No)	Yes	No	No	No	No
TOXICITY					
AMES toxicity (Yes/No)	Yes	No	No	No	No
Max. Tolerated dose (human) (log mg/kg/day)	0.832	0.371	0.152	0.363	0.128
hERG I inhibitor (Yes/No)	No	No	No	No	No
hERG II inhibitor (Yes/No)	No	No	No	No	No
Oral Rat Acute Toxicity (LD50) (mol/kg)	2.347	2.051	2.057	2.103	2.162
Oral Rat Chronic Toxicity (log mg/kg/day)	1.558	2.135	1.958	1.956	1
Hepatotoxicity (Yes/No)	Yes	No	No	No	No
Skin sensitization (Yes/No)	No	No	No	No	No
T. Pyriformis toxicity(log µg/L)	0.285	0.285	0.285	0.33	0.491
Minnows toxicity (log mM)	3.156	1.958	1.758	0.094	1.37

Figure 2. ADMET properties of the reference and lead compounds.

suggesting they have good drug-likeness properties. The docking results revealed that the lead compounds, namely Gibberellin A20, Gibberellin A44, Gomeric Acid and Andrographolide had binding affinity scores of -9.4 kcal/mol, -9.3 kcal/mol, -8.9 kcal/mol, and -8.7 kcal/mol, respectively, and performed better Roscovitine (-8.1 kcal/mol) which is a known Tat inhibitor (Shin *et al.,* 2020). ADMET analysis predicted the lead compounds to be non-hepatotoxic, non-mutagenic and non-carcinogenic, unlike Roscovitine, suggesting that they could be safer drug candidates for human use (Figure 2). In general, the lead compounds were predicted to have better absorption properties than Roscovitine.

CONCLUSION

Gibberellin A20, Gibberellin A44, Gomeric acid and Andrographolide had the most promising results as anti-HIV-1 Tat inhibitors based on their binding affinities, bioavailability and ADMET profiles. Further in vitro and in vivo studies are required to validate these findings.

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Fermentation of Corn Cob as a Feed Component using Co-Culture of *Bacillus Sp.* and *Saccharomyces Cerevisiae*

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INTRODUCTION

In recent years, the need for food production on a larger scale became obvious due to the increasing population. The process often generates wastes such as corn cob. This is commonly regarded as a waste product derived during agricultural processing but is known to be so due to its high cellulosic contents. In many parts of the world, they are left to decay on the farm after harvest some also burn them which adds to environmental pollution, depletion of ozone layers and more.

Statement of Research Problem: In many parts of sub-Saharan Africa, livestock productivity is influenced by environmental factors, especially the aspects of the feed which have the most impact. The main feed of ruminants is greenery but are now very limited, especially in the dry season which necessitates the provision of fodder from some agricultural wastes such as corn cub.

Justification: If this material is properly processed and harnessed, it could be utilized as an energy and protein source in feed formulation through controlled microbial fermentation because corn cob is made up of glucose molecules which could be obtained when microbial hydrolysis of the cellulose content is acted upon in a control manner.

Aim of the Study: This study was to determine the effect of control fermentation of corn cob on the nutritional components using co-culture of *Bacillus sp*. and *Saccharomyces cerevisiae* for animal feed base.

MATERIALS AND METHOD

The biomass (Corn cob) was pretreated with mild sodium hydroxide solution at a temperature of 80^{0}C for 3 hours. After rinsing, the biomass was further treated with 300 µL cellulase to convert cellulose to fermentable sugars at 50°C for 48 h. The samples were then divided into four; A was inoculated with *Bacillus sp*. B was inoculated with *Saccharomyces cerevisiae* only and C was inoculated with both cultures of *Bacillus sp*. and *Saccharomyces cerevisiae* (ratio 1:1) while D was uninoculated as control. The set-up, in triplicates and supplemented with mineral salts, was fermented for 5 days.

RESULTS AND DISCUSSION

The protein concentration of crude extract from all the fermented corn cob samples was for A, 0.273mg/ml, B 0.125 mg/ml, C 0.392mg/ml and D 0.178mg/ml respectively as shown in figure 2.
The protein content of the corn cobs fermented with the co-culture was relatively higher than the other samples. The result reveals that corn cobs are loaded with high-feed potential as an alternative feed for livestock if they are fermented to enhance their low nutritional quality.

Figure 1: Showing microorganisms and products after fermentation

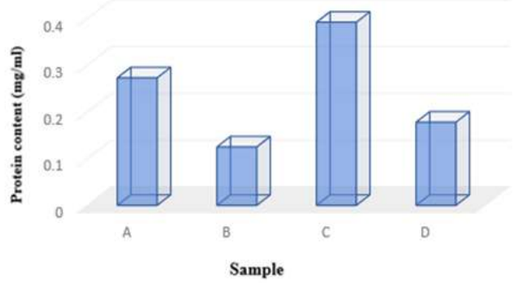

Figure 2: Effects of fermentation on the protein content of corn cobs: Protein concentration of crude extract from fermented corn cobs

CONCLUSION AND RECOMMENDATIONS

It was concluded that microbial co-culture fermentation of *bacillus* and *s. cerevisiae* is an effective and cheaper means of enhancing the nutritional quality of corn cob for use as an energy and protein source in livestock feed formulation. Therefore, this agricultural waste (corn cob) can be fermented to enhance its nutritional quality and improve animal feed components. Furthermore, enhancement of the product's quality should be explored via genetic improvement of the fermenting microorganisms as well as upscaling the product to the commercial application level.

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Exploring Anti-Prostate Cancer Potential of Actinomyces-Derived Compounds: A Network Pharmacology and Molecular Docking Study

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INTRODUCTION

Prostate cancer (Pca), a prevalent malignancy in men, is characterized by the growth of cancer cells in the prostate gland and is one of the leading causes of cancer-related morbidity and mortality globally (Bray et al., 2018). Despite the wide range of available PCa treatment options, their clinical utility is often restricted due to resistance to hormone therapy and chemotherapeutic approaches, recurrence, and severe side effects, hence, the search for newer and safer alternatives is still ongoing (Krause, 2023; Omoboyede, Ibrahim, et al., 2023). Actinomyces, a genus of gram-positive bacteria belonging to the phylum Actinomycetota, are notable for their ability to produce a plethora of secondary metabolites with pharmacological activities. Therefore, evaluating other compounds from the same genus for their potential as cancer therapeutics is a viable approach for identifying new anticancer drugs (Noor et al., 2022). Network pharmacology has emerged as a cutting-edge approach for identifying drug targets in complex diseases involving multiple pathways, repurposing existing drugs, and elucidating the mechanisms of action of drugs (Chandran et al., 2017; Omoboyede, Onile, et al., 2023). In this study, we aim to employ network pharmacology to identify the targets and mechanisms by which compounds produced by microorganisms of the genus Actinomyces can be utilized in the treatment of Pca.

METHODS

- **Drug-likeness Evaluation:** Assessing the drug-like properties of the compounds.
- **Pharmacokinetics and Toxicity Profiling:** Ensuring suitable ADMET profiles.
- **Target Prediction:** Predicting biological targets of the compounds.
- **Microarray Data Analysis:** Identifying dysregulated targets in Pca.
- **Protein-Protein Interaction (PPI) Network Construction:** Using the STRING database and visualizing with Cytoscape software.
- **Gene Ontology (GO) and Pathway Enrichment Analyses:** Revealing the biological processes and pathways mediated by the targets.
- **Molecular Docking:** Simulating the interaction between core targets and compounds to identify top binders.

RESULTS

The compounds were found to modulate 192 PCa-related targets involved in crucial processes such as positive regulation of cell communication, cell death, and signalling pathways including PI3K/AKT, MAPK, and Ras. Core targets identified include CDK1, HSP90AA1, BCL2, HSPA8, ESR1, PIK3R1, ITGB1, and PRKCA, all of which are implicated in PCa development, progression, and metastasis. Molecular docking simulations highlighted mitomycin and trehalamine as promising compounds capable of effectively binding and modulating these core targets.

DISCUSSION

Interestingly, all the compounds were evaluated as potential binders to more than one target associated with PCa development and progression, and enrichment analyses revealed that these targets mediate a crucial role in PCa development and progression. Specifically, the targets mediated biological processes which include programmed cell death, positive regulation of cell communication, positive regulation of signaling, and response to endogenous stimuli among others. It is worth noting that cell communication is crucial for maintaining homeostasis, regulating cell growth, differentiation, and ensuring proper functioning of tissues and organs, and in the context of cancer, dysregulation of cell communication plays a pivotal role in tumorigenesis, cancer progression, and metastasis –(Dominiak et al., 2020). Interestingly, the mechanisms via which cell communication is positively regulated include the activation of pathways such as the MAPK and the PI3K/AKT pathways some of these targets are also enriched (Loureiro et al., 2023). Hence, the modulation of these targets by the understudied compounds could lead to the restoration of normal cell communication in PCa cells, circumventing other processes that may lead to their metastasis. Additionally, these targets are involved in critical molecular functions, including serine/threonine/tyrosine kinase and transmembrane receptor protein kinase activities. In the context of cancer, particularly PCa, aberrant regulation of serine/threonine/tyrosine kinases is often implicated in the progression and malignancy of the disease (Chung et al., 2009). Dysregulation of these kinases can lead to uncontrolled cell proliferation, resistance to apoptosis, and increased metastatic potential, all of which are hallmarks of cancer. For instance, the overactivation of certain tyrosine kinases has been linked to the enhanced growth and survival of PCa cells (Shorning et al., 2020). Hence, the inhibition of these targets by inhibiting PCa progression. Molecular docking simulation revealed that both trehalamine and mitomycin exhibited consistently high affinities for the core targets identified in this study. Based on the results, trehalamine appears to possess a unique multi-target mechanism of action, potentially disrupting several key pathways involved in prostate cancer progression. Mitomycin, whose efficacy has been well-established in the treatment of breast cancer and low-grade upper tract urothelial cancer, also demonstrates a multi-target potential in the context of PCa. These findings suggest that trehalamine and mitomycin could be promising candidates for further investigations, either as standalone therapies or in combination with existing treatments for prostate cancer.

CONCLUSION

The findings of this study revealed that the compounds exhibit high binding affinities for the core targets associated with prostate cancer, indicating their potential as therapeutic agents. The compounds demonstrated a unique multi-target mechanism of action and the potential to disrupt several critical pathways involved in prostate cancer development and progression. Conclusively, two compounds, mitomycin and trehalamine, exhibited the highest potential among the compounds; however, further *in vitro* and *in vivo* studies are needed to validate the findings of this study.

ACKNOWLEDGMENTS

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Harnessing Bacteriocins: Innovative Applications in Industrial Biotechnology

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BACKGROUND

Bacteriocins, antimicrobial peptides synthesized by bacterial ribosomes, have garnered significant attention in industrial biotechnology attributable to their potent antibacterial properties and target specificity (Daba *et al*., 2022; Lozo *et al*., 2021). This paper provides a comprehensive review of the multifaceted applications of bacteriocins across various industrial sectors, with a focus on food preservation, pharmaceutical development, and bioprocessing. The review emphasizes the potential of bacteriocins as natural, effective alternatives to synthetic chemicals and antibiotics, underscoring their role in enhancing product safety and efficiency in industrial processes.

FOOD PRESERVATION

In the food industry, the demand for natural preservatives has surged in response to consumer preferences and regulatory pressures to reduce synthetic chemical use. Bacteriocins, with their ability to inhibit spoilage and pathogenic bacteria, offer a promising solution (Aljohani *et al*., 2023). This paper examines the efficacy of bacteriocins in extending the shelf life of perishable foods and enhancing food safety. Case studies highlight successful implementations where bacteriocins have significantly reduced microbial contamination and spoilage, demonstrating their economic and practical viability as natural preservatives.

PHARMACEUTICAL DEVELOPMENT

The rise of antibiotic-resistant pathogens presents a significant challenge in healthcare, driving the need for novel antimicrobial agents. Bacteriocins, with their unique mechanisms of action and effectiveness against resistant bacteria, are explored as potential next-generation antibiotics (Tarín-Pelló *et al*., 2022; Simons *et al*., 2020). This review delves into the therapeutic prospects of bacteriocins, discussing their application in treating infections that are unresponsive to conventional antibiotics. The potential for bacteriocins to be developed into new classes of pharmaceuticals is evaluated, including their role in targeting specific pathogens while minimizing disruption to the host microbiota.

BIOPROCESSING

In bioprocessing, microbial contamination poses a substantial risk to the yield and quality of bioproducts. Bacteriocins offer a strategic advantage in biofermentation processes by selectively inhibiting unwanted microbial growth (Soto-Reyes *et al*., 2022; Siddiqui *et al*., 2023)). This section of the paper reviews the integration of bacteriocins in bioprocessing, highlighting how they can enhance product yields and improve overall process efficiency. Examples of bacteriocin applications in industrial biofermentation illustrate their benefits in maintaining microbial control without resorting to chemical preservatives.

TECHNOLOGICAL INNOVATIONS

Advancements in genetic engineering and synthetic biology are pivotal in enhancing bacteriocin production and functionality. This paper discusses recent innovations that enable the tailoring of bacteriocin properties, such as spectrum of activity, stability, and production efficiency, to meet specific industrial needs. Genetic modifications and synthetic biology approaches are explored to optimize bacteriocin-producing strains, enhancing their suitability for large-scale industrial applications (Mugwanda *et al*., 2023).

CASE STUDIES

Several case studies are presented to demonstrate the practical application and benefits of bacteriocins in various industrial settings. These include examples from food preservation, pharmaceutical production, and bioprocessing, showcasing the

effectiveness and economic viability of bacteriocins. The case studies provide concrete evidence of the potential of bacteriocins to revolutionize industrial practices and contribute to sustainable and safe production processes.

CONCLUSION

This review offers an in-depth examination of the current status and future potential of bacteriocins in industrial biotechnology. Through highlighting their diverse applications, technological advancements, and economic viability, the paper underscores the transformative potential of bacteriocins in industrial settings. It also addresses the challenges and opportunities associated with their use, aiming to foster further research and development in this promising field. The insights provided in this review are intended to encourage the adoption of bacteriocins in industrial practices, promoting innovation and sustainability in biotechnology.

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Computational Identification of Potential HIV-1 Host Protein Cyclophilin A-Inhibitors from Edible African Plants.

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Keywords: HIV-1; Cyclophilin A; Inhibition; Binding affinity; Molecular docking

INTRODUCTION

HIV is one of the most widespread infectious diseases globally. In 2022, approximately 39 million people were living with HIV, many of whom were adults aged 15-49 years. The WHO African region remains the most severely affected, with about 1 in every 25 adults living with HIV. In 2022, 630,000 people died from HIV-related illnesses (WHO The Global Health Observatory, retrieved July 13, 2023 from https://www.who,int/data/gho/data/themes/hiv-aids). HIV quickly develops resistance to existing treatments and can hide in latent reservoirs, making it difficult to eradicate the virus completely. The global scientific community has researched more effective antiretrovirals that target different key factors at strategic stages of the viral lifecycle. Cyclophilin A, a cellular protein involved in many biological events and diseases, has been identified as an important host factor for HIV-1 infection. Cyclophilin A is the first host factor to be packaged within HIV-1 particles and functions by directly binding to the viral capsid (Padron *et al.,* 2023). Alisporivir, a Cyclosporine A analogue and inhibitor of Cyclophilin A, has been reported to significantly disrupt the replication of HIV-1(Daelemans *et al.,* 2010), although, with some underlying side effects like hyperbilirubinemia and hypertriglyceridemia. African plants with phytochemicals possessing pharmacological properties may also induce therapeutic effects and serve as potential natural inhibitors of Cyclophilin A. Therefore, this study was aimed at identifying potential natural inhibitors of Cyclophilin A, an important host protein in HIV-1 replication, from edible African plants.

METHODOLOGY

The methods described in Rowaiye *et al.* (2022) were employed in this study with slight modifications. Briefly, the 3D structure of Cyclophilin A (Figure 1) (PDB ID: 2RMB) was obtained from the Protein Data Bank, VADAR 1.8 was used to reveal the architecture, and Ramachandran plot was generated using the DiscoveryStudio visualization tool. A library of 1,040 small molecules derived from edible African plants was used for the study. All the compounds were pre-screened for Lipinski's (hydrogen bond donor (HBD) $\leqslant$ 5, hydrogen bond acceptor (HBA) $\leqslant$ 10, molecular weight $\leqslant$ 500, and logP $\leqslant$ 5) and Veber's (polar surface area (PSA) $\leqslant$ 140, and rotatable bonds $\leqslant$ 10) rules (Atatreh *et al.,* 2019). Ahead of the molecular docking, all the ligands were uploaded to the virtual screening software, PyRx (version 0.8) using the Open Babel plug-in tool and converted from sdf to Protein Data Bank, Partial Charge, & Atom Type (pdbqt) format. The AutoDock Vina plug-in tool in Pyrx was used to dock all ligands and the standard, Alisporivir, against the target protein, Cyclophilin A using the grid parameters described in Rowaiye *et al.* (2022). Virtual screening for oral availability was conducted using molecular descriptors and online tools like PubChem and SWISSADME. Further screening for pharmacokinetic properties and bioactivity were performed using pkCSM and Swiss Target Prediction.

RESULTS AND DISCUSSION

The binding affinity score in molecular docking measures the potentiality of the small molecule to find the optimal conformation within the protein binding pocket. Therefore, the ligand with the lower binding energy proposes a better binding affinity making it a likely drug candidate (Bell and Zang, 2019). Three lead compounds demonstrated greater potency as drug candidates as they all have a stronger binding affinity than the standard as shown in Table 1. However, cis-2a,3-Dihydroxy-3-methylcholanthrene has the strongest binding affinity of -9.7 Kcal/mol (Table 1). Additionally, subject to further screening, ellagic acid was left out because it had a PAINS value of 1 and a topological surface area above the accepted value of 140A^2. cis-2a,3-Dihydroxy-3-methylcholanthrene was positive for both mutagenicity and hepatotoxicity. This is a red flag for the drugability of any drug candidate. However, while Murrayazolinine tested positive for mutagenicity, as against the standard drug, it did not demonstrate hepatotoxicity, which is one of the drawbacks of Alisporivir. The results obtained also demonstrated that the lead compounds did not violate most of the Ghose, Lipinski, and Veber rules, and thus suggest that cis-2a,3-Dihydroxy-3-methylcholanthrene and Murrayazolinine have good oral bioavailability and permeability. However, the standard (Alisporivir) violated the Veber rule with a high topological surface area value (278.8A^2) and a molecular weight of 1216.64 g/mol. This suggests that Alisporivir would have considerably lower intestinal absorption, blood-brain barrier permeation, and cellular potency when compared to the lead compound (Clark, 2011). As shown in Figure 2, the lead compounds also demonstrated multi-protein target properties. Therefore, we suggest that these compounds may be good drug candidates having met some of the criteria for drug-likeness assessment (Al Wasidi *et al.,* 2020). Though, cis-2a,3-Dihydroxy-3-methylcholanthrene is an orphan compound, Murrayazolinine is a natural product found in *Murraya euchrestifolia* (Yohanes *et al.,* 2023).

Table 1. Molecular docking scores of ligands against Cyclophilin A

Ligand	Binding Affinity (kcal/mol)
Alisporivir (Standard)	-9.0
Ellagic acid	-9.2
Murrayazolinine	-9.3
cis-2a,3-Dihydroxy-3-methylcholanthrene	-9.7

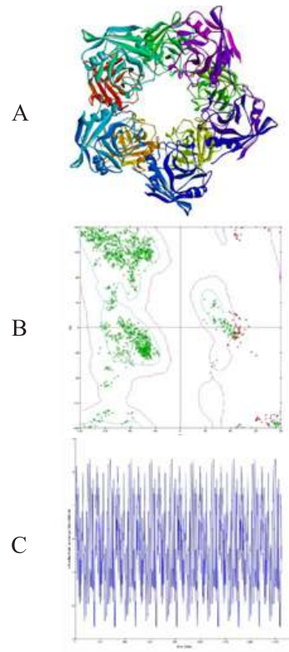
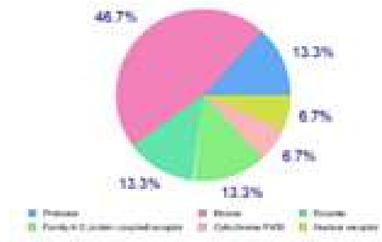
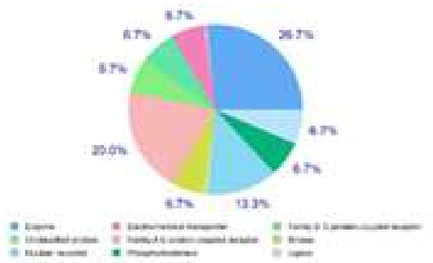


Figure 1.

The 3D structure (A), Ramachandran plot showing the amino acid residue conformation (B) and the hydrophobicity plot (C) of Cyclophilin A protein target.



cis-2a,3-Dihydroxy-3-methylcholanthrene



Murrayazoline

Alisporivir (Standard)

Figure 2. Target prediction of drug candidates and standard drugs.

CONCLUSION

Results obtained from this study suggest that the lead compounds, cis-2a,3-Dihydroxy-3-methylcholanthrene and Murrayazolinine possess inhibitory potentials against Cyclophilin A. However, these compounds also showed toxicological concerns. There is a need for further research to ascertain their inhibitory activities through comprehensive studies to evaluate their therapeutic potential effectively.

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Removal of Hydrocarbons from Kaduna Refining and Petrochemical Company Effluents using *Cladosporium.*

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INTRODUCTION

Bioremediation is defined as a process by which microorganisms are aided to degrade harmful organic pollutants to environmentally safe levels in water bodies. Microorganisms find food they eat in the oil or water where they live. However, if a contaminant is present it can become an additional food source for the microorganisms. The contaminants also provide energy for these microbes. The microbes obtain energy by breaking chemical bonds and transferring electrons away from the contaminants. This is known as an oxidation-reduction reaction. The contaminant that loses electrons is oxidized while that which accepts is reduced. Mycoremediation is a form of bioremediation where fungi are used to degrade or sequester contaminants in the environment. Fungal Mycelium Stimulates microbial and enzyme activity, reduces toxins, are hyperaccumulator and is capable of absorbing and concentrating hydrocarbons in their mushroom fruiting bodies. The decomposition of the fungi is usually performed by the mycelium. The mycelium secretes extracellular enzymes and acids that break down the organic matter. Petroleum-based products are the major source of energy for industry and daily life. Leaks and accidental spills occur regularly during the exploration, production, refining, transport and storage of petroleum products. The amount of natural crude oil seepage was estimated to be 600,000 metric tons per year with a range of uncertainty of 200,000 metric tons per year. Release of hydrocarbons into the environment whether accidentally or due to human activity is a main cause of water and soil pollution.

METHODOLOGY

Determination of total hydrocarbon concentration (Singh 2014).

To obtain the Total hydrocarbon concentration, the sample was properly mixed using a Vortex mixer, 50ml of the samples were transferred into a beaker, the pH was adjusted to 2 or less to acidify the sample, and the acidified sample was transferred into a 1000 ml graduated separatory funnel, 20ml of tetrachloroethylene was added to the sample in the separating funnel, the separatory funnel was covered and stirred thoroughly, the cap was removed at intervals to release pressure build-up, the separatory funnel was kept standing to allow the content to settle and separate, all emulsions were allowed to break before drawing the extract, the bottom layer was transferred into a clean 50 ml volumetric flask. Another 20 ml of tetrachloroethylene was added to the sample in the separatory funnel, the sample was fed into the quartz cell reagent to establish background spectra. The absorbance was recorded and the values obtained were entered into a graph to obtain the resultant concentration (Khan *et al*., 2013).

Isolation and characterization of *Cladosporium spp.* Hydrocarbon-contaminated water samples were done using the method of (Khan 2013).

RESULTS

Table 1: Total Hydrocarbon Concentration in (mg/l) before and after Bioremediation using *Cladosporium*

STERILIZED			NON-STERILIZED		%Removal(NS)	%Removal(s)
Absorbance (HC)	Before	After	(HC)Before	After		
A0.004	1.87	0.02	1.405	0.015	14	56
B0.035	1.64	0.02	1	0.03	45	11
C0.001	0.4	0.02	1.171	0.002	16	33

Key: mg/l- milligram per litre A, B, C refer to the sampling points; NS: Non Sterilized; S: Sterilized; S: Sample.

Effects of bioremediation using *Cladosporium* on the hydrocarbon concentration

After the introduction of the isolate as shown in Table 1, hydrocarbon concentration reduced from (1.87-0.02) mg/l for the first sampling point, also had 14% removal values for the sterilized and 56% for the non-sterilized, the other sampling point reduced in hydrocarbon concentration after bioremediation (Magdaline *et al.,* 2020). This reduction was also observed at all sampling points A, B and C.

CONCLUSION

This work has demonstrated the ability of *Cladosporium* in bioremediation as the concentration of hydrocarbon reduced with the introduction of the microorganism at all three sampling points. Therefore, Cladosporium can be used in cleaning and treating refinery effluents as it depicts positive results.

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Review on Recent Advances and Future Prospects in Post-Harvest Techniques used in the Management of Roots and Tubers: Potato and Yam as a Case Study

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INTRODUCTION

Root and tuber crops, such as potatoes and yams, are essential for food security and livelihoods worldwide. To address challenges in postharvest management, advancements have been made in storage technologies, including controlled atmosphere storage and modified atmosphere packaging (Asiedu & Sakyi-Dawson, 2019). Cold chain management, innovative packaging materials, postharvest treatments, and value addition through processing techniques have also contributed to reducing postharvest losses and extending the shelf life of these crops. These developments aim to ensure a sustainable supply of nutritious food while minimizing wastage (Aladdad *et al*. 2020).

