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BOOK OF ABSTRACTS

CONFERENCE THEME

IMPROVING NIGERIA'S ECONOMIC RESILIENCE THROUGH INNOVATIVE BIOTECHNOLOGY.

27TH–31ST AUGUST, 2023

Holding at the Sheda Science and Technology Complex,
Km 32 Abuja Lokoja Express way, Sheda Abuja.

The Sheda Science and Technology Complex (SHESTCO) Abuja Nigeria

Formation of the Sheda Science and Technology Complex

The Sheda Science and Technology Complex (SHESTCO)was established by an act of parliament on the 23rd of August, 1993 Cap S. 95 to be the foremost Centre to carryout high level research in Science and Technology with the main thrust on Nuclear Science. The establishment of the Nuclear Technology Centre is supported by the Advanced Research Centers (Biotechnology, Chemistry, Physics, Mathematics Simulation/information Technology). The complex is expected to provide the Nation with modern and sophisticated Facilities for use by national and international researchers at a comparable level as exist in the advanced world.

Function of the Complex

SHESTCO is saddled with the following operational functions;

1. Develop Facilities for the effective practice of applications oriented science and technology in Nigeria.
2. Carry out Research and Development activities involving the highest level of technologies available in the world with a view to strengthening the technological base of the Nigerian Economy.
3. In particular, operate a nuclear research reactor facility capable of providing service in the fields of agriculture, medicine, industry and basic sciences.
4. Operates an internationally accessible and comprehensive database in the area of science and technology.
5. Conduct Research and development activities in the field of conventional and non-conventional energy.
6. Carryout structured manpower development and training activities to meet the growing needs of Nigeria in the areas of high technology.
7. Provide avenues through which all the institutions of higher learning in Nigeria may carryout capital intensive research on a cost effective basis.

KEYNOTE ADDRESS

KA_01: IMPROVING NIGERIA'S ECONOMIC RESILIENCE THROUGH INNOVATIVE BIOTECHNOLOGY

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Nigeria's economic resilience has been a subject of concern, especially given its vulnerability to fluctuations in commodity prices and external shocks. It is reported that there’s a general decline in economic growth after covid-19, with the Gross Domestic Product (GDP) falling from 3.6% in 2021 to 3.3% in 2022 placing a huge burden on the economy. With over dependence on importation in virtually everything, Nigeria must as a matter of urgency embrace biotechnology in action and not by mouth. Biotechnology presents a promising avenue for economic diversification and increased resilience. This paper x-rays some practical strategies to apply biotechnology as the driver for sustainable development, enhanced agricultural productivity, promote healthcare advancements, and foster environmental sustainability, ultimately contributing to Nigeria's economic growth and resilience.

Keywords: economic resilience, vulnerability, gross domestic product, biotechnology, and diversification.

SUB-THEME 01: BIOTECHNOLOGY SOLUTIONS FOR EMERGING DISEASES CONTROL AND PREVENTION (BM - RED BIOTECH)

ST_001: Biotechnology/Genomic Solutions for Emerging Disease Control and Prevention

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The rapid development of biotechnology and genomics has revolutionized the landscape of disease control and prevention. This presentation explores the pivotal role of biotechnology and genomics in the field of emerging disease control and prevention, the intricate relationship between biotechnology, genomics and emerging diseases, and their collaborative potential to mitigate global health threats. Through historical perspectives, current applications, case studies and future projections, this presentation highlights the transformative impact of these technologies and the challenges they pose. Anticipated advances will be highlighted, along with insights into their potential impact on global health. However, by addressing ethical concerns, regulatory issues and funding constraints, we emphasize the need for responsible and inclusive application of biotechnology and genomics to safeguard public health. In conclusion, this discourse underscores the critical importance of biotechnology and genomics in the management and prevention of emerging diseases. Through an analysis of historical backgrounds, contemporary applications, illustrative cases and future projections, it highlights the revolutionary capacity of these technologies to ensure the protection of public health on a global scale.

SUB-THEME 02: BIOFUELS AND ENERGY SOLUTIONS (BE - GREY BIOTECH)

ST_002: South-South Co-operation and Collaborations on innovative biofuels and energy solutions

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There is a direct correlation between the level of development and energy consumption. Energy demand and consumption in most countries in the South are very low and there is a critical need for them to develop innovative energy sources to propel their economic development. Although fossil fuels are currently the major sources of energies driving the world economies, their limitations in terms of their non-renewability and non-sustainability, as well as the environmental degradation and pollution due to their exploration, distribution and utilization are driving the search for innovative alternatives. Renewable, especially biomass energies have very high potentials to complement or even replace some of the current fossil fuels. Although the average world renewable energy share was 19.1% in 2020, in most countries in the South, the share was well over 50%. Most of the renewable energy consumed in the South are from direct burning of biomass but a few countries such as Brazil have developed resources and technologies for large scale production of liquid biofuels such as bioethanol and biodiesel. In terms of availability of raw materials and cheap labour, most countries in the South have comparative advantages over most countries in the North for solar and biomass energies but do not have the technology and know-how to efficiently harness them. This requires international collaborations but currently, most of the cooperation and collaborations are between the North and the South. These South-North cooperation are hardly sustainable since the South present themselves, and are seen as beggars. Collaborations are sustained by the benefits that each party derives. Most of the relationships between the South and North are more or less donor-recipient type (aids) often attached with conditions that may not be the best for the receiving parties. The causes of energy deficiencies in the South are complex with technological, political, economics, cultural and social dimensions. Energy solutions in the South cannot be addressed without considering food security, environmental sustainability, resource management, land ownership systems, availability of infrastructures, and availability of suitable technology and knowhow. In most countries in the South, only a very small percentage of the arable land are under regular cultivation, the rates of unemployment are high, the climate conditions are very good for biomass production, and yet they are not able to produce enough food, and biomass feedstock for bioenergy industries. The energy problems in the South cannot be solved by simply adopting policies and introducing technologies used in the North. Most countries in the South have similar bioresources, are within the same climatic zone, have problems of food and energy security, have high rates of unemployment and thus will benefit equally from any collaborative efforts to solve these problems. Thus, South-South cooperation and collaboration are advocated for efficient production and conversion of biomass energies, harnessing of the abundant solar energy and production of other renewable and clean

energies that will propel their economic development. The notion that pursuit of clean energy development will slowdown economic development is not very true. The countries in the South should cooperate and collaborate to unlock their potentials in energy sector by exploiting their comparative advantages. The only way they can transit from followers to leaders in energy production is to share their experiences, develop their own roadmap and explore technologies for implementation. They can cooperate and collaborate to develop microgrids for de-centralized energy systems, using energy mix that takes into account the uniqueness of each region.

SUB-THEME 03: BIO-INNOVATIONS IN FOOD AVAILABILITY AND SAFETY (BF - GREEN & YELLOW BIOTECH)

ST_003: Bio-Innovation for Food Safety and Availability

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Bio-innovation is a singular and extremely important lens that sees through difficulties facing the food system and has promising solutions for addressing them. The global food system is under pressure considering the increasing population. The FAO Report 2023, estimated 900 million people to be food insecure in 2022. This implies that the four dimensions of food security that is; food availability, utilization, stability and access were not achieved. The concept of Bio-innovation combines Biotechnology which serves as the tool, economic models which refer to the interests of stakeholders interested in Biotechnology, and governance models which describe the set of rules that guide the application of the tools, in this context, Biotechnology. Although several biotechnological tools are currently employed in the improvement of crops to resist pests and diseases, these have been achieved with the use of gene editing, synthetic biology, advanced genomics etc. However, the safety of these food products and the processes that lead to their development requires regulation to ensure that they do not have adverse impacts on human health, animals, plants and the environment. In 2019, the National Biosafety Management Agency Act 2015 was amended to include the regulation of emerging biotechnologies such as Gene Editing, Gene Drive and Synthetic Biology. The NBMA food safety assessment of food and feed obtained from modern or emerging biotechnology to ensure food and feed safety and availability in Nigeria.

SUB-THEME 04: INDUSTRIAL PROCESSES AND APPLICATIONS (BI - WHITE BIOTECH)

ST_004: Industrial processes and applications: The Bioeconomy way

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Biotechnology has been recognized as a major tool that could lead to drastic changes in most developing and developed countries into industrialized nations most especially its application along the value chain to offer a huge sustenance to the development of the bio-based industries in manner to guarantee sustainability of the sector and to minimize the negative environmental influence. Furthermore, it has been established that biotechnology could help in the actualization of the UN sustainable development goals apart from being reliable sustainable tools that enhance diverse industrial growth. It has been established that the bioeconomy depends on renewable resources that could satisfy the society's need for industrial products, energy and food while it points out the function of material flows. The bioeconomy model is anticipated to decrease our reliance on fossil fuels in the long term. Therefore, this scientific talk will highlight the application of biotechnology in addition to the sequencing of microorganism genomes together with the mastery of fermentation processes will go a long way in enhancing several industrial biobased processes. Moreover, this scientific talk will elaborate on the development of strains, optimization, process of selection which permit the development of more industrial strains that could withstand the specific conditions of industrial processes and to meet precise objectives. The merits of integrating bio-based molecules into industrial processes can then be numerous includes reduction of transportation costs (in case of local sourcing), improvement of supply reliability, additional element for competitor differentiation, lessening of the environmental impact of the activity, reduction of production costs, reduction of toxicity both of the process and the final product, reduction of the volume of produced waste, lessening of the quantity of needed raw materials, development of new product features, improvement of process efficiency. Moreover, insight will be provided on some biotechnological techniques that could boost agribusiness development such as interventions that could improve competitiveness and productivity, packaging of perishable products, the promotion of food safety in the processing and regulatory environment; modern processing technologies, interventions could start from inputs and agricultural mechanization. Finally, a general overview on the current industrial biotechnology in relationship to inclusive and sustainable industrial development.

Keywords: *Industrial processes, Bioeconomy, sustainable development, bio-based molecules, microorganism genomes, fermentation processes, optimization.*

TECHNICAL ABSTRACTS

SUB-THEME 01: BIOTECHNOLOGY SOLUTIONS FOR EMERGING DISEASES CONTROL AND PREVENTION (BM - RED BIOTECH)

BM-001: Effect of Methanol Extract of Plumeria alba on Egg Albumin –Induced Inflammation in Rat

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Plumeria alba (Apocynaceae) has been found effective in traditional medicine for the treatment of microbial infections and cancers. This study aims at determining the effects of Plumeria alba leaves extract on egg albumin–induced inflammation in rats and the possible mechanism of action. The phytochemical content and antioxidant activities were determined in vitro using standard methods, while the anti-inflammatory activity was determined in vitro using membrane stabilization in human red blood cells (HRBC) and in vivo using egg albumin-induced paw oedema in rats. The results of the phytochemical screening showed the presence of Alkaloids, Flavonoids, Saponins, Tannins and Phenols. Plant extract showed a high level of antioxidant activities with DPPH, FRAP, and LPO levels at 500mg/ml recorded as 81.20±0.55, 90.97±0.47 and 75.94±0.60 respectively. The in vitro anti-inflammatory activity showed that various doses (100–800 µg/ml) of the extract significantly ($p < 0.05$) protected the HRBC against lysis induced by heat and hypotonic solution. There was no death recorded from the acute toxicity test making the extract safe for consumption. The in vivo anti-inflammatory activity showed a decreased level of paw oedema from 0 to 5 hours of egg albumin injection and was more effective after 2,3 4 and 5 hours. The percentage inhibition (%) of paw volume of P. alba for group 2 at dose 200mg/kg bw was significantly higher ($p < 0.0$ 5) than those of group 3 having a dosage of 400mg/kg bw). The obtained results from this study shows that P. alba possesses antioxidant and anti-inflammatory properties and this could be used as a potential drug in treatment of oedema and also effective in alleviating pain.

Keywords: *Antioxidant, inflammation, Plumeria alba, membrane stabilization*

BM_002: Investigating the Therapeutic Mechanisms of Astonia boonei (De Wild) in Diabetes Mellitus Ligand-Based Virtual Screening

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Several studies have established the antidiabetic properties of Astonia boonei, but only limited studies have elucidated their mechanism of action. TGR5, a membrane protein receptor has been implicated in boosting insulin signaling and is a valid drug target for the management of diabetes. However, to date, there is no available commercial drug with specificity for targeting TGR5. This study investigated compounds identified in A. boonei with therapeutic potential as agonists of TGR5. Compounds isolated from A. boonei were curated from the literatures and docked with TGR5 and GLP1 receptors. The compounds were filtered using Lipinski's rule of five (RO5) and consequently used for molecular docking analysis. The binding free energy of the best drug-like compounds was computed, then their pharmacokinetic and toxicological features were determined and compared with metformin. A 2D-QSAR model was constructed from an experimental dataset retrieved from the literature before confirming its robustness through validation. The prediction of the hit compounds drug-likeness, pharmacokinetic and toxicity properties by online web servers showed that the compounds are non-carcinogenic and showed moderate indices for ADMET parameters. This study thus provides insight into the potential of compounds from A. boonei that could be explored as therapeutic alternatives in diabetes treatment

Keywords: *citrus, diabetes mellitus, flavonoid, Inflammation.*

BM_003: Confirming Anopheles colluzzi as the Major Malaria Vector in Abraka Communities, Delta State, Nigeria

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This study was conducted to determine species composition, biting behaviour and abundance of mosquitoes with respect to seasons in the sampled mosquitoes in Abraka community of Ethiope East L. G. A, Delta State, Nigeria. Adult Anopheles mosquitoes were collected indoors and outdoors using CDC light traps for 10 months; from May 2022 to February 2023 and the entomological indices were examined. A total of 343 mosquitoes were obtained from the study and the difference between outdoor and indoor mosquitoes was significant ($p<0.05$). Anopheles mosquitoes collected were morphologically identified as Anopheles gambiae sensu lato. However, molecular screening using Polymerase Chain Reaction (PCR) confirmed them as Anopheles colluzzi. Wings lengths of the mosquitoes obtained outdoors were significantly ($p<0.05$) longer than the ones obtained indoors and may justify the reason for more outdoor mosquitoes. Furthermore, the biting peaks were observed between the hours of 8-9 pm and 2-3 am. The differences between the abundance of mosquitoes with time and traps were significant (F (biting time) = 6.10, p = 0.0028; F(trap)= 20.97, p = 0.0008). Generally, mosquitoes were more abundant in September (especially indoor) than in other sampled months and the lowest catch was in August. The mosquitoes obtained in the rainy months were significantly higher (F(seasons)= 6.56, p= 0.03) than the mosquitoes from the dry months. In conclusion, results from this study show that targeted control measures of A. colluzzi, which is a major vector that transmits malaria parasites, should be channelled outdoors before the month of September to reduce the malaria burden in the study area.

Keywords: *Anopheles mosquitoes, Entomological indices, Molecular confirmation, Delta State*

BM_005: Molecular identification of Rhabdolaimidae aquaticus in free – range chicken from a rural community in KwaZulu-Natal, South Africa

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Rhabdolaimidae aquaticus is a nematode belonging to the subfamily Rhabdolaiminae Family Rhabdolaimidae. The nematode R. aquaticus has been reported in marines, lakes, and soil; however, there is a paucity of information on its epidemiology, its intermediate hosts, and migratory route. This study aimed at shedding more light on the epidemiology of Rhabdolaimidae aquaticus. A cross-sectional study was designed to identify nematode species in free-range chickens (FRC). Forty-two FRC were randomly purchased from households owning chickens from willing sellers in four selected rural communities in the Northern [Gingindlovu, Ozwathini], and Southern Coasts [uMzinto, Shongweni], of KZN province. Chickens selected for the study were euthanized by decapitation according to guidelines approved by Animal Ethics of the University of KwaZulu-Natal South Africa. Tissue from various parts of each chicken such as the brain, heart, spleen, lungs, liver, kidney, crop, duodenum, oesophagus, intestines, thigh, breast, and pectoral were collected, digested, and examined for tissue larvae using the modified acid/pepsin digestion. The Rhabdolaimidae species larvae retrieved from the spleen of one of the chicken samples were subjected to molecular analysis using a QIAamp DNA Mini Kit (Qiagen Inc.) and used in subsequent PCR reactions. PCR reactions for the amplification of 18S rRNA were performed with nematode-specific primers Nem_18S_F (CGCGAATRGCTCATTACAACAGC (23 bases) and Nem_18S_R (GGGCGGTATCTGATCGCC (18 bases). The resulting nucleotide sequences were identified by aligning them with existing sequences of known genotypes from other countries in the GenBank databases using BLAST. The 810-bp 18S rRNA sequences of Rhabdolaimidae aquaticus from uMzinto showed 99.75% similarity and 100% query coverage with Rhabdolaimidae aquaticus FJ969139.1 from Germany. This result provides new insight into the epidemiology of Rhabdolaimidae aquaticus in chickens in South Africa.

Keywords: *Epidemiology, Free-range chicken, Rhabdolaimidae aquaticus, 18S rRNA, South Africa*

BM_006: Antibacterial Activity of Aloe vera Gel against Multidrug Resistant Staphylococcus aureus and Pseudomonas aeruginosa

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Staphylococcus aureus and Pseudomonas aeruginosa have been implicated as important nosocomial pathogens causing severe infections especially in hospitalized patients. The aim of the study was to assess the antibacterial activity of Aloe vera gel against multidrug resistant S. aureus and P. aeruginosa isolated from wound. Clinical isolates of S. aureus and P. aeruginosa from wound infection were collected from Microbiology laboratory of Barau Dikko Teaching Hospital (BDTH), Kaduna and re-confirmed using standard microbiological procedure. Antibiotic susceptibility pattern of the isolates was determined using Kirby Bauer disk diffusion method. Aloe vera gel was obtained fresh matured leaves of Aloe vera plant and was screened for the presence of phytochemical constituents. Antibacterial activity of the Aloe vera gel against Multidrug Resistant (MDR) Staphylococcus aureus and Pseudomonas aeruginosa isolates was determined by agar well diffusion technique. The result revealed that all the two isolates were resistant to more than three classes of antibiotics. The Staphylococcus aureus isolate was resistant to fluoroquinolone (ciprofloxacin), aminoglycoside (gentamicin), cephalosporin (cefaroline), folate pathway antagonist (trimethoprim-sulfamethoxazole), penicillin(cefoxitin) and macrolide (erythromycin) while the Pseudomonas aeruginosa isolate was resistant to βlactam (ticarcillin-clavulanate), fluoroquinolone (ciprofloxacin and norfloxacin), aminoglycoside (gentamicin) and cephalosporin (ceftazidime)hence regarded as MDR isolates. Phytochemical screening of the gel revealed the presence of saponins, flavonoids, terpenoids and alkaloids. The Aloe vera gel was found to have antibacterial activity against the test isolates with MIC and MBC values of 25µg/mL and 50µg/mL against MDR S. aureus 50µg/mL and 100µg/mL against MDR P. aeruginosa respectively. The study identified that Aloe vera gel possesses antibacterial activity against MDR S. aureus and P. aeruginosa isolated from wound infection.

***Keywords:** Aloe vera gel, antibacterial, MDR, Pseudomonas aeruginosa, Staphylococcus aureus.*

BM_007: Molecular Characterization of Pathogenic Dermatophytic Fungal Isolates from Children Attending Barau Dikko Hospital, Kaduna

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Dermatophytosis is a common infection of superficial keratinized epidermal layers, as well as hairs and nails that affects millions of people globally. This study was undertaken to isolate and characterize dermatophytes from children attending Barau Dikko Hospital Kaduna. One hundred (100) samples were collected from male children (3 to 10 years of age) clinically suspected with dermatophytosis. Ten samples were confirmed positive by microscopy. The specie identities of the fungal isolates were confirmed by PCR sequencing of the ribosomal DNA (rDNA) internal transcribed spacer (ITS) regions. Two out of the three fungal isolates were positive to PCR amplification of ITS regions, with amplicon sizes of 600 to 700 base pairs. The amplified sequences of each gene were submitted to GenBank and their accession numbers were assigned. The accession numbers of Fungi A and B are KY457576.1 and MK748313.1 respectively. The result revealed that fungus A isolate has a percentage (%) identity of 92.21% (which has a sequence similarity with the fungi Duitina rugosa), with fungus B isolate having a percentage (%) identity of 95.06% (which has a sequence similarity with the fungi Aspergillus niger), by aligning to reference sequences of GenBank. This study therefore revealed that the fungi Duttina rugosa and Aspergillus niger can be among the main fungal family that cause dermatophytosis locally.

Key words: *Dermatophytosis, DNA, ITS region, PCR.*

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BM_008: Antimicrobial Sensitivity Screening of Terminalia catappa Leaf and Stembark Extracts on Shigella sp., and Salmonella typhi.

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The Terminalia Catappa belongs to the Combretaceae family and is a very deciduous tree. For medicinal purposes in Nigeria, and many parts of the world, the aqueous extract from Terminalia Catappa leaves has been used as a folk remedy for various illnesses. In this study, 50g of leaves and stembark powder was macerated in an aqueous solution and allowed to stand on a shaker for 48 h at room temperature. Soxhlet Extraction was used to obtain pure plant extract, and used for antimicrobial screening against some pathogenic bacteria, with streptomycin as a control. The result showed that Shigella sp were not susceptible to the plant extract. Salmonella sp showed in vitro antimicrobial activity at a concentration of 90 mg/mL of the leaf extract against Shigella sp, with aqueous (21.72mm ± 0.38) and methanol (25.08 mm ± 0.12) extracts. Both aqueous and methanol extracts of this plant at concentration of 90 % showed 19.58mm ± 0.59 and 22.79mm ± 0.29, respectively against Shigella sp. Fourier Transform Infrared Spectroscopy was used to analyze the organic leaf and stembark samples. Results revealed the presence of C-H, N-H, O-H, and C-H functional groups for potential organic compounds. Therefore, Terminalia Catappa can be used in phytomedicine, such as being an effective treatment for dysentery, diarrhea, and other gastrointestinal disorders. It also has anti-inflammatory and antioxidant properties, which can help to prevent and treat various diseases. Further studies should be conducted to evaluate the potential phytochemicals present in the Terminalia Catappa plant.