Case Study 1: The Recent Advances in Postharvest Techniques Used in the Management of Potato

The recent advances in postharvest techniques for managing potatoes have significantly improved the way these crops are handled, stored, and preserved, leading to improved quality, reduced losses, and increased overall efficiency in the agricultural sector. Two key advances include using temperature and humidity sensors for potato storage and applying genomics in potato quality improvement (Foughali *et al*., 2019). The use of temperature and humidity sensors in potato storage allows for real-time monitoring and control of storage conditions, thus helping to maintain the quality of the potatoes, prevent spoilage, and reduce energy costs associated with storage (Mustika *et al*., 2022). However, sensor accuracy, durability, and potential interference issues need to be carefully addressed to ensure their effectiveness.

In potato quality improvement, genomics and advanced breeding techniques have enabled the precise selection of desirable traits in commercial potato varieties, such as disease resistance, tuber quality, and other complex characteristics (Slater *et al*., 2014). These advancements provide a more efficient and targeted approach to breeding and have the potential to significantly impact the productivity and quality of potato crops (Gebhardt *et al*., 2014). The use of temperature and humidity sensors in potato storage allows for real-time monitoring and control of storage conditions, thus helping to maintain the quality of the potatoes, prevent spoilage, and reduce energy costs associated with storage (Shen *et al*., 2019). However, sensor accuracy, durability, and potential interference issues need to be carefully addressed to ensure their effectiveness.

However, there are several challenges associated with controlled atmosphere storage, including temperature management, humidity control, gas composition, and pest and disease management. There are various solutions available to address these challenges, including insulation materials, temperature control systems, dehumidifiers, gas control systems, insect-proof storage containers, and fungicides and insecticides (Oyom *et al*., 2022). By addressing these challenges, the controlled atmosphere storage of potatoes can be optimized to provide a stable environment and extend their storage life.

Case Study 2: The Recent Advances in Postharvest Techniques Used in the Management of Yam

The recent advances in postharvest techniques for yam management include gamma irradiation and cold room storage. Gamma irradiation is a rapid and extensive method that can reduce post-harvest losses, extend shelf life, and maximize the nutritional value of yam flour (Verma *et al*., 2018). However, it is costly for wide use in practice. Cold room storage involves maintaining specific temperature and humidity conditions to preserve yams, with temperatures around 20°C effectively preventing sprouting and slowing down respiratory activities. However, extensive beneficial outcomes of using controlled atmosphere (CA) technology for large-scale storage of major yam varieties are still lacking (Tenadu, 2016).

Future Prospect and Emerging Trends in Post-Harvest Management of Root and Tuber Crops

An excellent overview of prospects and emerging trends in post-harvest management of root and tuber crops. The focus on efficient postharvest handling and storage techniques, sustainable and eco-friendly practices, the use of nanotechnology, and quality assessment and traceability demonstrate the industry's commitment to improving the quality, shelf life, and value of these commodities (Li *et al.,* 2019).

CONCLUSION

The conclusion emphasizes the importance of sustainable, cost-effective, and environmentally friendly approaches. Additionally, it discusses the integration of novel technologies, such as nanotechnology and precision farming, to revolutionize postharvest management. The utilization of biocontrol agents and bioactive compounds from natural sources is also highlighted as a safer and more sustainable alternative to synthetic chemical treatments. The conclusion underscores the need for a holistic approach across the postharvest supply chain, from production to consumption, to achieve enhanced postharvest management.

Understanding the complex physiological processes involved in the post-harvest life of tuber crops is identified as crucial for devising effective strategies to extend shelf life and enhance overall quality. Factors such as ethylene production, respiration rates, and water loss are mentioned as having a significant impact on the deterioration of crops after harvesting. The conclusion underscores the importance of studying these factors to gain insights and establish a foundation for targeted interventions, ultimately leading to improved resilience.

Furthermore, it acknowledges that optimizing these techniques for practical use is an ongoing process requiring further research and development. The translation of theoretical knowledge into practical solutions is identified as essential for increasing the market value of root and tuber crops and reducing post-harvest losses. The conclusion emphasizes the potential to create a sustainable and efficient post-harvest landscape by bridging the gap between scientific understanding and practical application, which can in turn strengthen the economic viability of these essential agricultural commodities.

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Assessment of Knowledge, Attitude, and Practice of Biosafety and Biosecurity (BSBS) among Staff in the National Biotechnology Research and Development Agency (NBRDA)

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Introduction

Biosafety and biosecurity are essential components of research in any institute that works with biological materials. Biosafety is the set of practices and procedures that are designed to protect laboratory workers, the public, and the environment from exposure to hazardous biological agents. Biosecurity is a set of systems and practices employed in research facilities to protect biological materials from unauthorized access, loss, theft, diversion, or intentional misuse (LSU, 2023). Biosafety and biosecurity knowledge is essential for safe and responsible conduct of research involving biological materials and toxins. A strong culture of biosafety and biosecurity is essential for any research institute that works with biological materials. This culture is built on a foundation of knowledge, attitude, and practice. The National Biotechnology Research and Development Agency (NBRDA) is a research institute that deploys biological techniques to meet national challenges in health, industry, agriculture, and the environment. Whereas, bio-techniques have produced beneficial products, the processes and products also have the potential to be used for harmful purposes including weaponization of biological agents and toxins to spread diseases and death on a large scale. Realizing the critical importance of robust biosafety and biosecurity measures, NBRDA has a Biorisk management (BRM) unit to ensure research is conducted safely and biological materials are secured. In addition, NBRDA has an institutional Biosafety and Biosecurity manual which was developed to serve as a guide for the researchers to work safely, securely and responsibly in the different facilities. Amidst all these efforts it became necessary to evaluate the impacts of the various efforts. Therefore, this study aimed to assess the knowledge, attitude, and practice of biosafety and biosecurity among staff of NBRDA.

Methodology

Study design and Sampling

The study was questionnaire-based and conducted between August and October 2023. The study participants included researchers, scientists, laboratory technicians, lab managers, and other lab users within NBRDA headquarters and the Bioresources Development Centre (BIODEC). A sample size of 100 was estimated but as the study was conducted using an online platform only 79 participated anonymously. A structured questionnaire was developed based on the biosafety and biorisk management guidelines from WHO with slight modifications from the researchers. The questionnaire consisted of four parts. The first part consisted of demographic information, the second part consisted of questions to assess their general knowledge of biosafety and biosecurity and the third part assessed their attitude towards biosafety and biosecurity. The fourth part consisted of 17 questions to assess the practice of biosafety and biosecurity. The scoring of responses was done following the method of Strengthening Laboratory Biosafety Programs (SLBP) Checklist 2015 with slight modifications.

Results and Discussion

Demographic information of the respondents

A total of 79 respondents consisting of scientific/research officers and laboratory technologists/assistants from technical departments of NBRDA headquarters and BIODEC participated in the survey. Table 1 shows their demographic information. A majority of the participants 38 (58.2%) had working experience of 5-10 years in the institution and 44 (55%) of the respondents were female. More staff 26 (32.9%) from the Environmental Biotechnology and Bio-conservation Department (EBD) participated in the survey as compared to other departments and BIODEC.

The study participants' knowledge of Biosafety and Biosecurity

Table 1: Demographic information of the 79 respondents from NBRDA

Variable	Number (%)
Gender	
Male	35 (44.3%)
Female	44 (55.7%)
Department/unit	
Agricultural Biotechnology Department (ABD)	15(19.0)
BIODEC	11 (13.9)
Environmental Biotechnology and Bio-conservation Department (EBD)	26(32.9)
Food and Industrial Biotechnology Department (FIB)	5 (6.3)
Genetic, Genomics and Bioinformatics Department (GGB)	6 (7.6)
Medical Biotechnology Department (MBD)	9 (11.3)
Not specific	8 (10.1)
Years of experience in the institute	
1-4	14 (17.7%)
5-10	36 (58.2%)
>10	19 (24.1%)

The knowledge assessment indicated a high degree of awareness, with 62.2% of participants showing a firm grasp of the concepts of biosafety and biosecurity (Figure 1). Although the majority showed excellent understanding, it is imperative to address 37.8% who did not show enough awareness to strengthen the BSBS culture.

The participants' attitude towards biosafety and biosecurity is

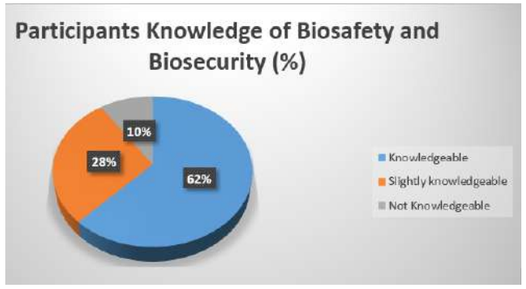

Figure 1: Study participants' knowledge of Biosafety and Biosecurity

shown in Figure 2. Among the participants 76.6% had a positive attitude while 5.8% had a bad attitude towards biosafety and biosecurity in NBRDA. The majority of the participants (97.5%) believe biosafety and biosecurity measures are important for protecting staff and the community. Also, 96.2% of the participants believe that regular training on biosafety and biosecurity is essential for all researchers. The survey looked at how NBRDA employees felt about biosafety and biosecurity protocols. Positive attitudes were demonstrated by a sizable fraction (76.6%), which is encouraging and highlights the significance of these behaviors. This optimistic outlook demonstrates a fundamental component of cultivating a culture of accountability and alertness.

A promising 58.9% of participants scored well on the biosafety and

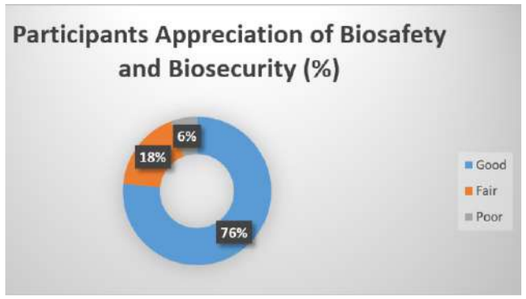

Figure 2: Attitude of the study participants regarding biosafety and biosecurity

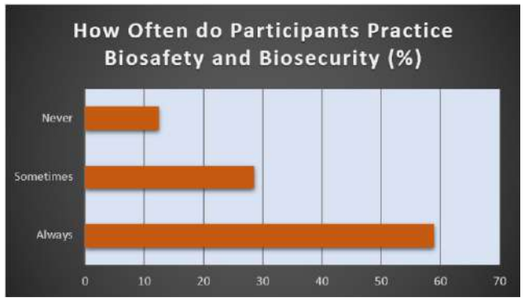

Figure 3: The study participants' practice of biosafety and biosecurity

biosecurity procedures assessment. These procedures covered several important topics, such as following protocol, handling waste, and reporting incidents. However, the study also pointed out some areas that needed improvement, such as the requirement for a more thorough risk assessment before the start of a study.

CONCLUSION

In general, the National Biotechnology Research and Development Agency is doing great in terms of Biosafety and Biosecurity. However, there is a need to address issues about KAP from the findings. The finding underlines the need to promote a culture of safety towards behavioral change through BSBS training and peer mentorship.

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Biorisk Assessment in Healthcare: Biotechnology Role and One Health Strategies in Mitigating Antimicrobial Resistance.

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INTRODUCTION

Antimicrobial resistance (AMR) is a critical global health issue, posing a significant threat to public health, food security, and economic development. The World Health Organization (WHO) identifies AMR as one of the top ten global public health threats facing humanity (WHO, 2020). AMR occurs when microorganisms such as bacteria, viruses, fungi, and parasites evolve to resist the effects of antimicrobial drugs, rendering standard treatments ineffective and leading to persistent infections and increased spread of disease.

ANTIMICROBIAL RESISTANCE (AMR)

Mechanisms of Resistance

Microorganisms develop resistance through several mechanisms,

including genetic mutations and the acquisition of resistance genes from other microorganisms. These mechanisms can include:

1. Enzymatic Degradation (Varela *et al*., 2021).
2. Alteration of Target Site (Hiramatsu *et al.,* 2001).
3. Efflux Pumps (Poole, 2007).
4. Reduced Permeability (Delcour, 2009).

Spread of AMR

The spread of AMR is facilitated by various factors, including inappropriate use of antibiotics in humans and animals, poor infection control practices, inadequate sanitary conditions, and insufficient regulatory frameworks. Horizontal gene transfer, where genetic material is exchanged between microorganisms, significantly contributes to the dissemination of resistance genes (Davies &Davies, 2010).

Global Impact of AMR

1. **Healthcare Systems:** Leads to increased morbidity and mortality rates, longer hospital stays and higher medical costs. This burden is much higher, in low- and middle-income countries (LMICs) (Laxminarayan *et al.,* 2013).
2. **Economic Consequences:** The economic impact of AMR results in increased healthcare costs, loss of productivity, and a negative impact on food security due to resistant infections in animals (World Bank, 2017).
3. **Food Security and Agricultur*e*** are negatively impacted due to the emergence of resistant strains that can be transmitted to humans through the food chain. Van Boeckel *et al.,* 2015).

Strategies to Combat AMR

- Antibiotic Stewardship (Dyar *et al*., 2017).
- Surveillance and Monitoring (WHO, 2015).
- Infection Prevention and Control (Allegranzi and Pittet, 2009).
- Research and Development (Wright, 2011)
- One Health Approach (Destoumieux-Garzón *et al.,* 2018).
- Policy and International Collaboration (Gibbs and Anderson, 2009).

Biorisk Assessment in Healthcare: involves the evaluation of risks associated with biological hazards, such as pathogens and toxins, to ensure the safety of healthcare workers, patients, and the broader community (WHO, 2020). Biorisk refers to the potential harm biological agents can pose to health and the environment. Biorisk assessment gauges the likelihood and severity of infections and exposures, leading to the implementation of control measures (CDC, 2021). Effective biorisk management encompasses hazard identification, risk characterization, exposure assessment, risk evaluation and risk Mitigation (WHO, 2004).

Tools and Frameworks for Effective Biorisk Assessment are Risk Assessment Matrix, Quantitative Risk Assessment (QRA), Biorisk Management Framework (BRMF), One Health Approach and Strength, weakness, opportunities and Threats (SWOT) Analysis.

Landscape of Antimicrobial Resistance (AMR)

- Global Prevalence: At least 700,000 people die each year due to drug-resistant infections. This number is projected to rise significantly if urgent action is not taken, potentially leading to 10 million deaths annually by 2050 (O'Neill, 2016).
- Regional Variations: Low and middle-income countries (LMICs) often face higher rates of resistant infections due to factors such as inadequate healthcare infrastructure, lack of regulatory enforcement, and the overuse of antibiotics in both humans and animals (WHO, 2020).
- Resistance Patterns: Common bacterial pathogens such as *Escherichia coli*, *Klebsiella pneumoniae*, and *Pseudomonas aeruginosa* have shown increasing resistance to multiple antibiotics. The Global Antimicrobial Resistance Surveillance System (GLASS) reports significant levels of resistance to fluoroquinolones, a key class of antibiotics for treating urinary tract infections caused by *E. coli* (WHO, 2020).
- Antibiotic Consumption: The WHO highlights that global antibiotic consumption increased by 65% between 2000 and 2015 (Van Boeckel *et al.,* 2014). In many countries, antibiotics are available over the counter without a prescription, exacerbating the problem.
- Resistance in Tuberculosis and Malaria: Drug-resistant tuberculosis (TB) is a major concern, with multidrug-resistant TB (MDR-TB) and extensively drug-resistant TB (XDR-TB) posing severe treatment challenges (WHO, 2020).

Impact of AMR on Healthcare systems and Patient outcomes

The impact of AMR on healthcare systems and patient outcomes includes:

1. Increased Morbidity and Mortality
2. Longer Hospital Stays
3. Increased Healthcare Costs
4. Compromised Medical Procedures
5. Impact on Vulnerable Populations
6. Global Health Security

Mitigating AMR through biotechnological innovative approaches

Biotechnology offers promising solutions to combat antimicrobial resistance (AMR). The combination of biotechnological innovations with the One Health approach provides a comprehensive strategy for biorisk assessment and AMR mitigation. This ensures coordinated efforts across human, animal, and environmental health, maximizing advanced technologies to tackle this global health threat (WHO, 2021)

Biotechnological Innovations

1) **Novel Antibiotics and Alternatives:**
   - Synthetic Biology: The use of CRISPR in developing new antibiotics.
   - Phage Therapy: Resistant bacteria targeting using bacteriophages.
   - Antimicrobial Peptides: Optimize natural peptides as antimicrobials.
2) **Advanced Diagnostics:**
   - Rapid Tests: PCR and CRISPR-based diagnostics for specific, sensitive and quick identification.
   - Point-of-Care Devices: Develop portable diagnostic tools (O'Neill, 2016).
3) **Microbiome Engineering:**
   - Probiotics/Prebiotics: Engineer beneficial microbes.
   - FMT: Use Fecal Microbiota Transplantation to restore healthy microbiota.
4) **Genomic Surveillance:**
   - Whole-Genome Sequencing: Continuously monitor bacterial genomes.
   - AI and Bioinformatics: Analyze large datasets to predict resistance patterns.

Concept of One Health Approach in AMR Mitigation

To effectively incorporate One Health principles in mitigating AMR, the following strategies have demonstrated successful implementation across different regions.

- **Integrated Surveillance***:* These systems monitor antibiotic usage and resistance patterns across human, animal, and environmental health sectors. This helps in identifying and addressing sources of AMR more effectively (Robinson *et al.,* 2016).
- **Antibiotic Stewardship Programs***:* includes guidelines for prescription, education campaigns, and regulatory measures. They help promote the rational use of antibiotics in humans and animals to reduce the emergence and spread of resistance. (Dyar *et al.,* 2018).

- **Education and Training:** Helps Provide interdisciplinary education and training for stakeholders professionals, veterinarians, farmers, and environmental scientists on the principles of One Health and the importance of AMR mitigation (Rüegg *et al.,* 2018).
- **Collaborative Efforts and Policy Making**

Interdisciplinary collaboration and policy-making are critical components of the One Health approach, essential for addressing complex health challenges such as AMR. (Rüegg *et al.,* 2018; Murray *et al.,* 2021).

- **Challenges and Solutions in Implementing Biorisk Assessments**

Resource constraints, data gaps and inconsistencies, interdisciplinary collaboration barriers, regulatory and policy challenges, public awareness and compliance.

Potential Solutions and Best Practices

- Resource Optimization and Capacity Building.
- Standardized Data Collection and Sharing.
- Strengthening Interdisciplinary Collaboration.
- Regulatory Harmonization and Policy Development.
- Public Engagement and Education

CONCLUSION

Biorisk assessments are essential for effectively identifying and managing biological hazards, enhancing preparedness, and safeguarding public health. These assessments are crucial in the fight against antimicrobial resistance (AMR), which poses a significant threat to healthcare systems globally. Integrating biotechnology innovations can significantly improve the detection and treatment of resistant pathogens. Concurrently, the One Health approach emphasizes the interconnectedness of human, animal, and environmental health, promoting interdisciplinary collaboration and integrated surveillance systems to address AMR comprehensively. Successful case studies demonstrate that combining these advanced biotechnological strategies with the holistic One Health perspective can lead to more effective risk management, better patient outcomes, and sustainable antimicrobial practices. By embracing these multifaceted strategies, healthcare systems can enhance their resilience, mitigate the impacts of AMR, and protect public health more effectively.

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The Role of Plasmid-Mediated Bacteria in the Biodegradation of Low-Density Polyethylene in Mitigating Climate Change

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INTRODUCTION

Plastic pollution, fueled by the persistent presence of low-density polyethylene (LDPE) wastes in the environment, has emerged as a pressing global concern. (Borrelle *et al.,* 2020). LDPE, a ubiquitous polymer used in various forms of packaging (Geyer *et al.,* 2017) contributes significantly to environmental degradation, posing threats to ecosystems, wildlife, and human health. (Kazeem *et al.,* 2012). In response to this environmental crisis, innovative solutions are being explored, with one promising avenue, being the use of plasmid-mediated bacteria (PMB) to degrade these pollutants in the environment (Venkata *et al.,* 2009).

Scientists employ genetic engineering techniques to introduce plasmids carrying specific polyethylene-degrading genes into bacteria (Saxena *et al.,* 2022). This genetic modification equips bacteria with the ability to produce enzymes capable of breaking down the complex structure of polyethylene, (Yoshida *et al.,* 2016), this aligns with the principles of green technology. (Allen *et al.,* 2011). Green technologies prioritize sustainability, environmental friendliness, (McDonough *et al.,* 2002*)* and reduced ecological impact, making it a noteworthy approach. (Prentice *et al.,* 2008). Understanding the intricate relationship between plasmid-mediated bacteria and polyethylene biodegradation is essential for comprehending the potential of this technology. (Varner and Gunsch, 2021).

METHODOLOGY

Source of Isolates and polyethylene samples: Isolates were retrieved from a previous culture known to have degraded LDPE in a recent study. LDPE films used were obtained from the Ekiti State University water factory.

Molecular Characterization of bacterial isolates, plasmid extraction, curing and biodegradation of LDPE: The isolates were identified through molecular characterization using 16S rRNA sequencing. The genomic DNA was extracted, and PCR

amplification was performed. The amplified products were analyzed using gel electrophoresis, and sequences were compared with known databases for identification. Plasmid isolation was carried out using the QIAGEN Plasmid Purification mini kit, followed by gel electrophoresis to confirm plasmid presence.
Prior to biodegradation, LDPE films were cut into small pieces to increase the surface area and subsequently disinfected with 70% ethanol. These films were then incubated with bacterial isolates in mineral salt medium (MSM) broth. Isolates with plasmid were duplicated, one of the duplicates was used for LDPE degradation and monitored over 30 days using spectrophotometric analysis. The second duplicate was used as a control, where the plasmids were cured by inoculating into 4 ml nutrient broth containing 25 µl of Ethidium bromide and incubated overnight in a shaker incubator at 37^{o}C and 200 rpm. (Rani *et al*., 2014).

RESULTS AND DISCUSSION

Molecular characterization identified six bacterial isolates from the polyethylene-polluted sites*: Lysinibacillus xylanilyticus* strain BN-1316S, *Rhodopseudomonas palustris* strain KRPR02, *Pseudomonas aeruginosa* strain JAY2N, *Stenotrophomonas maltophilia s*train T7D7, *Pseudomonas aeruginosa* strain SMVIT1, and *Achromobacter xylosoxidans* strain YEB. Four isolates were found to contain plasmids: *L. xylanilyticus* strain BN-1316S, *R. palustris* strain KRPR02, *P. aeruginosa* strain SMVIT1, and *A. xylosoxidans* strain YEB.

The biodegradation studies revealed that these plasmid-containing isolates effectively degraded LDPE films compared with the control. The four isolates were used to degrade the LDPE films and a peak of degradation was reached on the 21st day followed by a gradual declination on the 28th day. *L. xylanilyticus* strain BN-13(S6) exhibited the highest degradation of 0.898nm and *A. xylosoxidans* strainYEB (W11) exhibited the least degradation of 0.788nm. The result obtained revealed that PMBs are competent bio-degraders of polyethylene wastes and can be used as a better approach to reduce LDPE pollution in the environment and mitigate climate change.

Table 1: Showing optical wavelength of LDPE degradation using plasmid-mediated bacteria and Control (degradation of LDPE bacteria isolates without plasmids)

Interval (Days)	*L.xylanilyticus* strain BN-13 (S6) (nm)	*A.xylosoxidans* strain YEB (W11) (nm)	*P.aeruginosa* Strain SMVIT-1 SI (S1) (nm)	*R.palustris strain KRPR02* (W5) (nm)
1	0.853	0.603	0.728	0.824
7	0.867	0.662	0.863	0.830
14	0.888	0.736	0.636	0.842
21	0.898	0.788	0.820	0.887
28	0.518	0.748	0.501	0.873
CONTROL				
1	0.485	0.517	0.550	0.608
7	0.598	0.617	0.635	0. 673
14	0.693	0.644	0.852	0.734
21	0.826	0.710	0,820	0.876
28	0.806	0.508	0.619	0.607

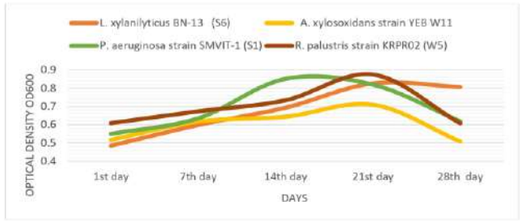
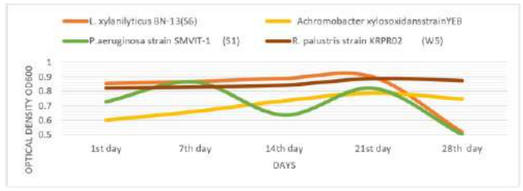


Fig 1: Growth pattern of LDPE degradation using plasmid-mediated bacteria



Control

Fig 2: Growth pattern of LDPE degradation using bacterial isolates without plasmids

CONCLUSION

The findings of this study demonstrate the significant potential of plasmid-mediated bacteria in the biodegradation of polyethylene waste. The identified bacterial strains, particularly those containing plasmids, showed considerable efficiency in degrading LDPE films. This suggests that PMB can be harnessed as a sustainable and effective approach to mitigate polyethylene pollution and its associated environmental impacts. The study underscores the importance of further research into the optimization and practical application of these bacterial strains for large-scale biodegradation processes.