Keywords: *Terminalia Catappa, FTIR, Salmonella typhi, Shigella*

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BM_009: Anti-Ulcer Activity of Beta vulgaris (Beetroot) in Indomethacin Induced Peptic Ulcer in Wistar Rats

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Peptic ulcer is a multifactorial disease. This study evaluated the antiulcer effect of Beta Vulgaris (beetroot). Thirty rats were grouped into 6 (n=5). All Groups were induced by administering indomethacin except group i. Beetroot was incorporated in their diets at 20%, 40% and 60% for 21 days. Omeprazole was administered at 40mg/kgBW and served as positive control (group 5). In vitro antioxidant activity, proximate and phytochemical screening of beetroot was carried out. Ulcer index, pH, total acidity, gastric volume, biochemical parameters (glutathione (GSH), superoxide dismutase (SOD), catalase (CAT), malondialdehyde (MDA), prostaglandin (PGE2)) and histopathology of the stomach tissue were determined by standard procedures. The in vitro antioxidant activity was concentration dependent, as the activity increased with increasing concentration of the plant material. Proximate results showed the presence of various major macronutrients at varying concentrations for both fresh and dried beetroot. The result showed that beetroot is rich in phytochemicals with flavonoids as the highest and glycoside lowest. The ulcer index were 5.20 ± 0.59, 3.97 ± 0.33 and 0.00 ± 0.00 (20%, 40% and 60%) respectively. Significant difference ($p< 0.05$) was observed in the body weight, pH, total acidity and volume of gastric secretions of experimental animals between the treatment and control groups. The beetroot demonstrated a significant ($P < 0.05$) dose-dependent decrease in inflammatory marker PGE2 and MDA, with an increase in the activity of antioxidant markers CAT, SOD, and GSH. Histological studies showed that beetroot was effective in the reversal of indomethacin-induced gastric mucosal injury in a dose dependent manner by preserving the architecture of the stomach, treat haemorrhagic gastric lesions, promote wound healing and reduce gastric inflammation in peptic ulcer as observed in the negative control group.

Keywords: *Beta Vulgaris, anti-ulcer, indomethacin, antioxidant activity, ulcer index*

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BM_010: Ameliorative Effect of Jatropha tanjorensis Tannin-Rich Leaf Extract on Methotrexate-Induced Hepatotoxicity in Rats

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Methotrexate (MTX) is a cytotoxic drug used in treatment of various malignancies. However, hepatotoxicity resulting from oxidative stress is one of the major complications of methotrexate therapy. This study was carried out to evaluate the ameliorative effect of Jatropha tanjorensis tannin-rich (Jt) extract on methotrexate-induced hepatotoxicity in rats. Rats were randomly divided into six groups as control, MTX treated (5 mg/kg intraperitonially (i.p) on day 1), MTX (5mg/kg i.p) on day 1 + sylimarin 100mg/kg for 14 days via oral gavage (o.g). The other three groups each received 5mg/kg of MTX (i.p) on the first day then treated with 100mg/kg, 200mg/kg and 400mg/kg of Jt extract respectively for 14 days (o.g). Aspartate aminotransferase (AST), alanine aminotransferase (ALT), alkaline phosphatase (ALP), lactate dehydrogenase (LDH), albumin and bilirubin were used as biochemical markers of MTX-induced hepatic injury. Levels of hepatic antioxidant enzymes such as catalase (CAT), superoxide dismutase (SOD), malondialdehyde (MDA) and glutathione peroxidase (GSH-Px) were used as markers of oxidative stress in liver sections. Histopathology of liver was evaluated by light microscopy. The results showed that MTX administration significantly increased ($p<0.05$) serum ALT, ASP, ALP, LDH, bilirubin and hepatic MDA levels. Administration of Jatropha tanjorensis lowered the enzyme levels in a dose-dependent manner. Similarly, serum albumin level and hepatic CAT, SOD and GSH-Px activity were decreased significantly in the methotrexate group compared with the Jt-treated, normal and sylimarin groups. Histological evaluation showed that MTX treatment induced enlarged hepatocytes sinusoids, centrilobular and periportal degeneration, hyperemia of portal vein, and severe necrosis, while all the histopathological changes were attenuated by Jt administration. Consequently, Jatropha tanjorensis administration can attenuate MTX-hepatotoxicity. The effect is partly mediated through the extract's antioxidant activity.

Keywords: *Antioxidant, Jatropha tanjorensis, Methotrexate, Hepatotoxicity*

BM_011: Effect of methanol leaf extract of Luffa aegyptiaca in mice infected with Chloroquine-sensitive Plasmodium berghei

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Malaria is a life-threatening disease of global concern affecting endemic countries, particularly in sub-Saharan Africa, most of which depends on medicinal plants to meet their primary health care needs. Researchers have discovered that Medicinal plants have great potential to provide new antimalarial substances. This study investigated the antimalarial, phytochemical, antioxidant and toxicological effects of 70% methanol leaf extract of Luffa aegyptiaca in mice infected with Chloroquine-sensitive Plasmodium berghei (P. berghei) NK65. Phytochemical studies of the extracts were carried out using standard procedures. The antioxidant activities of the extracts were studied using 2,2-Diphenyl-1-Picrylhydrazyl (DPPH), Ferric Reducing Antioxidant Power (FRAP) and Inhibition of Lipid Peroxidation (ILP). Acute toxicity study of the extracts was carried out as per the Organization for Economic Cooperation and Development (OECD) (425) guidelines. Antiplasmodial activities of crude extracts were assessed in P. berghei infected Swiss albino mice models using Rane's curative test. The haematological and biochemical parameters were also assayed. The phytochemical screening of the plant extracts indicated the presence of alkaloids, flavonoids, tannins, phenols and saponins. The antioxidant activities of the extracts increased in a dose-dependent manner. All doses of extracts exhibited no signs of toxicity at dose of 5000mg/kgbw. The parasitemia load of the treated groups (400, 200 and 100 mg/kg bw) decreased in a dose-dependent manner with 400 mg/kgbw Luffa aegyptiaca extract showing more activity. However, the parasitemia of the positive control group were significantly lower when compared with the extracts treated groups. The Hb and PCV of the negative group (mice that were infected with P. berghei and untreated) were significantly reduced as compared to other treatment groups. This study shows that the extract of Luffa aegyptiaca has significant effects against Plasmodium berghei induced-malaria which could be attributed to the presence of phytochemical compounds.

Keywords: *Antioxidant, Hematology, Luffa aegyptiaca, Malaria, Phytochemical.*

BM_012: Nephroprotective Effect of Tridax procumbens Phenol-Rich Plant Extract on Cisplatin-Treated Rats

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Cisplatin is one of the most potent and effective chemotherapies used to date but it is limited due to the severity of adverse side effects especially its dose-limiting factor nephrotoxicity. This research was designed to investigate the effects of phenol-rich extracts of Tridax procumbens on cisplatin-induced nephrotoxicity in albino rats. Rats were randomly divided into 6 groups (n=5) labelled Normal (normal control group), -control (Cisplatin group), +control (Cispatin+silymarin group), Tp-100mg, Tp-200mg and Tp-400mg treated with 100mg, 200mg and 400mg Tridax procumbens plant phenol-rich extract respectively for 14 days after administration of cisplatin. The rats were sacrificed on the 15th day and blood samples were collected into tubes for biochemical investigation of electrolytes (sodium, potassium, chloride, bicarbonate), urea, creatinine and uric acid). Renal tissue samples were also collected for investigation of antioxidant enzymes; catalase (CAT), superoxide dismutase (SOD, malonialdehyde (MDA), glutathione peroxidase (GSH-Px), total antioxidant capacity (TAC) and histopathology. The result revealed a significant decrease ($p<0.05$) in Potassium, TAC and MDA levels of treated and normal groups compared to the -control group. There was a significant increase ($p<0.05$) in sodium, chloride, bicarbonate, SOD, CAT and GSH-Px of -control compared to the treated, +control and normal groups. Significant decrease in serum urea, creatinine and uric acid levels of Tp-treated groups was observed compared to the -control. There was no significant difference in the serum chloride level of Tp-treated groups compared to the normal. The effects were dose dependent. Histological findings revealed effective renoprotection by different doses of the extracts when compared with the -control. The 400mg Tp-treated group showed normal architecture. In conclusion, Tridax procumbens phenol-rich extract has a nephroprotective effect against Cisplatin-treated rats.

Keywords: *Antioxidant, Cisplatin, Nephroprotective, Tridax procumbens*

BM_013: Molecular Identification of Bacteria Isolated from Tympanotonus fuscatus var. radula.

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Tympanotonusfuscatus var. radula periwinkles have great nutritional and culinary benefits; however, they are also a source of multidrug resistantfood pathogens hence theneed for proper identification to aid treatment and reduce cost.Total Bacteria Count (TBC), Total Coliform Count (TCC), Total Salmonella/Shigella count (TSSC) varied from 1.18 - 3.20 x 10 8 cfu/g, 1.20 - 2.80 x 106 cfu/g, 1.00 - 1.85 x 106cfu/g respectively.Pure cultures of the most frequently occurring bacteria:Escherichia coli6(24%),Bacillus sp 8((32%), Pseudomonas sp4 (16%) were subjected to molecular identification. ITS-1 and ITS- 4 primers were used at 94°C for 2 min, 52°C for 1 min, and 72°C for 2 min for the polymerase chain reaction before sequencing. Taxonomic identification of the gene sequence obtained was compared to known sequences in the NCBI gene bank using the BLAST search program. They showed similarity to Bacillus substilis strain TPS4 (96.60%), Pseudomonas asiastica strain CWCS NVNS (97.82%) and Escherichia colistrain ENOSE 10R (98.00%). Molecular identification is therefore the most accurate and reliable method of identification since it is to the strain level.

Keywords: *Tympanotonus fuscatus var. radula, Molecular, Bacteria, Markets, Sequences*

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BM_014: The Effect of Moringa oleifera Seed Powder on the Microbiological Characteristics of Abattoir Waste Water.

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As an attempt to find alternatives to the use of synthetic chemicals in wastewater treatment, a survey on the effect of Moringa oleifera seed powder on the microbiological characteristics of abattoir wastewater was carried out using standard microbiological and biochemical techniques. Total Bacterial Count (TBC), Total Coliform Count (TCC), Escherichia coli Count (ECC)and Total Fungal Count (TFC) before treatment at zero hour were 7.6 x 10^7, 3.6 x 10^5, 2.1 x 10^4 and 5.5 x10^4respectively. (1.0g, 2.5g and 5.0g) were used to treat 100ml of the wastewater resulting in a gradual change in colour from the initial very turbid reddish brown to slightly turbid white with increasing concentration of seed powder and time. After 72 hours, untreated samples (control) had a higher microbial load of TBC, TCC, ECC and TFC: 8.5 x 10^7, 4.0x10^5, 2.1 x 10^4 and 7.2 x 10^4respectively. Samples treated with 1.0g seed powder had TBC, TCC, ECC and TFC reduced to 2.1 x 10^7, 1.7 x 10^5, 1.5 x 10^4 and 3.0 x 10^4 respectively. Samples treated with 2.5g had TBC, TCC, ECC and TFC reduced to 2.0 x 10^7, 1.5x 10^5, 0.3 x 10^4 and 2.1 x 10^4 respectively. Samples treated with 5.0g gave the most significant reduction: TBC, TCC, ECC and TFC reduced to 2.0 x 10^7, 2.9 x 10^5, 0.9 x 10^4 and 1.3 x 10^4 respectively. This survey shows that M. oleifera seed powder can be used effectively for the treatment of abattoir waste water.

Keywords: *Abattoir, Microbial, Moringa oleifera, Treatment, Wastewater.*

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BM_015: Molecular Detection and Prevalence of Urinary Schistosomiasis among Schoolchildren in Sabon-Gari Local Government Area, Kaduna State, Nigeria

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Urinary schistosomiasis is the most prevalent form of schistosomiasis, affecting approximately 110 million individuals. This condition leads to terminal haematuria, and bladder wall pathology. The objectives of this study were to detect the eggs of Schistosoma haematobium in urine using sedimentation method, confirm the strain of S. haematobium using nested-PCR, determine the prevalence, and the risk factors associated with the transmission of the infection. A cross-sectional study was conducted using a non-probability sampling method, ethical approval was obtained from Ministry of Health Kaduna State. Total of 300 urine samples were collected from 169 males and 131 females (ages 5years-14 years). Detection of parasite's eggs was by sedimentation method. Genomic DNA was isolated using Phenol-Chloroform Isoamyl DNA extraction method (at ratio 25:24:1). The purified DNA were subjected to Nested-PCR and the amplicons were sequenced for phylogenetic analysis. Data on risk factors were collected using semi-structured questionnaires and analysed using Chi-Square test. Schistosoma haematobium was the leading cause of Urinary schistosomiasis among the study population with overall prevalence of 12.33%. The infection was higher among male schoolchildren (12%) than females (0.33%), and children between ages 11years-14 years were more susceptible to the infection than those between 5years -10 years. Schistosoma bovis was also detected in one of the urine samples. The sequences of the isolated S. haematobium were phylogenetically related to Malawi-LgHap2 with percentage identity of 96.07% (accession number EU-567128.1) and consistent with the predominant species in some African countries. Also, there was a cross between Schistosoma haematobium and Schistosoma bovis.

***Keywords:** Urinary Schistosomiasis, Haematuria, Prevalence, Sequencing, Schistosoma haematobium*

BM_016: Molecular Detection of E. coli O157:H7 From Well Water in Okene and Adavi Local Government Areas of Kogi State, Nigeria

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Water is essential for the survival of every life and the need for water is constantly increasing due to high rate of population growth and urbanization. The aim of this research was to detect the presence of E. coli O157:H7 from well water in Okene and Adavi local Government areas. The objectives were to determine the type of wells, the physicochemical parameters, the total coliform and faecal coliform counts from the water, detect the presence flic h7 and eae genes in E. coli O157:H7 and determine the antibiotic susceptibility pattern of E. coli O157: H7 isolated from the wells. A total of 240 samples were collected using simple random sampling method during the dry and wet seasons from ten sample locations within the study area. Physicochemical parameters and bacteriological quality were assessed. Polymerase chain reaction was carried out to detect flic h7 gene and eae gene in pure isolates of E. coli. The antibiotic susceptibility pattern of the isolates was analysed. Only 13% of the wells surveyed conform to World Health Organisation's standard. There was no significant difference in the Faecal coliform counts (P-value 0.164) and Total coliform counts (P-value 0.216) between the rainy and dry season. Out of the twenty six E. coli isolates confirmed, only 9 (34.6%) were non-sorbitol fermenters and through the detection of the presence of flic h7 gene, 6 (66.7%) of the 9 non-sorbitol fermenters were confirmed to be E. coli O157:H7 with a prevalence rate of 2.5%.

***Keywords:** E. coli O157:H7, Okene and Adavi Local Government, PCR, Prevalence, well water.*

BM_017: Evaluation of the In vivo Antioxidant and Antidiabetic Potentials of Green-synthesized Zinc Oxide Nanoparticle

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Diabetes mellitus has remained one of the greatest health concerns globally due to its increasing prevalence and associated complications. Synthetic antidiabetic drugs are not without side effects and diminished glycaemic control effect overtime. This study investigates the in vivo anti-oxidant and antidiabetic potentials of zinc oxide nanoparticle (ZnONP) synthesized from Mangifera indica leaves in alloxan-induced diabetic rats. The characterisation of the synthesised ZnONP, antioxidant and antidiabetic assays were carried out using standard procedures. ZnONP was characterised at UV-visible absorption peak of 329.07 nm. High resolution scanning electron microscopy scanning showed irregular square shape in clusters with average size of 200 nm. Selected area electron diffraction showed a continuous concentric ring. The X-ray diffraction patterns showed seven significant diffraction spikes in 100, 102, 101, 102, 110, 103, and 112 planes at 32^{o}, 35^{o}, 36^{o}, 47^{o}, 57^{o}, 63^{o} and 69^{o} respectively. The pattern was dominated by intense, sharp peaks, for oxygen (49.85%), Zinc (42.4 7%) and carbon (7.68%). There was significant reduction ($p < 0.05$) in the fasting blood glucose levels of rats administered 100 and 200 mg/kg bodyweight of ZnONP (27.30% and 42.52%), methanol extract of Mangifera indica (38.79% and 54.71%) and metformin (66.20%), compared to the diabetic control group at the end of the experiment. It was observed that the levels of some antioxidant enzymes (catalase, glutathione and superoxide dimutase) increased, while malondialdehyde levels decreased in the groups administered ZnONP when compared to the diabetic control group. This study shows the potential of ZnONP to be explored in the management of diabetes and oxidative stress.

Keywords: *Diabetes mellitus, fasting blood glucose, Mangifera indica, zinc oxide nanoparticle*

BM_018: Biochemical Diversity of Host-Plant Specific Weaver Ant (Oecophylla longinoida) in a Savanna Fruit-Tree Plantation, in North Central Nigeria

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The study was carried out to determine the influence of host-plant type on biochemical diversity of weaver ants (Oecophylla longinoida) in a typical savanna fruit crops plantation in North Central Nigeria. Weaver ants have been reported to be one of the best natural biological control agents and play a very significant role in protecting ripe fruits by colonizing the fruits trees. Weaver ant nests were collected and trapped undisturbed in black polythene bags. The polythene bag was quickly open into a standard killing jar containing chloroform. Sorted adult weaver ants and nest leaf materials were air dried at room temperature and homogenized separately to a fine coarse powder using an electric blender. Cold extraction method was used in order not to denature some bio-chemical components of the blended ant sample. Qualitative screening of bioactive metabolites in host plant leaf materials and colonizing adult weaver ants were carried out using standard procedures. Six bioactive metabolites viz, saponin, tannin, alkaloid, flavonoid, phenol and terpenoid were tested qualitatively in both host plant leaf materials and the adult weaver ants. The results revealed that saponin, flavonoid, phenol and terpenoid were present in adult weaver ant and the four host plant leaves namely Mango (Mangifera indica), Mahogany (Swietenia macrophylla), Cashew (Anacardium occidentale) and Shea butter (Vitellaria paradoxa) while, Tannin was present in only mango leaves and in adult weaver ant recovered from all host plants. Alkaloid was absent in mango leaves and present in all others. The findings of this study revealed strong relationships between biochemical constituents of weaver ants and their respective host plants that may be explored in sourcing for these metabolites, as well as, further understanding of the factors that influence the ecological productivity of this important biological control agent, the weaver ants.

***Keywords:** Alkaloid, Bioactive metabolites, Flavonoid, Tannin, Phenol*

BM_019: Detection of Antibiotic Resistance Genes Among Gram-Negative Bacteria Isolated from Lagos Lagoon and Creek

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The presence of antibiotic resistance genes (ARGs) among Gram-negative bacteria in the water bodies poses a profound threat to seafood as it contributes to the spread of the resistance genes among them and their consumers. This study aimed to detect the presence of antibiotic resistance genes in Gram-negative bacteria isolated from Ologe Lagoon and Badagry Creek, Lagos state, Nigeria. Eight multiple antibiotics resistance isolates obtained from the study sites and previously characterised in the Department of Microbiology, University of Ibadan, Oyo State, Nigeria. were used for this study. The isolates were subjected to conventional microbiological procedures to verify their identities. Antibiotic susceptibility testing (AST) was carried out using the Kirby Bauer disk diffusion method and six antibiotics including imipenem, ertapenem, ciprofloxacin, ceftazidime, kanamycin, and gentamycin were used. Conventional Polymerase Chain Reaction (PCR) was used to detect the presence of antibiotic resistance genes (blaCTX-M, blaSHV, blaTEM, and blaNDM) using specific primers. The isolates comprised Enterobacter cloacae (5), Aeromonas hydrophila (2), and Klebsiella pneumoniae (1). Antibiotic susceptibility testing (AST) showed that all the isolates were resistant to ciprofloxacin, ceftazidime, and ertapenem (multi-drug resistant), while seven were susceptible to imipenem. The multiple antibiotic resistance index (MAR) of the isolates ranged between 0.5 – 0.83. The PCR result showed that one Enterobacter cloaca harboured blaNDM gene while Klebsiella pneumoniae harboured blaTEM and blaNDM, showing multigene. None of the isolates harboured blaCTX-M and blaSHV genes. The high MAR index of isolates in this study shows high consumption of antibiotics and improper treatment of wastewater within the study areas before releasing into water bodies. Also, the harbourage of the ARGs among the isolates showed that water bodies can serve as reservoir of ARGs.

Keywords: *Antibiotic resistance genes (ARGs), Antibiotic susceptibility testing (AST), Multiple antibiotic resistance index (MAR), Polymerase Chain Reaction (PCR).*

BM_020: Plant Tissue Culture: An Important Biotechnology Tool in Drug Production

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In respect of the increasing demand for more availability, affordability and effectiveness in drug production, the need arises to embrace ‘Plant Tissue Culture’ technology for enhanced, large scale drug production. The use of plant source for drug production is a long established practice that is almost indispensable to human survival. Despite being the foremost and major source of therapeutics, plants utilization in drug production is highly threatened by a lot of biotic and abiotic factors that affect its reliance for stable pharmaceutical raw materials. Consistency in availability of the starting materials in good quantity and quality is crucial in drug development and production consideration. Most of the critical factors declining the dependence of botanical source in drug production culminate to extinction of the medicinal flora and/or low yields of the valuable medicinal content. Being unaffected by climate change or geographical conditions, tissue culture techniques ensures reliable, healthy and economical production of phytochemicals of pharmaceutical significance. With extended and promising uses of plants in the emerging area of “Plantivaccines,’ development, the importance plant tissue system is clearly emphasized. The significance of tissue culture technology in strengthening and improving the productivity of important plants /products of medicinal interests especially at industrial levels is the main focus of this article.

***Keywords:** Biotechnology, Drug, Plant, Tissue culture.*

BM_021: Unlocking the secrets of androgen receptors in prostate cancer susceptibility, progression, and treatment

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Prostate cancer (PCa) is a major cause of cancer-related mortality worldwide, with a rising incidence observed over the years. The androgen receptor (AR) signaling pathway plays a pivotal role in male development and maintaining masculine characteristics. Dysregulation of AR signaling in prostate cancer can lead to disease progression and resistance to standard therapies. Understanding the intricate regulation and function of AR in both healthy and diseased states is crucial for developing effective treatment strategies. This review comprehensively explores the role of androgen receptors in prostate cancer susceptibility, disease progression, and treatment response by analyzing recent literature. An extensive search of peer-reviewed publications in major databases, including PubMed, Scopus, and Web of Science, was conducted using specific keywords related to androgen receptor, prostate cancer, disease progression, and treatment resistance. Relevant conference abstracts and clinical trial reports were also included. The review presents an overview of the role of androgen receptors in prostate cancer initiation, progression, and treatment resistance. It highlights emerging biomarkers associated with AR signaling dysregulation such as TMPRSS2:ERG fusion, AR-V7, SPOP dysregulation, AR signaling-related genes, ctDNA mutations, PTEN loss, and specific long non-coding RNAs (lncRNAs), and their potential utility for early detection and personalized treatment approaches. Additionally, recent advances in targeting the AR pathway for novel therapeutic strategies to improve patient outcomes and overcome treatment resistance in advanced prostate cancer are discussed. The findings contribute to a comprehensive understanding of the AR signaling pathway in prostate cancer and offer insights into its multifaceted role in disease development and treatment response. They may pave the way for innovative therapeutic interventions and precision medicine approaches based on specific AR signaling profiles, enhancing patient care and reducing the burden of this lethal disease.

Keywords: *Androgen receptor, androgen deprivation therapy, AR signaling pathway, personalized treatment, prostate cancer*

BM_022: Chitosan: A biodegradable and biocompatible polymer suitable for encapsulation

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Chitosan is a natural biopolymer that is derived from chitin by deacetylation, which is found in the shells of crustaceans such as shrimp, crabs, lobsters, and cell walls of fungi. Due to its biodegradability, biocompatibility and ability to encapsulate drugs, chitosan is investigated for drug delivery systems. Encapsulation using chitosan serves many purposes such as controlled release of substances, protection from degradation, improved stability, and targeted delivery. To achieve these, spray drying, emulsification, coacervation, ionotrophic gelation, electrospining, polyelectrolyte complexation and others are methods that have been used to encapsulate bioactive plant extracts, essential oils and bioactive compounds using chitosan. Bioactive compounds that have been encapsulated using chitosan includes quercetin, luteolin, emodin, and carotenoids. Encapsulation using chitosan has been explored for drug delivery systems to improve efficacy of plant extracts and bioactive compounds against diseases like diabetes, cancer, inflammation, and oxidative stress. It has been employed in food technology for food preservation and packaging to help extend their shelf life, inhibit the growth of microorganisms, and improve food safety. Furthermore, it has been explored for the controlled release of agrochemicals (fertilizers and pesticides), to enhance the efficiency of the agricultural inputs and reduce environmental pollution. Chitosan-based materials have also been used to adsorb heavy metals, dyes, and other contaminants from water and so many more applications in water treatment.

***Keywords:** bioactive compounds, chitosan, drug delivery, encapsulation, and plant extracts*

BM_023: Wild Birds Possible Transmitters of Antibiotic Resistance Gene

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Wild birds are considered central to the spread of antibiotic resistance among humans, farm animals and the environment. This is due to their diverse ecological niche and migratory habits. Further evidence suggest wild birds can serve as reservoirs of antimicrobial resistance bacteria and can therefore be utilized as sentinels. This study was aimed at determining the incidence of antibiotic resistance genes of Escherichia coli isolated from fecal samples of wild birds in Plateau State, Nigeria. Fifty fecal samples were collected from identified wild birds. All samples were cultured on selective media for E. coli (Eosin methylene blue and MacConkey agar). Screening for potential Extended Spectrum Beta Lactamase (ESBL) producing E. coli isolates was done using disc diffusion method on nutrient agar followed by polymerase chain reaction (PCR) targeting the CTX, TEM and SHV genes. Also, PCR was carried out for resistance to qinolones (gyrA), tetracyclines (tetA), slphonamides ((sul1) and phenicols (cat1). Out of the fifty (50) samples collected, twelve (24%) were positive for E. coli whereas CTX(0%), TEM(90%), and SHV(10%) were positive for beta-lactamase resistance genes. Eight (16%) showed resistance for tetracycline (tetA-90%), sulphonamide (sul1-90%), quinolones (gyrA-90%) and non for Phenicol (cat1-0%). This study has shown the incidence of antibiotic resistance in E. coli from wild birds indicating the role these birds may play in the spread and maintenance of antibiotic resistance in the environment.

Keywords: *Wildbirds, antibiotics, resistance, gene*

BM_024: Bacterial Profile and Antibiogram of Doorhandles of Female Restrooms in Niger hall, Nile University of Nigeria

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Various bacteria have been isolated from public surfaces thereby providing information on the relative hygiene of commonly encountered public surfaces, identifying the environments with contaminants and risk of exposures. Gram positive and negative bacteria most especially are found to contaminate contact surfaces e.g; door handles, tables, chairs, windows, etc. The aim of this research is to identify and evaluate the prevalence of bacterial contaminants of door handles of female restrooms at Niger hall of Nile university of Nigeria. A total of 30 swab samples were collected from the door handles of female restrooms, using the swab-rinse method of the American Public Health Association. The swab sticks were introduced into test-tubes containing sterile peptone water (1ml) and were shaken and incubated at 37 ºC overnight. The samples were then streaked on MacConkey and nutrient agar and all the plates were incubated for 24 hours at 37 ºC. Observed bacterial growths were analyzed using cultural and biochemical techniques. The susceptibility testing with antimicrobial agents was done using Kirby Bauer disk diffusion method under Clinical Laboratory Standards Institute guidelines. The results showed that all samples (100%) had bacterial growths. Both Gram positive and Gram negative species were isolated from the samples. Staphylococcus species had the highest prevalence of 46.7% while Micrococcus had the lowest prevalence of 3.3%. Antibiotic susceptibility tests showed that Staphylococcus aureus had 100% susceptibility to the antibiotics used while E. coli had the lowest (60%). The findings of this research work indicate that hand contact surfaces such as door handles of restrooms are often colonized by several bacteria and may serve as a potential source of infections.

***Keywords:** Antibiogram, contact surfaces, door handles, prevalence, techniques.*

BM_025: In Silico Evaluation of Antidiabetic Activity of Bioactive Compounds from Oreganum vulgare Leaves Targeting PTP1B.

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Diabetes mellitus is a metabolic disorder associated with hyperglycemia due to alteration in insulin production/utilization. It continues to be a global burden despite the available therapeutic options to manage the condition, hence the need for safer and more effective alternatives. Medicinal plants are store houses for natural compounds with therapeutic potential against diabetes and Oreganum vulgare, commonly known as oregano has been used traditionally for managing elevated glucose levels and its extracts have been reported to possess antidiabetic potential. This study seeks to predict the phytochemical constituent of oregano plant that account for the reported antidiabetic activity of the extract using in silico approach. The 3-D structures of the chemical constituents of the plant and standard drugs were obtained from PubChem data base and 3-D structure for the drug target protein tyrosine phosphatase 1B (PTP1B) was obtained from RCSB-PDB database of proteins (PID: 4Y14). PTP1B was prepared for ligand-based screening using pymol and the bioactive compounds were minimized and converted to ligands. The Ligands were docked against PTP1B using autodock vina on PyRx while the drug-likeness, pharmacokinetic and toxicity properties of hit compounds were predicted using the SwissADME online server. From the study, four of the phytochemicals present in Oregano had lower docking scores than the standard drugs. α-bulnesene, δ-cadinene, γ-cadinene and β-sesquiphellandrene had lower docking scores of -8.1, -7.8, -7.5 and -7.5 respectively, when compared to the standard drug sitagliptin with docking score of -7.1. Pharmacokinetic properties of the four hit compounds were predicted to follow the Lipinski rule of druglikeness and are non-substrates of P-glcoprotein, suggesting that the compounds will not be eliminated quickly and thus better efficacy. The study revealed the phytochemicals present in Oregano that may be responsible for the antidiabetic properties of oregano plant extract.

Keywords: *Antidiabetic activity, Diabetes mellitus, In Silico, Oreganum vulgare, oregano*

BM_026: Combating the Prevalence of Diabetes Mellitus: Can Essential Oils Win the Fight?

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Diabetes is a non-communicable disease that occurs as a result of alterations in glucose metabolism due to defect in secretion or action of insulin and symptomatically characterized by chronic hyperglycaemia. It is one of the rapidly growing global health burdens affecting ~463 million people. Globally, about 50% of diabetes cases are undiagnosed, with low-income and middle-income countries accounting majorly for the figure. In Africa, over 70% of deaths as a result of diabetes occurred in persons below the age of 60. Pharmacotherapy, lifestyle and dietary modification are interventions used for the management of diabetes. However, side effects and non-compliance associated with these strategies have led to the search for better and safer alternatives. Essential oils (EOs) are complex mixtures of volatile organic compounds biosynthesized through the mevalonate pathway as secondary metabolites, conferring particular aroma, flavour and fragrance to plants. EOs are used in aromatherapy for treatment and management of metabolic disorders such as diabetes. Essential oils from leaves and/or seeds of Lavandula stoechas, Satureja khuzestanica, Nigella sativa, Brassica nigra, Melissa officinalis, Backhousia citriodora, Anonna muricata, Cinnamomum tamala, Rosmarinus officinalis, Citrus sinensis and others have been reported to possess antidiabetic properties. This antidiabetic activity of EOs have been reported in in-vitro studies and in-vivo studies using different rodent models. However, the volatile nature and non-aqueous solubility of essential oils impede its bioavailability and effectiveness as an oral antidiabetic agent. Hence, encapsulation and optimizing the use of EOs may be able to overcome these challenges and therefore provide an alternative to treating and managing diabetes.

***Keywords:** Antidiabetic properties, diabetes, essential oils, metabolic disorder*

BM_027: Acute Toxicity, Phytochemical Screening and Antiplasmodial Property of Extracts of Nelsonia canescens

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Malaria is a serious public health problem, especially in sub-Saharan Africa, with Nigeria having high cases. There is a constant search for drug and natural products that can serve as antimalarial targets. The study was set out to scientifically provide information on the use of Nelsonia canescens as a potent antiplasmodial plant as acclaimed by the trado-medicinal health practitioners. Plant materials were collected, washed, air-dried, and ground into fine powder. Ethanol and hydro-ethanol extracts were gotten by maceration in absolute ethanol and 50:50 v/v (ethanol and water) respectively, concentrated, freeze-dried, and kept until time of use. Acute toxicity test (LD50) was carried out using Lorke’s method, the extracts were screened for their phytochemical constituents using standard procedures. In vivo antiplasmodial property of the extracts were evaluated in Plasmodium berghei-infected mice by Peters’ 4-day suppressive test. Result of the acute toxicity test showed that the lethal dose (LD50) of the extracts were above 5000 mg/kg. Phytochemical screening of the extracts indicated the presence of flavonoids, tannins, saponins, phenols, coumarins, alkaloids, terpenoids, reducing sugars among others. Treatment with extracts significantly ($p < 0.05$) suppressed the levels of parasitemia in the parasitized mice and increased their mean survival time at all tested doses compared to the untreated infected control. However, chloroquine (CQ) treated mice showed 98% inhibition of the parasite with activity greater than the extracts treated groups. Total findings from this study suggest that some of the bioactive pytocompounds identified in the plant extracts may be responsible for the antiplasmodial property.

Keywords: *Antiplasmodial, Phytochemicals, Plasmodium berghei.*

BM_028: Anthelmintic Activities of Stem Bark of Parkia biglobosa on Goats Infected with Haemonchus contortus

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The anthelmintic effects of stem bark extracts of Parkia biglobosa was evaluated on West African Dwarf (WAD) goats. The extraction was done and yielded Crude Methanol Stem Bark Extracts (CMSBE), Ethyl acetate (EA) fraction and Aqueous (AQ) fraction. The anthelmintic potentials were studied in vivo in 18 WAD goats in six completely randomised groups, A, B, C, D, E and F with three animals per group. Group A was treated with 5mL/kg of distilled water as negative control, group B with 6.25mg/kg of Albendazole (ABZ)(positive control), groups C and D with 1000mg/kg and 2000mg/kg of CMSBE respectively and groups E and F with 1000mg/kg of EA fraction and AQ fraction each respectively. Faecal samples were collected for two weeks after treatment to evaluate faecal egg counts. After 16th day, one animal was euthanized from each group to determined percentage deparasitization. In vivo result showed significant ($P<0.05$) reduction in egg per gram (EPG) faeces in group B, C, D and E when compared to group A, all at 16th day post-treatment. Group F showed less efficacy in EPG reduction. The deparasitisation obtained in groups D and E were higher than group B, though without statistical significant difference. The study has shown that, CMSBE and EA fraction of P. biglobosa exhibited in vivo anthelmintic activities at 2000mg/kg and 1000mg/kg respectively that are sufficiently comparable to ABZ, hence, have potentials as a novel anthelmintic ethnobotanic preparation for control of H. contortus in WAD goats. It is therefore recommended to carry out further research on larger population size of goats.

***Keywords:** Egg counts, extract, faecal, goats, phytochemicals*

BM_029: Molecular Approaches to Malaria: Exploring Molecular Markers in Plasmodium falciparum Resistance to Four Front-line Antimalarials in Jos, Nigeria

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Malaria remains a life-threatening and most widespread infectious diseases. Although it is preventable and curable, nearly half of the world's population is at risk; about 247 million cases reported worldwide; and it spreads to non-endemic regions. This disease prevalence is highest in sub-Saharan Africa; Nigeria having 26.6% suffers the most followed by the Democratic Republic of the Congo (12.3%), Uganda (5.1%) and Mozambique (4.1%). Efforts to understand and develop means of eliminating malaria reached its peak with the molecular approaches. This study undertook molecular epidemiology and genetic studies for identifying molecular markers encoding Plasmodium falciparum resistance to some front-line antimalarials in Jos, Nigeria. The parasites' drug resistance is a challenge to the realization of the 'end malaria' vision. After being granted an ethical approval, two hundred clinically screened and confirmed (++ or more) malaria infected blood samples were collected from three hospitals in Jos, Plateau state, Nigeria. The samples were collected within a period of 8 weeks (October to December, 2019 when malaria was less rampant) and transported in EDTA bottles. DNA was extracted using Zymo Research extraction kits according to the manufacturer's instructions. PCR was used for detection of the parasite's genus, Plasmodium falciparum and four genes responsible for drug resistance namely: sulphadoxine resistant (540pfdhps), artemisinin resistant (Pfkelch13), chloroquine resistance transporter (pfcrt), and multi drug resistance (Pfmdr1) genes. PCR amplicons of resistant genes were sequenced and bioinformatics software used to analyze the sequences for mutations. The molecular approach revealed only 69.49% of the samples were positive for Plasmodium genus (1100bp) gene meaning about 30.51% constituted false positive malaria. The gene of the culprit, Plasmodium falciparum (205bp), was detected in 66.32% of true positive samples. This implies that 33.67% was non-falciparum infection. About 69.23% of the Plasmodium falciparum carried at least one resistant gene distributed as follows: 647bp 540pfdhps (12.3%), 848bp Pfkelch13 (16.92%), 145bp pfcrt (27.69%) and 418bp Pfmdr1 (12.3%). Worrisomely, about 21.54% of the parasites carried multiple resistant genes. This illustrates the density and complexity of plasmodium drug resistance in Jos, Nigeria. Malaria in Jos is caused by mixed infection, complex and densely resistant Plasmodium falciparum.

Keywords: *Malaria, Plasmodium falciparum, 540pfdhps, Pfkelch13, pfcrt and Pfmdr1 resistant gene*

BM_030: Physicochemical and Bacteriological Quality Assessment of Water from Reservoir in Nile University of Nigeria, Abuja.

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Water is one of the most essential natural resources needed by every living thing. Whether it is used for drinking, bathing, food production or recreational purposes, portable and accessible water supply is crucial for public health. This study was carried out to assess the physicochemical and bacteriological quality of water in the water reservoir in Nile University of Nigeria, Abuja. Water samples were collected from water reservoir in the study area using systematic random sampling technique and some of the physicochemical parameters such as temperature, pH, electrical conductivity, salinity, total hardness, Total dissolved solids, colour, odour and turbidity were measured. Heavy metals (Zinc and Lead) were analyzed using APHA standard method and bacteriological qualities were also analyzed. The total bacterial count was determined by dilution method. Bacterial identification was done using standard laboratory methods. The antibiotic susceptibility test was done using Kirby Bauer disk diffusion method under Clinical Laboratory Standards Institute guidelines. The physicochemical parameters of the water samples were all within the normal range of WHO limit. The two heavy metals tested were not detected in the water samples. The total bacterial count (TBC) in water samples was 2.1 x 104 CFU/mL. Escherichia coli, Staphylococcus aureus, and Klebsiella pneumonea identified. The antibiotic susceptibility tests showed that E. coli was resistant to all the antibiotics used for the study. K. pneumonia also showed 90% resistance while S. aureus showed the highest sensitivity of 40%. The bacteriological quality of the water sample is a public health issue especially with the level of antibiotic resistance demonstrated by the isolated bacterial species.

Keywords: *Electrical conductivity, Escherichia coli, heavy metals, physicochemical, reservoir.*

BM_031: Green microencapsulation: a sustainable solution to recrudescent malaria

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Lumefantrine, a component of artemisinin combination therapies, is an important antimalarial drug, used as the first line of treatment to combat residual malaria parasites in countries with high risks of malaria infections. However, its effectiveness against recrudescent parasites is limited by its poor aqueous solubility and oral bioavailability. A new extended formulation of lumefantrine was developed using a green and sustainable production process termed the supercritical fluid technology to address the unmet clinical need. Lumefantrine was formulated with polyethylene glycol and glycerol monostearate in supercritical carbon dioxide, co-precipitated as particles from gas-saturated solutions and micronized through a 500 µm nozzle. The particles were characterized and chemotherapeutic effectiveness was evaluated in Plasmodium berghei-infected mice model. Post-treatment analyses were carried out to assess the clearance of residual parasites. The formulated particles were spherical, micrometre range and had high encapsulation efficiency. The lumefantrine microparticles also had an extended-release rate in simulated physiological conditions. Treatment of infected mice with the lumefantrine microparticles resulted in complete clearance of the Plasmodium parasites. In summary, green microencapsulation enhances the effectiveness of lumefantrine against recrudescent parasites.

Keywords: *Drug Formulation, Lumefantrine, Malaria, Microencapsulation, Supercritical Fluid*

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BM_032: Investigating Alternative Daily Dose Regimens for Bedaquiline in Multidrug-Resistant Tuberculosis Treatment using model-based simulations and interactive Shiny application

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Tuberculosis (TB) remains a major global health concern, especially multidrug-resistant (MDR) TB. Bedaquiline (BDQ), is an effective drug for MDR-TB treatment and the current approved BDQ dose regimen in adults is a loading dose of 400 mg daily (QD) for 2 weeks followed by 200 mg thrice weekly (TIW) for 22 weeks with other drugs co-administered QD. The complex and different dosing schedules of BDQ could increase the risk of poor compliance, and missed doses, and may affect treatment outcomes. Therefore, a QD dose regimen of BDQ is required to simplify dosing, maintain therapeutic levels, and possibly facilitate a fixed-dose combination with other combination treatments in the future. The study aims to investigate an alternative daily BDQ regimen with the same loading phase as the approved regimen and implement a shiny tool for an interactive simulation of typical and population concentration profiles for different dose regimens. The NONMEM codes of the PK model were implemented in R-studio using the “mrgsolve” package integrated with other R package. Assuming patient characteristics of baseline body weight 53 kg, age 32 years, baseline albumin concentrations as 3.50g/dl and black and non-black race. The mrgsolve model was used to simulate three BDQ dose regimens of 24 weeks: approved regimen (400 mg QD for 2 weeks followed by 200 mg TIW for 22 weeks), TB alliance regimen (200 mg QD for 8 weeks followed by 100 mg QD for 16 weeks) and proposed regimen (400 mg QD for 2 weeks followed by 100 mg QD for 22 weeks). To compare regimens, PK metrics such as typical PK profile, trough PK profile, mean daily concentration (Cavg_daily), mean weekly concentration (Cavg weekly), cumulative area under the concentration-time profile (CumAUC), and PK profile after dosing at 2, 8, 24 weeks were plotted using the ggplot2 package. A shiny app was also implemented to enable researchers to explore different BDQ dose regimens using the shiny package in R to simulate a single regimen or compare three different regimens.

The typical PK profile including trough and peak BDQ and M2 concentrations overlapped for the approved and proposed dose regimen at week 2 (loading phase), followed by a rapid decrease in exposure at the start and different peak values at the end of week 22 (maintenance phase) for both races. The TB Alliance dose regimen showed a lower peak concentration at week 8 (loading phase) and a higher peak from week 10 to week 24 than the other two regimens for both races. The M2 concentrations were highest with the TB Alliance especially during the 8-week (loading phase) when compared to the other two regimens. The shiny app allows users to customize dosing, covariates, drug interactions, and simulation details for single regimen and regimen comparison panels. It will be published as open source. The proposed dose had a BDQ and M2 concentration similar to the approved dose regimen at the loading phase. In addition, the shiny app could serve as a basis for future expansion to enable explorations of other regimens and the inclusion of drug effects or safety targets of interest.

Keywords: *Bedaquiline (BDQ), Multidrug-resistant (MDR), Shiny tool, Interactive simulation*

SUB-THEME 02: BIOFUELS AND ENERGY SOLUTIONS (BE - GREY BIOTECH)

BE_001: Evaluation of selected heavy metal pollution in soil from auto-mechanic workshops in Delta State, Nigeria

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Increased activities associated with automotive repairs in a mechanic workshop would lead to an ecological imbalance via toxic heavy metal discharge from automotive parts. This study assessed the heavy metal content and the extent of pollution in the soil from 3 distinct locations of the major mechanic workshop in Warri, Delta State. The mean concentrations of soil metals via atomic absorption spectrometry (ice 3000 series) were Zinc (68.05-390.21 mg/kg), Copper (66.58 – 349.45 mg/kg), Chromium (5.31 – 28.44 mg/kg), Cadmium (8.35 – 10.36 mg/kg), Nickel (17.35 – 24.16 mg/kg), Lead (296.95 – 801.33 mg/kg). The mean geo-accumulation index (Igeo) values for Zinc, Copper, Chromium, Cadmium, Nickel and Lead were found to be (−0.97± 0.78), (1.24± 0.72), (−3.13± 0.77), (2.61±0.09), (-2.34±0.14) and (1.98±0.48) respectively. An Igeo $2 \leq 3$ assessment of Cadmium at all sampling locations was obtained. The contamination factor (Cf) of Cadmium at all locations exhibited high levels of contamination; 10.36, 8.79 and 8.35 respectively. The Cf for lead and Copper at location 1 displayed a high level of contamination (11.45, 6.99) whereas exhibited a considerable contamination degree to warrant future risk at locations 2 (4.28, 1.33) and 3 (4.24, 4.76). The degree of potential ecological risk index (PERI) revealed that Cadmium at all sampling locations exhibited high risk; 311, 264 and 251 respectively. All other sampling locations exhibited low risks on the potential ecological risk index. The data obtained suggests continuous monitoring and would also aid researchers to develop appropriate strategies for Cadmium remediation programs in the study area.