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Value Addition on Exported Cashew Nut, A Potential Fiscal Growth on Nigerian Economy; An Overview

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Introduction

The cashew, scientifically known as Anacardium occidentale L., which can be also referred to as 'wonder nut', is one of the most treasured processed nuts traded on the world commodity markets. It is a valuable tropical perennial tree crop, originally grown in coastal areas, but now spreading also far inland. It is one of the major export crops in terms of foreign exchange earnings in countries such as Brazil, Vietnam, India, Nigeria, Tanzania, Indonesia, Guinea-Bissau, Cote D'Ivoire, Mozambique and Benin. Cashew nuts are known to be a common appetizer, that is; peanuts and pistachio nuts. They are also use as raw materials in the food industry, and as a component in various confectionery products. The crop has not only been used for food for many years but it is also an important income generator. Value addition to cashew is a very competitive likewise a hypothetically productive activity that should be exploited by all processors. By adding value to cashew nut through processing, it ensures that the kernels are of high value luxury commodity. The main purpose of processing is to extract the valuable cashew kernel from the shell with little or no damage to the whole kernel command a higher price than the broken pieces. Cashew with value addition entails a series of unit operations essential to make available, the edible nut. Variations in processing methodology between different manufacturers are attributed to differences in cashew, available equipment, human power and fuel source
The importance of exportation to global businesses with trade and industry intensification is a mechanism indispensable for the improvement of a financial system, and hence the importance of exportation to the global business cannot be overemphasized (Timmer, 2002, Amao et.al., 2021). The development of the export sector will result in employment generation and will thus enhance living standards. Ever-increasing export income assists in reducing the strain on the stability of imbursement instability. Usman and Salami (2008) emphasized that exportation assists in growing the stature of collective trade and industry performance via its multifaceted effects on the level of nationwide earnings. Export is a determining factor in the development of both mature and maturing economies. The exports of maturing nations are composed chiefly of natural assets, but those of matured nations are largely composed of capital supplies.
Presently in Nigeria, products of the cashew tree (kernel and apple) are under-utilised for income generation. There is still much wastage of the fresh apples on farms since a negligible portion is consumed by the harvesters. This wastage reduces the household income. It is, thus, imperative that value addition to cashew apple and nut be explored.

Use of Cashew

Cashew nuts are known to be a common appetizer, that is; peanuts and pistachio nuts. They are also use as raw materials in the food industry, and as a component in various confectionery products. The cashew nut kernels have various nutritional values to human beings. Cashew is a rich source of protein (21.2 %), carbohydrates (22 %), fat (47 %) and minerals (Calcium, Phosphorous and Iron) (Sharma, 2004) and provides 575 kcal of energy per 100 g (Sathe, 1994).

Products of Cashew

Input	Products	Description and Uses
Nuts	Kernels	Raw nuts are processed inti kernels by boiling, cracking, decorticating and roasting
Apple	Prunes	Cashew prunes, produced by boiling the cashew apple in molasses in very similar to dehydrated prunes or dates
Apple	Juice	Cashew fruits is pulped by grating or pounding and the juice is pressed out and strained. Cashew juice have five times more citric acid than orange juice and is thus a good source of preservation acid medium when mixed with other fruit juices or vegetables
Apple	Wine	The juice from the cashew fruit can be processed into wine using the conventional method of producing fruit wine. The alcoholic content averages18%
Apple	Pulp	The fibrous pulp obtained after extracting Juice from the cashew apple can be used as animal feed or dried and processed into diet fibre biscuit
Shell	CNSL	Extracted from the cashew shell, Cashew Nut Shell Liquid (CNSL) is used in the manufacturing of paints, vanishes, resins and brake linings
Shell	Fuel Wood	After extraction of shell liquid, the spent shells are used as a processing fuel.

Cashew Production in Nigeria

The agriculture division has been the basis of the financial system since autonomy and regardless of copious problems; it lingers a supple sustainer of the common people {Amao et.al., 2021}. According to Lawal (2011), in his findings, discovered that Nigeria's position in the global cashew production has not been reflected in the development of the downstream value chain industry.

Market Dynamic

Nigeria's cashew nuts are highly sought after at the international markets due to their premium taste. Countries such as Vietnam, India and United State are among the importer of Nigerian Cashew Nuts. The demand for healthy snacks and ingredients in the food industry coupled with the rising popularity of plant based diets, has fuelled the global demand of cashew nuts, creating lucrative opportunities for Nigerian Exporters.

Opportunities of Local Farmers in Cashew Production

Cashew nut cultivation offers immense potential for local farmers in Nigeria. With proper training, access to quality seeds and supports from government initiatives and agricultural organisations, smallholder farmers can significantly increase their yields and income level. Additionally, cashew farming promotes sustainable agricultural practices and provides employment opportunities, especially in rural areas, thereby contributing to poverty reduction and economic development.

Challenges

Nigeria's cashew nut industry faced with several challenges which include; inadequate infrastructure, post-harvest losses and quality controlled issues. All these challenges require concerted efforts from various stakeholders, including government intervention in infrastructure development, investment in research and development, capacity building for farmers and processors and above it all, enhancing collaboration between the public and private sectors to facilitate the adoption of best practices and improve the competitiveness of Nigerian cashew nuts in the global market.

International Price Strategy for Nigerian Cashew Nuts

This can be influenced by various factors such as;

- **Market Demand and Supply:** The fundamental principle of demand and supply plays a significant role in determining the price of Nigerian cashew nuts at international market. For instance, changes in consumer preferences, population growth and dietary trend impact demand, while variables like weather conditions, crop yield and production cycles affects supply. Fluctuation in demand and supply levels can influence pricing strategies, with higher demand, typically leading to higher prices and vice versa.
- **Quality Grading:** Cashew nuts are graded based on various quality parameters, including size, colour, moisture content and Kernel integrity. Higher quality cashew nuts command premium price in the market, reflecting consumer preferences for superior taste, texture and appearance. pricing strategies may vary depending on the quality grading system used and market segments targeted with producers and exporters often seeking to differentiate their products based on quality attributes.
- **Cost of Production and Processing:** The cost of producing and processing cashew nuts differs, depending on the factors such as labour cost, agricultural inputs, transportation expenses, and overhead/handling cost. Pricing strategy need to take production cost into consideration to ensure profitability for growers, processors and traders along the supply chains. Efficient improvement, technological advancements and economies of scale can help in reducing production costs and enhance competitiveness in the global market.
- **Market Segmentation and Positioning:** Cashew nuts are sold in various market segments which include retails, wholesales, food services and industrial markets. Pricing strategies may be tailored into different market segments based on factors such as; product differentiation, brand positioning, distribution channels and customer's preferences.

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Comparative Advantage Of Cocoa Centered Rural Household In Nigeria

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Introduction

Cocoa is one of the important export crops in Ivory Coast, Ghana, Cameroun, Nigeria, Togo and Equatorial Guinea. In terms of world contribution, West African countries including Ivory Coast, Ghana, Nigeria and Cameroon contributed around 70 per cent of the world's cocoa beans. Nigeria, the third largest producer of cocoa in Africa generates about 6% of the world's production following Ivory Coast which produces 43% of the World's cocoa and Ghana with about 14% of the World's output (Amao *et al*., 2015,). At present, the production capacity of cocoa in Nigeria has reached about 385,000 tonnes per annum, an increase of 215,000 tonnes from the year 2000 production level (Erelu, 2008).

Prior to the oil boom in Nigeria, cocoa, cotton, groundnut, oil palm and rubber were the major export crops of the country (Amao *et al*., 2015). The agricultural sector was conversely neglected at the discovery of oil in the country, this oil discovery caused production and exportation of cocoa and other products to decline. The cocoa subsector offers a quite sizeable number of employment, both directly and indirectly (Amao *et al*., 2015). It is an important source of raw materials for industries, revenue to the government of cocoa-producing states and a significant contribution to the Gross Domestic Product (GDP) of the nation (CBN, 2007). Prior to the Structural Adjusted Programme (SAP) cocoa marketing was carried out by erstwhile highly regulated commodity Marketing Boards which were known to pay farmers less than the export price of cocoa (Folayan et.al., 2007, Amao *et al*.,2015). The Board had the responsibility to procure cocoa beans from all local farmers for exportation. It is evident that without the contributions of farmers in the production of cocoa, there will be nothing to deliberate on in terms of local use and exportation of cocoa. This research work showcases its uniqueness by revealing Nigerian cocoa farmers concerning the competitiveness of Nigeria's cocoa beans and their share in the world cocoa market. In other words, using the farmer's contributions as the index to measure the country's competitiveness.

Materials and methods

A multi-stage sampling procedure was adopted. The first stage involved purposive selection of the three local government areas known to be the largest Cocoa producing areas in the state which are: Ondo, Ile Oluji and Idanre Local government area of the study area. The second stage was a random selection of the three villages in each local government area while the last stage was a random selection of twenty Cocoa farmers in each village making the total number of 180 respondents.

Data Collection: Primary data collected were the cost of inputs used and cocoa yield obtained for both sole cocoa and mixed production. Secondary data were collected on the social cost of inputs and free on Board (FOB) price of cocoa at the international market from the Ministry of Agriculture, planning, research and Statistics, Central Bank of Nigeria.

Measure of protection: NPC is calculated by dividing the revenue in private prices (A) by revenue in social prices (E). It can be calculated for output and input.

$NPC_i = P_i^d / p_i^w$

NPC (on output) = A/E
NPC (on input) = B/F

Table 1: Policy Analysis Matrix model

Value of input				
Prices (Accounts)	**Value of output (Revenue)**	**Tradable input - cost**	**Non-tradable input cost (Domestic factor)**	**Profit**
Private prices	A	B	C	D
Social prices	E	F	G	H
Policy transfer (divergence)	I	J	K	L

If NPCO = 1, the domestic market price equals the world price and therefore, there is no protection and the price is efficient. If NPCO > 1, there is positive protection of output. If NPCO < 1, there is negative protection on output. If NPCI = 1, the domestic cost of input is expensive compared to imported inputs and it is preferred to use import for production, if NPCI < 1, it is profitable to use domestic input.

Effective Protection Coefficient (EPC): The EPC is defined as the ratio of value added in private prices to value added at social prices. It measures the ratio value added at domestic prices (A - B) to value added at world reference prices (E - F). Conceptually this ratio can be written as:

$EPC_i = Vid / V_i^w$

Where EPC_i = Effective protection coefficient of commodity I, V_i^d = value added at domestic prices and V_i^w = value added at world reference prices.

Using PAM elements, EPC = (A - B) / (E - F), if EPC > 1, it means net subsidy to value-added, if EPC < 1, it means net tax to value-added, if EPC = 1, it means no value added.

The EPC ignores the transfer effects of factor market policies like NPC.

Results and discussion

Tables 2 and 3 show that both sole and mixed cropping systems are profitable and competitively viable. Private profitability figures were positive for both systems, with sole cropping at N 69,986.13 and intercropping at N 91,246.33. However, intercropping was found to be more profitable, likely due to the additional income from other products alongside cocoa beans, consistent with findings by Neptune and Jacque (2007) in Trinidad and Tobago. Social profitability was also positive for both systems, with sole cropping at N 121,865.14 and intercropping at N 158,989.10, demonstrating efficient use of resources in cocoa production. Despite these profits, output transfers were negative, indicating that producers received lower prices than those available in the international market. On the other hand, input transfers were positive in both systems, suggesting that farmers were paid more for their output than the international market rates. Profit transfers, however, were negative for both systems, with sole production at -N 57,879.01 and intercropping at -N 67,742.77, indicating that producers earned less than they could have in the international market.

Table 4 displays the Nominal Protection Coefficients (NPCO) for cocoa production, revealing values below one for both production systems. Specifically, NPCO is 0.89 for sole production and 0.78 for intercropping. This suggests a scenario of negative output protection, indicating that domestic farm gate prices for cocoa are lower than international prices by 0.11 and 0.22 for sole and intercropping systems respectively, due to policy effects. In terms of Nominal Protection Coefficient on input (NPCI), values are above one, indicating an increase in tradable input costs influenced by policies. For sole production, NPCI is 1.37, and for intercropping, it is 1.39. Moving to Effective Protection Coefficients (EPC) shown in Table 4, values are also below one. EPC is 0.72 for sole production and 0.65 for intercropping, indicating that producers face taxes of 26% and 33% on value added compared to world reference prices. However, these findings highlight the policy impacts on cocoa production, including negative output protection and increased input costs relative to international benchmarks.

Table 2: Policy analysis matrix for sole cocoa production system.

Item	Revenue (₦/ha)	Cost of tradable inputs (₦/ha)	Domestic factors (₦/ha)	Profit (₦/ha)
Private price	174, 630.38	70,443.16	34,201.09	69,986.13
Social price	195,383.55	51,253.89	22,264.52	121,865.14
Effect of policies and other divergences	-20,753.17	19,189.27	11,936.57	-57,879.01

Source: Field survey, 2011.

Table 3: Policy analysis matrix for mixed cocoa production system.

Item	Revenue (₦/ha)	Cost of tradable inputs (₦/ha)	Domestic factors (₦/ha)	Profit (₦/ha)
Private price	169,241.52	5,4198.88	23,791.31	91,246.33
Social price	215,793.13	38,918.35	17,885.68	158,989.10
Effect of policies and other divergences	-46,551.61	15,280.53	5,910.63	-67,742.77

Source: Field survey, 2011.

Table 4: Four indicators of policy effects and comparative advantage

Indicator	Sole production	Mixed production
Nominal protection coefficient of output (NPCO)	0.89	0.78
Nominal protection coefficient of input (NPCI)	1.37	1.39
Effective protection coefficient (EPC)	0.72	0.65
Private profit (₦)	69,986.13	91,246.33
Social profit (₦)	121,865.14	158,989.10
Domestic resources cost (DRC)	0.15	0.10
Social cost-benefit ratio (SCB)	0.38	0.26

Source: Field survey, 2011.

Conclusion

It is evident that cocoa production is profitable in the study area in terms of private and social. Recommendations from this study are: Tax policies on tradable inputs should be reviewed to ensure farmers are fairly compensated for their production costs. Government intervention is crucial to align commodity prices with international levels, thereby reducing poverty among cocoa farmers.

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The Chemo-Preventive, Ameliorative and Molecular Effects of *Cucurbita maxima* Leaf-Supplemented Diet on Streptozotocin Induced Diabetes Mellitus in Male Albino Rats

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INTRODUCTION

Diabetes mellitus is a chronic condition that affects almost all cell types in the body (Nutakor *et al.,* 2021). It is associated with severe complications and is extremely difficult to manage. The condition is yet to have a permanent cure and therefore still poses a severe burden to the sufferer and society in general (Oguejiofor *et al*., 2014). Hence, preventing this disease condition is perhaps a better alternative. The plant in view is squash-like belonging to the family *Cucurbitaceae* and genus *Cucurbita* with other species like *Cucurbita mixta, Cucurbita pepo* and *Cucurbita moschota* (Mohamed *et al*., 2014). *Cucurbita maxima* (C.*maxima)* plant has shown great potential in the treatment of several other disorders, as evidenced by previous scientific studies (Yongabi *et al.,* 2001). The current study investigated the chemo-preventive and ameliorative effects of a *C. maxima* leaf-supplemented diet and its further effects on the INS gene expression at the molecular level in streptozotocin-induced diabetic rats. Fresh leaves of *C. maxima* were collected from Ejule, Ofu LGA of Kogi State, and were taken to the standard Herbarium of the Department of Biological Science, Ahmadu Bello University Zaria, for identification, authentication and a voucher number of 1077 was obtained**.**

MATERIALS AND METHODS:

The leaves were rinsed in clean water, dried at room temperature and ground to powder. Experimental dietary inclusions at 5%, 10%, 15% and 20% w/w for the experimental groups were prepared using the leaf powder of *C. maxima* (Onuche and Abu, 2021). Sixty rats were randomly assigned into 6 (six) groups of five animals each (n=5) in both preventive and ameliorative trials. For preventive purposes, the rats were initially fed with the various inclusions of *C. maxima* leaf for four weeks, and thereafter, diabetes induction was carried out on day 28 of the fourth week. Inversely, The STZ induction was carried out first on animals in the ameliorative group on day 1 of the first week, followed by feeding with *C. maxima* supplemented diets (5%, 10%, 15%, and 20%) for four weeks. The plant leaf powder used for the dietary supplementation as well as the supplemented diet was evaluated for proximate composition, phytochemicals and antioxidant capacity by Diphenyl-1-picrylhydrzyl (DPPH), and active component through GC-MS The weekly blood glucose levels and body weight were estimated. The liver, kidney functions, lipid profile and haematological parameters were determined using standard methods. At the end of the experiments (preventive and ameliorative studies) the animals were sacrificed; blood and tissue samples (liver, kidney and pancreas) were collected. Histological examination was carried out on the liver, kidney and pancreas, while the pancreas was examined for any possible effect on expression levels of the INS gene.

RESULTS

Preliminary analysis of the plant revealed appreciable levels of antioxidant constituents, with any IC_{50} for DPPH scavenging activity of 3.1 µg/mg. A significantly ($p < 0.05$) higher blood glucose value was observed in the negative control group in week 4 compared to the supplemented groups in the preventative treatment. In the ameliorative treatment, the glucose level in the negative control group increased significantly ($p < 0.05$) from week 2 to week 4 while the levels in the groups receiving C. *maxima* leaf-supplemented diets decreased or significantly ($p < 0.05$) from week 2 to week 4. The liver function parameters in the groups whose diets were supplemented with *C. maxima* leaves did not show significant ($p > 0.05$) alteration as compared to the normal control group in both preventive and ameliorative treatments. The levels of liver markers (ALT, AST, ALP, TB, and DB) were significantly ($p < 0.05$) lower or stable in the groups receiving *C. maxima* leaf-supplemented diet in the preventive and ameliorative treatments than in the negative control group, although the levels of total protein were significantly ($p < 0.05$) higher in these groups receiving the supplemented diets than in the negative control group. It was observed also that *C. maxima* significantly ($p < 0.05$) decreased the elevated kidney function parameters in the blood sample, and reversed lipid profiles as well as haematological parameters. The biochemical changes that took place in the liver, kidney and pancreas tissues were further supported by restored histology by *C. maxima* leaves in the diet-supplemented groups.

Cycle threshold (CT) values of INS gene in the STZ control group of both trials showed significant ($p < 0.05$) higher value when compared to supplement groups. Furthermore, enumeration of mRNA copies of insulin gene using qRT-PCR showed reasonable and consistent expression folds in 15% leaf-supplemented groups in both trials (preventive and ameliorative) as compared to the STZ control.

CONCLUSION/SUMMARY

In both trials, it can be concluded that the *C. maxima* leaf exhibited anti-hyperglycaemic and anti-hepatotoxic potential. The findings suggest that *C. maxima* resist (prevented and reverse STZ-induced hyperglycaemia, abnormal lipid production, and protection for special organs. These effects may be mediated by interaction and protection of relevant gene and multiple receptors from free radical attack and boosting the levels of antioxidant enzymes in the system.

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Biotechnology, a Yardstick to Economy Sustainability in Nigeria: Review

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Introduction

Biotechnology is a field of science and technology with an interdisciplinary outlook that deals specifically with the changes encountered by living and non-living matter using active organisms (Tonukari, 2023). Products derived from these biological processes are of useful basic knowledge as well as prototypes for the creation of goods and services (Tonukari, 2004, 2011; Acquaah *et al*., 2006; Dubin, 2007; Tonukari *et al.*, 2010). It encompasses a wide range of applications, including genetic engineering, pharmaceuticals, agriculture, environmental conservation, and more.

Economy refers to the system of production, distribution, and consumption of goods and services within a society or a country. It encompasses all economic activities, including the buying and selling of goods, the creation of wealth, the allocation of resources, and the management of financial transactions. There are different types of economies, such as market economies, command economies, mixed economies, and traditional economies. In a market economy, decisions regarding production, consumption, and investment are primarily made by individuals and businesses based on supply and demand in the market. While in a command economy, the government controls the production and distribution of goods and services. Mixed economies combine elements of both market and command economies.

The economy is influenced by various factors, including government policies, market forces, consumer behaviour, technological advancements, global trade, and economic indicators such as inflation, unemployment rate, GDP (Gross Domestic Product), and interest rates. Understanding the economy is essential for policymakers, businesses, investors, and individuals to make informed decisions that can impact economic growth, stability, and prosperity.

Sustainable Economy

A sustainable economy is an economic system that aims to meet the needs of the present generation without compromising the ability of future generations to meet their own needs. It focuses on promoting economic growth, social equity, and environmental protection in a way that is environmentally responsible, socially inclusive, and economically viable in the long term.

Key principles of a sustainable economy include:

- **Environmental sustainability**: Ensuring that economic activities do not deplete or degrade natural resources, harm ecosystems, or contribute to climate change. This involves promoting renewable energy sources, reducing waste and pollution, and protecting biodiversity.
- **Social Equity**: Ensuring that economic benefits are shared fairly among all members of society, including marginalized and vulnerable populations. This involves promoting social justice, reducing income inequality, and providing access to basic services such as healthcare, education, and housing.
- **Economic Viability**: Ensuring that economic activities are financially viable and contribute to long-term prosperity. sThis involves promoting sustainable business practices, investing in innovation and technology, and fostering a diverse and resilient economy.
- **Inter-generational Equity**: Ensuring that current economic activities do not compromise the ability of future generations to meet their own needs. This involves taking a long-term perspective in decision-making, considering the impacts of economic activities on future generations, and promoting sustainable development practices.

Achieving a sustainable economy requires collaboration and coordination among governments, businesses, civil society organizations, and individuals. It involves integrating environmental, social, and economic considerations into decision-making processes and policies to create a more resilient and equitable economy that can thrive for generations to come.

Correlations between Biotechnology and Sustainable Economy

Nigeria has a large scientific potential to pursue a significant improvement of the biotechnology industry and enterprises with specialty on the creation of pioneering solutions Biotechnology can bring a sustainable economy by leveraging biological processes and organisms to develop innovative solutions that promote environmental, social, and economic sustainability. This includes:

- **Sustainable Agriculture**: Biotechnology can enhance crop yields, reduce the need for chemical inputs, and improve resistance to pests and diseases, leading to more efficient and environmentally friendly farming practices.
- **Renewable Energy**: Biotechnology can be used to develop biofuels from organic materials such as algae, crop residues, and waste products, providing a sustainable alternative to fossil fuels.
- **Waste Management**: Biotechnology can help in the treatment of wastewater, solid waste, and industrial by-products through processes like bioremediation and bioconversion, reducing pollution and promoting resource recovery.
- **Healthcare Innovation:** Biotechnology enables the development of new drugs, vaccines, and diagnostics that improve health outcomes and reduce healthcare costs, contributing to social well-being and economic growth

However, biotechnology plays a crucial role in advancing sustainable development by harnessing the power of nature to address global challenges such as food security, climate change,

resource scarcity, and public health. By integrating biotechnological solutions into various sectors of the economy, we can create a more resilient, equitable, and environmentally responsible society for present and future generations.

Hindrances/Limitations

While biotechnology holds great potential for promoting economic sustainability, there are several limitations and hindrances that can impede its progress. Some of these include:

1. Incompetence Researchers: An important limitation of the development of the biotechnology sector is the low availability of experienced entrepreneurs among members of the scientific and research team who understand what is necessary to establish and develop a successful company in the field of biotechnology (Shimasaki, 2009)
2. Regulatory challenges: Biotechnological innovations often face stringent regulatory requirements and approval processes, which can be time-consuming and costly. Uncertainty around regulatory decisions can also create barriers to market entry and investment in biotechnology projects.
3. Intellectual property issues: Protecting intellectual property rights in biotechnology can be complex, especially when it comes to genetic resources, gene sequences, and biotechnological processes. Disputes over patents and licensing agreements can hinder collaboration and innovation in the field.
4. Public perception and acceptance: Biotechnology is a rapidly evolving and sometimes controversial field, with concerns about GMOs, gene editing, and bioengineering raising ethical, environmental, and safety considerations. Public scepticism and resistance to biotechnological applications can limit market acceptance and adoption of innovative products.
5. Access to resources: Biotechnological research and development require specialized infrastructure, equipment, expertise, and funding, which may be limited in certain regions or for smaller companies. Access to skilled personnel, research facilities, and financial support can be barriers to realizing the economic potential of biotechnology.
6. Market competition: The biotechnology industry is highly competitive, with large multinational corporations dominating the market and setting high entry barriers for smaller players. Limited market access, distribution channels, and partnerships can hinder the commercialization of biotechnological products and services.
7. Technological challenges: Biotechnological innovations often rely on complex biological systems and processes, which can be unpredictable, difficult to scale up, or prone to technical failures. Developing reliable and cost-effective biotechnological solutions requires continuous research, experimentation, and optimization.

Addressing these limitations and overcoming hindrances to economic sustainability in biotechnology will require collaboration among stakeholders, investment in research and development, supportive regulatory frameworks, public engagement, and strategic partnerships to harness the full potential of biotechnological advancements for sustainable economic growth.

Strategies to prevent Limitations

The know-how of biotechnological knowledge is the creation of fundamental and gradual improvements as well as applications that create wealth for countries (Aghmiuni *et al*., 2020). A government policy encouraging the establishment of biotechnology companies is urgently needed in Nigeria. The followings can be of help:

- **Build strong partnerships and collaborations**: Biotechnologists can overcome limitations by forming strategic partnerships with other research institutions, industry players, and government agencies. Collaborating with experts in complementary fields can help leverage resources, expertise, and infrastructure to accelerate innovation and commercialization.
- Invest in continuous research and development: To stay competitive and address technological challenges, biotechnologists should prioritize ongoing research and development efforts. Investing in cutting-edge technologies, equipment, and talent can help drive innovation, improve product quality, and enhance market competitiveness.
- Engage with regulatory authorities: Proactively engaging with regulatory authorities and staying abreast of changing regulations can help biotechnologists navigate the complex regulatory landscape. By ensuring compliance with regulatory requirements and standards, biotechnologists can mitigate risks, build trust with stakeholders, and facilitate market access.
- Enhance intellectual property protection: Biotechnologists should prioritize protecting their intellectual property through patents, trademarks, and licensing agreements. Developing a robust IP strategy can safeguard innovations, create barriers to entry for competitors, and attract investment for further growth and expansion.
- Promote public awareness and acceptance: Addressing public concerns and promoting transparency around biotechnological applications can help build trust and acceptance among consumers, policymakers, and other stakeholders. Engaging in dialogue, educating the public about the benefits and safety of biotechnology, and soliciting feedback can foster a supportive environment for economic sustainability.
- Diversify revenue streams: Biotechnologists can mitigate market competition and financial risks by diversifying their revenue streams through product diversification, licensing agreements, partnerships, and international expansion. Exploring new markets, applications, and business models can help capture untapped opportunities and drive sustainable growth.
- By implementing these strategies and proactively addressing limitations in achieving economic sustainability, biotechnologists can unlock the full potential of biotechnological advancements and contribute to a more sustainable and prosperous future.