***Keywords:** Heavy metals, AAS, Geo-accumulation, Contamination-Factor, PERI*

BE_002: Isolation and Characterization of Heavy Crude Oil degrading bacteria obtained from Gut of Bos taurus africanus (Sanga cattle)

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Methanogenic bacteria obtained from a range of environmental niches play essential roles in the degradation of petroleum hydrocarbons, attracting considerable interest for its application across a diverse range of petroleum products. In this study, the fastest growing mesophilic bacteria, designated VG6 was obtained from the fecal gulp of Bos taurus africanus using pyrene as a screening source of carbon. Pure cultures of VG6 exhibited good growth on mineral media supplemented with glucose; 2.1 X 103 to 7.7 X 103 (cfu/ml), starch; 1.8 X 103 to 5.9 X 103 (cfu/ml) and engine oil; 3.8 X 102 to 1.2 X 103 (cfu/ml) respectively over a 96-hour incubatory period. Furthermore, pure culture VG6 targeted and degraded C23-C38 heavy aliphatic fractions of heavy crude oil as well as the overall total petroleum hydrocarbon (TPH) component of the oil, exhibiting a 27% reduction in the latter with excess of 82% reduction in components of the former. The VG6 pure bacterial culture also degraded several polycyclic aromatic hydrocarbons (PAH) compounds of the heavy crude oil, reducing selected 3, 4 and 5 ringed PAHS. The overall viscosity of the heavy crude oil was reduced by over 41% by this strain. Biochemical analysis using an API20e kit coupled with 16S rRNA sequencing revealed that pure VG6 bacterial pure culture shared a 99.18% sequence similarity with Acetobacter pasteurianus. This report therefore indicated that bacterial culture VG6 could be applied not only to degradation of crude oil but could also be targeted towards enhanced oil recovery.

Keywords: *Bos taurus africanus, Heavy Crude oil, Acetobacter pasteurianus, bio-degradation*

BE_003: Assessment of heavy metal contamination in Ivo Local Government Area of Ebonyi State.

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This research work was focused on evaluating the concentration of heavy metals (i.e., Cr, Zn, Co, Ni, Pb, Mn, Cu, Cd and Fe) in soil samples collected from the local mining sites at Ivo local government area of Ebonyi State, Nigeria. The heavy metals in obtained samples were ascertained by the atomic absorption spectrophotometer (AAS). This study revealed that the elemental concentration for chromium (82.98 – 282.42 ± 31.82 mg/kg), sodium (-0.49 – 195.29 ± 31.76 mg/kg), zinc (272.74 – 650.37 ± 55.27 mg/kg), calcium (24.63 – 4,581.29 ± 729.23 mg/kg), Magnesium (74.05 – 338.76 ± 46.95 mg/kg), iron (5,733.21 – 6,997.64 ± 198.38 mg/kg), cobalt (8.40 -31.49 ± 4.23 mg/kg), potassium (249.38 – 1,010.22 ± 118.34 mg/kg), lead (481.17 – 9,303.08 ± 1379.33 mg/kg), manganese (764.53 – 1,735.21 ± 210.94 mg/kg), copper (3.48 – 47.58 ± 5.78 mg/kg). Cadmium was not detected in the samples. Soil contamination was assessed on the basis of geo-accumulation index (Igeo) and contamination factor (CF). Igeo values were in the range chromium (-0.12 to 1.65) zinc (0.64 to 1.89), cobalt (-2.57 to -0.46), nickel (-1.34 to -0.11), lead (2.78 to 7.05), manganese (-0.15 to 1.10) and copper (-3.85 to -0.07) respectively. The Igeo values of lead suggested almost all sampling locations were extremely polluted. The CF values were in the range chromium (0.92 to 2.31) zinc (1.56 to 3.72), cobalt (0.31 to 0.73), nickel (0.40 to 0.93), lead (6.87 to 132.90), manganese (0.90 to 2.15) and copper (0.07 to 0.95) respectively. The Cf for all samples exhibited high risk for lead contamination. Physicochemical analysis revealed a range of pH (5.03 to 6.63), conductivity (42.62 to 521.70 μS/cm), nitrates (6.814 to 21.486 mg/L), chlorides (69.449 to 148.819 mg/L), sulphates (15.876 to 117.687 mg/L). The findings in this study indicate that the problem of lead poisoning is ongoing in Ivo local government area. Ebonyi State authorities should address the challenge through sustained periodic assessment and cleanup of affected areas. Implementation of safer mining practices should be enforced immediately.

***Keywords:** AAS, Contamination-Factor, Geo-accumulation, Heavy metals, Mining*

BE_004: Harnessing Microbiome-Based Biotechnologies for Improvement of Soil Health

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The use of microbiome-based biotechnologies to enhance soil health is explored in this research. The soil microbiome is the totality of microorganisms in the soil environment which is essential for performing a variety of functions that support plant growth, including nutrient fixation, solubilization, and mobilization, hormone and antibiotic synthesis, and pathogen and insect suppression. The soil microbiome can be exploited in a variety of ways to enhance agriculture. Additionally, carbon sequestration, greenhouse gas emissions, and soil nutrient cycling are all impacted by soil microbiota. However, the natural equilibrium of soil microbiota has been disturbed by contemporary agricultural practices, resulting in soil degradation and decreased productivity. In order to repair and improve soil health, this study discusses current developments in microbiome-based biotechnologies, such as microbial inoculants, biofertilizers, biostimulants, and other bio-innovations. The potential advantages and disadvantages of the approaches are examined, along with the significance of taking the ecological context and long-term sustainability of microbiome-based technologies into consideration in the use and deployment of these approaches. In general, the review reveals that utilizing microbiome-based biotechnologies have considerable promise for enhancing soil health and advancing sustainable agriculture.

***Keywords:** Microbiome, Biotechnologies, Soil Degradation, Soil health and Sustainable Agriculture*

SUB-THEME 03:
BIO-INNOVATIONS IN FOOD AVAILABILITY AND SAFETY
(BF - GREEN & YELLOW BIOTECH)

BF_001: Enhancing Pearl Millets' Resilience in Nigeria: CRISPR-Cas9 Promising Prospects

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Pearl millet (Pennisetum glaucum L. R. Br) is one of the most important cereal crops in Nigeria, it is a major source of food and beverage for over 40 million subsistence farmers living in the most marginal agricultural lands of Northern Nigeria. It is a crop of choice because of its nutritional benefits and ability to withstand drought and adverse agro-climatic conditions. Nigeria is the second-largest producer of pearl millet globally, with a tremendous amount of pearl millet diversity. However, there are challenges still affecting pearl millet production. Low yields are mainly due to the effects of climate change such as short and unreliable rainy seasons, frequent dry spells, droughts, declining fertility of soils and poor crop management. Recently, climatic conditions are causing the frequency and severity of drought events. The United Nations declared 2023 the year of millet, bringing more focus on millet improvement. There is a need to improve pearl millets resilience for food security in the future. CRISPR/Cas9 has brought revolutionary changes to agricultural and plant science research. CRISPR-Cas9 technology is the most effective gene editing system for functional genomic studies, trait improvement, and breeding in common cereal crops like rice, maize, and wheat. The development of a highly efficient gene editing system using the CRISPR/Cas9 system has been reported for foxtail millet, it is the only millet in the gene editing works for now. The potential application of CRISPR-Cas9 holds great promise for improving drought tolerance in pearl millet. This paper highlights the potential of CRISPR-Cas9 in enhancing drought tolerance in pearl millet cultivars adapted to Nigerian agro-ecological conditions.

***Keywords**: CRISPR-Cas9, Drought Tolerance, Food Security, Gene Editing, Pearl Millet*

BF_002: Assessment of Factors Mitigating Farmers' Adoption of New Varieties of Cassava in Benue State

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Most farmers lose interest in the adoption of new varieties of agricultural products globally due to fear of uncertainties such as low yield, consumer acceptability, post-harvest losses, and others. The study evaluated constraints against farmers' adoption of new varieties of cassava in Benue State with the use of a structured randomly cohort questionnaire and interview, 336 farmers were selected from four (4) Local government areas of Benue State and factors militating the adoption of the new varieties of cassava TMS 98/0505, TMS 0581, TMS 30572, TMS 01/1368, TMS 96/1632, TMS 92/0326, TME 419, NR 8082 were identified and ranked. A high percentage (93%, 342) of the improved varieties could not be stored for a long period of time (1st) and no market to sell increased quantity of cassava roots (93%, 342) (2nd). Poor extension contact (88%, 321) was a prevalent factor hindering adoption (3rd); followed by lack of access to credit facilities [(87%, 319) (4th)]. Also, the use of crude implement [(86%, 316) (5th)] was identified as part of the constraints. The farmers complained that the improved varieties were too watery [86%, (300)] ranked 6th, while poverty (80%, 283) ranked 7th. High cost of labor and inadequate technical knowledge, which were 78% (287) and 78%, (287) respectively ranked 8th and 9th, while scarcity of farm inputs (58%, 212; 11th) was the least ranking factor. Adoption of new varieties of cassava has a significant impact on farmers' output and increased income in Benue State but its acceptability is influenced significantly by some factors such as availability of inputs/materials, affordability of the technology, funding, farming experience, acceptability/marketability and others which could be addressed.

Keywords: *Cassava, new varieties, mitigating factors, Benue State.*

BF-003: Comparative Assessment of Cassava Yield Before and After Introduction of New Varieties

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A comparative assessment of cassava yield after introduction of new varieties in Benue State was carried out using a structured randomly cohort questionnaire and interview, 336 farmers were selected from four (4) Local government areas of Benue State. Demographic assessment showed that 29% (106) of cassava farmers were within the age bracket of 40-49 years with mean age of 47 years. Gender distribution also showed that 57% (208) were male and 70% (256) of them married. Only 39% (144) had secondary education; with a mean farming experience of 14 years. A total of 54% (197) of the farmers had no extension visit, and 56% (206) had farm sizes between 1 to 5 hectares. A total of 74% (271) of farmers had cassava yield of 10,000kg and above. On the quantity of cassava produced before the adoption of improved cassava technologies, 33% (121) of the farmers produced 1001 – 5000 kg of cassava root, 45% (164) produced 5001-10000 kg and 22% (81) of the farmer produced above 10,000kg of cassava per year. The result showed that after the introduction of the new varieties of cassava, 74% (271) of the farmers had output of above 10,000kg; 19% (68) had outputs of about 5001kg - 10000kg and only 7% (27) of the respondents had output of about 1001kg - 5000kg. This implies that there was an increase farmers output as a result of adoption of the newly introduced varieties of cassava in Benue State.

Keywords: *Comparative assessment, cassava yield, new varieties, Benue State.*

BF_004: Morphological Characterisation and Cyanide Content Determination in Phaseolus lunatus Linn. (Lima Beans) Accessions

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Lima bean (Phaseolus lunatus Linn) is one of the important legumes in developing countries. A total of 15 Lima bean accessions were laid out in Complete Randomised Design with three replicates. Morphological characters/traits were evaluated based on the descriptors proposed by the International Plant Genetic Resources Institute, while six of the accessions having the best yield, moderate yield, and lowest yield were selected for cyanide determination. The result showed that the accessions varied morphologically. The highest yielding accessions were TPl-2429, 2005- 014, 2006-003A, and 2005-011, while 2006-003B and TPl-178 had moderate yields. Accession 2005-014 had the highest growth characters, followed by 2006-015 and 2006-003A which showed good quality. Lower amounts of cyanide were detected in 2005-014 and PS-16 accessions, while 2006-003A, 2006-003B and 2006-005A accessions did not show cyanide contents. Therefore, TPl-2429, 2006-003A and 2005-011 accessions which showed higher growth and yield characters with no cyanide content could be further improved in breeding of lima beans.

Keywords: *Breeding, cyanide, lima beans, morphological traits*

BF_005: Application of silver nitrate and silver nanoparticles on Fusarium wilt severity and fruit yield of tomato

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Fusarium oxysporum f.sp lycopersici is a serious causal agent of Fusarium wilt that reduces the yield of tomato in many growing regions of the world. This study was conducted at the Federal University of Agriculture, Abeokuta, Ogun State in 2022 to examine the influence of silver nanoparticles (AgNPs) and silver nitrate (AgNO3) in managing Fusarium wilt on wilt-endemic sites. Data were collected on plant height (cm), number of leaves, branches, tomato fruits, fruit yield (t/ha), disease incidence, and severity. The experiment was laid out in Randomized Complete Block Design with three replicates. Results indicated that, at the 8th week after transplanting (WAT), the highest plant height of 206.67 cm in AgNPs-treated UC82-B was significantly different from plant height of 54.43 cm and 71.17 cm, recorded for Roma VF and UC82-B in untreated control plots, respectively. Also, the highest number of leaves (65.33) recorded in the UC82-B tomato plot treated with AgNPs, was significantly different from the number of leaves (31.00) observed in the UC82-B untreated control tomato plot. The least disease severity (2.00) recorded for AgNPs-treated UC82-B tomato was significantly lower than the highest disease severity of 6.00 recorded in untreated control plots for both Roma VF and UC82-B, respectively. The highest tomato fruit yield (3.25 t/ha) observed when UC82-B was treated with Carbendazim, followed by 3.21 t/ha with Carbendazim-treated Roma VF, were not significantly different from 1.92, 2.85, 1.99 and 2.90 t/ha fruit yield for AgNO3-treated Roma VF, AgNPs-treated Roma VF, AgNO3-treated UC82-B and AgNPs-treated UC82-B, respectively. Data were subjected to analysis of variance (ANOVA) using Statistical Analysis System (SAS), 9.1 package, and means were separated using the Duncan's Multiple Range Test ($p \leq 0.05$). Though both AgNO3 and AgNPs exhibited promising potential against Fusarium wilt and increased fruit yield compared with untreated control plot, AgNPs was more effective and comparable to the standard fungicide.

Keywords: *Nanoparticles, nitrates, silver, tomato, wilt.*

BF_006: Optimization of Loop-Mediated Isothermal Amplification (LAMP) Assay for Detection of Yam Mosaic Virus

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The traditional polymerase chain reaction (PCR) is time-consuming because of its multiple thermocycling stages and is not suitable for urgent pathogen detection in food security. To overcome these limitations, this study aimed to find an optimal and practical method for on-field detection of yam mosaic virus (YMV) using Loop-Mediated Isothermal Amplification (LAMP). Six YMV primers were designed based on the published sequences of the virus (GenBank accession no. MT542849.1) using the NEB® LAMP Primer Design Tool. The primers included forward and backward inner primers (YMVFIP and YMVBIP), two outer primers (YMVF3 and YMVB3) and two loop primers (YMVLF and YMVLR). A 10X LAMP primer mix was prepared by reconstituting the primers. Infected yam plant leaves were collected and used as samples. The samples were divided into two groups, one re-suspended with distilled water and the other with extraction buffer. Controls were included, and all samples were centrifuged. Each sample was prepared in triplicates. The reaction mixture (25µl) contained Warm-Start Colorimetric LAMP 2X Master Mix (New England BioLabs), LAMP primers, plant samples, and molecular-grade water. The reaction tubes were then placed in a heating block at 37°C for 1 hour, and positive samples showed a colour change from pink to yellow. Notably, no difference was observed between samples diluted with extraction buffer and those diluted with water, which offers an extra advantage for on-site detection. Based on the results, this single-tube LAMP method can effectively detect suspected yam mosaic virus infections in the field. It holds promise in facilitating prompt decision-making for virus control measures, benefiting farmers and enhancing food security.

Keywords: *Loop-Mediated Isothermal Amplification (LAMP), Yam mosaic virus, Pathogen detection, Food security*

BF_007: Evaluation of Nutrients and Functional Properties of Jatropha tanjorensis and Telfairia occidentalis Leaves

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Jatropha tanjorensis and Telefairia occidentalis are common plants used locally as nutraceuticals. Freeze-dried powdered Jatropha tanjorensis (FDJ) and Telfairia Occidentalis (FDT) leaves were analyzed for proximate, vitamins (A and C), minerals (Fe, Zn, and Cu), functional properties [water absorption capacity (WAC), swelling property (SP), and wettability (WT)] and microbial count. The analyses were conducted in a laboratory, following AOAC standard procedures. The proximate showed that FDT had significantly ($p<0.05$) higher proteins (34.99 %) and fibre (10.00 %) contents than FDJ (29.89 %) and (9.51 %) while FDJ had higher moisture (6.25 %), and carbohydrate (40.39 %) content than FDT (3.00 %) and (37.97%) respectively. The ash for FDJ (12.98 %), FDT (13.00 %), and fats contents FDJ (1.00 %), FDT (1.05 %) were not significantly different. The FDT had higher vitamin A (9.63 mg/100 g) than FDJ (8.57 mg/100 g) while FDJ had higher vitamin C content (12.15 mg/100 g) compared to FDT (6.72 mg/100 g). Iron contents for FDJ (4.20 mg/100 g), copper (1.03 mg/100 g) and zinc (10.25 mg/100 g) were significantly higher than FDT (3.10 mg/100 g), (0.98 mg/100 g) and (4.93 mg/100 g) respectively. FDT showed significantly higher WAC (3.90 g/cm) and WT (2.79 s) compared to FDJ (3.20 g/cm) and (1.95 s), FDJ however, had significantly higher SP (3.55 %) than FDT (2.25 %). The bacterial and fungal counts for both plants were within the range of 10^5 CFU/g, no physical mould growth was observed throughout the 4 weeks of the experiment period. These findings highlight Jatropha tanjorensis and Telefairia occidentalis as nutraceuticals that can provide essential nutrients for health enhancement and management of diseases such as anaemia.

Keywords; *Nutrients, Neutraceutical, Anaemia, Jatropha tanjorensis, Telfairia occidentalis*

BF_008: Rice Flowering Locus T1 (RFT1) Gene Delay Flowering in MR219 Indica Rice

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Rice is one of the staple foods that contribute significantly to global food security. In countries, rice occupies the commanding height of staple food basket. However, local rice production fails to satisfy domestic demand which is hampered by the low yield and poor amenability to genetic transformation. This study sought to address these challenges by identifying the most efficient method for indica rice transformation to transgenic recovery. MR219 Malaysia wetland rice was used for shoot apex induction. RFT1 gene from Wai upland rice was constructed into pCAMBIA1305.2 expression vector. The construct was further mobilized into Agrobacterium tumefaciens LBA4404. Five-day-old shoot explants were used for transformation with A. tumefaciens LBA4404 harbouring pCAMB::RFT1 construct. The transformants were analyzed for transient expression and stable integration of transgenes and histochemical analysis. Optimum shoot apices regeneration frequency of 71.64±0.74% was recorded in MS medium supplemented with 3 mg/L TDZ and genetically transformed. pCAMB::RFT1 construct was successfully developed and transformed into MR219 rice. The molecular analysis of the transgenic rice confirmed the integration of the RFT1 transgene, hpt and GUS gene into the To plant. Histochemical and PCR analyses of established transgenic MR219 also confirmed the presence of the transgenes. Total transformation efficiency was recorded in the range of 12.5±5.37% to 17.5±4.91%. Fully matured transgenic rice with well-developed tillers was obtained but with no panicle at 16 weeks, while MR219 shows ranges of flowering duration between 72 to 93 days. This is the first report of full-length RFT1 gene isolation from upland rice cultivar and transformation into MR219 shoot apex. The findings from this study could serve as insight for further genetic manipulation and a fundamental stage for producing transgenic rice.

Keywords: *MR219 Rice; Wai upland rice; Shoot Apex; RFT1 Gene; Flowering*

BF_009: Advancements in Cowpea Research: Exploring Insect Resistant Genes for Improved Production in Nigeria

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Cowpea, a native African crop, holds great significance as the primary grain legume in Nigeria. As a vital source of affordable protein and animal feed, it plays a crucial role in nutrition. However, the production of cowpea in Nigeria faces significant challenges due to the prevalence of pre-harvest and post-harvest insect pests, including Aphids, Maruca pod-borers, and Bruchids. Numerous approaches have been employed to control pest infestation, including the use of pesticides, cultural practices, and biological control methods. However, these methods have not proven entirely effective. Consequently, host plant resistance through genetic control emerges as the most promising and efficient strategy for managing insect pests in cowpea production. Research focused on screening the wild variety of cowpea has revealed the presence of genes conferring resistance to pests within the gene pool. Notably, Nigeria has made significant advancements in developing cowpea varieties with resistance against pod-borer. SAMPEA 20-T, a transgenic variety, has been successfully created, providing an affordable, safe, and economically viable solution against the pod-borer pest. However, challenges remain in finding effective solutions for other insect pests and stored grain pests, such as bruchids or cowpea weevils. This review highlights the progress of research conducted in Nigeria, showcasing recent advancements in addressing cowpea production challenges and the integration of gene editing techniques to develop improved cowpea varieties resistant to insect pests.

***Keywords:** Cowpea, Insect resistance, Gene editing, Insect pests*

BF_010: The Dynamics of Indigenous Wild Yeast Behaviours during Fermentation and their Suitability for Local Food Industry

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Owing to the relevance of small and medium scale industries in Nigeria, the increasing cost of foreign importations and urbanization, we studied the dynamic behavior of some wild yeasts during spontaneous fruit juice fermentation at a flask shaken level using standard model in the laboratory. Twenty-eight (28) wild yeasts were isolated and characterized from spontaneous fermentation of seven (7) homemade fruit juices (Sweet Orange, Pineapple, amongst others) respectively. Nine (9) had some unique characteristics that could be considered for industrial applications which were further investigated using culture-dependent method in a shaken flask fermentation as well as Durham's tube in test tube in order to determine their CO2 production abilities. In order of occurrence and dominance were Saccharomyces cerevisiae, Kluyveromyces marxianus, Rhodotorula mucilaginosa, Pichia caribbica, Candida tropicalis. Saccharomyces cerevisiae strains SC02, SC13, SC09 and SC11 had high dough-raising capacity, versatile sugar utilization profile, high-temperature ethanol fermentation ability, non-hydrogen sulphide producing, remained active at high salt and sugar concentrations. Rhodotorula mucilaginosa RT07 and RT15 were also found. In conclusion, the result was that chemical leavening agent could be replaced with these isolated yeast strains owing to their records. Also, the isolated R. mucilaginosa could be utilized in other functional bio-products.

Keywords: *Bio-ethanol, Dynamics, Fermentation, Yeasts, Spontaneous.*

BF_011: The Assessment of Yield and the Nutritive Value of Capsicum Varieties in Keffi, Nasarawa State

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Capsicum species are essential for their economic value and nutritional benefits. These versatile peppers can be used in various ways - fresh or dried, ground or whole, and alone or in combination with other flavourings. Recent yield improvement programs have shown that certain genotypes of Capsicum perform better than others under specific environmental conditions, including temperature, climate, soil type, and disease resistance. This research was carried out to assess the yield of different varieties and the nutritional value of Capsicum varieties in Keffi, Nasarawa State, Nigeria. The research was conducted at the Plant Science Farm of the Nasarawa State University in Keffi in 2015 cropping season. Four (4) pepper varieties, namely 'Shombo', 'Atarugu', 'Tatase' and 'Chili', were evaluated for yield and nutritive content. The different varieties were grown separately in a nursery, transplanted and nurtured to maturity in the main field in a Randomized complete block design (RCBD) with three replications, and each replicate contained four plots. Proximate analysis was conducted on the peppers at harvest to determine its nutritive content. Data were collected on growth and yield parameters such as plant height (cm), number of fruits per plant (no), number of leaves (no), number of flowers (no), number of branches(-no), fruit length (cm), fruit weight at maturity (g),yield (kg/ha). The collated data were analyzed statistically using the Analysis of Variance (ANOVA) and significant means separated using Least significant difference (LSD) at ($P \leq 0.05$) with the Statistical Analysis System (SAS) version 9.0 Software. Results showed farmers could optimize their yields and produce high-quality peppers for various applications by carefully selecting suitable Capsicum cultivars. All four pepper varieties had good yields however Tatase produced the highest yield with 845.6kg/ha and chili had the least at 622.2kg/ha. Tatase is recommended for commercial production in Keffi, Nasarawa State.

***Keywords:** Capsicum spp, Nutrition, Yield, Varieties*

BF_012: Morphogenetic Studies of Northern Nigeria Garlic for Breeding Programmes, Sustainable Food Availability and Security

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Garlic is an important crop grown in the Northern part of Nigeria, which is consumed by every household for its various benefits. This study aims at determining the relationship among the garlic accessions using their phenotypical characteristics such as plant height, number of days to maturity, number of leaves per plant, leaf length, leaf area, leaf area index, plant stem external diameter, clove width, 100 clove weight, clove length, bulb length, bulb width, bulb neck, total bulb weight, shoot dry weight, shoot fresh weight, bulb fresh weight, bulb dry weight and emergence percentage. The bulb of 45 garlic accessions were purchased from the local farmers from Bauchi, Bornu, Kaduna, Kano, Sokoto and Zamfara States. The bulbs were sown at the Institute for Agricultural Research Horticultural Unit experimental field, ABU, Samaru, with one bulb per hole in a randomized completely block design with three replications. The mean performance value for each morphological character at maturity was used to construct the dendrogram using the SAS GLYM 2 R-Square stat (R version 4.1.2). The results revealed two main groups with four subgroups, which exhibited significant genetic variation and fractional similarities among the accessions. Group one possessed significant trade processing value, while group two had the least. The classification for the groups cut across different locations, which makes it ideal cultivars for investigating heritage and diversity for food production and improvement. Hence, the characteristics (plant height, number of leaves, leaf length/area, clove weight/length, bulb length/width, bulb weight and dry weight can be use for selection and assessment in Northern Nigeria garlic in the breeding program.

***Keywords:** Garlic, Phenotype, Diversity, Breeding, Food sustainability*

BF_013: Evaluation of Pests and Diseases on the Yield of Watermelon Varieties in Keffi, Nasarawa State

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Watermelon (Citrullus lanatus Thumb.) is a delicious and nutritious fruit that is highly appreciated by consumers due to its high water and carbohydrate content, as well as its delicate texture and sweet taste. The fruit is susceptible to diseases and pest attacks, especially if planted in soils with previously recorded pest infestations or if planting operations are improperly handled. To further understand the effect of pests and diseases on the growth and yield of watermelon varieties, a study was conducted at the Biotechnology Garden of Nasarawa State University, Keffi, during the 2015 cropping season. Four varieties were used for the study: Kaolack, Crimson Sweet, Super Tresor and Sugar Baby, and examined for resistance to the Melon aphid pest (Aphis gossypii Glover). The experiment was laid out in a Randomized complete block Design (RCBD) with three (3) replicates, each replicate containing four beds. Growth and yield parameters such as number of leaves (no), number of fruits per plant (no), average fruit length (cm), average fruit width (cm), and yield per hectare (kg/ha) were collected, subjected to analysis of variance (ANOVA) and significant means separated using Least significant difference (LSD) at ($P \leq 0.05$) with the Statistical Analysis System (SAS) version 9.0 Software. The results showed that Super Tresor had the highest resistance to the Melon aphid pest, with a yield of 752.33 kg/ha, while Kaolack had the lowest resistance and yield of 519.77kg/ha. In the overall, this research demonstrates that watermelon is a fruit that can be grown successfully in Keffi, Nasarawa state, under good growth and soil conditions and provide substantial nutritional benefits in the study area.

Keywords: *Watermelon, Pests, Diseases, Yield*

BF_014: Attributes of Stored Human Urine in Soil on Talinum fruticosum L. Plant

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The amelioration of stored human urine on Talinum fruticosum growth is dependent on the quantity applied to the soil. This study evaluates the function of 17 days of stored human urine applied to the soil in improving Talinum fruticosum planted in 620.10 and 360.10-mL soil compared to control (0 mL) soil. The urine was urinated by the Correspondent Author and the counting started after 4 days of urination (5:30 – 6:00 am) until 17 days, 0, 360.10, and 620.10 mL of the urine were prepared, each solution (mL) was measured, and applied to each pot containing 9.0 Kg soil, and 21.50 cm depth. The parameters acquired before commencing the experiment were soil: pH (4.0), sulphur, phosphorus (mg/Kg), nitrogen (%), chloride, nickel, manganese, lead, iron, vanadium, cadmium, boron (mg/Kg), and further soil parameter was obtained for cation exchange capacity: calcium, magnesium, potassium, sodium (1.54 meq/100), and microbial population. Plant parameters at 30 days of growth were: height, stem girth, number of leaves, number of branches, leaves chlorophyll content, and morphology. The results obtained showed that: 620.10 and 360.10 mL of the stored urine soil enhanced the plant height and stem girth when measured with a centimeter tape, enhanced number of leaves and branches when counted, significantly enhanced the leaves chlorophyll content when measured with a spectrophotometer, and enhanced the plants morphology when visually observed. The study revealed that the application of specific stored human urine to unfertile agricultural soil will enhance Angiosperms plant growth. Farmers who are harvesting low-farm produce can apply this study methodology to a bigger plot of farmland to achieve great economic production.

***Keywords:** Attributes, human urine, soil, and Talinum fruticosum*

BF_015: Zinc Oxide Nano Packaged Films Maintained Quality And Post-Harvest Fungi Contamination Of Beans

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Bean is one of the most important sources of dietary protein for human and animal nutrition. Packaging of beans is done to prevent fungi infestation which is detrimental to human health and can reduce its market value leading to economic loss. Therefore, this study is aimed at evaluating the proximate composition and the mycological assessment of beans packaged with Zinc oxide nano-composite film. Approximately 50g of beans were packaged using biosynthesized zinc oxide nano-composite film, polyethene, starch film, Neem and zinc oxide nanoparticle and were stored for 30 days. The proximate and fungi analysis were carried out using standard procedures and serial dilution technique procedures respectively. The result obtained showed that the polyethene packaged beans had the highest moisture content than others (16.50 ± 0.50%), compared to the control (unpackaged beans) (4.33± 0.02%). The unpackaged beans had the highest ash content, protein content and carbohydrate content (4.40± 0.10%, 24.17± 0.15% and 61.23± 0.21%). However, beans packaged with zinc oxide nano-composite film had (3.73± 0.12%, 22.10± 0.10% and 60.77± 0.76%). The unpackaged beans with the beans packaged with polyethene, starch film and Neem had the total fungal count (23.5×104 cfu/g, 1.5×104 cfu/g, 28×104 cfu/g and 1×104 cfu/g) respectively, with no microbial growth in the zinc nanofilm packaged beans. The microorganisms isolated include Mucor species, Aspergillus niger, Aspergillus flavus, Aspergillus fumigatus. Therefore, this study suggests that the zinc oxide nano-composite film was a better packaging material because of its anti-microbial activities.

***Keywords:** Mycological assessment, proximate analysis, common beans.*

BF_016: Screening of Lactic Acid Bacteria Isolates from Some Fermented Foods for Potential to Produce Bacteriocins

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Bacteriocins from lactic acid bacteria are ribosomally synthesized low-molecular-weight peptides or proteins with potential use in food preservation due to their bactericidal effects on food spoilage and pathogenic organisms. This study was carried out to obtain strains of lactic acid bacteria from some Nigerian fermented foods (Nono, Daddawa, wara, Kunun zaki, Kunun aya) with the potential for the production of bacteriocins. Fifty (50) isolates of LAB were obtained from the fermented foods based on colonial, cell morphology, and biochemical characteristics. The research was conducted in the Centre for Genetic Engineering and Biotechnology, Federal University of Technology Minna, Niger state. The research was carried out within six months. The isolates were tested for inhibitory activity against food-borne bacterial pathogens (FBBP) (Staphylococcus aureus, Pseudomonas aeroginosa, Escherichia coli, Bacillus subtilis) by agar well diffusion assay. Lactic acid bacteria having the highest inhibitory activity were identified using 16SrDNA sequencing. Lactic acid bacteria having an inhibitory activity (3 isolates) in the FBBP were identified as Lactococcus lactis, Lactococcus garvieae, and Lactococcus hordniae. It was observed that the antibacterial activity ranged from 9.0 mm to 15.0mm after 24 hours of incubation, with Lactococcus hordniae having the highest summed-up inhibitory activity of 52mm, followed by Lactococcus garvieae,(49mm) and Lactococcus lactis (48mm). The bacteriocins elaborated by lactic acid bacteria can be used as a biopreservative in fermented foods.

Keywords: *Bacteriocins, Fermentation, Lactic acid L*

BF_017: Intra-Specific Flavonoid Classes, Content and Relationships in African Yam Bean (Sphenostylis stenocarpa [Hochst ex A. Richmond] Harms] Tubers

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Tubers of African Yam Bean [Sphenostlis sternocarpa (Hochst. ex A. Richmond) Harms], from family Fabaceae, are under-exploited especially in West Africa by human. The tuber holds varying quantitative bioactive properties. The present study seek to unveil inherent flavonoid compound in different accessions of African yam bean (AYB) tubers. Fresh tubers were obtained from 17 accessions of AYB. The same were dried and flour samples were prepared. Flour samples from the 17 accessions were analyzed and 38 flavonoid compounds were obtained for each using high performance liquid chromatography (HPLC). The 17 accessions differed in the proportion of each of the 38 flavonoid contents. The highest flavonoid was observed to be Apigenin (2.393g/100g), Didymin (2.353g/100g), Daidzein (2.232g/100g), Luteolin (1.743g/100g), Isorharmmetic (1.370g/100g). Hesperidin (0.001g/100g), Fisetin (0.002g/100g), Rhamnazin (0.003g/100g), Genistein (0.004g/100g), Glycitein (0.004g/100g) and Eriodictyol (0.005g/100g) were found to be the least. These were further grouped into six sub-classes. Flavones were found to be the highest (55%) and anthocyanidin was the lowest (1%) in the tubers of African yam bean. Within each sub-class, all paired correlations were positive and their proportion of significance were: Flavon-3-ol (100%), isolafove (100%), flavone (69%), flavonone (64%) and flavonol (20%). Flavonoid in AYB was significantly higher than most tuberous crops, hence its alternative use as the industrial crop is much more promising for health benefits. TSs 57 had the highest (14.037g/100g) total flavonoid composition, hence its cultivation and utilization are highly encouraged.

Keywords: *African yam bean, bioactive compounds, flavonoid, health benefits, tubers*

BI_018: Development and Optimization of Crosslinked Starch/Graphene Oxide Bioplastic Film for Fruits and Vegetable Packaging

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The environmental hazards associated with non-biodegradable plastic materials is a huge global challenge which has prompted research into the development of different biodegradable plastic materials. The use of starch films for packaging has been recommended, however they are characterized by poor mechanical properties and low water stability. This study was aimed at improving the properties of cassava starch films using a combination of green crosslinking and the introduction of graphene-oxide nanoparticles for potential application in fruits and vegetable packaging. Cassava starch was crosslinked with oxidized sucrose and the effect on some physicochemical properties was determined. Graphene oxide was synthesized using hummers method and optimization was carried out using Design Expert software for different responses including mechanical properties, barrier properties, film solubility and antimicrobial activity. The results of the physicochemical parameters showed that an amylose content of 20.78 %, a degree of substitution of 0.406, a degree of crosslinking of 27.4 % and a thermal degradation residual weight loss of 19.58 % (thermogravimetric analysis) were obtained after the crosslinking of cassava starch. In addition, the crosslinked starch had significantly ($P < 0.05$) lower solubility (20.85 %) and swelling power (5.62 g/g) indicating that crosslinking improved the properties of cassava starch associated with film strength and water stability. The average particle size of the synthesized graphene oxide was 65.2 nm and the optimal formulation for the crosslinked starch/graphene oxide (CS/GO) film as determined by the software had a model desirability of 73.1%. The film displayed antimicrobial activity with zones of inhibition between 6.2 and 23.7 (mm) against microorganisms isolated from deteriorated tomato fruit. This work concludes that the combination of green crosslinking and graphene oxide nanoparticles improved the properties of the cassava starch films for potential application in fruits and vegetable packaging.

Keywords: *Crosslinking, graphene oxide, optimization, oxidized sucrose*

BF_019: Nutritional Composition and Phytochemical Analysis of The Leaves Of Monkey's Potato (Solenostemon monostachyus (P. Beauv) Briq.)

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The nutritional composition and phytochemical analysis of the leaves of monkey's potato (Solenostemon monostachyus (P. beauv.) Briq.) was investigated in this study. The leaves were collected from the Biological garden at College of Education, Warri, Delta State, identified, air dried, powdered and then stored in airtight containers for analysis. Standard methods for proximate analysis were employed to determine the moisture content, total ash, crude protein, crude lipid and crude fibre composition. Standard methods for qualitative and quantitative phytochemical analysis were also used to determine the presence of reducing sugar, terpenoids, triterpenoids, steroids, phenolic compounds, flavonoids, tannins, alkaloids, saponins, anthraquinones as well as cardiac glycosides in S. monostachyus. Results from the proximate analysis of the leaves of Solenostemon monostachyus revealed the presence of moisture (9.29 %), total ash (5.23 %), crude lipid (4.27 %), crude fibre (7.00 %) and crude protein (5.55 %). Results from the qualitative analysis of the phytochemical constituents of the leaves of Solenostemon monostachyus detected the presence of Flavonoids, Tannins, Cardiac glycosides, Steroids, Saponnis, Phenolic compounds and Alkaloids in various concentrations. Quantitatively however, flavonoids had the highest concentration (26.59±0.01) followed by cardiac glycosides (20.58±0.18), Tannins (12.29±0.17), Steroids (4.44±0.06) and Saponins (2.72±0.02). Phenolic compounds had the lowest composition with 0.73±0.02. The presence of various nutritional and phytochemical components obtained in this study justifies the use of Solenostemon monostachyus leaves as a medicinal plant and also as a nutritious vegetable. Based on the result obtained, it is therefore recommended that S. monostachyus should be cultivated for its various nutritional and medicinal potentials rather than being treated as a weed.

Keywords: *Medicinal potential, Monkey's Potato, Nutritional Composition, Phytochemical Analysis.*

BF_020: Optimization of In-Vitro Micropropagation of Pineapple (Ananas Comosus)

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Pineapple (Ananas comosus) is an economically significant tropical fruit crop priced for its sweet flavor, high sugar content, and nutritional value. The demand for natural fruit concentrates to meet the needs of the expanding fruit juice industry in Nigeria requires the application of efficient rapid multiplication techniques to produce clean, high-yielding and elite planting materials. The in-vitro regeneration potentials of two pineapple parts; pineapple crown and pineapple sucker explants were assessed using varying concentrations and time of exposure to ethanol and sodium hypochlorite for sterilization; on full and half strength of the Murashige and Skoog (MS) medium. The leaves and stem were washed thoroughly and sterilized with ethanol (70% for 1 minute 95 % for 1 minute) and sodium hypochlorite (10 %v/v + tween 20 for 20 minutes, 50 %v/v + tween 20 for 10 minutes). Meristems were carefully excised from the sterilized plants under HEPA filter laminar flow-hood cabinet to ensure aseptic conditions. The meristem explants were then cultured on full strength MS medium supplemented with 5 mg/L BAP (6-benzylaminopurine) and transferred to the growth room. After four weeks, in-vitro plantlets were sub-cultured in full and half strength MS medium with varied concentrations of BAP (3.5 mg/L and 5 mg/L) for shoot multiplication. The results demonstrated that meristem explants from pineapple crown on half strength MS medium supplemented with 3.5 mg/L BAP yielded the most desirable outcome, with maximum shoot proliferation. The sterilized treatment with 95 % ethanol for 1 minute gave better results for both crowns and suckers.

Keywords: *Ananas comosus, crown, sterilization, sucker, BAP, shoot proliferation.*

BF_021: Distribution and Prevalence of Parasitic Nematodes of Cowpea (Vigna unguiculata) in Abuja, FCT

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Cowpea grain is a major food crop in sub-Saharan Africa, particularly in the dry savannah regions of Nigeria, high in protein (25%) and other nutrients including carbohydrate and vitamins. It is particularly vulnerable to root knot nematode and suffers from enormous infections, causing major economic loss. A survey was carried out on three (3) locations – Gwagwalada, Giri and Iddo all in Abuja, FCT, during rainy season to identify the prevalence and distribution of parasitic nematodes affecting cowpea root and the rhizospheric soil. Analysis was carried out on cowpea plant roots using direct examination method while sieving and decanting method was used for the rhizospheric soil samples. The nematode species were extracted and identified using a compound microscope at 10 x magnification. Images were then compared with documented literatures, Meliodogyne icognitta was the most prevalent nematode spp. in the roots and rhizospheric soil of the cowpea in the three (3) locations observed. For cowpea roots, Meliodogyne icognitta was 25 % in Gwagwalada, 24 % in Giri and 50 % in Iddo while for cowpea rhizospheric soil samples, Meliodogyne icognitta was 40 % in Gwagwalada, 50 % in Giri, and 55 % in Iddo. This result shows the predominance of Meliodogyne icognitta and may be responsible for the observed symptoms in the roots and rhizospheric soil samples of cowpea. This survey result has also shed light on the nematode's ecology and can be utilized to guide future study and control efforts.

***Keywords:** Meliodogyne icognitta, Microscope, Root, Soil, Vigna unguiculata*

BF_022: Assessment of the Effect of Boiling Time on Anti- Nutritional Compounds of Sweet Potatoes (Ipomi batata) and Cocoyam (Colocasia esculenta)

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Sweet potato, Ipomoea batatas is one of the main root and tuber crops commonly grown in the tropical and subtropical parts of the world. It was described as the seventh most important food crop in the world. Cocoyam is reported to have superior nutritional value over major root and tuber crops, especially in terms of their protein digestibility and mineral composition. In many tropical areas, cocoyam plays major role in the lives of many as a food security crop, mainly for smallholder farmers. These tubers with a considerable importance for food security are categorized under neglected and underutilized crops. This research was aimed to assess the effect of boiling time on antinutritional ccomponents of sweet potatoes and Cocoyam. The anti-nutrient was determined Quantitatively using standard procedure. The experiment was compltely randomizd. The results of the findings confirmed that anti-nutrient composition of boiled tubers of cocoyam for total and soluble oxalate contents ranged from 7.65±0.07 mg/100 g dw (dry weight) to 1.35±0.07 mg/100g dw for the cocyam and from 1.5±0.6 mg/100 g dw to 4.5±0.1 mg/100g dw during boiling times respectively. The flour from boiled cocoyam tuber at 10 hr had the highest total and soluble oxalate contents of 7.65±0.07, while the lowest total and soluble oxalate contents were obtained within the flour from cocoyam at 1hour with 1.35±0.07 mg/100 g. Furthermore, the reduction of soluble Oxalate content after the hydrothermal treatment seemed remarkable.

***Keyword:** Cocoyam, Sweet potatos Oxalate, tannin and phytate.*

BF_023: Red Pigment Dye Extracted from Beetroot (Beta vulgaris L.) as Alternative for Morphological Identification of Nematodes

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Laboratory experiment was conducted at the Biotechnology Advanced Research Centre, Sheda Science and Technology Complex, Abuja in June, 2023. Dyes are stains used to add colours to tissues and microbes to make them optically distinct. The harmful effects of some synthetic dyes evoked great enthusiasm in the scientific sphere to search for eco-friendly and natural colorants for morphological study and identification of microorganisms. Therefore, the objective of the study was to develop an alternative dye from the red pigments extracted from beet root (Beta vulgaris L.) The extract provides an eco-friendly alternative to chemical based stains, with an additional incentive of being cost effective comparatively.Dye was extracted from the roots using different concentrations of ethanol at 100, 80, 70, and 50%, respectively. Yam sample (Dioscoreacommunis) infected with nematode was extracted in a suspension and a drop of the extracted dye was used to stain the sample. The slides were visualized under a binocular microscope. The aim was meant to assess the ability of each dye concentration to visualize the presence of nematodes and their ova from the sample and to clearly define their morphology. The result revealed that absolute ethanol (100%) extraction of the plant gave the best clear view of the nematode stained with the extracted dye while 80%, 70%, and 50% ethanol concentrations stain gave a fair visualization. Therefore, it could be recommended that the alternative eco-friendly dye which providedthe best support to environmental sustainability be adopted by farmers.