Policies that help Biotechnology in Sustaining Economy

- **Establish Supportive Regulatory Frameworks**: The government can create policies that provide a clear and predictable regulatory environment for biotechnologists. This includes streamlining approval processes for new biotechnological products, ensuring consistent enforcement of regulations, and promoting innovation-friendly policies that foster growth and investment in the sector.
- **Provide Financial Incentives and Support**: Governments can offer financial incentives such as tax credits, grants, and subsidies to encourage research and development in biotechnology. Funding programs for biotechnological startups, innovation hubs, and technology transfer initiatives can help accelerate commercialization and market adoption of biotechnological products.
- **Invest in Infrastructure and Talent Development**: The government can invest in building infrastructure such as research facilities, laboratories, and technology parks to support biotechnological research and development. Additionally, policies that promote education and training in biotechnology-related fields can help develop a skilled workforce to meet the growing demands of the industry.
- **Support International Collaboration and Partnerships**: Governments can facilitate international collaborations and partnerships by promoting trade agreements, joint research initiatives, and technology transfer programs. By fostering global cooperation, biotechnologists can access new markets, resources, and expertise to drive innovation and competitiveness.
- **Promote Sustainability and Responsible Innovation**: Governments can implement policies that promote sustainable practices in biotechnology, such as promoting the use of environmentally friendly technologies, reducing waste and emissions, and supporting ethical considerations in research and development. By encouraging responsible innovation, biotechnologists can contribute to long-term economic sustainability while minimizing negative impacts on society and the environment.
- **Advocate for Intellectual Property Rights Protection**: Governments can advocate for strong intellectual property rights protection through patent laws, enforcement mechanisms, and international agreements. By safeguarding intellectual property, biotechnologists can secure their innovations, attract investment, and incentivize continued research and development in the sector.

By implementing these policies and supporting biotechnologists in achieving economic sustainability, governments can foster a thriving biotechnology sector that drives innovation, economic growth, and societal benefits.

World Benefits in Economy with Biotechnology

- **Improved Healthcare**: Biotechnology advancements in the healthcare sector can lead to the development of new treatments, therapies, and diagnostic tools that can improve the quality of healthcare services and contribute to better health outcomes for citizens.
- **Enhanced Food Security**: Biotechnology can help increase crop yields, improve resistance to pests and diseases, and enhance nutritional content in food products. This can contribute to ensuring food security and addressing hunger and malnutrition challenges in society.
- **Environmental Sustainability**: Biotechnological innovations such as biofuels, biodegradable materials, and waste management solutions can help reduce environmental impact, promote sustainable practices, and mitigate climate change effects for the benefit of citizens and future generations.
- **Economic Growth and Job Creation:** The expansion of biotechnology across various economic sectors can stimulate economic growth, attract investment, and create job opportunities in research and development, manufacturing, healthcare, agriculture, and other related fields, benefiting citizens through increased employment and income generation.
- **Increased Access to Innovative Products and Services**: Biotechnology advancements can lead to the development of innovative products and services in areas such as personalized medicine, bio-based materials, renewable energy, and more. Citizens can benefit from access to cutting-edge technologies that improve their quality of life and enhance overall well-being.
- **Addressing Societal Challenges:** Biotechnology can play a crucial role in addressing pressing societal challenges such as infectious diseases, environmental pollution, food insecurity, and aging populations. By leveraging biotechnological solutions, citizens can benefit from improved public health, environmental protection, and social welfare outcomes.
- **Empowering Scientific Research and Education**: The integration of biotechnology across economic sectors can support scientific research, innovation, and education initiatives. This can empower citizens with knowledge and skills in biotechnological fields, fostering a culture of innovation, lifelong learning, and technological advancement within society.

Overall, allowing biotechnology to flourish in all economic sectors can bring about a wide range of benefits for citizens, including improved health outcomes, environmental sustainability, economic prosperity, access to innovative products and services, and solutions to societal challenges.

Advancement of Biotechnology in Developed Countries

- **Precision Medicine**: Biotechnology has enabled the development of personalized treatments and therapies tailored to individual genetic profiles, leading to more effective and targeted healthcare interventions in developed countries.
- **Agricultural Productivity**: Biotechnological innovations have improved crop yields, enhanced resistance to pests and diseases, and increased nutritional content in food products, contributing to food security and sustainable agriculture practices in developed countries.
- **Biopharmaceutical Industry Growth**: The biotechnology sector has spurred the growth of the biopharmaceutical industry in developed countries, leading to the production of advanced medicines, vaccines, and medical devices that address a wide range of health conditions and diseases.
- **Environmental Sustainability:** Biotechnology advancements have facilitated the development of biofuels, biodegradable materials, and waste management solutions that promote environmental sustainability and reduce carbon footprint in developed countries.
- **Industrial Applications**: Biotechnology has revolutionized various industries in developed countries, including energy, manufacturing, and textiles, by enabling the production of bio-based materials, renewable energy sources, and sustainable products that reduce reliance on fossil fuels and contribute to a greener economy.
- **Research and Innovation**: Biotechnology has fueled research and innovation in developed countries, leading to breakthrough discoveries, novel technologies, and cutting-edge solutions that drive economic growth, competitiveness, and technological leadership on a global scale.
- **Job Creation and Economic Impact**: The biotechnology sector has created new job opportunities, attracted investment, and stimulated economic growth in developed countries by fostering a culture of innovation, entrepreneurship, and collaboration across industries.

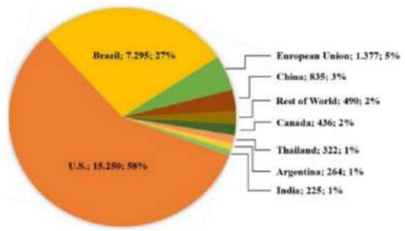
The advancements in biotechnology have significantly contributed to the advancement of developed countries by improving healthcare outcomes, promoting sustainable practices, driving economic growth, and fostering innovation and competitiveness in various sectors.

Wastes Converted to another Useful Products

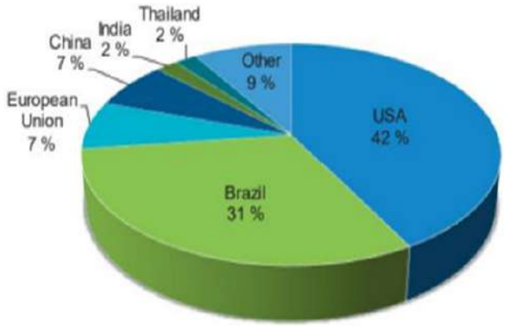
- **Food Waste**: Can be converted into bioplastics, biofuels, and animal feed through processes like anaerobic digestion and fermentation.
- **Agricultural Waste**: Crop residues and by-products can be converted into bio fertilizers, bio pesticides, and biofuels through processes like enzymatic hydrolysis and microbial fermentation.
- **Industrial Waste**: Waste from industries like paper mills, breweries, and textile factories can be converted into biogas, bioethanol, and biopolymers through bioremediation and biochemical processes.
- **Municipal Solid Waste**: Household waste can be converted into compost, biogas, and recycled materials through processes like composting, anaerobic digestion, and pyrolysis.
- **Plastic Waste**: Non-biodegradable plastics can be converted into biodegradable plastics, biofuels, and other valuable products through processes like plastic pyrolysis and microbial degradation.
- **Sewage Sludge**: Waste from wastewater treatment plants can be converted into bio fertilizers, biogas, and soil amendments through processes like anaerobic digestion and composting.
- **Electronic Waste**: E-waste can be converted into valuable metals, plastics, and other materials through processes like mechanical recycling and chemical extraction using biotechnological methods.

Nigerian academics and researchers must take a leading role in establishing bio-based industries and leveraging the knowledge

Countries Benefiting Biotechnology in their Economy



Bioethanol production by country, million gallons, 2017 (RFA, 2017).



Prediction of world bioethanol production by 2024.

gleaned from research for the manufacturing of innovative products and processes as well as in generating employment and creating values (Tonukari, 2023). Realizing the dream of an industrial biotechnology revolution in Nigeria will take a lot of courage and imagination. This will add value to the citizens and reduce the level of importation, hence gives a sustainable economy of the country.

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Identification of Fish Ficolin in a Primitive Chondrostean Sturgeon, *Acipenser baeri:* Molecular Characterization and Evolution

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Introduction

The innate immune system stands as the body's primary defense mechanism against invading pathogens, with a newfound specificity highlighting its evolution for effective pathogen defense in teleosts. Within the diverse components of innate immunity, the complement system (CP) occupies a central role as an ancient defense mechanism present in invertebrates and vertebrates. This system is activated by three pathways: alternative, classical and lectin, generating functions such as opsonization, lysis, inflammation, and modulation of the innate and adaptive immune responses. The lectin pathway is activated through the binding of mannose-binding lectin (MBL) and ficolins (FCNs) to carbohydrates present on the surfaces of pathogens. Both FCNs and MBL are lectins characterized by the presence of collagen-like and carbohydrate-binding domains (carbohydrate recognition domain for MBL and fibrinogen-like domain for FCNs). Ficolins are structurally and functionally homologous to mannose-binding lectin (MBL) and can activate the lectin pathway of the complement cascade a crucial part of the immune response in mammals. However, the molecular identity of ficolins in teleosts remains unknown.

The ligand specificities for the FCNs and MBL differ. Whereas MBL reacts strongly with carbohydrate ligands including mannose, fucose and N-acetylglucosamine (GlcNAc), FCNs react with N-acetylated molecules including GlcNAc etc. (Fujita 2002; Endo *et al*; 2011). From an evolutionary perspective, numerous studies have been conducted on ficolins, particularly in mammals, such as humans, which have led to the identification of various prototypes. These ficolin denoted as M-ficolin (FCN-1, NP_001994.2), L-ficolin (FCN-2, NP_004099.2), and H-ficolin (FCN-3, NP_003656.2) (Howard et al., 2018; Matsushita, 2013; Santi et al., 2018) all share a common affinity for acetyl group but differ in their specific binding characteristics. however, there is no evidence of ficolin in teleost fish. Sturgeons, particularly the Siberian sturgeon (*Acipenser baerii*), are essential for evolutionary studies due to their unique position between cartilaginous and bony fish, offering insights into vertebrate evolution and the molecular adaptations of their immune systems.

Given the above background, our current study aims to achieve the following objectives: (1). The identification of ficolin in teleost primitive fish, *Acipenser baerii* by molecular cloning. (2). Determination of their structural and evolutionary relationships, by comparing its amino acid sequence with mammalian ficolin and other orthologs using bioinformatics analysis, thereby gaining insights into its possible function in fish. (3). Unraveling the origins and evolution of identified ficolin through phylogenetic analysis. (4) To elucidate the expression profile of the ficolin gene in *Acipenser baerii* through quantitative reverse transcription polymerase chain reaction (qRT-PCR), to facilitate comprehensive functional analysis.

Methodology

cDNA was synthesized from pooled head kidney and liver tissues of three juvenile sturgeons. RNA was extracted using Trizol, and 2 µg total RNA was reverse transcribed with oligo dT primers. FCN cDNA was identified and analyzed in silico, followed by PCR amplification, TA cloning, and sequencing. The structural analysis included ORF finding, domain analysis, and 3D-structure prediction, while multiple sequence alignment and phylogenetic tree construction used Clustal O and MEGA 11, respectively. Tissue distribution of FCN mRNA was examined across nine tissues using RT-PCR and qPCR, with data analyzed by the Livak method.

RESULTS AND DISCUSSIONS

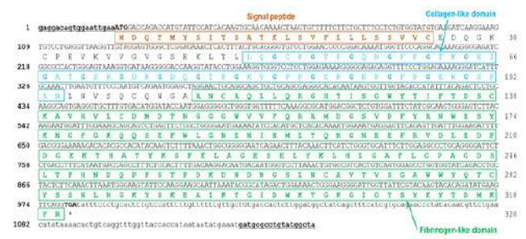

Figure 1: The representative *Ab*FCN cDNA sequence comprised 1,145 bp containing an ORF protein comprising 320 amino acid residues with a signal peptide (Met[1]-Cys[25]), a collagen-like domain (Leu[47]-Asn[111]), and a C-terminal fibrinogen-like domain (Arg[121]-Arg[320]), indicating the *Ab*FCN protein has a typical ficolin domain architecture.

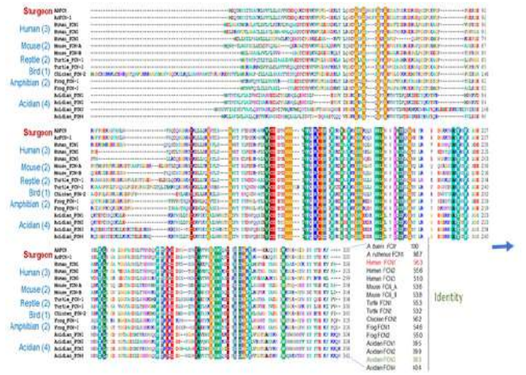

Figure 2: Multiple sequence alignment of identified *Ab*FCN with other FCN orthologs. Their identity matrix is indicated. *Ab*FCN had high sequence similarity (>50%) with mammalian ficolins specifically Human-FCN 1 with an identity of 56.3%.

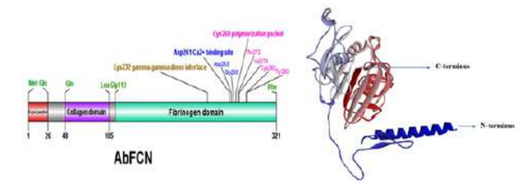

Figure 3: Domain architectural analysis of cloned sequences of candidate *Ab*FCN and the Schematic diagram showing *Ab*FCN predicted tertiary structure built based on template c2j61B_**(Phyre2) and constructed by Robetta online tool.** A comparison of the domain structural analysis with the Human Ficolin was consistent with existing research within the human ficolin.

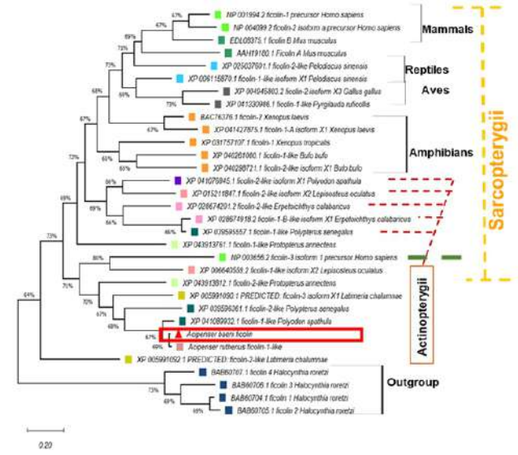

Figure 4: Phylogenetic analysis of the *Ab*FCN protein showed a high branch support which indicates high homology with the sarcopterygians and as well as actinopterygians and shares evolutionary origin with Human ficolin 3.

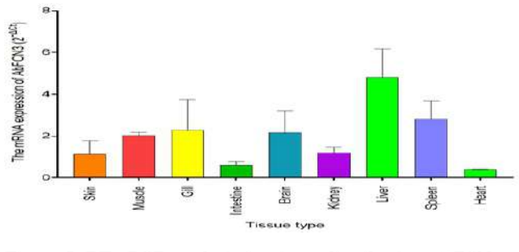

Figure 5: RT-qPCR analysis for tissue distribution. *Ab*FCN showed significant tissue distribution patterns in the tissues, liver and spleen were most predominant. The highest expression was seen in the liver and the lowest expression in the heart.

Conclusions

Collectively, the identified FCN gene shows the same characteristics as human FCN, findings from this study provide useful information not only to bridge gaps in our knowledge on the ficolin gene in teleost and vertebrates but also to gain better insights and provide a steppingstone to unravel the functional intricacies of ficolins in the context of fish's innate immunity.

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Prevalence of Direct Acting Antiviral Resistant Variants among HCV Infected Individuals in Kaduna State, Nigeria

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INTRODUCTION

Despite the paradigm shifts in the treatment of hepatitis (alpha interferon to Direct Acting Antivirals (DAAs) therapy), there is an increase in resistance to these antiviral agents (Bhatia and Gupta, 2020). Direct-Acting Antivirals (DAAs) act by inhibiting enzymes which are crucial in the replication of HCV in the hepatocytes. This results in > 90% sustained virological response (Bhatia and Gupta, 2020).
Multiple variants of HCV (quasispecies) have emerged as a result of: lack of proof-reading ability of the viral polymerase, high rate of HCV replication and selective pressures (Bhatia and Gupta, 2020). These variants are genetically distinct and some might harbour baseline resistance-associated substitutions (RASs), which can result in DAAs resistance at varying degrees (Lontok *et al*., 2015).

MATERIALS AND METHODS

Collection of samples

Blood samples (5 mL) were aseptically collected from HCV positive blood donors who are DAAs naïve. After clotting, the samples were centrifuged for 2 mins at 2000 rpm and the sera were stored at a refrigerating temperature (-4°C) for further analysis.

RNA extraction and cDNA Synthesis

Hepatitis C virus RNA was extracted from the ELISA seropositive serum samples using the Quick-RNA Viral Kit as per the manufacturer's instruction. The extracted RNA was used to synthesize complementary DNA (cDNA) using the ProtoScript II First Strand cDNA Synthesis Kit.

PCR amplification conditions and sequencing of HCV *NS3*, *NS5A*, and *NS5B* genes

Amplification of HCV *NS3*, *NS5A*, and *NS5B* genes was achieved by nested PCR using primers designed in this study and amplification conditions described by Li *et al*. (2017).

NS3, NS5A, and NS5B Sequence analysis for detection of RAVs

Resistance Associated Substitution (RAS) analysis to detect RAVs was carried out using the Geno2pheno HCV tool (https://hcv.geno2pheno.org/index.php).

RESULTS

Four (4) RASs were identified in HCV belonging to subtype 1b (T54S, Y56F, V170T and L159F) while two (2) RASs were identified in HCV belonging to subtype 1a (N174S and M28V) (Table 1). Frequency and Prevalence of Resistance Associated Variants (RAVs) are shown in Table 2. The frequency and prevalence of NS3 RAV were 4 and 36.36% respectively. While the frequency and prevalence of NS5A RAV and NS5B RAV were 1 and 9.09% each. Overall, four of the blood donors were infected with RAV strains of HCV, giving a prevalence rate of 36.36% (4/11).

DISCUSSION

Table 1: Distribution of Resistance Associated Substitution (RAS) based on HCV subtypes

Genes	Resistance Associated Substitution (RAS) GT1a	GT1b
NS3	N174S	T54S, Y56F, V170T
NS5A	M28V	None
NS5B	None	L159F

Table 2: Frequency and Prevalence of Resistance Associated Variants (RAVs)

Region n = 11	Frequency of RAV	Prevalence (%) of RAV
NS3	4	36.36
NS5A	1	9.09
NS5B	1	9.09

In this study, numerous amino acid substitutions were identified, some of which were associated with resistance (namely V170T and T54S) or reduced susceptibility (namely M28V, Y56F, N174S and L159F) to one or more DAAs. However, most of the substitutions were not associated with DAA resistance. This observation is in line with the report of Malandris *et al.* (2021).
RASs were observed to be more common in subtype 1b (4) compared to subtype 1a (2) in this study. This might due to the fact that only one (1) subtype 1a was identified in this study compared to subtype 1b that were ten (10). Similarly, Sayana *et al.* (2020) reported that the prevalence of RAS was higher in HCV subtype 1b compared to HCV subtype 1a.
In this study, 36.36% of blood donors with PCR positive samples were found to be infected with HCV RAVs i.e. strains that harbour at least one RAS in one of the three DAA targeted regions namely NS3, NS5A and NS5B. NS3 RASs were identified as the most frequent RASs in this study. This is contrary to the findings of Li *et al.* (2017) and Bertoli *et al.* (2018) where NS5B RASs were the most frequent and the report by Chen *et al.* (2016) that RASs to NS5A inhibitors are frequently detected in HCV genotype 1. In conclusion, the prevalence of Resistant Associated Variants of HCV among blood donors in Kaduna state was 36.36%.

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Impact of Wastewater on Aquatic Organisms in Selected Water Bodies within Lagos Mainland.

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INTRODUCTION

The integrity of our water resources is one of the most essential environmental issues of the 21st century and wastewater disposal is a major contributing factor (Giri, 2021). The discharge of wastewater without proper treatment to remove pharmaceuticals may lead to contamination of drinking water (WHO, 2011). Based on the potential deleterious effects of most of these contaminants and the relatively few studies available, the occurrence and associated adverse effects must be investigated. This study evaluated the toxicological effects of wastewater in selected water bodies within Lagos Mainland on Nile Tilapia (*Oreochromis niloticus*).

METHODS

Water samples were collected from four locations in Lagos, Nigeria: Iganmu (E1), Isolo (E2), Maryland (E3) and Ipaja (E4). The physicochemical properties were evaluated. Acute and subacute toxicity testing was carried out in African Nile Tilapia fingerlings. Antioxidant, biochemical and histopathological analyses were evaluated. Comparisons between the control and treatment groups were performed using analysis of variance followed by Tukey's post-hoc tests at $p<0.05$ significance level (Akaahan *et al*., 2015).

RESULT AND DISCUSSION

The toxic unit (TU) approach (von der Ohe &de Zwart, 2013; Parkerton *et al*., 2023) was used to estimate the potential toxicity of test samples. Samples testing positive for toxicity had TU values > 1.0 (Logue *et al*., 1989; Harbi *et al*., 2017). In this study, the water samples had toxic units >1 in aquatic test animals (1.59, 2.00, 1.69 and 1.58 toxic units) which is in agreement with studies which have shown that aquatic organisms are more sensitive to the acute effects of most water contaminants (USEPA, 2002). Furthermore, other factors such as BOD, COD and DO could also be responsible for mortalities in fish as they were beyond their prescribed standards (Somanath, 2002). Mallatt (1985) suggested that the effect of short-duration exposure of water samples on fish gills is responsible for mortality in fish. This may account for the non-lethality in rodents. However, due to the scarcity of potable water within this environment, there is a high potential for non-aquatic organisms to be exposed.
Biochemical oxygen demand (BOD) and chemical oxygen demand are important water quality parameters. They affect the amount of dissolved oxygen (DO) in rivers and streams. The larger the BOD, the more quickly oxygen is depleted in the stream. Physicochemical characteristics of the water bodies sampled in this study showed high COD and BOD which is also indicative of pollution (Ohe and Zwart, 2013). Due to the considerable burden of organic matter in these water bodies indicated by high COD values, they are bound to have a good growth of decomposer organisms in them, which would demand oxygen greatly for their respiration (Gryzywna and Sender, 2021).

Table 1: Physicochemical parameters of water samples and standard values

Location	1.1 (R)	1.2 (I)	1.3 (I)	2.1 (R)	2.2 (I)	2.3 (R)	3.1 (R)	3.2 (R)	4.1 (I)	4.2 (I)	4.3 (R)	NESREA	WHO
TS (mg/L)	155.00±2.00	1730.67±4.33	1873±6.00	66.67±3.33	82.33±1.33	111.00±1.00	75.33±0.67	75.67±0.33	272.00±1.00	455.00±2.00	217.00±2.00	NS	NS
DO (mg/L)	2.50±0.05	1.60±0.03[a,b]	2.58±0.05	1.85±0.05[a,b]	0.90±0.08[a,b]	1.17±0.03[a,b]	1.82±0.06[a,b]	2.31±0.06	1.99±0.03[a,b]	0.93±0.03[a,b]	1.11±0.05[a,b]	<2	<2
Cl	434.00±1.00	3574.67±9.33	3294.67±3.33	225.87±1.87	271.60±8.40	226.80±2.80	224.93±0.93	169.87±1.87	143.73±3.73	170.80±2.80	167.07±0.93	NS	10
COD (mg/L)	287.49±0.02	285.93±0.03	256.86±0.01	266.15±0.00	275.84±0.02	266.12±0.01	282.54±0.01	278.28±0.02	268.36±0.02	287.05±0.01	276.60±0.01	90	80
BOD (mg/L)	154.25±0.02	143.65±0.01	144.13±0.02	153.83±0.01	153.07±0.02	143.15±0.01	144.09±0.01	154.74±0.01	154.13±0.01	143.76±0.00	153.60±0.02	50	15
Lead (Pb) mg/L	0.089±0.00	0.035±0.003	0.062±0.00	0.009±0.003	ND	0.071±0.000	0.043±0.001	0.025±0.001	ND	0.025±0.003	0.009±0.003	2.00	0.01
Cadmium (Cd) mg/L	0.004±0.004	ND	0.004±0.01	0.001±0.00	0.005±0.000	0.004±0.000	0.012±0.000	0.004±0.000	0.005±0.01	ND	0.002±0.000	9.02	0.003
Nickel (Ni) mg/L	0.07±0.00	0.01±0.00	0.03±0.00	0.01±0.00	0.02±0.00	0.02±0.00	ND	0.03±0.00	ND	0.01±0.00	0.01±0.00	0.05 20	0.02

Table 2: Physicochemical parameters of water samples

Location	1.1 (R)	1.2 (I)	1.3 (I)	2.1 (R)	2.2 (I)	2.3 (R)	3.1 (R)	3.2 (R)	4.1 (I)	4.2 (I)	4.3 (R)	NESREA	WHO
DO (mg/L)	2.50±0.05	1.60±0.03	2.58±0.05	1.85±0.05	0.90±0.08	1.17±0.03	1.82±0.06	2.31±0.06	1.99±0.03	0.93±0.03	1.11±0.05	<2	<2
COD (mg/L)	287.49±0.02	285.93±0.03	256.86±0.01	266.15±0.00	275.84±0.02	266.12±0.01	282.54±0.01	278.28±0.02	268.36±0.02	287.05±0.01	276.60±0.01	80	80
BOD (mg/L)	154.25±0.02	143.65±0.01	144.13±0.02	153.83±0.01	153.07±0.02	143.15±0.01	144.09±0.01	154.74±0.01	154.13±0.01	143.76±0.00	153.60±0.02	50	15

National Environmental Standards and Regulations Enforcement Agency (2009) Nigeria, maximum permissible limits for wastewater discharge. World Health Organization (2002) Guidelines for drinking water recommendation.