Keywords: *Alternative dye, Beet root, Ethanol, Red pigments, Yam.*

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BF_024: Molecular Variation and Genetic Divergence in T. Aman Rice Genotypes Using SSR Markers

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Transplanted (T.) aman rice (Oryza sativa L.) covers the largest cultivated area in Bangladesh whilst very little information on the molecular level characterization of T. aman genotypes persists. The major aim of this study was to dissect molecular characterization and genetic diversity of 25 T. aman rice genotypes using twelve simple sequences repeats (SSRs) markers. The rice genotypes comprised local landraces that were collected from twelve districts of Bangladesh. A total of twelve SSR primer pairs covering all 12 chromosomes of rice were selected for the study. The molecular characterization, genetic diversity, population structure, and principal component analysis were estimated and the results revealed a total of fifty alleles across 12 loci ranging from 2 (RM411) to 7 (RM252) per locus. The maximum gene diversity was exhibited in RM252 (0.7) while the minimum was in RM320 (0.15). The polymorphism information content (PIC) values ranged from 0.14 to 0.67 while RM252 and RM206 were identified as the most suitable markers. Clustering based on unweighted pair group method with arithmetic mean (UPGMA) analysis clustered 25 genotypes into six major clusters (I-VI) with a similarity coefficient value 0.34. Cluster V contained a maximum of seven genotypes with 5 sub-groups. Again, the population structure displayed 3 populations namely populations 1, 2, and 3. These populations were clustered into the 3 major groups in the Principle Component Analysis (PCA) 2D plot. Here, PC1 and PC2 contributed 32.7% variations. Overall, the hybridization suggested between the genotypes of populations 1 and 3, specifically between clusters I and cluster VI. Again, between the diverse parents such as, genotypes Bohi Trimota and Ranga, Bohi Trimota and Purple Rice-2, Bohi Trimota and Purple Rice-3. These diverse clusters and genotypes identified through SSR makers lay the foundation for molecular characterization of T. aman rice genotypes in Bangladesh and further marker-assisted studies will be suggested.

Keywords: *Molecular variation, genetic divergence, aman rice, genotypes, landraces*

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BF_025: Achieving Optimal Soybean Yields through Inoculation and Phosphorus Efficiency in the Southern Guinea Savannah of Nigeria

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Soybean, scientifically known as Glycine max (L.) Merrill is a remarkable crop as it holds significant global economic importance because of its versatility and high market value. Field experiments were conducted during 2020, 2021, and 2022 cropping seasons at the Research farm of the Faculty of Agriculture, University of Abuja, Gwagwalada, located in the Southern Guinea Savanna of Nigeria. The study aimed to evaluate how inoculation (Bradyrhizobium japonicum) and Phosphorus rates affected the optimal production of different varieties of soybeans. The treatments consisted of three Soybean varieties: TGX 1485-1D, TGX 1448–2E and TGX 1987–10F. Two levels of inoculant (control, with inoculant) and three levels of Phosphorus fertilizer (0 kg/ha, 20 kg/ha, 40 kg/ha). The experiments were laid in a 3 x 2 x 3 factorial in a randomized complete block design, with three replicates and 54 plots. Growth parameters such as the number of leaves, number of branches, leaf area index, Stem diameter (cm), plant height (cm), and yield parameters such as number of nodules, number of pods per plant, number of seeds per pod, biomass (kg/m2), 100 seed weight (g), grain yield (kg/ha) were collected. Collated data were subjected to analysis of variance (ANOVA) using the ‘agricolae’ package in the R Statistical Programme (R version 4.2.2), Duncan Multiple Range Test (DMRT) and Standard error (SE) were used to separate means at ($P \leq 0.05$). Correlation studies was also conducted to know the relationship within the parameters. Varieties TGX 1987-10F or TGX 1448-2E, in combination with inoculation, and a Phosphorus rate of 40 kg/ha, produced the highest yield of up to 30% above control. Therefore, this could be recommended for optimal yield and profit for Soybean farmers within the study area.

Keywords: *Soybean, Inoculation, Phosphorus efficiency and Varieties*

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BF_026: DNA Barcoding of Sesame Accessions from the Six Geo-Political Zones in Nigeria

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This research aims at closing the gap on DNA barcoding of Nigerian sesame. In achieving this, twenty five accessions of sesame were collected from the six geopolitical zones and five improved accessions were also obtained from National Cereal Reseach Institute, Badeggi, Niger State. DNA extraction and amplification using chloroplast DNA (cpDNA); ribulose-1, 5-bisphosphate carboxylase (rbcL) marker was carried out. Phylogenetic relationships were determined using neighbor joining method. The rbcL sequences were further subjected to authentication through the National Center for Biotechnology Information (NCBI) using Nucleotide Basic Local Alignment Search Tool (BLASTN). Total length of sequence alignment of 568, conserved sites of 566 and variable sites of 2 were observed in this study. Transversional mutation of A/C at consensus position of 11 was observed in four accessions while ten accessions exhibited deletion at position 385. BLAST analysis of total bit score, query coverage, and percentage identity were in the ranges of 974 - 1009, 99% to 100% and 98.93% to 100%, respectively. BLAST hits obtained for the 29 accessions considered in this study showed high level of similarity matches to Sesamum indicum already annotated and deposited in NCBI database. This revealed the need to consider other molecular markers for proper identification of Nigerian sesame.

Keywords: *DNA barcoding, rbcL, Transversional, BLAST, Sesamum indicum*

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BF_027: Metabolomics evaluation and health impacts of small-scale gold mining on local avifauna (Gallus Gallus domesticus) in Osun state

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Artisanal and small-scale gold mining (ASGM) operations can significantly harm animal health by causing environmental changes. As a result, the levels of metabolites involved in energy metabolism might be altered over time. This is because energy that should be utilized for maintenance or other objectives may instead be used to deal with stress. While metabolomics techniques are increasingly being used to analyze environmental stressors, their use to study stress in birds is still in its early stages. We examined the metabolic response in free-ranging hens (Gallus Gallus domesticus) in the Ilesha gold mining areas using proton Nuclear Magnetic Resonance (NMR) spectroscopy. Robust metabolic pathway analysis was performed using Metaboanalyst 5.0. In accordance with this study, physiological stress causes free-ranging hens from Ilesha gold mining locations to shift their energy metabolism and create distinct metabolite profiles from control chickens. A metabolic investigation found that the metabolites glucose, pyruvate, lactate, glutamine, -hydroxybutyrate, succinate, oxoglutarate, alanine, valine, leucine, and 6-phosphogluconic acid were perturbed due to ASGM activities. The disturbance of these metabolites in the study animals affects the energy-producing metabolic pathways that use them as substrates or intermediates. As a novel technique, metabolomics holds promise for detecting and explaining the physiological responses of free-range chickens to stressors.

***Keywords:** Artisanal and small-scale gold mining, energy metabolism, stress physiology, metabolomics*

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BF_028: NMR-Based Metabolomics in Food Microbiology: Unveiling the Hidden Biochemical Landscape

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Nuclear Magnetic Resonance (NMR) spectroscopy has become a crucial analytical technique in food microbiology, notably for metabolomic profiling. This study provides a thorough analysis of the use of NMR-based metabolomics in investigating the biochemical aspects of food microbiology. NMR offers important insights into microbial metabolic pathways, their reactions to environmental changes, and interactions between different microbial communities in food matrices due to its potential to simultaneously detect and quantify a large range of tiny organic compounds. The following are some of the main areas of focus: (1) Finding microbial metabolites that serve as indicators of fermentation and spoilage processes, which helps determine the safety and quality of food; (2) Deciphering microbial metabolic pathways, which aids in optimizing fermentation processes for higher product yield and quality and (3) analyzing possible pathogenic metabolites in food products which in turn ensure food safety. The advantages of NMR over conventional analytical techniques are also highlighted in this study, including non-destructive sampling, little sample preparation, and the capacity to provide comprehensive metabolomic profiles. Nevertheless, problems, including overlapping spectra, limited sensitivity for specific metabolites, and the requirement for sophisticated statistical methods for data interpretation, continue to exist. Finally, NMR-based metabolomics provides a unique window into the complex world of microbial metabolism in food systems, enabling a greater knowledge of food quality, safety and the ability to enhance food processing methods. It is predicted that NMR will play a bigger part in determining the direction of food microbiology research as technology advances.

***Keywords:** NMR, Metabolomics, Food Microbiology, Metabolic Profiling, Fermentation, Food Safety.*

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BF_029: Improving the Nutritive value of Weaning food (pap flour) Fortified with Defatted Nuts

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Pap, a traditional fermented weaning food, is mainly starch with limiting nutrient quality and can be fortified using protein-rich crops like groundnuts and almond nuts in order to prevent infant malnutrition. This research aims to produce and assess the nutritive value of pap flour from sorghum fortified with defatted nuts flour. The flour was formulated in ratio 80:20, 70:30, 60:40 and 50:50 sorghum to nuts. While the control was constituted using 100% sorghum. There was an improvement in protein, fat, ash and fibre content as the concentration of the almond nuts were increasing (14.86-28.03, 6.86-11.71%, 1.38-1.71%, 3.95-4.02%,). While moisture and carbohydrate content reduced from 3.58-3.24% and 69.34-51.30%. Pap fortified with groundnuts had protein, fat and moisture content values of (15.74-22.76%, 11.64-20.27%, 2.08-2.63%). While the ash, fibre and carbohydrate content reduced from 1.04-0.48%, 4.63-2.64% and 64.87-51.50%. Fortifying the pap with the nuts also increased the samples' mineral contents (calcium, magnesium, iron). The functional properties (water absorption capacity, oil absorption capacity, bulk density, emulsion activity and foam capacity) of pap fortified with almond nuts ranged from 1.80-2.80g/ml, 1.86-2.55g/ml, 0.32-0.83g/ml 49.00-51.00% and 3.70-11.50%, while the samples fortified with groundnut ranged from 1.50-3.00ml/g, 0.78-1.37ml/g, 0.31-1.05g/ml, 54.00-55.00% and 5.60-13.60% respectively. The nutritional quality of pap flour was improved when fortified with almond nuts more than groundnuts. This is an alternate way of meeting the macro and micronutrient needs of infants in developing countries for a better complimentary weaning food which is able to handle nutritional deficiency during the weaning stage of development.

Keywords: *Weaning food, pap flour, almond nuts, malnutrition*

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BF_030: Biotechnology: building innovative pipelines of economic resilience

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Biotechnology's innovation pipelines, from basic and translational research, commercial product and process development, to bio-converging solutions and services, can potentially create a new wave of billion-dollar businesses and assure economic resilience. The global biotech market is expected to grow at a rapid pace in the coming years driven by advancements in the medical and agricultural sectors. The market size is predicted to increase at a compound annual growth rate of 13.9% from its present $1.6 trillion value to $3.9 trillion by 2030. The revenue generated from biotech products and services in the medical industry between 2016 and 2021 increased by 55% to $217 billion. Investments in medical biotech research and development which is helping to drive the growth of the market are also on the increase, significantly rising by 48% to $89 billion within the last five years. Many African medical biotech start-ups are also worth hundreds of millions of dollars. Despite the prospects of biotech companies such as 54gene in Nigeria, the sector faces significant challenges, including volatile markets, supply chain disruptions, and global competition. These factors have limited the development of indigenous biotech companies. However, the agricultural sector holds great potential for the impactful application of biotech in the country, which could lead to improved food security and poverty reduction. National projects and programmes conceptualised to combat poverty, hunger, and malnutrition using genetic engineering strategies to develop crop varieties resilient to abiotic stress and diseases are ongoing. Barriers to the acceptability and commercialisation of genetically modified crops need to be removed to ensure food and nutrition security. In addition to government policies and interventions, private sector investment in biotech research is required to establish disruptive and innovative pipelines that will guarantee economic growth and sustainable development.

Keywords: *Biotechnology, Economy, Innovation, Nigeria, Research*

BF_031: Effects of exposure time to Acute Heat and Fasting stress on Performance and Histology of Major organs in two Broiler chicken strains in Tropical Environment

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Four weeks old broiler chickens [200 Arbor Acre (AA) and 200 Hubbard strains (HB)] were used to study the effects of acute heat and fasting stress for four weeks. The completely randomized design experiment was conducted with the control kept under normal environment, while the experimental treatment groups were kept at higher environmental temperature (40±2oC) under a locally constructed heat chambers for 30, 60 and 90 minutes, and fasted for 2 hours. Parameters measured were vital signs, body weight, performance, blood parameters, carcass traits and histology of the heart muscles and kidney. The combined effects of subjecting the broiler strains to both stress for 3 consecutive days during their last four weeks were significant ($p<0.05$) on rectal temperature, rapid respiratory rate and breath rate. The results showed that different rate of acute heat and fasting stress had no significant ($p<0.05$) effect on the body weight of AA strain, but differ significantly ($p<0.05$) within the HB strains. The control had the best performance indices with respect to feed conversion ratio and percentage mortality by eight weeks of age in both strains, while HB strains had the highest percentage mortality across the treatments. Time of exposure to acute heat and fasting stress had no significant ($p<0.05$) effects on most carcass trait; but there was an elevated creatinine and phospholipids in both strains. Exposure to different rate of acute heat and fasting stress caused cellular hyperplasia of the heart muscles and degeneration of kidney cells in both strains of broiler chickens studied.

Keywords: *Blood parameters, Histology, Production, Vital Signs.*

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BF_032: Potentials of Nano-Genome Editing Technology in Advancing Crop Improvement

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Climate change poses a great threat to food security. New plant varieties with quality traits such as better yield, early maturing, disease resistance, insect resistance, high nutritional content, drought resistance, and with improve agricultural productivity is important for a growing global population. Several genome editing technologies: electroporation, microinjection, sonoporation, particle bombardment, gene gun, Agrobacterium-mediated delivery, and the novel CRISPR-Cas9 have been developed over the years to facilitate nucleic acid and protein delivery in any biological system. These have recorded success in some crops. However, significant bottlenecks prevent efficient plant gene delivery due to genotypes, random insertion of genes, complicated protocols, potential tissue damage, DNA incorporation in the host genome, transformation efficiency, and long breeding seasons. Nanomaterials could address some of the most critical challenges of CRISPR genome editing in plants through improvements in cargo delivery, species independence, germline transformation, and gene editing efficiency. This review identifies barriers preventing effective and seamless plant genetic engineering in CRISPR and other gene delivery methods from reaching its full potential in the application of nanotechnology to plant genetic manipulation, including the development of nanocarriers for the delivery of genetic cargos and advances in nano-mediated plant regeneration and recommend ways that nanoparticle technologies can lower or eliminate these barriers. We also describe advances needed in nanotechnology to facilitate and accelerate plant genome editing. Timely advancement of gene delivery technologies in plant engineering is crucial for our ability to feed and sustain the growing human population under a changing global climate.

Keyword: *genome editing, Nanotechnology, food security, climate change*

SUB-THEME 04: INDUSTRIAL PROCESSES AND APPLICATIONS (BI - WHITE BIOTECH)

BI_001: Microbial Conversion of Agrowastes for Lactic Acid Production using Bacteria Isolated from Agro-Waste Dumpsite

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Lactic acid is an organic compound produced via fermentation by microorganisms that can utilize a wide range of carbohydrate sources and has gained relevance in the food, pharmaceutical, textile, medical, leather and chemical industries. This study focused on isolating and screening bacteria from agrowastes (corn cob, sugarcane bagasse, plantain peduncle and groundnut shell) dumpsites for lactic acid production. Soil samples were obtained from agro-waste dumpsites, serially diluted and plated using the pour plate technique. The LAB were isolated using MRS agar. The LAB were identified based on their cultural, morphological, biochemical and molecular characteristics. The LAB isolate with the best ability for lactic acid production was ascertained using the spectrophotometric method. The supernatant (100µL) obtained from the centrifugation of the fermentation broth was reacted with 4 ml of Iron (III) chloride; the absorbance value was taken at a wavelength of 390nm. Eleven (11) isolates were obtained from the agro-wastes. Lactiplantibacillus plantarum (accession number OM510300) from plantain peduncle dumpsites had the highest potential for lactic acid production (1.9558g/L). The lactate dehydrogenase (d-ldh) gene was detected as the gene responsible for the production of lactic acid. The study revealed that plantain peduncle can be used as an alternative substrate for the production of lactic acid.

***Keywords:** Lactic acid, LAB, Agro-wastes, Plantain peduncles, and Lactiplantibacillus plantarum.*

BI_002: Physicochemical and Antioxidant Properties of Purple Sweet Potatoes (Ipomoea batatas (L.) Lam) Flour and Wine

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Purple sweet potato, Ipomoea batatas (L.) Lam, is a specie of sweet potato with low glycemic index and high health benefits. The aim of this study was to evaluate the physicochemical and antioxidant properties of purple sweet potato flour and wine. The estimation of secondary metabolites, proximate analysis, antioxidant activities alongside glucose concentration and microbial activities were carried out using standard methods. The wine was produced using potatoes only, potatoes and zobo, potatoes and tsamiya, and lastly, potatoes, zobo and tsamiya samples. The results of the quantitative phytochemical composition of the were: Glycosides (62.69±0.00) flavonoids (57.05±0.12) alkaloids (49.26±0.59) phenol (41.70±0.03) carotenoid (34.20±4.80) saponin (30.15±1.62), anthocyanin (15.85±0.00) and tannins (11.15±0.30) while the proximate composition values (%) were: moisture (6.28±1.20), crude protein (0.49±0.01), ash (17.21±1.38), fat (1.25±0.08), crude fibre (14.25±0.42) and Carbohydrate (60.73±0.81). The purple sweet potato extract produced significant ($p<0.05$) inhibition of Ferric Reducing Antioxidant Power (FRAP) with the highest activity when compared to 2,2-diphenyl-1-picrylhydrazyl (DPPH) and Inhibition of Lipid Peroxidation (ILP). The rate of consumption of glucose in the wine samples decreased with time the potatoes and tsamiya wine samples having the best rate of consumption. All the wine samples had high DPPH radical scavenging activities and zero ethanol content levels. Hence, consumption of purple sweet potatoes and wine produced from it can provide the body with several health benefits.

Keywords: *Purple sweet potatoes, wine, antioxidant, proximate composition*

BI_003: Urease Producing Capability of Microorganisms Isolated from Refuse Dump Sites and Urine Polluted Soils

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The urease enzyme has diverse applications in the industries such as the production of wine, vaccines, in the treatment of cancer and plays an important role in nitrogen metabolism. Urease hydrolyses urea in the soil to ammonia and carbon dioxide. Microorganisms may provide a natural source of a more stable enzyme with more diverse properties. The study, therefore, investigated the urease-producing potential of some bacteria and fungi isolated from some soil samples in Abraka, Delta State. Standard microbiological methods were used to isolate, characterize and identify the microorganisms. The bacteria isolated were Bacillus sp, Staphylococcus sp, Escherichia sp, Klebsiella sp, Micrococcus sp, Proteus sp, Enterobacter sp and Pseudomonas sp while the fungal species were identified as Aspergillus niger, Mucor sp. and Rhizopus sp. Screening for urease production showed that Proteus, Klebsiella, Enterobacter, Proteus and Aspergillus niger were urease producers. Assay for the urease activity showed that Proteus sp. Enterobacter and Klebsiella were potent in the conversion of urea to ammonia. Proteus sp. was the most potent, producing 1838.24 µmol of ammonia per minute while Aspergillus niger was found to be the least efficient in the conversion of urea to ammonia (producing 900.00 µmol of ammonia per minute). Proteus sp. and Enterobacter sp. isolated from soil can serve as potential sources of urease which can be applied in diverse industries.

Keywords: *Bacteria, Enzyme Activity, Fungi, Urease, Soils*

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BI_004: Screening of Bacteria from Snail gut for Laccase Production

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Laccases (benzenediol: oxygen oxidoreductases, EC 1.10.3.2), are multi-copper enzymes belonging to blue oxidase, which catalyzes the oxidation of a wide variety of naturally occurring as well as synthetic compounds like phenolic, diamines and aromatic amine compounds. Laccases are of great significance in various industries including pulp and paper, textile, cosmetics, pharmaceutical and food industries. Exudates were collected from the gut of a garden snail in Minna Nigeria. The gut of the garden sail was cut open using sterile fin forceps and a sterile swab stick was used to collect a portion of its exudates, this was streaked on a nutrient agar plate and incubated at 37°C for 24 h. Individual colonies were observed and sub-cultured on nutrient agar plates for another 24 h. Isolates were screened for laccase production on a mineral salt medium agar supplemented with guaiacol (0.01%). Two bacterial isolates from the exudates of the snail were positive for laccase production indicated by the brown-coloured growth of the organism on the medium amongst other organisms. The isolates were both identified as Bacillus subtilis. The result of this study showed that laccase-producing bacteria can be found in exudates from the gut of a snail and can be developed for the industrial production of laccase.

Keywords: *Bacillus subtilis, Garden snail, Guaiacol, Laccase*

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BI_005: Conventional and Molecular Identification of Gluconobacter oxydans for Partial Production of Biomaterial (Vegan Leather) using Black Tea as Substrate

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The high volume of garments provided at low cost has made clothing expendable and led to the widespread disposal of fabrics. This practice has negatively affected the environment, and research has been focused on developing sustainable textile materials for use in the clothing production sector. The isolation, conventional and molecular identification of the Acetic Acid Bacterium (Gluconobacter oxydans) was carried out using standard techniques. The biocellulose was partially produced using black tea as a substrate. Kombucha tea was used as a starter culture for biocellulose (BC) production. The carbon and nitrogen requirements of the bacteria in the medium were met by sucrose and caffeine present in black tea, respectively. The fermentation medium was produced by preparing black tea, in which 10 g/L of tea and 50 g/L of sucrose were used, and fermentation was carried out for two weeks. The segment size of bacterial DNA was observed to be between 700 and 800 bp. The BLAST sequence query showed that the isolate had a 97.02% identity (% homology) to be Gluconobacter oxydans in several trials where kombucha starter cultures were added to the prepared tea substrate in proportions of 10, 48, 50, and 100% v/v. The kombucha culture revealed that trials 1–3 produced no BC film, while trials 4 and 5 yielded a thin layer of biofilm which can be used to produce the vegan leather. Biocellulose film for vegan leather production can be obtained from the fermentation activities of acetic acid bacteria using black tea as preferred substrate.