The consequences are that fishes and other aquatic organisms become stressed, suffocate, and die as DO levels between 0-2 mg/L are not enough to support higher aquatic life (Yan *et al*., 2020). Tables 1 and 2 show the physicochemical parameters of water samples and standard values. Dissolved oxygen values were consistently low in all the locations sampled (0.90-2.58 mg/L) while chemical oxygen demand and biochemical oxygen demand levels were high.

Subacute exposure significantly increased (p<0.05) serum liver enzymes, creatinine and urea levels in the treatment groups relative to the control. A significant decrease (p<0.05) in antioxidant enzymes and significantly higher MDA levels (p<0.05) in the gills, liver and kidney of the exposed tilapia groups was also observed. Histologic sections of the gills showed necrosis of either or both primary and secondary lamellae in the treatment groups.

Table 3: Biochemistry (Sub-acute toxicity in *O. niloticus*)

Groups	AST (IU/L)	ALT (IU/L)	ALP (IU/L)	Creatinine (µmol/L)	Urea (mmol/L)	Bilirubin (mg/dl)	TP (g/L)	Albumin (g/L)
E1	258.50±6.82*	6.30±0.61*	18.67±3.56	23.30±0.56	1.20±0.06	0.17±0.07	3.47±0.07*	0.20±0.06
E2	531.60±105.80*	12.00±1.12**	45.17±25.47	23.93±0.81	1.20±0.20	0.43±0.03	3.50±0.31**	0.17±0.03
E3	235.50±90.27*	3.53±1.07	47.23±35.40	24.63±0.99	1.47±0.03*	0.33±0.13	3.33±0.03***	0.10±0.06
E4	301.40±31.90**	14.93±1.70**	52.24±2.53*	26.78±1.39*	1.47±0.12**	0.13±0.03	2.23±0.09***	0.17±0.03
E5	531.60±105.80*	12.00±1.12**	45.17±25.47	23.93±0.81	1.20±0.20	0.43±0.03	3.50±0.31**	0.17±0.03
Control	177.3±50.86	2.33±0.46	26.42±14.02	21.01±0.39	0.80±0.06	0.43±0.19	4.80±0.44	0.43±0.12

Values are expressed as mean ± S.E.M. (n=5). *p<0.05, **p<0.01, ***p<0.001 vs. Control (one-way ANOVA with Tukey's post test).

CONCLUSION

This study established the pollution impact of wastewater on the aquatic environment.

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Molecular Detection of Beta Lactamase Genes from *Salmonella typhimurium* Isolated from Poultry droppings in Nyanya- Abuja.

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Introduction

Poultry and poultry meat products are considered as some of the main carriers of *Salmonella* Species and represent a significant share of the attributed sources of *salmonellosis* in Humans. The widespread occurrence of *Salmonella* in natural environments and the Intensive husbandry practice used in the meat, fish and shellfish industries have been a significant problem in public health (Brenner et al, 2010).

Beta-lactamases are ancient bacterial enzymes that attack the beta-lactam ring. The class B beta-lactamases (the metallo- beta-lactamases) are divided into three subclasses: B1, B2 and B3. Subclasses B1 and B2 are theorized to have evolved about one billion years ago and subclass B3s are theorized to have evolved before the divergence of the Gram-positive and Gram-negative eubacteria about two billion years ago (Andrews et al., 2011).

Penicillinase was the first β-lactamase to be identified. It was first isolated by Abraham and Chain in 1940, Among Gram-negative bacteria, the emergence of resistance to expanded-spectrum cephalosporins has been a major concern. *Salmonella* infections are one of the major global public health problems (Okoli et al., 2015).

Methods

Study Area

The study was carried out in the satellite town in Abuja called Nyanya which is under the Abuja Municipal `Area Council, it is bordered on the north and northeast by a range of hills, to the east and southeast by the Mararaba district of Nasarawa state to the south by Federal housing, Karu site and to the west by Abuja city

Media

Bacteriological media that was used, Methyl Red Voges Proskauer Medium, xylose-lysine deoxycholate (XLD) agar, Bismute sulphate agar (BSA) and *Salmonella-Shigella* agar (SSA), Nutrient Agar, Simmon's Citrate Agar, Urea broth, and Peptone Water, Mueller-Hinton Agar (MHA)

Sample collection- A total of one hundred and eighty (180) poultry faecal droppings samples were collected using sterile screw tubes. The samples were then transported to the microbiology laboratory department of Nasarawa State University Keffi for analysis.

Biochemical tests

The conventional and commercial (Microgen Bioproducts) biochemical identification tests were used. Conventional biochemical tests were carried out according to the methods of Cheesbrough and observed for reactions typical of *Salmonella* such as Triple Sugar Iron Agar (TSI); Indole Test; Lysine Decarboxylase Test: Methyl Red Test; Citrate Utilization test; Urease test; Motility Test

Molecular Detection of Extended-Spectrum Beta-Lactamase Resistance

DNA Extraction

The DNA was extracted from ESBL-producing isolates using the boiling method as described by Ibrahim et al. [13]. Briefly following, 1 pure colony of ESBL-producing isolate, was inoculated into 2 ml of LB broth and incubated at 37ºC for 8 h and 200 µl of LB culture was transferred into an Eppendorf tube and centrifuge in a microcentrifuge at 3200 rpm for 2 min at room temperature and the supernatant was discarded living the cells and the cells were washed twice with washing buffer. About 0.5ml of sterile phosphate buffer was added to the pellet and vortex for 5 sec after which it was heated at 90ºC for 10 min rapid coiling was done by transferring the tubes into the freezer for 10 min and thereafter it was centrifuged at 3200 rpm for 1 min to separate the DNA and the cell containing the DNA debris and 300 µl of supernatant, was transferred into 2 ml Eppendorf tube and stored at -10ºC until use.

DNA Amplification of Extended Spectrum β-Lactamase Genes

Multiplex Polymerase Chain Reaction (PCR) was performed in order to amplify the ESBL genes present in the isolates. The presence of blaCTX-M, blaSHV and blaTEM genes was tested using previously published primer sets and conditions. The primer sequences and expected amplicon size for each gene are listed in Table 1. The reactions were carried out in 20 µl reaction volume made up of 10 µl of Mastermix (Qiagen), 0.32 µl of primers (0.16 µl each of forward and reverse primers), 3 µl of DNA and 6.68 µl of nuclease-free water. The primer concentration stood at 0.2 M. The reaction tubes were placed in the holes of the thermal cycler and the door of the machine was closed. Conditions during the reactions were set as: 3 minutes of initial denaturation at 95°C, followed by 35 amplification cycles of denaturation at 95°C for 30 sec, annealing at 56°C for 40 sec, initial extension at 72°C for 50 sec, final extension at 72°C for 3 min and hold at 4°C infinitely.

Results

Isolation and identification of Salmonella typhimurium

The cultural, Morphological and Biochemical characterization of *Salmonella typhimurium* from poultry droppings in some selected poultry farms in Nyanya- Abuja, as shown in Table 2, shows that *Salmonella typhimurium* is Gram-negative staining, the morphology of the isolated bacterium was small, Gram-negative rod shape bacteria, On xylose lysine Deoxycholate (XLD) plates, the presumptive *Salmonella typhimurium c*olonies appeared red with black centre appearing shows the presumptive and the biochemical characteristics of the *Salmonella* isolates.

Multiple Antimicrobial Resistance (MAR) index

The MAR index of the isolates from Selected Poultry Farms is shown in Table 6. The isolates were distributed into different MAR indexes and the commonest MAR index was 0.8(33.3%) from farm A and (36.3%) from farm B,

Occurrence of ESBL resistance genes

The occurrences of the ESBL resistance genes in the 4 cefuroxime, cefotaxime and amoxicillin-clavulanic acid-resistant isolates are given in Table 7. The order of occurrences of the 4 genes detected was: *blaCTX*-M-9 and *blaSHV* (75.0%) > *bla CMY2* and *Bla CTX*-M (50.0%).

Table 6. Multiple Antibiotic Resistance (MAR) Index

			No. (%) of isolates	
No. of antibiotics resistance to (a)	No. of antibiotics tested (b)	MAR Index (a/b)	Farm A (N-9)	Farm B (N-11)
10	10	1.0	1(11.1)	0(00.0)
9	10	0.9	1(11.1)	3(27.2)
8	10	0.8	3(33.3)	4(36.3)
7	10	0.7	1(11.1)	2(18.1)
6	10	0.6	1(11.1)	1(9.0)
5	10	0.5	1(11.1)	1(9.0)
4	10	0.4	0(00.0)	0(00.0)
3	10	0.3	0(00.0)	0(00.0)
2	10	0.2	0(00.0)	0(00.0)
1	10	0.1	0(00.0)	0(00.0)

Conclusion

In this study, *Salmonella typhimurium* was isolated from two poultry farms sampled. The occurrence of the isolates was high from farm A. The isolates were highly resistant to most commonly used antibiotics to treat infection caused by *Salmonella* species. Most of the isolates were multidrug-resistant and beta-lactam-producing isolates. The beta-lactam-resistant genes detected were *blaCTX*-M-9 and *blaSHV*, *bla CMY2* and *Bla CTX*-M.

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Cost-Effectiveness of Oil Palm Marketing in Kogi State, Nigeria.

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Introduction

The oil palm provides one of the leading vegetable oils produced globally, accounting for one-quarter of global consumption and approximately 60% of international trade in vegetable oils (World Bank, 2010). The oil extracted from these palms is included in numerous products used all over the world such as margarine, baked foods, detergents, sweets, and cosmetics (UNESCO, 2007). It is of note that estimated 74% of world palm oil usage is for food products and 24% is for industrial purposes (USDA, 2010). Since the 1990s, the area occupied by oil palm cultivation has expanded worldwide by around 43%, driven mainly by demand from India, China and the European Union (RSPO 2011). Oil palm is very useful for biodiesel all over the world. Oil palm is among the most productive and profitable of tropical crops for bio-fuel production. High-yielding oil palm varieties developed by breeding programs can produce as much as 20 tons of fresh fruit bunches/ha/year under ideal management, which is equivalent to 5 tones oil/ha/year (excluding the palm kernel oil). The oil forms 10% of the total dry biomass produced by the palm, but the 90% left might be a source of fiber and cellulosic material for second-generation bio-fuel production (Basiron, 2005).

In Nigeria, the oil palm tree is an important crop that is relevant in all aspects of life with socioeconomic and socio-cultural values. According to Ibitoye *et al*., (2011) oil palm is a versatile tree crop with almost all parts having economic value and useful for everyday livelihood. The different parts of oil palm include: the fronds, leaves, trunk and roots. These parts give a wide range of products which are of benefit to mankind. The most important product of oil palm is the palm fruit, which is processed to obtain three commercial products. These include palm oil, palm kernel oil and palm kernel cake. The palm oil is rich in carotene and contains vitamin A. It is also used in the manufacture of soaps and other detergents (Agwu, 2006). The palm kernel oil is used in the manufacture of margarine, cooking fats, lubricants, pomade and a source of glycerin (Ajie, 2013).

Materials and Methods

Study Area

A multi-stage sampling technique was used to select the respondents for this study. The first stage involved a purposive selection of Kogi and Edo States of Nigeria. The second stage was a purposive selection of three Local Government Areas from each state due to their predominant activities in oil palm value chain activities. The third stage was a random selection of villages in each LGA and this are Ofu LGA (Ofakaga, Ejule, Aloma), Dekina LGA (Egume, Ocharu, Ayingba), Ijumu LGA (Iyamoye, Ayetoto Gbede, Iluagba), Oredo LGA (New Benin 1 & 2, Gelegele,), ikoba-Okha LGA (Ogbeson, Aduwawa, Ekiuwa), Egor LGA (Evbouguide, use, Uwelu) and lastly, a snowball selection of women oil palm fruits actors each from the selected villages to give a total sampling size of 309 respondents due to some unfilled and incomplete questionnaire. The response rate of the interview schedule is 85.83%.

Data Analysis

This study employed Costs and Returns and Gross Margin Analysis The budgeting technique was used to evaluate costs, returns and profits in oil palm fruits Value chain. Gross Margin Analysis is one budgeting technique which was used to analyze the profitability of an enterprise. Gross Margin is a measure of the difference between gross returns from the enterprise and the variable costs associated with its production.

RESULTS AND DISCUSSION

The mean age of the oil palm fruits processors as shown in table 1 were found to be 44 years which shows that they are fairly young and are expected to be very active in their various oil palm fruits processing activities. Marital Status revealed that most of the value chain actors were married (96.3%) which indicated that there are some levels of responsibilities on them. Educational status indicated about 62.8% had formal school education which is a factor that is expected to positively impact information seeking behavior of respondents in their various oil palm fruits processing. This result agrees with the finding of Ibitoye *et al.,* (2011) which stated that the level of farmer's education is crucial to the understanding of value and use of oil palm innovation. The mean of the household size of the processors were found to be about 46.6%, that is less than 5 and 43.3% is between 6-10 persons which implies that they had moderate household size. This agrees with Udoh (2015) who observed that under the system of subsistence farming in palm oil and kernel, labor was provided mostly by women and by the extended family. The average experience of respondents in oil palm value chain activities was 15 years for processor. The finding therefore implies that most of the Oil palm fruit processors entrepreneurs in the study area have vast years of experience in their respective activities which will improve their level of operation, performance and profitability in the enterprises.

Average income from oil palm fruits processors was found to be N33, 500. This finding could be assumed to be small amount, especially for those who did not have other means of income generation. They may find it difficult in meeting all their household basic needs but supports from their husband and household can help them cope in their profitability.

The results of the various oil palm fruits value chain activities (table 2) indicates that majority of the farmers are frequently involved in all the important production activities such as Nursery management (86.7%), Planting (89.6%), Weeding (95.1%), Fertilizer application(90.3%), Labor (84.5%).

Table 1: Summary of Activities involvement/participation level in oil palm fruits value chain in the study area

Involvement/participation level of women in oil palm fruits production	Involvement Level								
Variables	Frequently			Occasionally			Rarely		
	F	%	Mean	F	%	mean	F	%	Mean
Nursery management	268	86.7	89.2%	15	4.9	5.5%	26	8.4	5.2%
Planting	277	89.6		10	3.2		22	7.1	
Weeding	294	95.1		12	3.9		3	1.0	
Fertilizer application	279	90.3		9	2.9		21	6.8	
Labor	261	84.5		39	12.6		9	2.9	

Source: field survey, 2023

Table 3 showed the result of regression analysis between the respondent socioeconomic characteristics and the profits realized from oil palm fruits was significant. The results revealed that there was significant difference between Age (t= 0.168), farm size (0.136) at 5%, also Experience (0.199) at 10 % and their profits from oil palm fruits value chain in the study area.

Table 2: Summary of Result of Pearsons Product Moment Correlation (PPMC) between Socio-economic Characteristics of Oil Palm Processor and their profits in Kogi and Edo state

Socioeconomic	r value	P value	Decision
Age	0.168**	0.003	Significant
Household size	0.006	0.909	Not Significant
Experience	0.199**	0.000	Significant
Farm size	0.136*	0.017	Significant

Source: field survey, 2023

Conclusion and Recommendation

Conclusively, the results showed that the actors of the oil palm fruits value chain are young, experienced and married. It can also be concluded that oil palm fruits value chain is a profitable and lucrative means of livelihood in the study area. Access to credit facilities by relevant government and non-government organization should be provided to improve oil palm fruits production.

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Toxicological Impact of Waste Plastic Bottles Recycling Plants at Three Sites in Abuja, Nigeria

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INTRODUCTION

The ubiquitous presence of waste plastics (polyvinyl chloride, polystyrene, polyrthylene and polyethylene terephthalate) has drawn the attention of ecotoxicologists to its toxicity in the environment (ecosystem). Waste plastics have become a serious environmental problem worldwide as they are not easily biodegradable, hence they are recalcitrant. The environmental impact of microplastics can be due to their small size, which facilitates internalization by biota (microbes, plants and aquatic organisms), leading to resultant accumulation in the food chain and affecting organisms in their ecological niches. Studies have shown microplastic accumulation in molluscs, birds, turtles, aquatic organisms and mammals. They can adsorb pollutants on their surfaces, which makes them good carriers of persistent toxic pollutants such as heavy metals, and polycyclic aromatic hydrocarbons (PAHs) and form complex pollution. They also contain additives such as lead heat stabilizers (tribasic lead sulphate, dibasic lead sulphate and lead sulphate), phthalate plasticizers (diisononyl phthalate, disodecyl phthalates and di (2ethylhexyl) phthalates) and flame retardants (polybrominated diphenyl ethers). This study aimed to evaluate the toxicological impact of activities at three waste plastic bottle recycling plants in Abuja, Nigeria. The investigation involved collecting liquid effluent, soil samples, and a plant species *Vernonia amygdalina* from three recycling sites: Lugbe (Site A), Area 1 (Site B), and Giri (Site C).

METHODS

Toxicological evaluations were conducted using 40 catfish (*Clarias gariepinus*) exposed to liquid effluents for four weeks, assessing liver marker enzymes and oxidative stress marker enzymes.

RESULT AND DISCUSSION

The soil samples from the three waste plastic recycling sites recorded different pH levels where waste plastic recycling site B of Area (1) village showed the lowest pH of 5.6 ± 0.10, while waste plastic recycling site A of Lugbe village and C of Giri village recorded 6.2 ± 0.10 and 6.9 ± 0.10 respectively. The control samples recorded 6.83 ± 0.10. The Electrical conductivity (EC) was highest in waste plastic recycling site B of Area (1) village with a value of 1.89 ± 0.36 mS cm^{-1}, when compared to waste plastic recycling site A of Lugbe village which had (1.52 ± 0.24 mS cm^{-1}) and C of Giri village which had (1.63± 0.24 mS cm^{-1}). The control recorded for EC showed higher values (1.95 ± 0.24 mS cm^{-1}) to test samples. The waste plastic recycling site B of Area (1) village showed the lowest total organic carbon (TOC), 1.45± 0.10%, when compared to site A of Lugbe village and C of Giri Village, which had 1.86 ± 0.10%, and 1.78 ± 0.10% respectively. The control values for total carbon content recorded 2.31 ± 0.20%. The Total organic matter (TOM) evaluated for the waste plastic recycling sites was all lower than the control while waste plastic recycling site B of Area (1) village recorded the least TOM. Soil total nitrogen showed 1.40 ± 0.04%, 1.24 ± 0.01% and 2.48 ± 0.27% for sites A of Lugbe village, B of Area 1 village and C of Giri village. Liquid effluents showed varying levels of physicochemical properties.

The effluent from waste plastic recycling site B of Area (1) village recorded the lowest pH of 6.01 ± 0.10 when compared to the standard (6.5 – 8.5) and the other waste plastic recycling sites. The Electrical conductivity (EC) values for all liquid effluents from the three recycling sites recorded 213.03± 10.32 mS cm^{-1}, 240.16± 12.11 mS cm^{-1} and 232.10± 18.26 mS cm^{-1} respectively. They were all below the standard (1000 mS cm^{-1}) stipulated by WHO. Total solids (TS) evaluated showed that effluents from site B of Area (1) village recorded the highest value (290.40± 21.00mg/l). Magnesium, chloride and nitrate levels were observed to be lower than the WHO standard across the three liquid effluents except for effluents for site B of Area (1) village that recorded 256.78± 0.14 and was higher than the standard (250mg/l). Phosphate levels showed that site A of Lugbe village, B of Area 1 village and C of Giri village recorded 0.56± 0.01, 0.84±0.01 and 0.84± 0.01 respectively. The biological oxygen demand (BOD) levels investigated showed that they were all lower (between 11 to 18 mg/L) compared to the standard which is 20 - 40 mg/L. The dissolved oxygen (DO) showed that effluents from waste plastic recycling site B of Area (1) village recorded the least amount of DO (6.13 ± 0.10 mg/L) when compared to the other samples. The soil samples from the waste plastic recycling sites were evaluated for plasticizers [phthalates, polybrominated biphenyls (PBDEs) and polychlorinated biphenyls (PCBs)]. The phthalates evaluated showed that Di ethyl Phthalate (DEP) recorded high levels in all the soil samples when compared to the control 0.05±0.00 mg/kg. BBP (Benzyl butyl phthalate) was detected in site A of Lugbe village and B of Area (1) village but was BDL in site C of Giri village. The DBP (Di-n-Butyl phthalate) present in soil samples from the 3 waste plastic recycling sites recorded 0.34±0.33mg/kg, 0.41±0.018 mg/kg and 0.28±0.10 mg/kg for A of Lugbe village, B of Area 1 village and C of Giri village respectively. They were not detected in the control. The Di (2-ethylhexyl) phthalate (DEHP) showed the highest level in waste plastic recycling site B of Area (1) village as 0.04±0.00mg/kg compared to the control which had 0.01±0.00mg/kg. (DiNP) Di-isononyl Phthalate levels were higher in Dump sites B of Area (1) village and C of Giri village but was BDL in site A of Lugbe village however, it was below detectable limit (BDL) in the control. Heavy metal analysis of soil samples showed the presence of Arsenic (As), Iron (Fe), Zinc (Zn), Lead (Ld), and Cadmium (Cd). Mercury (Hg). Chromium (Cr), Cobalt (Co), Copper (Cu), Nickel (Ni) and Aluminium (Al) in varying concentrations. Arsenic (As) in soil samples from the three waste plastic recycling sites recorded 0.80±0.10mg/kg, 1.40±1.01mg/kg and 0.52±0.01mg/kg for sites A of Lugbe village, B of Area (1) village and C of Giri village respectively however, it was BDL in the control.

Iron (Fe) appeared in moderate levels in all the samples from the 3 recycling sites, while Zinc had high levels in all the 3 soil samples from the 3 waste plastic recycling sites when compared to the WHO standard, with site B having highest value 11.76±0.56 mg/kg. They all exceeded the permissible limit (5 - 10mg/kg) except the control. Lead, cadmium and Mercury levels detected were all above the standard including the control however, cadmium was not detected in the control and mercury was not also detected in site C of Giri village. Cobalt and Nickel recorded the highest level in soil sample B of Area (1) village which was 5.10±0.26mg/kg, and 4.89±0.21mg/kg respectively. They were all higher when compared to their standards of 0.1mg/kg for both. Heavy metals were also evaluated in Liquid effluents from the waste plastic recycling sites, as Arsenic showed the highest level in Liquid effluents from site B of Area 1 village with a value of 0.21±0.01mg/L when compared to the WHO standard of 0.01mg/L. Iron and Chromium were found in high levels as Iron showed a level of 0.82±0.10mg/L, while sites A and C had 0.58±0.10mg/L and 0.62±0.10mg/L respectively compared to the WHO standard, and chromium having sites B and C in high levels as 0.38±0.20mg/L and 0.38±0.18mg/L, respectively. Polybrominated biphenyl ether (flame retardants) in soil samples were also detected in varying high levels, such as Congener-99, and Congener-47. Congener-183, Congener-100, and Congener-153 showed highest levels in soil samples from waste plastic recycling site B of Area (1) village as 28.2±0.36 µg/kg. 35.3±1.75 µg/kg, 42.4±0.34 µg/kg, 38.6±0.23 µg/kg and 31.32±0.01 µg/kg respectively. Polychlorinated biphenyl ether (flame retardants) also showed the highest levels of Congener -75, Congener-81 and congener-114 in site B as these levels were detected as 1.56±0..12 µg/kg, 1.40±0.10 µg/kg and 1.13±0.10 µg/kg respectively.

Microbial analysis for soil samples showed varying levels of microbial colonies, as site A of Lugbe village recorded *E.coli, Acromobacter sp, Aspergillus sp., Rhodotorula sp.* and *Bacillus sp.* Waste plastic recycling sites site B of Area (1) village recorded varying levels of Aspergillus, *Rhodotorula sp., Bacillus, E.coli,* and streptomycetes. Site C of Giri village also showed varying levels of *Rhodotorula sp., Aspergillus Sp., E. Coli, Bacillus Sp*., and *Pseudomonas Sp*. Heterotrophic counts for soil samples from the sites also showed coliform and viable counts as well as that of the effluent samples. There was a significant decrease ($p<0.05$) recorded for Dehydrogenase in soil enzyme level for waste plastic recycling sites B of Area (1) village and C of Giri village. They had 2.31±0.42 (µg TPF g^{-1} soil h^{-1}, and 2.75±0.33µg TPF g^{-1} soil h^{-1}) respectively compared to 3.47±0.24 (µg TPF g^{-1} soil h^{-1}) for site A of Lugbe village. Catalase was recorded least in site B of Area (1) village as it had a level of (0.72±0.26 mL KMnO4 g^{-1} Soil h^{-1}) and highest in PET recycling site A with a level of 1.22±0.24 mL KMnO4 g^{-1} Soil h^{-1}) compared to the control which had (1.10±0.24 mL KMnO4 g^{-1} Soil h^{-1}). Urease had normal levels for all soil samples. while phosphatase and invertase were detected highest in waste plastic recycling site A of Lugbe village for Phosphatase as (0.38±0.20 µg Phenol g^{-1} Soil h^{-1}) and site B of Area 1 village for Invertase as (1.86±0.52µg Glucose g^{-1} Soil h^{-1}).

Heavy metal levels for plant samples from these waste plastic recycling sites were within normal standards except for cobalt which had a significant ($p<0.05$) high level in site B of Area (1) village with a level of (0.31±0.10mg/kg). Polybrominated diphenyl ether (flame retardants) in Plant samples showed the highest levels of Congener-99, and Congener-47. Congener-100, Congener-153, Congener-28, Congener-154, and Congener-183 in site B of Area (1) village as compared with WHO standard. There were recorded levels of plasticizers in plant samples from the three recycling sites as plant samples from site B recorded the highest level of (DiNP) Di-isononyl Phthalate and (DIBP) Di-iso-butyl phthalate as 0.13±0.10mg/kg and 0.15±0.01mg/kg respectively. Alanine transaminase (ALT), Aspartate transaminase (AST) and Alkaline phosphatase (ALP) levels of fish samples showed varying levels due to the contamination with PET liquid effluents at different concentrations. They all increased significantly ($p<0.05$) across all the groups that were grown. The effects of effluent samples from the three PET sites on stress markers such as Catalase (CAT), Glutathione (GSH), Glutathione peroxidase (GPx) and Malondialdehyde (MDA) levels of fingerlings results showed a significant difference in test groups when compared to the control. They all increased significantly ($p<0.05$) across all the groups grown.

CONCLUSION

The ecotoxicological assessment showed the extent of harm and possible adverse effects these waste plastic recycling sites could cause to the environment. It has also shown the bioaccumulation of plasticizers and heavy metals in edible plants beyond standards stipulated by WHO which can become detrimental to humans. Therefore, it is necessary to continue to enlighten these farmers about the dangers of cultivating and fishing in nearby waste plastic recycling sites.

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Effect of Leaf Extracts and Incidence of *Cylas formucarius* (Weevil) on Sweet Orange Potato (*Ipomoea batatas*) in Abuja, FCT, Nigeria

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INTRODUCTION

Root and tuber crops play a significant role in agriculture and facilitate food security in many developing countries. Worldwide, sweet potato is the sixth most important food crop after rice, wheat, potatoes, maize and cassava. Sweet potato is the crop with the highest potential for commercial exploitation (Kenneth, 2009) From 2010 to 2022, the global production of sweet potatoes amounted to approximately 86.4 million metric tons, a decrease of about one million metric tons from the previous year (Shahbandeh, 2024). Sweet potato comes in various varieties with skin and flesh color that range from white to yellow, orange, and deep purple.

Sweet orange flesh is an important source of beta-Carotene, the precursor of vitamin A. Just 125g of fresh sweet potato root from most sweet orange varieties contain enough beta-carotene to provide the daily pro-vitamin A needs of a preschooler, (FAO, 2021). The rich sources of nutrient from the intake of SOP has decreased the risk of obesity, diabetes, heart disease and overall mortality while promoting its intake. Unfortunately, the SOP is highly susceptible to the weevil known as Cylas. *Cylas spp*, is a very serious pest of sweet potato, especially the sweet orange varieties. They feed on the tubers, leaving behind numerous small black holes on the affected tubers which render its qualities (taste and market value) useless. This study is intended to achieve the following objectives to compare the effects of the different levels of Moringa leaf extract on the Sweet orange potato production and to determine the effect of different levels of application in the control of cylas weevil.

MATERIALS AND METHODS

The study was conducted in 2022 cropping season at the Teaching and Research Farm of National Biotechnology Research and Development Agency, Abuja. Abuja, the federal capital territory is located in the Guinea savannah of Nigeria. The sweet orange potato was sourced from the potato farmers association, Abuja. The SOP is a high yielding variety and has been under pre-release evaluation for recommendation to farmers in Nigeria. The treatment levels were 0, 20, 50& 100ml of MLE where 0ml was the control. The Moringa fresh leaves was sourced from the research farm of the experimental site. Four treatment combinations was used with randomized complete block design and replicated thrice. Each replicate contained 4 plots and plot size was 3m×3m and planting spacing was 1m×0.3m. plant stands per plot was 30 and inter plot spacing was 1m. During planting, 2/3 of the length of each line (20cm long) was inserted into the soil, at angle of 60^0.The soil around the vine was firmly pressed to ensure proper contact to the soil for easy establishment. First and second weeding was done three and seven weeks after planting using hoes respectively and the extract was applied after weeding before the vine leaves covered the ground surface, suppressing weed in the process.

Data collected were stand count at harvest, root weight (Kg/plot), mean marketable and unmarketable roots/plot , mean root with cylas weevil incidence (i.e total number of roots with cylas weevil). Mean root cylas weevil severity score where 1) All tubers clean of cylas damage across the plot. 2) < 20% of each tuber in the plot damaged. 3) 21-50% of each tuber in the plot damaged. 4) 51 -50% of each tuber in the plot damaged. 5) >80% of each tuber in the plot damaged. Data collected were subjected to analysis of variance (ANOVA) using Duncan multiple ranges tests to separate means

RESULTS AND DISCUSSION

Table I showed the fertility status the site of experiment before the onset of the experiment. The result indicates that the soil fertility was relatively poor and that may be attributed to the continuous cropping in the area as indicated by cropping history. Esu, (2010) classified the soil in the area as alfisols, well drained and strongly acidic giving credence to the pre-planting soil analysis that showed a soil pH value of 5.3. Also, after the experiment, postharvest soil analysis was done and the status of some basic elements (N, P, K, Mg and Ca) was enhanced significantly in the plots with 100ml and 50ml application (Table 5). Percent nitrogen and phosphorus were relatively higher in control plots. The large concentration of phosphorus was observed in control plot, pH was significantly improved with the application of moringa leaf extract especially in the highest level of treatment. pH values tend to increase the cation exchange capacity of the soil under this situation of basic cations which are significantly available to the plant for their nutrition. Moringa has been reported to significantly improve soil fertility if used as a green manure, (Davis, 2000) while there was a decline in control plots.

Table 2 showed that the yield components of the sweet orange potato with different levels of treatments. Stand counts showed that stands amended with different levels were higher than the control plots. Phiri (2003) reported that *Moringa oleifera* leaves have high zeatin content. Zeatin is a plant growth hormone from the cytokinin group. It plays an improved role in cell division and cell elongation (Taz & Zeiger, 2006). Root yield was significantly improved (P>0.05) on treated plots. Plots amended with 100ml of moringa extract produced 74% more root yield than the control, 50ml by 70% and 20ml by 58% respectively. Marketable number of roots significantly (P<0105) was improved with treated plot while unmarketable was highest in the control plots. In Zambia, Moniga has been reported to increase crop growth and yield (Foidl *et.,al,* 2001). In terms of severity of infection by Cylas on the roots, stands treated with MLE showed very mild to moderate symptoms than the control (Table 3). Fugile, (2001) reported that MLE improves resistance to pests and diseases.

CONCLUSION AND RECOMMENDATION.

Table I: Pre-planting physical/chemical properties of the experimental site.

Parameters	Before Planting
PH in meter(1:25)	5.3
%Organic matter	0.52
Total N	0.43
P(PPM)	10.3
K(CmolKg^{-1})	0.47
mg(CmolKg^{-1})	2.38
Na(CmolKg^{-1})	1.44
Clay%	36.6
Silt	16.9
Sand	4

Table 2: Mean root yield & yield components of Sweet orange potato

Potato	Application	Stand counts	Marketable	Unmarketable	Root/yield
SOP	O ml	20 d	7 gh	16 f	4i
SOP	20 ml	25 c	21 d	21 d	7 gh
SOP	50 ml	24 c	23 c	10 g	8 gh
SOP	100 ml	28 b	39 a	8 gh	19 e

DMRT (p>0.05)

Table 3: Severity of infection of Cylas Weevil on the storage roots of the sweet orange potato.

Potato	Application	No of roots with cylas	Severily Score
SOP	0 ml	18	4
SOP	20 ml	12	3
SOP	50 ml	8	2
SOP	100 ml	5	2

Mean SPVD Severity score at 10weeks after planting where
1.No visible SPVD symptoms on all plants in the plot
2.Very small symptoms on all plants in the plot
3.Moderate symptoms on all infected plants
4.Severe symptoms on infected plants and
5.Very severe symptoms on infected plants(plants are stunted, leaves shriveled)

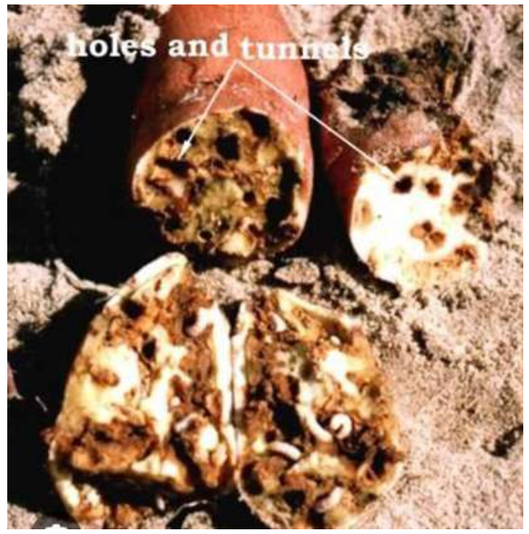

Fig 3;Severe cylas infestation on SOP

Table 4: Post harvest soil properties on the effect of leaf extracts and incidence of Cylas weevil.

Potato	Application	Physical properties			Elements			%organic matter		
Clay	Silt	Sand	pH	N	P	K	Mg	%	ppm	<-
cmolkg^{-1}->										
SOP	20	38	18	43	6.7	0.12	12.4	0.57	2.61	0.43
SOP	100	37	18	40	5.8	0.41	8.6	0.51	2.37	0.58
SOP	50	37	17	40	4.8	0.53	14.7	0.51	1.88	0.37
SOP	0	38	17	40	4.5	0.21	9.5	0.34	1.10	0.11

The results of the study showed that the 100ml moringa treated plots increased yield and had mild symptoms of infestation of Cylas weevils, thus farmers can adopt the use of this extract to increase yield with easy and simple managements of pests and diseases.

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Prevalence of *Trypanosoma Spp.* Infection and Associated Factors among Cattle in North-West Region, Cameroon

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Abstract
African trypanosomiasis is a parasitic disease of man and livestock which results in immeasurable economic losses and public health problems, however, its current prevalence in parts of Cameroon is yet to be determined. This research was, therefore, aimed at evaluating the prevalence of *Trypanosoma* spp. infection among cattle in the North-West region, of Cameroon. Blood samples were collected from cattle in six divisions of the northwest region of Cameroon. A part of the sample was used for microscopic diagnosis in the field. The other part was centrifuged and the buffy coat was used for molecular analysis. Gudali, Red Fulani, White Fulani, Mboro and Holstein were the breeds of cattle observed. The knowledge, attitude, and practices of herders revealed Animal African Trypanosomiais as the most vital limitation to cattle production in the region. The results showed that 30.3 % of the animals were anaemic and a greater percentage of the cattle were female (63.4%), older (71.8%), of median body condition score (61.6%) and of the Gudali breed (40.8%). The study established an overall prevalence of 7.1%, which varied with season (rainy season (4.4%) and dry season (2.7%). The species of trypanosomes identified in the study area were: *T. simiae* (3.8 %), *T. grayi* (2.2%), *T. congolense* (1.1%), *T. vivax* (1.1%) and *T. brucei* (1.1%). Older cattle were observed to present a higher trypanosome prevalence than younger ones. The results suggests that Animal African Trypanosomiasis is still prevalent in the North-West region of Cameroon.

Keywords: Trypanosome, Cattle, Prevalence, Infection, Cameroon

Background of Study
African trypanosomiasis is a parasitic disease of man and livestock which results in immeasurable economic losses and public health problems. Cameroon is recognized as one of the largest producers of beef in the Economic Community of the Central Africa States (CEMAC) region with an estimated ten million cattle (Mamoudou *et al.,* 2015). In Cameroon, about 90 % of the population of the estimated cattle are at risk of trypanosome infection (Paguem *et al.,* 2019). Moreover, cattle are noted to play an important role in improving food security and alleviating poverty (Molina *et al.,* 2020). However, its current prevalence in parts of Cameroon is yet to be determined. This research was, therefore, aimed at evaluating the prevalence of *Trypanosoma* spp. infection among cattle in North-West region, Cameroon.

Method
A cross-sectional survey was carried out from March to April (early rainy season) and from November to December (Early Dry season) in six divisions in the North West region, of Cameroon. Questionnaires were used on the field before the blood sample collection process from cattle. A part of the sample was used for microscopic diagnosis in the field. The other part was centrifuged and the buffy coat was used for molecular analysis. Nested PCR was carried out using the ITS-1 primers. Data generated were analyzed using the Chi-square test at a 95% confidence interval, and the Epi info 7 test.

Result

Table 1. Number of Cattle and their Breed identities in the North-West Region of Cameroon

Division	Number of Herds/Number of Herds men	Number of Cattle	Breed
Boyo	3	240	Red Fulani
Donga Mantung	10	876	Gudali, Red Fulani
Menchum	3	203	Gudali, Red Fulani, White Fulani
Mezam	6	174	Gudali, Red Fulani, White Fulani
Momo	4	326	Gudali, Red Fulani, White Fulani, Mboro, Holstein
Ngoketunjia	4	775	Red Fulani, White Fulani, Mboro
Total	**30**	**2217**	

The breeds of cattle observed were Gudali, Red Fulani, White Fulani, Mboro and Holstein (Table 1).
The results revealed that 30.3 % of the animals were anaemic and a greater percentage of the cattle were female (63.4%), older (71.8%), of median body condition score (61.6%) and of the Gudali breed (40.8%). The study established an overall prevalence of 7.1%, which varied with season (rainy season (4.4%) and dry season (2.7%). The species of trypanosomes identified in the study area (Table 2) were: *T. simiae* (3.8 %), *T. grayi* (2.2%), *T. congolense* (1.1%), *T. vivax* (1.1%) and *T. brucei* (1.1%). Older cattle were

Table 2. Prevalence of Trypanosome by Specie in the North-West Region of Cameroon (n=183)

Parasite species identified	Number of infected cattle	Prevalence (%)
Single parasite species		
T. simiae	2	1.1
T. congolense	2	1.1
T.vivax	2	1.1
T. brucei	1	0.5
T. grayi	1	0.5
Mixed parasite species		
T. simiae + T. grayi	4	2.2
T. simiae + T. brucei	1	0.5

observed to present a higher trypanosome prevalence than younger ones.
Conclusion This study established the occurrence of Trypanosomiasis in the Boyo, Donga Mantung, Menchum, Mezam, Momo and Ngoketunjia divisions in the North-west region of Cameroon, with an overall prevalence of 7.1%.

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Influence of Agrarian Export Products to Fiscal Growth in Nigeria

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Introduction
Agricultural resources have historically been significant in the Nigerian economy and continue to be a major sector despite the dominance of the oil industry. It provides job opportunities for the growing population, helps alleviate poverty, and contributes to economic growth (Oji-Okoro, 2011). Since independence, the agricultural sector has been the backbone of the economy and remains a resilient supporter of the populace despite various challenges. In 1960, Nigeria was a leading global exporter of groundnuts, cocoa, palm produce, rubber, and cotton (Sekunmade, 2009). Currently, agriculture employs about two-thirds of Nigeria's workforce, significantly contributes to GDP, and generates a substantial portion of income outside the oil sector (Odetola and Etumnu, 2013). The agricultural sector in Nigeria has vast untapped potential for expansion and improvement, given the availability of land, water resources, and a large domestic market (Ewubare, 2015). While approximately 84 million hectares of Nigeria's land are suitable for farming, only around 40% is currently utilized for agriculture (Ewubare, 2015; FMARD, 2012). However, the efficiency of cultivated land is limited due to small farm sizes and outdated agricultural practices. As a result, Nigeria heavily relies on food imports (Odetola and Etumnu, 2013). Despite having diverse vegetation that can support a large livestock population and irrigation potential with significant surface and underground water resources, Nigeria's agricultural sector faces challenges. The country's growing population presents an opportunity for a vibrant internal market for increased agricultural output (Odetola and Etumnu, 2013). Yet, the state of agriculture in Nigeria remains poor and fundamentally weak, with a continued reliance on outdated practices to support a growing population without efforts to add value (Odetola and Etumnu, 2013). This has negatively impacted the sector's productivity, contribution to economic growth, and ability to fulfill its traditional role in food production, among other agricultural benefits (Odetola and Etumnu, 2013).
Materials and Methods
The study employed an uncomplicated production function: Y = AK (Y represents productivity, A represents technical advancement while K represents assets and adopts non-diminishing returns towards assets). This research adopted the Solow–Swan production function, a financial model used for long-term financial development fixed in a structure of neoclassical economics – like a foundation towards improving financial development representation in support of the present research. The representation aims to clarify long-standing financial expansion by considering asset accretion, workforce, and technical development, owing to its predominantly smart mathematical features. Solow– Swan proved to be a suitable preliminary stage regarding several expansions:
$Y = f(L, K)$ (1)
The manufacturing function should be extended by the addition of agricultural exports:
$Yt = f(LEBt, DCFt, POPGt, AGRIC\_Et, \mu)$ (2)
The representation can be altered by inclusion of both exchange rate and foreign direct investment as regulator variables:
$GDPt = f(LEBt, OERt, FDIt, DCFt, POPGt, AGRIC\_Et, \mu)$ (3)
where
GDPt is the yearly gross domestic product.
LEBt denotes life expectancy at birth.
OERt represents the official exchange rate.
FDIt denotes foreign direct investment.
DCFt is domestic credit provided by a financial institution.
POPGt is population growth.
AGRIC_Et is agricultural export while μ is the error term
Statistical Analysis
The study utilized the General Method of Moments (GMM) to investigate the impact of agricultural export products on Nigeria's trade and industry development. Data were sourced from reputable institutions such as the Central Bank of Nigeria (CBN), the Nigerian Bureau of Statistics (NBS), and the World Bank to ensure the credibility and reliability of the information used. The analysis focused on the relationship between agricultural export products and trade and industry development, with a specific examination of their effects on agricultural revenue, export products, total output, and subsectors within the agricultural sector.
Result and discussion
In Table 1, all other sectors show a negative but significant impact on total output (GDP_O) except LEB ($t = 14.72$, coef = 1.079 at $p < 0.01$) that is positive and significant regarding GDP_O. The total agricultural export product ($t = -1.34$, coef = –0.1321 at $p > 0.1$) is negative and insignificant regarding GDP_O. Looking at the subsector impact on agricultural export product under FLA_E, all other factors except LEB are negative but significant ($t = 13.45$, coef = 1.0698 at $p < 0.01$), which is positive and significant. FLA_E itself is negative and significant ($p < 0.1$). The impact of BETO is negative ($t = -2.72$, coef = – 0.1195) but significant ($p < 0.01$), while other factors are also negative but significant. Looking at the impact of CMINE_E, CMINE_E itself is negative and insignificant ($t = -1.45$, coef = –0.1141 at $p > 0.1$), LEB is positively significant while all the other factors are negative but notably effective. The effect of AVOF_E is progressive but negligible ($t = 0.19$, coef = 0.0126 at $p > 0.1$). Consequently, the F-statistic for Table 1 shows that all explanatory variables, including the agricultural export subsector, are sufficient to explain the dependent variables while R2 shows the reliability of explanatory variables not <90% i.e they at significant at 1%, 5% and 10%.
Table 2 shows that all factors contributing to agricultural production in their monetary value, the result revealed that the availability of Tractor to the farmers is negative but significantat 1% (t= -3.70, coef

= -0.7860), official Exchange rate, OER was significant to the monetary value of agricultural products (t= 6.3, coef =0.03), the total output (yield) have a negative relationship with the monetary value of agricultural products together with Direct Credit facilities. Looking at population growth, it has a positive impact which shows the the larger the number of people engaged in agricultural production, the more the output hence, an increase agricultural fiscal value.

Table 1: Performance of Agricultural Export Products on Nigeria Economy

	LNGDP_O		LNGDP_O		LNGDP_O		LNGDP_O		LNGDP_O	
	"Coef".	"T-test"	"Coef".	"T-test"	"Coef".	"T-test"	"Coef".	"T-test"	"Coef".	"T-test"
FDI	-0.3774	-3.41***	-0.3764	-3.47***	-0.3424	-2.80***	-0.3638	-3.16***	-0.3145	-2.17**
OER	-0.0091	-2.87***	-0.0094	-2.84***	-0.0126	-3.34***	-0.0086	-2.73***	-0.0077	-1.92*
LEB	1.0790	14.72***	1.0698	13.45***	1.2416	14.61***	1.0807	14.82***	1.0156	10.55***
DCF	-0.0300	-3.04***	-0.0273	-2.60***	-0.0235	-2.06**	-0.0341	-3.35***	-0.0256	-2.08**
POPG	-2.7534	-4.65***	-2.6667	-4.37***	-3.6638	-6.25***	-2.8921	-5.08***	-2.8429	-4.38***
LNAGRIC_E	-0.1321	-1.34								
LNFLA_E			-0.1310	-1.84*						
LNBETO					-0.1195	-2.72***				
LNCMINE_E							-0.1141	-1.45		
LNAVOF_E									0.0126	0.19
CONSTANT	-26.5136	-9.63	-26.4517	-9.04	-32.6996	-11.01	-26.5811	-9.91	-25.4614	-6.80
Adj R-Square	0.903		0.903		0.910		0.902		0.896	
F-Statistics	52.38 (0.000)		52.53 (0.000)		53.64 (0.000)		51.66 (0.000)		48.86 (0.000)	
Number of Obs.	34		34		32		34		34	

Note: *** rep significancy at 1%
** rep significancy at 5%
* rep significancy at 10%

	Coef	Standard Error	t-test
LNTRACTOR	-0.7860	0.2456	-3.20***
OER	0.0300	0.0047	6.37***
LEB	0.0848	0.1146	0.74
DCF	-0.0589	0.0142	-4.15***
POPG	5.0435	0.8771	5.75***
LNYIELD	-4.8772	0.6334	-7.70***
CONSTANT	30.0058	4.2084	7.13

Note: *** rep significancy at 1%
** rep significancy at 5%
* rep significancy at 10%

CONCLUSION AND RECOMMENDATIONS

The results of this study shows that the overall exportation of agricultural products has a very minimal impact on Nigeria's economy.

Value addition should be prioritized before agricultural products are exported. Also improved or hybrid inputs should be provided to farmers at affordable rates.

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Effectiveness of Cocoa Promotion in Osun State, Nigeria.

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INTRODUCTION

Cocoa, scientifically known as Theobroma cacao and belonging to the Sterculiaceae family, is classified as a beverage crop. Originating from the tropical rainforests of South America, cocoa was introduced to various West African countries during the 19th century. It became a significant export crop in nations such as Ivory Coast, Ghana, Cameroon, Nigeria, Togo, and Equatorial Guinea. African countries collectively produce around two-thirds of the world's cocoa, with Nigeria ranking as the third-largest producer in Africa, contributing approximately 6% of global production. Currently, Nigeria's cocoa production capacity has reached about 385,000 tonnes per year, showing substantial growth from the 2000 production levels. Agriculture serves as the largest non-oil export earner in Nigeria, playing a crucial role in wealth creation, and poverty reduction, and serving as a major employer. Cocoa's contribution to the economic development of the nation is significant, as it has been highlighted in various studies. In terms of foreign exchange earnings, cocoa stands out as a key commodity, providing raw materials, and revenue to cocoa-producing states' governments and making a notable contribution to the Gross Domestic Product (GDP).

Marketing is a vital process in which the demand for products, services, and ideas is anticipated, managed, and satisfied. It encompasses all business activities involved in planning, pricing, promoting, and distributing goods and services to meet the needs of current and potential customers. Prior to the Structural Adjustment Programme (SAP), cocoa marketing in Nigeria was managed by regulated commodity Marketing Boards that often paid farmers less than the export price for their cocoa beans. These boards were responsible for procuring cocoa beans from local farmers for exportation, utilizing Licensed Buying Agents appointed by the boards to purchase, bag, store, and sell the beans.

Efficient marketing is crucial for economic development, as it plays a key role in poverty alleviation, reducing consumer prices, earning foreign exchange, and eliminating economic inefficiencies. The shift towards more efficient marketing practices is essential for enhancing the economic development of any nation. The Nigerian Cocoa Marketing Board (NCMB) used to oversee the grading and transportation of cocoa beans to the Board's Port Store. This was done to stabilize the prices received by cocoa farmers and shield them from fluctuations in the world market. However, with the abolition of the NCMB, the orderly marketing of cocoa came to a halt. This led to an increase in the number of individuals involved in buying and selling cocoa, resulting in a variety of channels for farmers to market their produce.

The marketing process for cocoa in Nigeria involves several intermediaries, including small traders and wholesalers. Small traders purchase cocoa beans directly from farmers and then sell them to wholesalers. The wholesalers, in turn, sell the beans to exporters or cocoa processors. Some farmers' cooperatives also directly sell to exporters or export the beans themselves. Once the cocoa beans reach the port for export, they are graded and stored in warehouses before being loaded onto cargo vessels.

Currently, there are approximately 123 registered cocoa exporting firms in Nigeria, but a few of them handle the majority of cocoa exports. Initially, after the abolition of the NCMB, there was a chaotic market with numerous exporters, but over time, a few large corporations have emerged and are now integrating into various stages of the cocoa supply chain.

Over the past two decades, there has been a global trend towards market liberalization, affecting both international and domestic markets. In developed economies, this has led to concentration and vertical integration, with a small number of large corporations dominating the market. In contrast, in developing countries like Nigeria, market liberalization has resulted in de-concentration and specialization, leading to lower market prices for producers. Since the abolition of marketing boards in 1986, Nigerian farmers and marketers have faced challenges in selling their produce in the global market, particularly for crops like cocoa, cotton, and rubber. This has led many farmers and marketers to diversify into other sectors of the economy.

Despite past efforts by Nigerian governments to support agriculture through institutional programs, success has been limited due to poor implementation and inconsistent government policies. Efficiency in the agricultural industry is crucial for measuring market performance and ensuring sustainable development in cocoa marketing activities in Nigeria. The cause of these, this research work tends to analyze the effectiveness of cocoa marketing in Ile-Ife and Modakeke-Ife of Osun State. Seeking the socio-economic characteristics of cocoa marketers, examining marketing activities, analyzing the profitability and marketing efficiency, and identifying the challenges to marketing activities of respondents. The hypothesis of the study will seek the significant relationship between selected market variables and revenue generated by respondents.