Keywords: *Kombucha tea, bacterium, leather, biocellulose, biofilm*

BI_006: Bioremediation potential of a cellulose-degrading consortium from the digestive tract of the Bayelsa suya larvae

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Bioremediation of agricultural waste and effluents of the cassava and pulp industries represents a significant challenge in Africa's sub-Saharan countries. In this study, we show that the microbiome of the Bayelsa suya larvae digestive tract is diverse and rich in cellulose and lignocellulose degrading organisms; 107 to 109 colony-forming units g-1 biomass on Carboxy Methyl Cellulose (CMC)-Congo Red-Agar plates. Using selective media, every single CMC degrading colony was composed of at least four different groups of organisms, namely, Streptococci, Lactobacilli, Enterococci, including Yeast and Fungi species living synergistically. Interestingly, Streptococci, Lactobacilli, and Enterococci could not degrade CMC or cellulose individually. In contrast, the yeast and fungi could, albeit slower than the whole colony. The CMC-degrading colony readily degraded cellulose (Whatman paper number 1) and the Yam peels, which demanded slightly longer incubation period, in minimal liquid medium, thus opening the door for the exploitation of this stable consortium for the treatment of agricultural waste and effluents of the cassava and the pulp industries.

Keywords: *Cellulases, Lignocellulases, Bayelsa suya, Microbial consortium, Bioremediation*

BI_007: Purification of Pineapple (Ananas comosus) Fruit Bromelain by Polyethylene glycol/Ammonium sulphate Aqueous Two-Phase System.

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Bromelain is the pineapple's fruit or stem cysteine protease. It is used widely in food, cosmetics and pharmaceutical industries due to its proteolytic and therapeutic properties with little or no side effects. Polymer-salt aqueous two-phase systems (ATPS) is a fast, cheap and eco-friendly purification method that offers ease of scale-up, and little denaturation, thus, a high yield to protein. The ammonium sulphate fractional precipitation profile of bromelain was assayed. Based on a 24-1 fractional factorial design, ATPS (5g) was prepared with polyethylene glycol (PEG) (concentration: 15–20 %; molar mass: 4,000 – 8,000), 200 mM of phosphate solution (pH 6-8), ammonium sulphate saturation level of 25-35 % and 20 % bromelain crude extract (v/v). The bromelain's protein concentration and enzyme activity were determined in the two separate phases formed. The partitioning behaviour of bromelain in ATPS was quantified in terms of partition coefficient, purification factor, and yield. The most significant ($p<0.05$) portion of bromelain precipitated at 20-40 % ammonium sulphate saturation level. Optimal conditions of pH 8, (NH4)2SO4 concentration of 35 %, PEG concentration of 15 % and PEG molar mass of 4000 g/mol yielded 98.85 % bromelain with a purification factor of 15.23 folds. Nigeria ranked eighth among the ten top pineapple-producing countries. A vast quantity of this plant that goes to waste annually in the country because of its short shelf life can be purified into value-added products like bromelain using polymer-salt aqueous two-phase systems (ATPS) that offer close to absolute recovery as a first purification step.

***Keywords:** Bromelain, Purification, Precipitation, System, Yield.*

BI_008: Isolation and Molecular Cloning of a GH3 β-glucosidase from the Filamentous fungus Penicillium funiculosum

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Cellulases are an important class of enzymes produced by filamentous fungi and secreted into the cultivation medium. Recent research has revealed that fungi from the Penicillium genus exhibit a highly effective cellulase-producing system similar to the renowned model industrial biofactory "Trichoderma reesei." To enhance enzyme production, there is a need to obtain functional enzymes with improved characteristics using genetic and engineering approaches with the aim of reducing cost of enzyme production. In this study, the peptide sequence of one of the major glycoside hydrolase family 3 β-glucosidases from the fungus Penicillium funiculosum was isolated and cloned. The fungus was cultivated in a modified cellulose-inducing medium at 28°C and pH 5.5. Genomic DNA was extracted, and the open reading frame of the β-glucosidase gene, along with 500 bp upstream and downstream regions, was amplified through PCR using specific PfBgl primer sets. The PCR product was purified via agarose gel electrophoresis and subsequently cloned into a pJET blunt vector containing an ampicillin resistance gene. The cloned gene was later excised from the shuttle vector by restriction digestion and inserted into pCambia1302 at the XhoI/MauBI restriction sites between the left and right T-DNA borders. Finally, the cloned vector was transformed into E. coli DH5α and was spread on an LB agar plate containing kanamycin for selection. Subsequent clone analysis by PCR and plasmid isolation confirmed positive transformants. The generated clones will facilitate future gene expression and genetic engineering investigations in the fungus.

Keywords: *β-glucosidase, Cellulases, Filamentous fungi, Genetic engineering, Penicillium*

BI_009: Isolation and Screening of Amylase-Producing Microorganisms at a Cassava Production Site

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Amylases are vital enzymes that break down starch into glucose and play crucial roles in numerous industrial processes, including the food and pharmaceutical industries. This study focused on the screening and identification of amylase-producing microbes obtained from a soil sample collected at a cassava production site. To identify potential amylase producers, serial dilutions of the soil sample were cultured on starch media. Incubation was carried out at 37°C for bacterial growth medium and 25°C for fungal growth medium. The microbial isolates capable of producing amylase were distinguished by the formation of a clear zone around their colonies when exposed to a 1% iodine solution. Enzyme activity assays were performed using the dinitrosalicylic acid (DNSA) reagent method. The results indicated the presence of seven microbial isolates, comprising five bacterial strains (B1-B5) and two fungal strains (F1 and F2), all exhibiting amylase-producing potential. The amylase activities of these isolates varied from 4.65 U/ml to 6.89 U/ml. Among them, the highest activity was observed in B2 (6.89 U/ml) and F1 (6.88 U/ml), while the lowest activity was recorded in B4 (5.75 U/ml) and F2 (4.65 U/ml). These amylase-producing bacteria and fungi exhibit promising potential as valuable sources of industrial enzymes. Future work may involve the genetic identification of these microbes to further explore their industrial applications.

Keywords: *Amylases, Fungal strains, Industrial enzymes, Microbes, Screening.*

BI_010: Characterization of a Cyclodextrin Glucanotransferase and Its Application in Bread Making

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Cyclodextrin glucanotransferase (cyclomaltodextrins glucanotransferase, cycloamylase, CGTASE) is a unique enzyme produced by some microorganisms that are capable of acting on starch and related carbohydrates. Soil samples was obtained from cassava producing sites around Bosso, Minna, and Niger State. A total of 10 bacterial isolates was obtained. The bacteria showing the yellow halo zone were considered producers of CGTase. The highest enzyme activity was observed at 72 h with Alkalihalobacillus Oshimensis strain wahaha MZJ-1 with an activity of 10.95 U/ml. the optimum temperature and pH was observed at 10.0 and 35 oC. The crude enzyme was purified using 80 % ammonium sulphate precipitate and starch adsorption on DEAE-Sepharose 6B The enzyme had a purification fold of 5.2 with a percentage recovery of 44.64. Cycloamylase production was optimized by supplementing the production medium with different starches obtained from tubers. The maximum cycloamylase activity was observed in the medium supplemented with sweet potato starch (15.68 U/ml). Maximum cycloamylase production was obtained at 72 hrs of fermentation with the concentration of peptone, yeast extract, sweet potato starch at 0.65 %, 0.65 %, and 1 % respectively with an agitation of 250 rpm. The influence of the enzyme, starch and temperature on the production of cyclodextrin was determined with statistical central composite factorial design. The highest β-cyclodextrin (91.70 g/L) was obtained with from 150 g/L enzyme, 50 g/L starch and 50oC temperature. The effects of the addition of cycloamylase at concentrations of 5 U, 10U, and 20 U was studied. Crumb moisture of the crust, crumb and whole bread was significantly improved with 10 U addition.

Keywords: *Alkalihalobacillus oshimensis, central composite, cyclodextrin glucanotransferase, β-cyclodextrins.*

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BI_011: Assessment of Amylase Production Potentials of Lactic Acid Bacteria Isolated from Wheat Sourdough

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Consequent from increasing demand for amylase enzyme in the food industry, this study assessed the amylase production potentials of lactic acid bacteria (LAB) isolated from wheat sourdough. LAB were isolated from wheat sourdough samples and screened for amylolytic ability using the plate assay method. Isolates that were amylolytic were characterized and identified using standard methods. Submerged fermentation was carried out using the amylolytic lactic acid bacteria (ALAB) isolates at 30°C for 120 h. Reducing sugar yields and amylase activity were determined using the 3, 5-dinitrosalicylic acid method. The lactic acid bacteria isolates and their occurrences were as follows: L. plantarum 3(27.3%), L. brevis 3(27.3%), L. fermentum 2(18.2%), L. pentosus 1(9%), L. mesenteroides 1(9%), and P. pentosaceus 1(9%). A total of 11 isolates exhibited amylolytic activity with zones of starch hydrolysis in the range of 18-46 mm. L. plantarum TM3 and L. brevis KT1strains produced the highest reducing sugar concentrations (0.63mg/ml and 0.61 mg/ml respectively). Peak amylase activities of the ALAB isolates were observed at 24 h incubation time and ranged from 8.76 to 30.67 µmol/min/ml with L. plantarum TM3 and L. brevis KT1strains recording the highest amylase activities of 30.67 µmol/min/ml and 30.20 µmol/min/ml respectively. Findings from this study show that wheat sourdough is a good source of amylase-producing LAB strains such as L. plantarum TM3 and L. brevis KT1that could be exploited in starch degradation processes especially in the food industry.

***Keywords:** amylase, lactic acid bacteria, sourdough, wheat*

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BI_012: Evaluation of Lycopene and Vitamin C Content in Fresh and Dried Tomatoes

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Tomato (Solanum lycopersicon L.) and its products play a significant role in modern human diet as important sources of vitamins, minerals, and antioxidants as well as their being relatively easily accessible foods. It is consumed in many forms, such as fresh, cooked, condensed, and dried. This study was conducted to investigate the vitamin C and lycopene content in fresh and dried tomatoes. The tomatoes sample were sliced and dried in a solar dryer for six days. The sample were extracted and spectrophotometry analysis was carried out on both the fresh and dried samples to estimate the vitamin C and lycopene content. The fresh tomatoes had high levels of vitamin C (7.72 ± 0.26) and lycopene (32.34± 0.01) as compared to the dried tomatoes which had a value of 7.57 ± 0.20 and 7.72 ± 0.26 for vitamin c and lycopene respectively. It was observed that the lycopene content in fresh tomatoes was three times that of the dried tomato. It is then concluded that fresh tomatoes can be a significant source of dietary lycopene and vitamin C. In addition to the specific nutritional benefits of tomato consumption, encouraging greater tomato and tomato product consumption may be a simple and effective strategy for increasing overall vitamins and lycopene intake.

***Keyword:** lycopene, vitamin C, antioxidants, tomatoes*

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BI_013: Microbial Succession-Profile, Biochemical and Mechanical Properties of Biofilm from Cassava-Effluent: From Processing Waste to Edible-Package

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Plastics are part of our everyday life as they have a wide range of applications. The increase in the use of this largely non-biodegradable polymer has in recent years increased global concerns due to its health implications arising from several associated diseases. In this study, biodegradable plastic was produced from agricultural waste (Cassava effluent). Cassava peels and potato peels, avocado, moringa, and almond oils were used as fillers and additives respectively. The bioplastics were characterized to determine their respective mechanical, biochemical properties and structural observations. Using scanning electron microscopy (SEM) and functional groups using FTIR spectrometers were carried out. The microbial succession profile across the days of degradation was also determined. Biofilm formation without fillers using moringa oil as an additive showed the best properties with tensile strength (109.42 M Pa), elongation at the break of 30.22% and Young's modulus of 23 M Pa. The degradation time of the biofilms was 7 days (biofilm with cassava peels) 15 days (biofilms with potato peels) and 28 days (biofilms without fillers). Using molecular identification, the microbial succession profile of the selected biofilm showed the abundance of Bacillus pumilus, Aspergillus niger, Pseudomonas spp, Enterococcus species, Clasdosporium sphaerosperum and Candida species. While A. niger and B. subtilis are dominant microbes. The biofilms were able to package fruits for one week without visible damage. The application of microbiome analysis can further improve the understanding of their microbial succession profile. Interestingly, the properties obtained for these biofilm formations revealed that they can be applied in various biotechnology industries such as food packaging.

***Keywords:** Bioplastics, cassava effluent, microbiome, biofilms, food packaging, biodegradation*

BI_014: Phytoextraction of Heavy Metals using Endemic Plants Grown on Contaminated Soils in Urban Kano

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The research focused on phytoextraction and assessment of Heavy metals (HMs) accumulated in organs of Amaranthus hybridus and Racinus communis grown on contaminated soils obtained from three sites in urban Kano. The physicochemical parameters of the soil samples before and after the experiment were analysed using Near-Infrared spectrometer (NIRS D-2500) and other standard procedures. The concentrations of HMs in the soil samples and plant organs were analyzed using Micro Plasma Atomic Emission Spectrometer (MPA-ES, Model 4210). The level of HMs pollutants was evaluated using Mueller Geoaccumulation Index (Igeo). The plants were evaluated using biological indices, bioaccumulation factor and Translocation Factor. Data were statistically analysed using one way Analysis of Variance at $P < 0.05$. The physicochemical results revealed that all the soil samples were sandy-loam in texture and slightly acidic with pH values ranging between 6.11±0.02-5.02±0.06. The concentrations of Organic Matter (OM), Electrical Conductivity, Available Phosphorous, Available Nitrogen (AN) and Cation exchange Capacity (CEC) vary across the soil samples, with higher OM, CEC and AN revealed in soil collected from site C (3.87±0.14%, 86.04±0.28 cmol/kg and 4.21±0.02% respectively). The results of the HMs analyses across the soils revealed highest concentrations of Fe (311.02 ±0.04 mg/kg), Cu (208.62±0.01 mg/kg) and Zn (112.04±0.04 mg/kg) in soil site A, Pb (34.03±0.16 mg/kg) and Cr (4.63±0.03mg/kg) were observed to be higher in soil samples site C, while the highest concentration of Cd (1.20±0.00 mg/kg) was recorded in soil site B. Relatively all the concentrations of HMs in the contaminated soil samples were above WHO permissible limit. The HMs accumulated in plant organs ranked in order of Leaf > Root > Stem. The findings provide scientific evidence that R. communis and A. hybridus species may be used to decontaminate HMs polluted soils via phytoextraction and HMs accumulated may also be recovered for other industrial applications.

Keywords: *Biological indices, Contaminated soils, Heavy Metals, Plant Organs, Phytoextraction.*

BI_015: Socio-Cultural Values and Risk Factors Associated with Endemic Plants Used for Phytoremediation of Heavy Metals

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Contamination of environments with Heavy metals (HMs) is a common problem worldwide, with location and level of development playing essential roles in the various approaches used in managing these contaminations. The development and testing of numerous bio-physicochemical strategies of HMs decontamination such as soil incineration, excavation, landfilling, soil washing, solidification and microorganisms, have resulted in varying degrees of success and limitations. However, phytoremediation is a relatively new technology that has gained popularity for its ability to effectively remove HMs from soil, water and the atmosphere. The technology is also unique, eco-friendly, solar-driven, and cost-effective. Heavy metals contaminants have the potential to harm or destroy organisms, including human and ecosystem. Their concentrations rise when organisms move from lower to higher trophic levels (biomagnification). The effects of this phenomenon are felt at social, economic, and developmental levels. Endemic plants with phytoremediation potentials produced high biomass, high bioaccumulation and translocation factor of target HMs from soil, tolerance to the HMs toxic effects, good adaptation to environmental and climatic conditions in the respective areas, repulsion for herbivores to avoid contamination via food chain, increased resistance to pests and pathogens, ease of cultivation and with no effects on the ecological balance. Thus, using endemic plant species is generally more advantageous for phytoremediation while taking the risk factors into considerations. This review paper focuses on the risks associated with such endemic plant species used as food or medicine (Nutriceutical) within the global community on specific HMs. The bibliography searches focused on keywords related to indigenous and/or native plants species used for phytoremediation studies globally.

Keyword: *Bio-physicochemical, Contamination, Endemic plants, Phytoremediation, Risk factors.*

BI_016: Biodegradable Plastics: a promising approach to curb the menace of plastic pollution

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The advent and rapid development of the industrial sector as well as modern technology have simultaneously ushered in an unprecedented level of demand and usage of plastics in the world. Over the years, the primary source of plastic driving the industrial revolution has always been petroleum based formulated plastics which are foreign to the natural environment and takes umpteenth years to degrade naturally in the environment. Degradation of any organic substances in the environment is primarily mediated by the activities of microorganisms who use these substrates as a source of food in the process converting them to environmentally friendly fragments beneficial to man and environment. The unending years it takes petroleum-based plastics to naturally degrade has made it a pollutant all over the world. In recent years, there is an increasing quest for alternative sources of plastics from biological sources, as an environmentally friendly option. Available bioplastics are made from natural polymers of corn-starch, potato starch, cassava starch, rice, wheat and agar as well as gelatin. To give the bioplastic elasticity, sorbitol, glycerol, castor oil, fractionated coconut oil etc. are employed as plasticizers. This combination at different permutation resulted in production of varied categories of bioplastics with major differential properties of thermal stability, water degradability, tensile strength and biodegradability when tested using standard procedures. With corn-starch as the major material for bioplastic production, the use of plants that grow in the wild and underutilized crops may be considered as an alternative to this source. These will ensure that the raw materials for bioplastics production will not compete with staple food and also encourage the cultivation of plants that grow naturally in the wild.

Keywords: *Biodegradable plastics, corn-starch, natural polymers, and plastic pollution*

BI_017: RAPD and HPLC Analysis of Clerodendrum capitatum (Verbenaceae)

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Clerodendrum capitatum is a famous medicinal plant used traditionally in the treatment of various ailments such as inflammation, diabetes, malaria, antidotes for venomous bites and stings in Nigeria and other parts of Africa. The present study aims to evaluate the molecular and phytochemical properties that could be of value in the standardization and quality assessment of C. capitatum. The randomly amplified polymorphic deoxyribonucleic acid – polymerase chain reaction (RAPD - PCR) analysis was carried out on the leaf sample. The high-performance liquid chromatography (HPLC) was carried out on 80% (aq) ethanol leaf extracts, N-hexane fraction, Dichloromethane fraction, Ethyl acetate fraction and N-butanol fraction. the decamer oligonucleotide primers A (GGTGCGGGAA), B (GTTTCGCTCC) and E (CCCGTCAGCA) sequence revealed the presence of 30 scorable bands for the three primers with their corresponding size ranges from 10 to 10,200 bp. Primer A showed total of 11 bands, 2 ranging between 1999 to 1000 bp and 9 bands ranging between 999 to 200 bp. Primer B showed a total of 9 bands, a band ranging between 1999 to 1000 bp, 6 bands between 999 – 200 and 2 bands ranging between 199 to 10 bp. Primer E showed 2 bands with size range between 10,200 to 2000 bp while 3 bands between 1999 – 1000bp and 5 bands between 999 to 200 bp. The HPLC analysis revealed the presence of 14 compounds in the 80% (aq) Ethanol extract (EE80), 16 compounds in the hexane fraction, 19 compounds in the Dicloromethane fraction, 9 and 12 compounds in n-butanol and ethylacetate fractions respectively. The HPLC chromatograms of the extracts of leaf of C. capitatum showed some similarities and differences in the type, number and concentration of the compounds in the various fractions. The DNA and HPLC fingerprints obtained from this research can be useful in the identification and
authentication of C. capitatum and thus may be useful in the standardization of this plant.

Keywords: *C. capitatum, HPLC, RAPD-PCR, decamer oligonucleotide primers*

BI_018: Development and Optimization of Crosslinked Starch/Graphene Oxide Bioplastic Film for Fruits and Vegetable Packaging

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The environmental hazards associated with non-biodegradable plastic materials is a huge global challenge which has prompted research into the development of different biodegradable plastic materials. The use of starch films for packaging has been recommended, however they are characterized by poor mechanical properties and low water stability. This study was aimed at improving the properties of cassava starch films using a combination of green crosslinking and the introduction of graphene-oxide nanoparticles for potential application in fruits and vegetable packaging. Cassava starch was crosslinked with oxidized sucrose and the effect on some physicochemical properties was determined. Graphene oxide was synthesized using hummers method and optimization was carried out using Design Expert software for different responses including mechanical properties, barrier properties, film solubility and antimicrobial activity. The results of the physicochemical parameters showed that an amylose content of 20.78 %, a degree of substitution of 0.406, a degree of crosslinking of 27.4 % and a thermal degradation residual weight loss of 19.58 % (thermogravimetric analysis) were obtained after the crosslinking of cassava starch. In addition, the crosslinked starch had significantly ($P< 0.05$) lower solubility (20.85 %) and swelling power (5.62 g/g) indicating that crosslinking improved the properties of cassava starch associated with film strength and water stability. The average particle size of the synthesized graphene oxide was 65.2 nm and the optimal formulation for the crosslinked starch/graphene oxide (CS/GO) film as determined by the software had a model desirability of 73.1%. The film displayed antimicrobial activity with zones of inhibition between 6.2 and 23.7 (mm) against microorganisms isolated from deteriorated tomato fruit. This work concludes that the combination of green crosslinking and graphene oxide nanoparticles improved the properties of the cassava starch films for potential application in fruits and vegetable packaging.

Keywords: *Crosslinking, graphene oxide, optimization, oxidized sucrose*

BI_019: Evaluation of Physicochemical and Heavy Metals Load of selected Metal Scraps Dumpsites in Gwagwalada Area Council, Abuja.