METHODOLOGY

The research was conducted in Ile-Ife and Modakeke-Ife, both located in Osun State, Nigeria. Data for this study was obtained using purposive sampling methods. Structured interviews were conducted to collect information on the socio-economic status of cocoa marketers, their marketing practices, channels, experiences, costs and returns on their business, as well as any problems encountered during the marketing process. The collected data was analyzed using two main analytical tools: Descriptive analysis and Budgetary analysis. Descriptive statistics were used to analyze the socio-economic characteristics of the respondents. Budgetary analysis was employed to determine the profitability and efficiency of cocoa marketing. Budgetary analysis aimed to examine how profitable cocoa marketing is by utilizing specific equations:

Total Revenue (TR) = P*Q
Where P = Price/ton and Q = Quantity sold/ton
Total Cost (TC) = Total Variable Cost (TVC) + Total Fixed Cost (TFC)
Gross Margin = TR – TVC
Profit (π) = TR – TC
Profitability Efficiency = TR/TC

Benefit Cost Ratio (BCR) = ΣTR/ΣTC
When BCR > 1
The enterprise is profitable. Otherwise, it is not

Marketing Efficiency = BCR * 100%, Also, when TR>TC, there is profit, When TR <TC, there is loss, and When TR=TC, there is a break-even point in business.

Regression Analysis: This shows the relationship between the dependent variables (XL_1 – LX_9). The regression function postulated for cocoa bean marketers in the study area is implicitly presented by the following equation.

$Y = f(X_1,X_2,X_3,X_4,X_5,X_6,X_7,X_8,X_9,N_i)$

Y = Revenue; X_1 = Sex; X_2 = Number of children; X_3 = Age; X_4 = Marital Status; X_5 = Level of Education; X_6 = Year of Experience; X_7 = Source of fund; X_8 = Total Cost; X_9 = Total Return; N_i = Error terms

Presentation and Discussion of Results

Socio-economic Characteristics of Respondents: The result shows that 82% of the respondents were male while 18% were female. All marketers were married with an average household of 6.02. The average age of the respondents was 45.5 years with 13.5 years of experience in the marketing of cocoa.

BUDGETARY ANALYSIS

Cost and Returns data supplied by the respondents were analysed below:

Total Revenue (TR) = Selling Prince * Quantity Sold

Variable Cost (VC) = N1,25,749,960.00

$$AVC = \frac{N125,749,960}{70 \text{ Respondents}} = N1,796,428.00$$

$$\text{Average Fixed Cost} = \frac{N52,099,950}{70 \text{ Respondents}} = N744,285.00$$

ATC = AVC + AFC

= N(1,796,428 + 744,285)

= N2,540,713.00

$$\text{Total Return (TR)} = \frac{N195960730}{70}$$

= N2,799,439.00

Gross Margin = TR – VC

= 2,799,439.00 – 1,796,428.00

= N1,003,011.00

Net Return = TR – TC

= N(2,799,439 – 2,540,713)

= N258,728.00

Profitability Ratio (Benefit Cost Ratio)

TR = N2,799,439.00 TC = N2,540,713.00 TR > TC (i.e 2,799,439 > 2,540,713)

Profitability Efficiency = TR/TC

$= \frac{2,799,439}{2,540,713} = 1.102$

BCR > 1 reveals that cocoa marketing in the study area is profitable. Challenges Associated with Cocoa Marketing in the Study Area: Based on the data collected, it was revealed that the majority of the marketers were faced with a lack of capital, poor sorting and grading of the cocoa beans, inadequate storage facilities, and deterioration in quality as well as poor transportation due to bad roads.

Table 1: Challenges associated with cocoa marketing, n = 70

Challenges	Frequency	Percentage (%)
Financial challenge	70	100.00
Deterioration in quality	54	77.1
Poor sorting and grading	52	74.3
Poor transportation	70	100
Inadequate storage facilities	56	80.0
Pest and Diseases	59	84.3

TEST OF HYPOTHESIS

Ordinary Least Square analysis was employed to test the hypothesis which stated that, there is no significant relationship between market variables and revenue generated by respondents. The variables selected were sex, family size, age, level of education, year of experience, source of funds, total cost, and total returns. The Cobb-Douglass functional form was found to be best fitted considering the number of statistically significant estimated variables and signs carried by the coefficient of the variables. All the independent variables were found to be significantly influencing revenue generated by respondents. Adjusted R square indicates a 73.4% variation in revenue could be estimated variables. F-value of 27.9 which was significant at 1% revealed the goodness fit of the model employed.

RESULT AND DISCUSSION

The findings indicated that the cocoa marketing business is profitable and efficient. The study revealed a significant relationship between the socioeconomic characteristics of marketers and their income. It was also found that there has been an increase in returns from sales for these marketers. Moreover, market competitive forces do not dictate the price of cocoa.

CONCLUSION AND RECOMMENDATION

It is evident that the Nigerian Agricultural Sector experienced a setback both in production and exportation but the marketers are still finding their ways to obtain their profit from the sales of cocoa beans. These marketers are the middlemen between farmers or local buyers of cocoa beans and the exporters, and they are maximizing the opportunity available for them to meet their ends needs. It is recommended that commercial and merchant Banks should cooperate with the government by providing loans for farmers involved in cocoa marketing. The government should focus on developing rural areas and providing social amenities for farmers and marketers. Encouraging the formation of cooperative societies among cocoa marketers would benefit wholesalers as they can collectively make decisions on matters that directly affect them. Regular reporting of prices to farmers and buying agents is crucial for the effective functioning of the marketing system.

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Molecular Genotyping of the Voltage Gated Sodium Channel (VGSC) Gene Mutation (l995f) in *Anopheles Coluzzii*

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INTRODUCTION

The knockdown resistance (kdr) gene, also known as the voltage gated sodium channels (VGSCs) gene, is impacted by the mutations (Labbé *et al*., 2017). The target-site insensitivity of *A. coluzzii* is related with two dissimilar mutations in the transmembrane segment 6 of domain II (DIIS6) of para type sodium channel at position 995. The results of the mutations include leucine (TTA) to phenylalanine (TTT) (L995F) or leucine (TTA) to serine (TCA) (L995S) substitutions (Aboulfadl *et al*., 2023). The former mutation, known as kdr-west, was shown to be widespread in West Africa (Aboulfadl *et al*., 2023), whereas the later mutation, known as kdr-east, was first identified in East Africa (Acford-Palmer *et al*., 2023). Notwithstanding, studies have indicated that the 995F allele is located in East Africa and West Africa (Sagbohan *et al*., 2021). These imply that the regional distribution of the two mutations is not what was previously stated. In *A. coluzzi*, the African malaria vector, these two-point mutations confer resistance against DDT and pyrethroid insecticides (Ibrahim *et al*., 2019). Both the M molecular form of *A. gambiae* (*A. coluzzii*) and S molecular form of *A. gambiae* (*A. gambiae* s. s.) have been found to carry the L995F mutation. However, according to Souza *et al*. (2023) the L995S was only seen in the M-form. Both types of mutations have been linked to pyrethroid resistance; yet, in *A. coluzzii*, a high frequency of the 995F kdr allele has been strongly linked to resistance to lambda-cyhalothrin (Ibrahim *et al*., 2014).

Knowing the mutation profile and the genotypes of both the resistant and susceptible mosquitoes will guide in understanding how transgression of genes often occur among the mosquitoes. The objective is to identify the contribution of knockdown resistance (kdr) mutation L995F in voltage-gated sodium channel and profile resistance to the pyrethroid insecticides.

METHODOLOGY

Mosquitoes genomic DNA was extracted from *An. coluzzii* species according to protocol prepared (Lekeufack-folefack *et al*., 2020). Molecular identification of Mosquitoes was according to (Caputo *et al*., 2022). The protocol used for the detection of the L995F kdr alleles was adapted from the protocols developed by (Aboulfadl *et al*., 2023).

RESULT AND DISCUSSION

A. coluzzii were the members of the *A. gambiae* complex identified in the study area during the rainy season (Period of peak malaria transmission). The genotypic frequency showed that there are more homozygous individuals than heterozygous individuals in the Permethrin resistant phenotype while little disparity was observed in Deltamethrin resistant phenotype. Clearly from our result, homozygous mutants indicated higher chances of survival under Permethrin treatment. Although, equal chances of survival between homozygous and heterozygous mutants under Deltamethrin treatment was indicated. Also, heterozygous mutants were observed in susceptible phenotype (very small percentage). This heterozygosity may result in the removal of susceptible individuals, leaving the first resistant. This could happen via consanguinity and preferential mating, which will only pass on the resistance allele (995F) to their progeny, ensuring the spread of mutation within the population [38]. For improved validation, more research with a bigger sample size is necessary.

The limitation of this study is that we did not sequence the VSGC gene to check for novel mutations.

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Comparative Bactericidal Effect of Aqueous and Ethanolic Extracts of Lawsonia inermis (Henna) on Some Selected Bacteria.

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INTRODUCTION

The increasing use of plant extracts in the food, cosmetics and pharmaceutical industries suggests that to find their active compounds, a systematic study of medicinal plants is very important (Nostrol et al., 2002). The acceptance of traditional medicine as an alternative form of health care and the development of microbial resistance to the available antibiotics has led researchers to investigate the antimicrobial activities of medicinal plants (Lisbachin and Deans, 1996; Maoz and Neeman, 1998; Hammer et al., 1999). In recent times, naturally occurring bioactive compounds from medicinal plants have been used as chemo-preventive agents to treat diseases without risk assessment. The finding of antibacterial activity presents an easy in vitro system that can be used for assessing the antibacterial activity of plants. To substitute synthetic antibiotics, many of today's modern and effective drugs have their origin in traditional folk medicine (Natarajan et al., 2003). Plants have been used to treat human, animal and plant diseases from time immemorial. Also, herbal medicines have been known to man for centuries (Goun et al., 2003). Therapeutic efficacies of many indigenous plants for many disorders have been described by practitioners of traditional medicine (Almaqbool et al., 1985; Khattak et al., 1985). This paper aims to determine the bactericidal properties of the leaves of henna (Lawsonia inermis) using the aqueous and ethanolic extracts and their efficacy against different bacterial strains.

MATERIALS AND METHODS

The leaves of Lawsonia inermis were collected from the University of Abuja main campus and they were botanically authenticated in the herbarium of Biological Sciences Department. After proper identification, the leaves were air-dried for 28 days, at room temperature after which they were pulverized into fine powder using an electric grinder and the powder obtained was stored in an air-tight container until further use. Pure clinical isolates of Escherichia coli, Staphylococcus aureus, Pseudomonas aeruginosa and Salmonella typhi were obtained from the Department of Medical Microbiology, University of Abuja Teaching Hospital, Gwagwalada, Abuja, Nigeria. The identities of the organisms were confirmed by standard biochemical tests and proper gram-staining

techniques. The organisms were subcultured on nutrient broth in bijou bottles and incubated at 370C for 24 hours. The organisms were then stored at 40C until needed and the cultures were checked for viability and purity by regular plating.

RESULTS AND DISCUSSION

The Results of the bactericidal properties of the leaves of henna are presented as follows:

Table 1: Showed the result of the Percentage yield of *Lawsonia inermis* using the aqueous and ethanolic solvent.

PARAMETER	AQUEOUS	ETHANOLIC
Weight of powdered extract	80g	80g
Value of weight extracted	4.95g	6.49g
Percentage yield (%)	6.2%	8.1%

80g of the henna powder resulted in 4.95g in aqueous and 6.49g in ethanolic solvents yielding 6.2% and 8.1% respectively.

Table 11**: Zone Diameter of Inhibitions (mm)**

Sample Extracts	Conc. (mg/ml)	*Escherichia Coli*	*Salmonella Typhi*	*Staphylococcus Aureus*	*Pseudomonas Aeruginosa*
Aqueous	50	22	20	15	14
	100	23	25	16	19
	200	25	30	20	20
	250	30	32	24	22
	500	32	37	28	24
Ethanol	50	26	29	17	21
	100	26	27	25	21
	200	27	36	26	24
	250	30	37	30	28
	500	35	39	31	30
Ampiclox (control)	50	26	18	14	16
	100	31	24	15	17
	200	32	27	21	19
	250	25	29	24	22
	500	20	36	18	15

The results above showed that *Lawsonia inermis* extracts could effectively inhibit the growth of these bacteria. Among individual extracts, the alcoholic (ethanol) was more active against *Escherichia coli, Salmonella typhi, Staphylococcus aureus* and *Pseudomonas aeruginosa.* This result is in agreement with Ahmad *et al.,* (1998) who stated that alcohols are a better solvent for the extraction of antimicrobial substances as compared to water.

Table 111**: DETERMINATION OF MINIMUM INHIBITORY CONCENTRATION (MIC) USING AQUEOUS AND ETHANOLIC EXTRACTS**

Sample Extracts	Conc. (mg/ml)	*Escherichia Coli*	*Salmonella Typhi*	*Staphylococcus Aureus*	*Pseudomonas Aeruginosa*
Aqueous	500	-	-	-	-
	250	-MIC	-	-	-MIC
	100	+	-MIC	-MIC	+
	50	+	+	+	+
Ethanolic	500	-	-	-	-
	250	-	-	-	-MIC
	100	-	-MIC	-MIC	+
	50	-MIC	+	+	+

-=Clear; +=Turbid

From the table above, *Staphylococcus aureus* and *Salmonella typhi* had the least minimum inhibitory concentration (MIC) at 100mg/ml, while the minimum inhibitory concentration of *Escherichia coli* and *Pseudomonas aeruginosa* were 250mg/ml using the aqueous extract. Also, *Escherichia coli* had the lowest minimum inhibitory concentration (MIC) at 100mg/ml concentration, while the minimum inhibitory concentration of *Staphylococcus aureus* and *Salmonella typhi* were at 100mg/ml using the ethanolic extract. Turbidity indicates growth, the lowest concentration showing no growth is the MIC of the antimicrobial agent for the organism.

Table 1V**: DETERMINATION OF MINIMUM BACTERICIDAL CONCENTRATION USING AQUEOUS AND ETHANOLIC EXTRACTS**

Sample Extracts	Conc. (mg/ml)	*Escherichia Coli*	*Salmonella Typhi*	*Staphylococcus aureus*	*Pseudomonas Aeruginosa*
Aqueous	500	-	-	-	-MBC
	250	-MBC	-	-	+
	100	ND	-MBC	-MBC	ND
	50	ND	ND	ND	ND
Ethanolic	500	-	-	-	-MBC
	250	-	-	-	+
	100	-MBC	-MBC	-MBC	ND
	50	+	ND	ND	ND

+= Clear; - = Turbid; ND= Not Determined

Staphylococcus aureus and *Salmonella typhi* had the lowest minimum bactericidal concentration (MBC) at 100mg/ml using the aqueous extract, while the minimum bactericidal concentration of *Escherichia coli* and *Pseudomonas aeruginosa* were at 250mg/ml and 500mg/ml respectively. Also, *Escherichia coli*, *Salmonella typhi* and *Staphylococcus aureus* had the least minimum bactericidal (MBC) at 100mg/ml using the ethanolic extract, while the minimum bactericidal concentration of *Pseudomonas aeruginosa* was at 500mg/ml. The results obtained showed that water which was commonly used as a solvent by the traditional healers to extract the pharmacologically active compounds due to its easy availability, is not the best and most effective solvent for extracting the bioactive components of *Lawsonia inermis* (El-Olemyl *et al*., 1994). All the extracts of the leaves (aqueous and ethanol) affected the selected microorganisms with different zones of inhibition at the same concentration.

CONCLUSION

The present research has shown the efficacy of the leaves of the plant use: for the treatment of bacterial disease. It was observed that extracts of the leaves of *Lawsonia inermis* possess higher antibacterial activity in most cases than the control-ampiclox. This plant could be a fairly economical therapeutic agent and antibacterial. The study also indicated the existence of antimicrobial compounds in the crude aqueous and ethanol extracts of this plant and it also showed a good correlation between the reported uses of this plant in traditional medicine against infectious diseases. Further studies on *Lawsonia inermis* may help to discover new chemical classes of antibiotics that could serve as selective agents for the maintenance of health.

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Bio-Efficacy Studies of *Cry1Ab* Transgene Against *Maruca Vitrata* in Different Cowpea (*Vigna unguiculata*) Genetic Backgrounds

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INTRODUCTION

Cowpea [*Vigna unguiculata* (L.) Walp.] (2n = 2x = 22) is one of the most ancient human food sources and has probably been used as a crop plant since Neolithic times (Horn and Shimelis, 2020). Cowpea is commonly referred to as "niebe," "wake," and "ewa" in much of West African countries, and "caupi" in Brazil. In the United States, other names include "southern peas," "black-eyed peas," "field peas," "pink eyes," and "crowders." These names reflect traditional seed and market classes that developed over time in the southern United States. The name cowpea probably originated from the fact that the plant was an important source of hay for cows in the southeastern United States and other parts of the world (Timko *et al.,* 2007). Cowpea is commonly cultivated as a nutritious and highly palatable food source in the southern United States, the Middle East, Africa, Asia, and throughout the tropics and subtropics. The seed is reported to contain 24% crude protein, 53% carbohydrates, and 2% fat (FAO, 2012). Despite the great importance of cowpea, its productivity is very low due to various biotic and abiotic stress factors (Singh *et al.*, 2000). Insects are the major constraint to cowpea production, attacking every developmental stage of the crop and post-harvest stages (Daoust *et al*., 1985). *Maruca vitrata*, one of its most devastating post-flowering pests can sometimes cause up to 80% yield loss leading to loss or poor cowpea harvest running into billions of dollars (Foltz, 2007). Therefore, this study is to re-validate the efficacy of the introgressed transgene against *Maruca* pod borer in generations of transgenic cowpea lines.

Materials and Methods

Sample Collection: A transgenic Bt cowpea line 709A with three non-transgenic cultivars namely Sampea 6, Sampea 8 and Sampea 9 were selected for this study.

Development of Genetic Populations: The hybridization process was effected by crossing the selected transgenic *Bt* cowpea line 709A with each of the three commercial cultivars to develop three sets of F_1 populations Sharma, (2006). Staggered planting of the genotypes was adopted to synchronize the flowering and subsequent pollination. The F_1 populations were advanced to second filial generation (F_2) by selfing and backcrosses were generated through the processes of emasculation and pollination of the F_1 progenies to their respective parents to generate (BC_1P_1) and (BC_1P_2). The progeny derived from backcrossing the F_1 to the female parent were designated as BC_1P_1 and those from backcrossing to the male parent as BC_1P_2.

Experimental Design: Developed populations were evaluated and the experiment was laid out using a Randomized Complete Block Design (RCBD) with two replications. Non-segregating parental lines were evaluated with ten plants at 0.25m intra-row and 0.75m inter-row spacing for each replication, twenty plants for each replication of first filial generation (F_1), eighty plants for each replication of backcrosses and one hundred and twenty for each replication for the second filial generations (F_2).

Maruca Rearing for Artificial Infestation: *Maruca vitrata* larvae were reared on an artificial diet in the Department of Crop Protection, IAR Zaria for bioassays as described by Jackai and Raulston, (1988). Deposited eggs were incubated to hatching to provide the first laboratory generation. Insect colonies were maintained on a 12-hour light (L): 12-hour dark (D) cycle and room temperatures were 25°C (L) and 20°C (D); relative humidity (RH) was 60 ±10%. First instar larvae were transferred with a small camel hairbrush into a small round plastic containing a synthetic diet. Each cup contained only one larva to avoid cannibalism. Healthy pupae were subsequently removed, transferred and kept in a cup containing vermiculite until adult emergence.

Screening of Genetic Population for Efficacy against *Maruca*

Developed genetic populations consisting of transgenic and non-transgenic parents, f_1, f_2 and backcrosses were evaluated under field conditions by subjecting them to artificial infestation to determine the resistance status of each plant. Ten (10) 1st instar *Maruca vitrata* larvae were placed directly on the leaves and flower bud to cover the entire floral development and pod formation at 45 days after planting and five infestation events were carried out at three days intervals. Data on pod damage were recorded at harvest. Insect damage on pods was visually scored on the infested pods after harvest by identifying the healthy pods from damaged pods which were separated and counted. The percentage damage of pods was calculated based on healthy and damaged pods by *Maruca* larvae as described by (Akhtar *et al.,* 2010).

$$\%PDI = \frac{\text{Number of infected/damagedpods}}{\text{Total number of pods of that generation}} \times 100$$

RESULTS AND DISCUSSION

The results on the total number of pod damage were presented in Tables 1, 2 and 3.

Table 1: Frequency of damaged pod and undamaged pod derived from the cross Sampea 6 x 709A Generations

Generation	Total NOP	Pod Damaged	Pod Undamaged	%Pod Damaged	%Pod Undamaged
Sampea 6	212	202	10	95.28	4.72
709A	472	0	472	0	100
(Sampea 6 x 709A) F_1	792	5	787	0.6	99.4
(Sampea 6 x 709A)F_2	5040	1079	3961	21.41	78.60
Sampea 6 x (F_1)	2233	1170	1063	52.40	47.60
709A x (F_1)	3584	0	3584	0	100

Table 2: Frequency of damaged pod and undamaged pod derived from the cross Sampea 8 x 709A Generation

Generation	Total NOP	Pod Damaged	Pod Undamaged	%Pod Damaged	%Pod Undamaged
Sampea 8	351	341	10	97.15	2.85
709A	462	0	462	0	100
(Sampea 8 x 709A)F_1	770	4	766	0.5	99.5
(Sampea 8 x 709A)F_2	5263	768	4495	14.60	85.41
Sampea 8 x (F_1)	2989	1575	1414	52.69	47.31
709A x (F_1)	3482	0	3482	0	100

Table 3: Frequency of damaged pod and undamaged pod derived from the cross Sampea 9 x 709A Generations

Generation	Total NOP	Pod Damaged	Pod Undamaged	%Pod Damaged	%Pod Undamaged
Sampea 8	351	341	10	97.15	2.85
709A	462	0	462	0	100
(Sampea 8 x 709A)F_1	770	4	766	0.5	99.5
(Sampea 8 x 709A)F_2	5263	768	4495	14.60	85.41
Sampea 8 x (F_1)	2989	1575	1414	52.69	47.31
709A x (F_1)	3482	0	3482	0	100
Generation	Total NOP	Pod Damaged	Pod Undamaged	%Pod Damaged	%Pod Undamaged
Sampea 9	401	387	14	82.9	17.1
709A	475	0	475	0	100
(Sampea 9 x 709A)F_1	873	2	871	0.20	99.80
(Sampea 9 x 709A)F_2	5173	1895	3278	36.63	63.37
Sampea 9 x (F_1)	3341	1694	1647	50.70	49.30
709A x (F_1)	3616	0	3616	0	100

Total number of pods (TNP) produced by Sampea 6 was drastically reduced when compared to the TNP of the resistant parent 709A (table 1). The loss observed in the susceptible parent Sampea 6 due to pod damage (PD) was 95.28% and 4.72% pod undamaged (PUD) while the percentage of pod damage of the transgenic parent (709A) was 0% PD and 100% PUD. The F_1 had a considerably low pod damage percentage as observed in the result of the resistant parent with 0.63% pod damaged and 99.37% pod undamaged which shows the dominance of the transgene and subsequent resistant character. The segregating F_2 population with the highest total number of pods of 5040 had a percentage pod damage of 21.41% and a percentage pod undamaged of 78.59%. The percentage of pod damage to pod undamaged observed in the backcross means of the F_1 to the susceptible parent Sampea 6 gave 52.40% and 47.60% respectively while the backcross means of F_1 to the transgenic 709A parent had a percentage pod damage of 0% and percentage pod undamaged of 100% indicating a total dominance of resistant gene for pod damage. The same trend of the result was observed for the crosses derived from Sampeas 8 and 9 by 709A (tables 2 and 3). The results showed that losses on pod damage were more prevalent in the susceptible non-transgenic parents ranging from 82.9% to 97.2% compared to resistant transgenic parents that recorded no damage. Also, the percentage pod undamaged (PUD) for the hybrids (F_1) in the three crosses ranged between 99.4% - 99.8%. This indicates and further confirms the efficacy of the Cry1Ab gene against the targeted *M. vitrata* in the transgenic parents. This confirms the earlier report by Ishiyaku *et al.* (2010) who reported complete protection of some transgenic cowpea lines expressing Cry1Ab gene against *M vitrata* damage under field conditions. The few undamaged pods observed in the susceptible parents could be due to chance or escape. The F_1 hybrids resulting from the cross between susceptible lines and the transgenic line (709A) showed low to no pod damage of *M. vitrata* which indicates the complete dominance of resistance gene over susceptible. This result corroborates the findings of Rasco *et al.,* (2013) who found Bt corn hybrids to be effective against Asian corn borer (ACB) (Ostrinia furnacalis) under natural field infestation. Insignificant pod damage was observed in F_1 hybrids indicating total dominance of the resistant gene and further confirmed gene stability in F_1 plants. The results obtained for pod damage from the F_2 segregating progeny test further confirmed the inheritance of the *Cry1Ab* gene and its efficacy against *M. vitrata.* It was observed that the result of percentage pod damage and pod undamaged for backcross to the susceptible parents (BC_1P_1) skewed towards the susceptible parent P_1. Also same was observed for the backcross of resistant transgenic parents (BC_1P_2) which skewed towards the resistant transgenic parent 709A, thus indicating the resistance/tolerance of the transgenic gene *Cry1Ab* on the pod survival against the *Maruca* pests in the corresponding generation. This corroborates the studies done by Peter *et al.* (2015) who reported that means for emerged *Striga* counts and *Striga* damage rating for BC_1P_1 were skewed towards the resistant parent P_1 and susceptible parent (BC_1P_2) was skewed towards the susceptible parent P_2.

CONCLUSION

The information obtained in the pod damage data of this study has confirmed stable inheritance and integration of the *Cry1Ab* gene into the genomes of different cowpea backgrounds. Therefore, the insect-resistance character is governed by a single dominant nuclear *Cry1ab* gene. These transgenic cowpea lines can be used not only for the production of *M vitrata-resistant* hybrids but also as an exotic donor source in conventional recombination breeding. This result further confirms the effectiveness and efficacy of the *Cry1Ab* gene as it conferred total resistance to the *Maruca pod borer* pest.

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A Review Study On Genetic Engineering In Bioremediation Of Petroleum Contamination: Opportunities, Challenges and Economic Implications

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Introduction

Over the years, scientific and technological advancements have been reliant on the development of new tools which are significant for the improvement of socioeconomic values and even so on a national and global scale, as far as sectors such as agriculture, environmental protection, healthcare, finance, industrialization, etc. are concerned (Okonko *et al.*, 2006). These developments crucial to socioeconomic development, regardless may however come at impedimental cost(s). Although the petroleum industry activities have driven nations to economic heights, nonetheless some of these activities have undoubtedly brought about some challenging events whose impact may directly or indirectly involve high-cost implications if the status quo needs to be ransomed effectively. The resulting outcomes cannot be overemphasized – the net outcome of oil contamination of the environment could constitute a chain effect that may result in a relatively long-term socioeconomic retrogradation. This has been evident in the adopted conventional techniques and practices of numerous nations such as the United States of America (U.S.A) which as a result of cleaning up hazardous wastes has confronted ginormous projects – including projects involving petroleum contamination such as cleanups of the 1989 Exxon Valdes and the 1991 Persian Gulf oil spills (Fayad *et al.*, 1992).

Accordingly, all around the United States of America (U.S.A) numerous polluted sites, running into thousands were discovered with estimated cleanup costs of over USD 1.7 trillion if extant technologies other than bioremediation have to be employed in recovering them (Pritchard *et al*, 1992). In Nigeria, the terrestrial and aquatic environment of the oil-rich Niger Delta and its adjourning regions are frequently plagued with enormous pollution (Ifeadi and Nwankwo, 1989; Olagbinde *et al*., 1999; NNPC, 2004; Okonko *et al*., 2006; Nnadi *et al*., 2018; Osuagwu and Olaifa, 2018). Apart from being socio-culturally problematic, these, however, pose a serious threat to public health in such affected regions (Nwachukwu and Ugorji, 1995; Mishra *et al*., 2001; Abed *et al.,* 2002; Page and Page, 2002; Anejionu *et al*., 2015; Oladipupo *et al*., 2016; Kornom-Gbaraba & Aenan, 2020), which nonetheless, have coincidental economic consequences in the form of the cost incurred for healthcare. Ordinioha and Brisibe (2013) analyzing the direct impact the quantity of spilt petroleum in ecosystems has on human health and household food security in the regions around the Niger Delta revealed that an average of 240,000 barrels of crude oil is spilt around the Niger Delta annually leading to a 60% reduction in household food security and its contact with living organisms (especially humans) could be hemotoxic and hepatoxic, which could result in infertility and cancer. In fact, before oil contamination, it is clear that these regions' primary sources of income are land farming and fishing. However, after oil contamination, they are confronted with not only health challenges but also economic struggles as their means of livelihood are threatened.

Oil contamination accounts for the: loss of microbial consortium and habitats, diminishing of the available farmlands and areas of vegetation meant for agricultural purposes; destruction of wetlands and as well causes the death of aquatic species when they invade water bodies and coastal areas, etc. Nonetheless, the diversity of microbial communities and their ecological and metabolic functions have the potential for remarkable scientific, social and economic impact (Snow *et al* (2005)). In an attempt to eradicate oil contaminants from surface soils and possibly mitigate further slippage into the water table bioremediation has sprung up, and through the practice of genetic engineering has advanced and over the years continuously proven to yet be not only the most environmentally benign, but also the most economically viable way to mitigating contamination.

In a bid to strengthen the national economy, many entities have leveraged the scientific development of GEMs, using it as an incentive, a local content for enhancing the national economy. The aftermath of adapting bioremediation and principal use of GEMs for environmental cleanup in cases of the oil spill (such as the Exxon Valdes and others) bespeaks of their great potential for solving economic challenges by tackling issues relating to food insecurities, health, etc., (Stephen *et al*., 1997; Irons *et al.,* 2000; Chorom *et al*., 2010; Rebello *et al*., 2021) – benefits that demonstrate the viability of GEMs in both environmental protection and economic growth when applied. The potential of genetic engineering to contribute significantly to GDP growth cannot be downplayed. From the investigations of Bakshi *et al* (2018) as a result of oil contamination the buildup of HMs in the soil causes a resultant diminish in the specific adsorption of other cations by increasing the (super) saturation of the cation exchange sites by HM cations, thereby displacing the protons in the soil solution and causing a resultant lowering of soil pH (i.e. acidification) in the reduction process. In excess, HMs become immobile and destroy soil microbiota, making it less inhabitable for agricultural and economically valuable microbes. Furthermore, the experimental investigation of Gimba *et al* (2021) revealed that certain microorganisms can reduce the mobility of most metals, but may however not eliminate the risk and toxicity caused by such metals in soil. However, the use of GEMs is plausibly the best alternative cost and time economical technique employable for effective remediation (Wu *et al*., 2021; Daâssi and Almaghribi, 2022).

Bioremediation and genetic engineering have not only health improvement potential through waste eradication and conversion (Pritchard, *et al*., 1992; Timian and Connolly, 1996) but also can facilitate economic growth through the vantage of cost reduction (Fayad *et al.,* 1992; Hamilton, 1995; Aguilar *et al.,* 2009; Aguilar *et al*., 2013). As a result, the global industry related to bioremediation services has systematically spread, becoming an industry whose worth grew to about USD 35 billion in the year 2009 (Singh *et* al., 2009). In recent pasts, the growth of the global bioremediation market has accelerated: reaching USD 91.0 billion in 2018; and had an expected growth to USD 186.3 billion in 2023 (BCC, 2021), all owing to the part involvement of advanced techniques like genetic engineering. The Exxon Valdes oil spill and the Gulf War cleanups (Pritchard *et al*., 1992), are two good examples of historical events buttressing claims that bioremediation and genetic engineering have played key roles in environmental and economic sustainability. It's estimated that there are 500,000 and 340,000 contaminated sites in the U.S. and Europe, respectively (Liedekerke *et al.,* 2014), however, according to Hamilton (1995) "*a variety of bioremediation techniques (including the use of GEMs) had been successfully employed at over 400 cleanup sites throughout the U.S. at a cost approximately 80-90% lower than other cleanup technologies*".

The cost efficiency of the bioremediation technique may not be considered systemic in some cases such as the use of GEMs. Consider, for instance, a comparative experimental-cost analysis by Orellana *et al* (2022) where projected costs were compared against an extensive database of 130 soil bioremediation projects of petroleum-contaminated soils in Chile and results showed that biostimulation-based treatments have lower costs than their counterparts using bioaugmentation. Specifically, the comparison between all bioaugmented treatments and biostimulation with 10% of compost revealed that the latter, though effective in hydrocarbon biodegradation regardless of the degradation of heteroatoms (Liedekerke *et al.,* 2014)), showed a significant reduction in direct material costs, provision and covering assets. The high cost of bioaugmented treatments resulted from the cost implication for culturation and, the need for sophisticated machinery and facilities, making the estimated cost for bioremediation range as high as USD 310.4 per m^3 (from USD 50.7 per m^3) of contaminated soil. For biostimulation approaches, manufacturing overhead cost was the second largest contribution to the total costs. Bioaugmentation approaches (including the use of GEMs), provision and covering assets were the second and the third largest item costs, suggesting that the technological level of bioaugmentation has a contrastingly significant impact on economic growth. The provision cost of bioaugmentation treatments is almost two-fold higher than the provision cost of biostimulation. This is mainly due to an increase in monitoring and quality control and an additional high level of costs for equipment and machinery for the culture of microbial strains which may discourage its adoption. Nonetheless, these research experimental findings are based on short-term studies. It has been found that some GEMs are not only capable of degrading hydrocarbons and their heteroatoms in highly unfavourable environments, but are highly tolerant and also economical as they require little to no stimulation processes to function (Hussein *et al.,* 2005; Xu *et al*., 2022; Tarek and Ali, 2023).

Furthermore, the environmental cost can be classified into three: preventive cost, internal failure cost and detection cost (which includes cost incurred for contamination testing and measure of contamination levels) (Ifurueze *et al*., 2013; Ezeagba *et al*., 2017; Kornom-Gbaraba and Aenan, 2020). The examination and tracking of a bioremediation process can be tedious and time-demanding since consistent qualitative and quantitative laboratory analysis may have to be carried out periodically to ascertain certain dynamic properties whose values and alterations over time determine the state of the process and as well render any analytical result conclusive. The use of GEMs has time economic advantage. However, specifically, the use of *bioluminescent* GEMs in biosensing has made it easier to study and track the bioremediation process averting detection costs with even lesser time and labor implications. This eludes and possibly discards the need for some of the age-long adopted laboratory and analytical methods requiring the use of reagents, materials certain equipment and facilities, etc.; which are more or less multiple-steps-engaging and uneconomical approaches. However, the economic implication of any project to be undertaken is of key importance. Withal, economic viability cannot be the direct and sole criteria for judgment on its credibility – i.e. judgment based on the cost implication of the adopted technique

and its immediate short-term effects. The practice of employing GEMs for petroleum remediation has proven to be an effective and efficient technique. Practices otherwise, because of the inestimable cost incurrable from battling the long-term aftereffect of xenobiotics persistence in the environment may incur unfathomable costs considering health and other factors such as diseases that may by chance become pandemic.

The use of GEMs in environmental remediation has a chain effect on the economy. Although its implications on the global economy may not be pointed out directly, via application, the impacts have been manifested in its uplifting many other sectors of national economies such as agriculture – through the recovery of previously contaminated farmlands and water bodies, healthcare – through aversion of aftereffects of xenobiotics, etc. Aside from environmental biotechnology and genetic engineering bearing numerous benefits that are of ecological advantage (such as pollution control, waste reduction as well as conservation of biodiversity, and cost-time efficiency) it has created a knowledge-based market for researchers and scientists and its application has consequently created jobs for a wider range of fields of studies outside the field of environmental sciences. For example, in the multidisciplinary fields of law and criminology (Ihemeson (2024)), GMOs have been applied innumerably, not only in the eradication of chemical wastes but to study and clean-up crime and accident scenes (including rig blowout scenes) where body fluids and organic remains are found to be persistent, presenting a cost-effective way to prevent possible nemesis that may arise. In addition, apart from the direct cost of employing the conventional bioremediation, traditional physical, chemical and thermal processes, the significant reduction in environmental impact also prevents potential costs associated with environmental damage and its subsequent repair. Some chemicals have the potential to disrupt soil biodiversity and destroy soil structure: the physical method of excavation may be less effective and may have less viscous and persistent (xenobiotic) contaminants remnant for the incapacitated microbial community to degrade; the use of heat and chemicals may potentially destroy soil micro consortium and liberate volatile contaminants into the atmosphere, thereby compounding the environmental problems.

Conclusion

Genetically modified bacteria's potential for widespread usage in the natural environment is still up for debate, given the potential negative impact they might have on human health and the biological ecosystem's delicate balance. With the world rapidly plunging into an era where nations will greatly depend on environmental biotechnology and genetic engineering for economic improvement and sustainability through applications not only in various science-related aspects such as medicine, health, agriculture, ecosytemology and environment studies. An initial guide for the evaluation of costs of different bioremediation approaches is relevant not only to compare advanced alternatives to projects based on other techniques (such as conventional bioremediation, physical excavation and disposal, use of chemical, heat, etc.) which are rather easy to grasp but to integrate this information through management practices to ensure the technical and economic feasibility of advanced bioremediation projects, where decision making is empirical rather than knowledge-based.

In addition, over time, as we traverse into the next millennium – with growing populations, rapid changes in levels of urbanization and industrialization with the consequential need for effective and more efficient techniques to address waste production for environmental sustainability becoming paramount, this technology will become even more vital. However, risk assessment cannot be pushed aside. Considering alternative courses of action, and selecting the most appropriate option after integrating the results of risk assessment with engineering, social, economic, and political concerns to reach an approbatory decision is important. This will help check future probable losses in economic output and also direct costs incurrable in combating invasions in cases of later defective employment of GEMs in vie for environmental sustainability. It, therefore, stands that political policies and concepts, socioeconomic factors, societal standings and approval are largely (and probably the ultimate) determinants of which scientific attainabilities will eventually become a reality and hence must be satisfied accordingly. Also, to check and mitigate possible constraints and challenges that may arise as a result of societal counter-beliefs and opinions there is a need to adequately educate the larger society. On a final note, the traditional methods of remediation are considered as primary methods of remediation, while the use of GEMs is a primary and secondary/tertiary remediation technique, yet the issue of environmental remediation of petroleum contamination would not colossal if safety is ought most and paramount over other considerations. Nonetheless, with the end goal of finding an effective and economically viable method for restoring petroleum-contaminated environments, genetic engineering has provided a reliable and environmentally benign variety of techniques towards transcending and surmounting the hurdles of oil and other related contaminations eradication in the environment, with the added advantage of economic sustainability.

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Screening of Aspergillus Species isolated from different soil samples in Jos metropolis for protease, amylase, lipase and cellulase enzymes production potential.

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ABSTRACT

Aspergillus is a genus of filamentous and cosmopolitan fungi that includes important species for medical mycology, food, and basic research and agro-industry areas. Aspergillus species are utilized in the fermentation industry. *Aspergillus* spp are efficient producers of hydrolytic enzymes. This investigation is aimed at screening aspergillus species for protease, amylase, lipase and cellulase production potential. Soil samples were collected from ten different locations (in triplicates) in Jos metropolis of Plateau state, Nigeria, and used for isolation and identification, by plating, pure culturing, incubating, staining, inoculating techniques. The mycelia and cytoplasm are stained using Lactophenol and cotton blue (provides light blue background). The stained specimens are observed under the microscope for identification and photographs are taken. To visualize the enzyme activity, specific substrate of each enzyme was added to the culture medium as a carbon source. After inoculation and incubation of cultures for 2-5 days depending on the growth rate of the strains, the appearance of a clear halo around the thallus indicates enzyme production. Cultures indicated that the isolates (*A niger*, *A flavus* and *A fumigatus*) show various levels in cellulase, Amylase and lipase production potential. Protease however showed no conspicuous zone of hydrolysis. *A flavus* from AE (Abatoir effluent) among the fungi isolates isolated, produced the highest cellulase activity (70mm) base on the zone of clearing to colony diameter followed by *A niger*, from ND (NASCO Detergent Wastes) wastes for cellulase (68.5mm) and *A niger* from ND as the highest for Amylase (34.5mm). Lypase showed the least zone of hydrolysis, 4.5mm by a niger from ND, followed by *A nidulans* (3mm) and the least 2mm by *A flavus*.

Key Words:*Aspergillus species, Isolation, Enzyme activity, Substrate, Hydrolysis.*

INTRODUCTION

The role of many enzymes has been known for a long time. Their existence was associated with the history of ancient Greece, where they were using enzymes from microorganisms in bakery, brewing, alcohol production, cheese making etc., (Chapman,2018). Nowadays enzymes are used in large scale in the textile (amylase, cellulose, oxidoreductase); detergents (protease, lipase, cellulose, amylase and oxidoreductase), food (pectinase, protease, cellulose and oxidoreductase); paper (xylanase, oxido-reductase and lipase) and leather (protease and lipase) industries. The major classes of enzyme offering immediate application are the hydrolytic enzymes (Chapman, 2018).

Among all industrial enzymes, hydrolytic enzymes account for 85%. Microbial enzymes are preferred to those from plants and animal sources because they are cheaper to produce and their enzyme contents are more predictable, controllable and reliable (Sindhu,2018) and also because of their broad biochemical diversity, feasibility of mass culture and ease of genetic manipulation. Today, the new potential of using microorganisms as biotechnological sources of industrially relevant enzymes have stimulated renewed interest in the exploration of extracellular enzymatic activity in several microorganisms (Singh, et al 2019).

Selection of the right organism plays a key role in high yield of desirable enzymes. Fungi are microorganisms which are well known for their wide range of novelty of enzymes they produce and enzymes of fungal origin are used in the industrial process for which, amount to billions of dollars of revenue annually (Dewan, 2017). Due to their diversity, fungi have been recognized as a source of new enzymes with useful and/or novel characteristics (). Filamentous fungi are particularly interesting due to their easy cultivation, and high production of extracellular enzymes of large industrial potential (Singh,et al 2019).

Soil provides a heterogeneous and complex environment for all soil inhabitants. Soil is also known to harbor different microorganisms including diverse group of fungi. Jos Metropolis are considered as one of the locations for biodiversity including microbial diversity. Hence the soils can be a source of fungi of industrial importance. Screening of microorganisms with enzymes production potential could facilitate the discovery of novel enzymes suitable to new industrial applications. The present work, involved screening of *aspergillus species*, isolated from different soil samples in Jos Metropolis, for protease, amylase, lipase and cellulose production potential.

MATERIALS AND METHODS

COLLECTION OF SOIL SAMPLES

Soil samples were collected from ten different locations (in triplicates) from Gardens, Mechanic workshops, Industrial Areas, Abattoir and Palm oil selling areas in Jos Metropolis, Plateau state, Nigeria. The upper part of the soil and other soil debris were removed and the soil was dug to depth of about 3 cm from where the soil samples was collected aseptically using sterile hand gloves into clean polythene and taken to the laboratory for culturing and isolation.

Isolation and Identification of *A.spp*

The fungi were isolated by the method reported by Raja, Praveena & John William (2017). 1.0 g of soil sample was mixed with 9.0 ml of sterile distilled water in a test tube and shaken vigorously. Series of dilutions were made until 1:1000 dilutions. Then 0.5ml was pipetted, poured and dispersed by swirling on potato dextrose agar (PDA) and incubated at 30°C for five days.

PURIFICATION OF FUNGI SPECIES ISOLATED

All the fungi colonies that developed were adequately sub-cultured several times until pure cultures were obtained.

IDENTIFICATION OF FUNGI

Characterization method was employed for the identification of the fungal isolates by both the inspection of colonial features, cellular characteristics at X100 and X40 microscopic magnification. Identification by employing the method Raja, et al 2017 and conventional techniques of isolation; and by allowing them to grow and produce colonies.

EXTRACELLULAR ENZYMES PRODUCTION

To visualize the enzyme activity, specific substrate of each enzyme was added to the culture medium as a carbon source. After inoculation and incubation of cultures for 2-5 days depending on the growth rate of the strains, the appearance of a clear halo around the thallus indicates enzyme production (Rajaa et al., 2019).

ENZYME	REAGENT	SUBSTRATE
Lipase	Sudan lll	Groundnut oil
Amylase	Iodine	Starch
Protease	--	Skimmed milk
Cellulase	Congo red	CMC (carboxymethylcellulose)

AMYLASE
Amylase activity was evaluated on nutrient agar medium supplemented with 2 g L^{-1} of soluble starch. The media was composed of 1% starch (7.0 g L^{-1} KH_2PO_4, 2.0 g L^{-1} K_2HPO_4, 0.1 g L^{-1} $MgSO_4.7\ H_2O$, 1.0 g L^{-1} $(NH_4)_2SO_4$, 0.6 g L^{-1} yeast extract, 10 g L^{-1} starch and 10g L^{-1} agar) After incubation, the cultures was flooded with a solution of iodine and rinsed with distilled water. Clear zone around the thallus reveals the presence of enzymes activity.

CELLULASE
Cellulase activity was evaluated on nutrient agar medium supplemented with 1% (w/v) carboxymethyl cellulose powder. The media was composed of 1% cellulose (7.0 g L^{-1} KH_2PO_4, 2.0 g L^{-1} K_2HPO_4, 0.1 g L^{-1} $MgSO_4.7\ H_2O$, 1.0 g L^{-1} $(NH_4)_2SO_4$, 0.6 g L^{-1} yeast extract, 10 g L^{-1} microcrystalline cellulose and 15 g L^{-1} agar) (Abe *et al*. 2015).After incubation, the culture was flooded with Congo red. Clear zone around the thallus reveals the presence of enzymes activity.

PROTEASE
Protease activity was detected on milk agar medium containing 30% skimmed milk and 2% agar. After incubation, the degradation of casein was reflected by a clear zone around the thallus.

Result and Discussion
Isolation and Identification Aspergillus Species such a *A niger*, *A fumigatus*, *A flavus* and A nidular (Table 1) were Isolated from 10 different areas in Jos metropolis, isolates were identified on the basis of morphological and microscopic morphology.

The most commonly occurring species were *A niger* (IA, ND. KO and HG), A*flavus* (AE, MGF), *A Fumigatus* (TO) (Table 1)

Table 1: **Organisms Isolated From Different Soil Samples in Jos Metropolis**

S/N	AREAS	ORGANISMS
	IA (Industrial area wastes)	*A niger*
	ND (Nasco Detergent waste area)	*A niger*
	AE (Abattoir Effluent)	*A flavus*
	KO (Kugiya oil selling market)	*A niger*
	TO (Terminus oil selling market)	*A Fumigatus*
	MG (Mazaram garden)	*A nidulans,A flavus*
	HG (Home garden)	*A niger, A mich;fr*

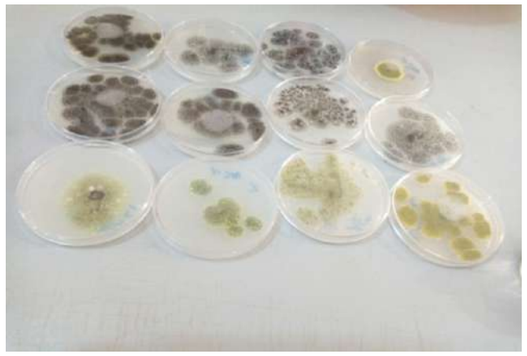

Plate 1. Plate Culture of Organisms Isolated.

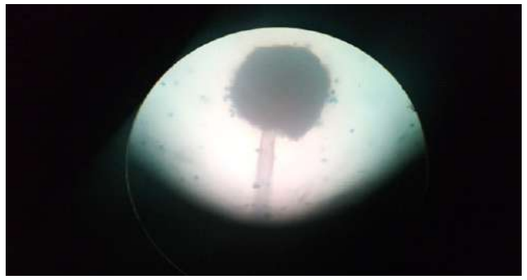

Plate 2. Microscopic Slides of *A. niger*

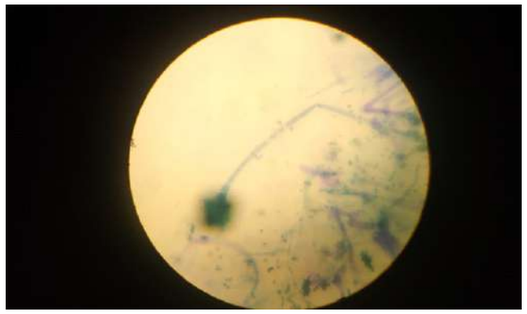

Plate 3 Microscopic Slides of *A. flavus*

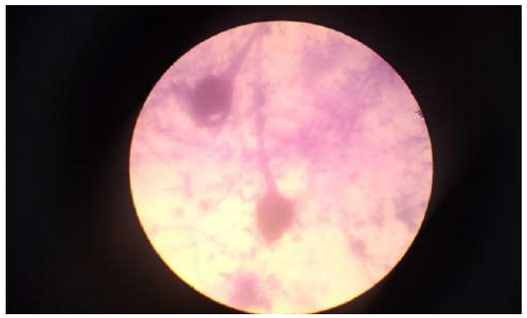

Plate 4 Microscopic Slides of *A. fumigatus*

Result of Qualitative Analysis (Enzyme Production Potential)
Cultures indicated that the isolates (*A niger*, *A flavus* and *A fumigatus*) show various levels in cellulase, Amylase and lipase production potential (Table 2, 3, 4 and Figure. 1) protease however showed no conspicuous zone of hydrolysis.

Table 2 Zone of Hydrolysis for Amylase

	Organisms base on Areas	Zone of hydrolysis (mm)
1	MG (*A nidulans*)	41.5
2	HG (*A niger*)	45.5
3	ND (*A niger*)	34.4
4	AE (*A flavus*)	5.5
5	KG (*A niger*)	2.5
6	IA (*A niger*)	2.5
7	TO (*A fumigatus*)	-
8	KO (*A niger*)	4.25

Plates 5 Showing Zone of Hydrolysis for Amylase

Table 3. Cellulase Zone of Hydrolysis

Organisms based on Areas	Zone of Hydrolysis (mm)
1. MG (*A nidulans*)	**67.5**
2. HG (*A niger*)	**61**
3. ND (*A niger)*	**68.5**
4. AE (*A flavus*)	**70**
5. KG (*A niger*)	**56.5**
6. IAa (*A niger*)	**58.5**
7. IAb (*A niger)*	**57**
8. KO (*A niger)*	**4.25**
9. TO (*A fumigatus)*	**7.85**

***A flavus* from AE among the fungi isolates isolated, produced the highest cellulase activity (70mm) base on the zone of clearing to colony diameter followed by *A niger*, from ND wastes for cellulase (68.5mm) and *A niger* from ND as the highest for Amylase (34.5mm), (Table3).**

Table 4 Zone of Hydrolysis for Lypase Enzyme

Organisms Based on Areas	Zones of Hydrolysis (MM)
• MG (*A nidulans*)	3
• HG (*A niger*)	2
• ND (*A niger)*	4.5
• AE (*A flavus*)	2
• KG (*A niger*)	-
• IA (*A niger*)	-
• KO (*A niger)*	-
• TO (*A fumigatus*)	-

Plates 6 Zone of Hydrolysis for Cellulase

CONCLUSION
The result of this study shows that *Aspergillus species* (Isolated and identified according to their macroscopic and microscopic morphology) from soil in Jos metropolis can produce enzymes of industrial importance.
Cultures indicated that the isolates (*A niger*, *A flavus* and *A fumigatus*) show various levels in cellulase, Amylase and lipase production potential (Table 2, 3, 4 and Figure. 1) protease however showed no conspicuous zone of hydrolysis.
Vast microbial biodiversity of some areas in Jos such as the mining sites are yet to be exploited so that the indigenous soils can be screened for the Isolation of other novel fungi with the ability of production of some important enzymes, antibiotics and other bioactive compounds.

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