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Rapid urbanisation and population growth has improved garbage production proportionally. The need for environmental quality has risen due to the threat that some organic and inorganic toxic pollutants such as heavy metals (HMs) pose to human health, ecosystems as well as reduction of soil quality for agricultural production. Using systematic sampling technique soil samples were collected from the study sites: park road (PKR) metal scrapyard, metal scraps dumpsites at social democratic party (SDP) junction as well as soil from undisturbed area as control (Cnt). The soils were processed and subjected to physicochemical analysis using standard procedures. The concentrations of HMs were analyzed using Atomic Absorption spectroscopy (AAS). The results of physicochemical parameters revealed; pH [Sdp (7.5), Pkr (7.09), Cnt (7.05)], EC [Sdp (114.60%), Pkr (360.50%), Cnt (67.63%)], CEC [Sdp (Na 3.1312, K- 0.852, Ca-0.111, Mg-0.488), Pkr (Na- 3.61, K-0.488, Ca-0.411, Mg-0.641), Cnt (Na-3.213, K-0.198, Ca-0.086, Mg-0.438)], Moisture [Sdp-0.13%, Pkr- 4.41%, Cnt-0.14%]. However, the result of the HMs analyses showed that Pb, Cr and Cd were significantly higher at Sdp scrapyard 0.02mg/l, 0.018m/l and 0.002mg/l respectively. Results obtained from Pkr were Pb (0.02mg/l), Cr (0.011mg/l) and Cd (0.001mg/l). Whereas, the control was Pb (0.0043), Cr (0.003mg/l and Cd (0.0003mg/l) and other analyzed HMs were insignificant. Juxtaposed against Igeo values, Sdp and Pkr metal scrap yards were moderately polluted with Pb, Cd, and Cr. The concern of the environmentalists is the quantity and toxic level posed by the wastes produced for environmental monitoring and policy making. Thus, the findings recommend proper policy on HMs pollution and control by appropriate authorities.

Keywords: *Atomic Absorption spectroscopy, Dumpsite, Heavy metals, Physicochemical.*

BI_020: DNA Barcoding of Securidaca longepedunculata fresen (Polygalaceae) and Securinega virosa (Roxb) Baill (Euphorbiaceae)

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The demand for medicinal plants is astronomically growing, hence, assertions of their properties and accurate identification has become vital for safe usage. DNA barcoding has shown to be a valuable molecular identification tool for medicinal plants, ensuring the safety and efficacy of plant materials of therapeutic significance. We evaluated the capability of the nuclear plastid DNA barcodes rbcL to identify two important medicinal plants, Securidaca Longepedunculata Fresen (Polygalaceae) and Securinega virosa (Roxb) Baill (Euphorbiaceae). They are popular medicinal plants used in traditional medicine for the treatment of various diseases. The present study aims to develop DNA barcode for Securidaca Longepedunculata and Securinega virosa. The total genomic DNA were extracted from the young leaves, the isolated total genomic DNAs were PCR amplified using the forward and reverse rbcl marker and the PCR products were resolved on agarose gel electrophoresis. The amplified bands were sequenced and studied using Basic Local Alignment Tool (BLAST). The primer (rbcl) gave good amplifications and produced a barcode region of 555 bp and 556 bp in S. Longepedunculata and S. virosa respectively. The results showed that the use of these conserved DNA sequences as barcodes and chemical profiles would be an accurate way for species identification and discrimination.

Keywords: *DNA barcoding, Securidaca Longepedunculata, Securinega virosa, rbcl marker.*

BI_021: Screening of Some Native Filamentous Fungi Species for Industrial Dyes, Food Colourants, Cosmetics and Textiles Production.

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Colours are pleasant to modern man owing to the beautiful outlook they create. Natural dye is often referred to as any dye, pigment, or other substance derived from natural sources such as plants, animals, microorganisms and minerals. They are renewable and sustainable bioresource products with minimum environmental impact. Several of these products have been known since antiquity for their use in coloring of textiles, food substrates and so on. Fungi are an understudied, biotechnologically valuable group of organisms that are capable of production of array of natural dyes. The aim of this research was to isolate and screen some species of filamentous fungi for their colour metabolite-producing abilities. Decayed wood/liter samples were collected from some sites at the National Biotechnology Development Agency, Lugbe, Abuja, Nigeria. The fungi were identified using standard microbiological methods such as colonial morphological identification studies and by comparison with mycological atlas. The pure cultures of the respective fungi were grown in liquid media (Potato Dextrose Broth) at 280C for 72 hours for extracellular colour metabolite production. The supernatant of the respective fungal was separated using clean muslin cloth and the residue was ground after drying to a constant weight in the hot air oven set at 450C. Afterwards, the dried residue was divided into portions and each part was added water, acetone and ethanol as extraction media and then shaken at 130 rpm methanol for 60 min. The products obtained were studied as prospect compounds for color production from fungi on sustainable bases. The results showed that out of the eight fungal strains identified, six strains produced colours, viz; deep red pigment produced by Penicillium purpurogenum MS2, yellowish colour by Aspergillus terreus MS12, Pinkish colour by Fusarium sp., MS03, Penicillium sp. MS14, Black colour by Cladosporium sp. MS17 and Blue colour by Penicillium sp. MS05 respectively.

***Keywords:** Natural dye, fungi, bioresource. Metabolites and residue*

BI_022: Determination of Tannin Content of Selected Food and Agricultural Wastes from FCT, Nigeria

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Tannins provide several advantages like being as good biomaterial, antimicrobial, antioxidant, pharmaceutical, biopesticide, and nutraceutical agent. The objective of this study is to analyse and compare tannins of eight selected food & agricultural wastes and synthetic tannin. Wastes such as sugar bagasse, cocoa pods, banana peel, plantain peel, rice husk, coconut husk and corn cob were obtained from Sheda village and Gwagwalada in FCT in Abuja, Nigeria. They were air-dried and blended. The tannin content was estimated using UV-Visible Spectrophotometric method. The FTIR analysis of the samples was also carried out. Results obtained revealed that the tannin content of samples was found to decrease in the order: coconut husk> plantain & banana peel> cocoa pod> sugarcane bagasse> corn cob> rice husk. The highest amount of tannin (5.06mg/g) was obtained from coconut husk while the lowest amount of tannin (2.688mg/g) was obtained from rice husk. The FTIR analysis showed a broad band at 3285-3216 cm-1 for all the samples representing bonding –OH groups. The samples displayed peak around 2928-2917cm-1 represents aliphatic chains, -CH2- and –CH3. The peak around 1616-1576 cm-1 corresponds to C-O vibrations. The peak around 1363-1256 cm-1 corresponds to C (O)-O stretching vibrations and –OH in plane vibrations. These peaks correspond to peak values obtained from pure synthetic tannic acid. Results from this study indicate that some food wastes may be utilised as source of cheap, readily available tannin for various industrial applications.

***Keywords:** Coconut husk, Food wastes, FTIR, Sugar bagasse, Tannin*

BI_023: Isolation and Molecular Characterization of Microorganisms from Fermented Rice Gruel (Ogi)

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Research has revealed some local rice varieties as worthy alternatives to maize in the production of ogi (a cereal-based fermented gruel). However, the microorganisms responsible for the fermentation process have not been characterised. More understanding of the microbial profiles of local rice ogi is necessary to guide its adoption and optimization as a novel variant of breakfast meal or weaning food. In this study therefore, ogi was produced through the spontaneous fermentation of Tapa rice, and microorganisms involved in the process were isolated. This was followed by a microbial identification using a polymerase chain reaction. Microbial loads recorded were 14.7–1.6x105cfu/g for bacteria and 4.0x102–1.2x103cfu/g for fungi. Microbial isolates were characterized as Lactobacillus plantarum, Leuconostoc mesenteroides, and Aspergillus oryzae, with 98.74%, 96.68% and 94.49% percentage identification levels, respectively. It was concluded that lactic acid bacteria were the predominant microorganisms involved in the spontaneous fermentation of Tapa rice for ogi production. Further research may investigate and compare the single and combined effects of the identified microorganisms on the physicochemical and sensory properties of Tapa rice ogi.

Keywords: *local rice, fermentation, ogi, identification*

SUB-THEME 05: GENOMICS AND BLUE ECONOMY (BB - BLUE & GOLD BIOTECH)

BB_001: Comparative ISSR Marker and Principal Coordinate Analysis of Two Ecotypes of Nigerian Indigenous Chicken (NIC)

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In order to determine the genetic diversity of Nigerian Indigenous Chicken (Naked neck strain) from two ecotypes (Calabar and Obudu) in Cross River State, Inter Simple Sequence Repeat (ISSR) using four primers and Principal Coordinate analyses were performed. Genomic DNA extraction was carried out using the CTAB protocol, followed by PCR amplification and observation by gel electrophoresis. The power maker software (ver. 3.5) was used to analyze genetic diversity. Results obtained showed the major allele frequencies as 0.3, 0.4, 0.5, and 0.5 respectively. Genetic diversity ranged from 0.62 to 0.82 while polymorphic information content (PIC) ranged from 0.547 to 0.797. PCoA results showed that the total percentage contribution to the variability was 40.26%. The three coordinates contributed differently to the total variability thus: Axis 1, 2, and 3 contributed 14.52%, 13.58%, and 12.16% respectively. Clustering on the chart also seemed to be population dependent. The results of the genetic evaluation can be used as baseline genetic information on the variation of both ecotypes of naked neck chicken, which can be assimilated with genetic information programs, to implement further genetic studies and breeding of the naked neck strain local chicken.

Keywords: *Ecotypes, Genetic Diversity, ISSR, NIC, Principal Cordinate Analyses*

BB_002: Molecular identification of bacterial flora from Clarias gariepinus gastro-intestinal tract within Abuja Metropolis

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Cat fish (Clarias gariepinus) production in Nigeria has reached an all-time high in recent years as the single largest staple for dietary protein after plants. The key to improving production yield and profitability in aquaculture is dependent on establishing and maintaining stable, well-balanced microbiota in the digestive system. Determination of the microbiota of fish gut is essential for enhanced valuation and management of the growth environment and fish health. Molecular biology assays proffer excellent sensitivity and ability to test a wide range of microorganisms useful as prebiotics and probiotics to its host. Bacteria from the gastrointestinal tract was assayed from fresh fish purchased from the Jabi Lake resort, Abuja, Nigeria. The bacteria cultures were serially diluted on fluconazole supplemented Bennett's media using 0.15% sterile peptone water. Following repeat streaking to obtain 9 pure cultures designated ECG 1-9, DNA was extracted using CTAB extraction method. Genomic DNA purity ranged from 1.85 to 1.98 (A260:A280) using a UV-Vis Spectrometer. Amplification was done using the 27F and 1492R universal bacterial primers. Taxonomic identification of the 16S rRNA gene sequence obtained was compared known sequences in the NCBI genebank using the BLAST search program. Pure cultures ECG1 and ECG3 were identified as different strains of Hafnia paralvei (97.82%, 98.47%), pure cultures ECG2, ECG4 and ECG10 were identified as Bacillus vallismortis (98.82%), Bacillus velezensis (96.22%) and Bacillus subtilis (97.75%) respectively. Pure cultures ECG5 and ECG8 were identified as Pseudomonas putida (97.88%). Pure cultures ECG7 and ECG9 were identified as Acinetobacter pittii (98.65%) and Aeromonas dhakensis (94.59%). The results confirm the presence of beneficial bacteria known to aid in nutrition, bacteriostasis and immune-regulation. DNA technology serves as an effective tool in the biosafety assessment of commercially available seafood.

Keywords: *Clarias gariepinus, molecular Identification, PCR, BLAST.*

BB_003: Unraveling temporal gene expression patterns during the diauxic shift in saccharomyces cerevisiae using an artificial intelligence model

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The diauxic shift is a critical metabolic transition in saccharomyces cerevisiae, characterized by a switch from fermentative to respiratory metabolism during glucose depletion while utilizing an alternate carbon source. To comprehend the temporal gene expression patterns driving this transition, we analyze DNA microarray data, which captures gene expression levels at various time points during the diauxic shift process. A machine-learning technique is then applied to identify differentially expressed genes and define temporal gene expression patterns. However, the study revealed intricate patterns in the saccharomyces cerevisiae gene expression profiles. The model identified co-expression modules of functionally related genes, elucidating potential regulatory pathways and biological processes. Furthermore, we observed that the neural network-based approach outperformed traditional statistical methods in capturing non-linear relationships and predicting gene expression patterns during the diauxic shift. The current technique contributes to our understanding of gene regulation and functional interactions within the yeast transcriptome, offering new insights into fundamental cellular processes and paving the way for potential biotechnological applications.

***Keywords:** Diauxic shift, machine-learning technique, saccharomyces cerevisiae, temporal gene expression patterns, neural network-based approach*

BB_004: Stacking neural networks for consensus multi-class protein secondary structure prediction

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The prediction of protein secondary structure plays a crucial role in clarifying their functional properties, aiding in understanding their three-dimensional structures, and allowing insights into their biological functions. With the rapid expansion of protein sequence data due to advancements in high-throughput sequencing techniques, accurate and efficient prediction strategies are in high demand. While various machine-learning approaches utilized this task, intrinsic intricacy and heterogeneity of protein sequences present a formidable obstacle in attaining a high prediction accuracy level. The current study proposes a novel ensemble approach, termed stacking neural networks for consensus multi-class protein secondary structure prediction (SNN-CMSP), which aims to leverage the strengths of individual neural network models to attain enhanced predictive performance. The SNN-CMSP method involves constructing a multi-layered ensemble architecture that combines multiple base neural networks to reach a consensus prediction. Each base network is carefully designed to capture distinct features and patterns inherent in protein sequences, including local and global sequence information, evolutionary profiles, and physicochemical properties. The observed results demonstrate that the proposed ensemble consistently outperforms individual base models, achieving substantial improvements in prediction accuracy, sensitivity, specificity, and Matthew's correlation coefficient. Furthermore, by exploiting the complementary strengths of diverse neural network models, SNN-CMSP exhibits superior predictive capabilities compared to traditional single-model methods. The proposed approach shows an enhancement potential to understanding protein structure-function relationships, advancing various fields, such as drug design, molecular biology, and bioinformatics.

Keywords: *Ensemble approach, high-throughput sequencing techniques, machine-learning approaches, protein secondary structure, stacking neural networks.*

BB_005: Metagenomic analysis of microbial communities in residential soil adjacent a mechanic workshop

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Soil pollution occurring at auto-mechanic workshops has adverse impacts on soil microbial diversity beyond its immediate environment. New approaches, such as metagenomics approach, have become a powerful tool to investigate biodiversity of soil microbial communities. In the current study, metagenomics approach was used to investigate the microbial diversity of soils contaminated with arsenic (As) via leaching from a mechanic site. The contaminated soils were collected from a residential estate. The soil total DNA was extracted using a ZymoBiomics DNA Miniprep kit and 16S rDNA genes were amplified using universal primers 27F and 1492R, targeting the V3-V4 region of the bacterial 16S rRNA gene. Samples were sequenced on the Sequel system by PacBio and raw sub-reads were processed through the SMRTlink (v11.0). Further data processing taxonomic information was determined based on QIMME2. The results revealed a high abundance of Proteobacteria (27.49%), Chloroflexi (18.25%), Firmicutes (16.49%), Actinobacteriota (15.20%), Acidobacteriota (5.85%), Nitrospirota (2.92%), Gemmatimonadota (2.46%), Cyanobacteria (2.11%) and Myxococcota (1.99%) in the metagenome retrieved from the soil sample. Unclassified bacteria (3.16%) represented a significant portion of the metagenome. Detection of a higher novel UTCFX-1 bacterium abundance to that of Perlucidibaca spp., and Smaragdicoccus niigatensis amongst the known species suggested a heavy metal-associated risk to environment. Inductive Coupled Plasma Optical Emission Spectrophotometric (ICP-OES) analysis revealed a 1.0804 mg/kg Arsenic concentration, double its acceptable limit for residential areas. While the present study highlighted the microbial community structure present in a residential environment close to an active mechanic workshop, it solicits the adoption of metagenomics in exploration of microbial diversity in unique environmental niches as part of a comprehensive environmental impact assessment tool whilst identifying bacteria useful to the ecosystem.

Keywords: *Metagenomics, Next-generation sequencing, Diversity, Soil, Heavy-metal*
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BB_006: Evaluation of Genetic Variations in Growth Hormone Secretagogue Receptor (GHSR) Gene and Performance Trait in Four Chicken Genotypes

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Understanding the role that genes play in the control of economic traits of farm animals has aided selection and breeding improvement in breeding programmes. This research was carried out to evaluate the association between single nucleotide polymorphisms (SNPs) in growth hormone secretagogue receptor (GHSR) gene and performance traits in four chicken genotypes (normal feather, frizzle feather, naked neck and exotic. A total of forty birds comprising 10 each of the genotypes for normal feather, fizzle feather, naked neck and exotic breed were used for the study. Blood samples were obtained from all the chicken and used for molecular assessment of variation in GHSR gene while growth performance of the different chicken genotypes were measured at 8 weeks. Following the sequencing of GHSR gene, was performed using the primers: GHSR1 F-GTCGCCTGCGTCCTCCTCTT and R-ACGGGCAGGAAAAGAAGATG. 20µl reaction comprising approximately 20ng of purified PCR product as template DNA, 8µl of Big Dye Terminator Reaction Mix (dNTPs, ddNTPs, buffer, enzyme and MgCl2), 8µl of deionized water, 2µl of primer programmed as 25cycles at 96oC for 10 seconds, 60oC for five seconds and 60oC for four minutes. Multiple sequence alignment was performed using MEGA. Genetic polymorphism was determined using DnaSP while Codoncode aligner was utilized to evaluate SNPs in GHSR gene sequences. Association between SNPs and growth performance was determined using multiple correlation. Results of the growth performance revealed that the exotic chicken genotype had significantly higher body traits than the three indigenous genotypes. Genetic polymorphism revealed the highest sequence polymorphism from exotic genotype with 127 polymorphic sites. The number of haplotype diversity was highest in exotic genotype (0.946±0.0001) followed by frizzle feather (0.644±0.023). While nucleotide diversity was highest in normal feather (0.131±0.0001) which was similar with nucleotide diversity of the naked neck genotype. Evaluation of SNPs in the GHSR showed that majority of the identified SNPs resulted in transversion and non-synonymous mutations.

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Phylogenetic relationship among the four chicken genotypes resulted in two major clusters with naked neck and frizzle feather in the same sub-cluster. The association between SNPs and growth performance of the chicken genotypes revealed significant association between SNPs and body length of all the genotypes except naked neck. Similarly, there was significant association between SNPs and body weight of all the chicken genotypes. The different SNPs identified in the GHSR gene of the chicken genotypes can be utilized in the selection and breeding of indigenous chickens for grow*th improvement.*

Key words: *Growth hormone, Genotype, Secretagogue receptor, Performance trait, Chicken*

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BB_007: Phenotypic and Molecular Assessments of Accessions and Landraces of Sphenostylis stenocarpa (Hochst. ex A. Rich) Harms (African Yam Bean)

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African yam bean (AYB) is an important neglected leguminous crop with dual benefits of edible tuber and seeds. There is limited information on the characterization and traits inheritance. Therefore, morphological and molecular assessments of twenty-one accessions and four landraces of AYB were investigated in this study. The experiment was laid out in a complete randomised design with three replicates. The morphological traits were evaluated using standard procedure. Genomic DNA was extracted from the seeds and amplification was done using simple sequence repeats primers obtained from black gram. The result showed that TSs-86 accession matured earlier for both number of days to 50 % flowering (97 days) and number of days to pod maturity (127 days). The highest number of pods per plant and seed weight per pod were recorded in TSs-87 (14) and TSs-104 (7 g), respectively. The highest number of seeds per pod (20) was shown in accession AYB 94. The highest broad sense heritability (99 %) was expressed in plant height, number of leaves, and internode length, while twenty traits had higher genetic advance (> 20). Seed width was positive and highly correlated with seed length and seed thickness at r = 0.95. The principal biplot showed that two components accounted for 99.92 % and 61.19 % of variations in growth, and agronomic and yield traits, respectively. Primer CEDG284 had the highest number of 90 amplicons, while CEDG010 primer had the highest gene diversity (0.50), heterozygosity (0.78) and polymorphic information content of 0.38. The four landraces were found to be grouped with the twenty-one accessions in two clusters. This study elucidated the importance of combining morphological and molecular markers in assessing genetic diversity for selection and improvement of African yam bean.

Keywords: *Simple sequence repeats, characterisation, heritability, genetic advance, morphology*

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BB_008: Computational-based Comparative Physicochemical Characterization of Smooth Cayenne Fruit Bromelain

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Bromelain is a sulfhydryl proteolytic protein extracted from the pineapple plant and extensively reported as a phytomedicine with antiedematous, antithrombotic and anti-inflammatory activities. The pharmacokinetic properties of drugs are governed by their physicochemical properties because the ability to convert a biologically active compound to a therapeutically effective drug depends significantly on their physiochemical properties. This study sequenced a novel fruit bromelain (SCFBRM) via Sanger's method and manually edited it using the BioEdit sequence alignment editor. BLASTn and phylogenetic tree were used to determine its homolog. The physicochemical properties of SCFBRM and its homolog (MN299329.1) were determined via the ProtParam tool and compared. Amplified SCFBRM comprising 761 nucleotide bases produced six highly similar top hits (with 98% query cover and 91-99 % percentage identity) that diversified into three major clades. SCFBRM showed nine single nucleotide polymorphisms (SNPs) that translated into 13 amino acid variations. Physicochemical parameters of SCFBRM predicted were: Amino acid residues (248), Atomic number (3895), Molecular weight (28310.79g/mol), Theoretical pI (5.81), Instability index (43.62), Aliphatic index (67.98) and Grand Average of hydropathicity (- 0.447). Sequence analysis is a fundamental element of bioinformatics that gives insight into biomolecules' molecular and biochemical mechanisms. Thus, this computational analysis has provided intuition into the functional diversity of SCFBRM that can be modified in drug development and delivery for emerging disease control and prevention.

***Keywords:** Bromelain, Physicochemical, Sequence, Computational. Homolog*

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BB_009: Genotoxicological Evaluation of Some Plants Grown on Crude Oil Polluted Soil using Comet Assay

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The ecosystem hosts a myriad of persistent genotoxins ranging from petroleum hydrocarbons to heavy metals, which directly or indirectly stretch into the food chain jeopardizing the biotic community. As a result, genotoxicological evaluation is highly important and comet assay remains a standard, sensitive, cheap, and simple technique usually employed to detect single and double stranded DNA breaks in eukaryotic cells. In this study, we evaluated the genotoxic effect of crude oil on three vegetables (Allum cepa, Telfairia occidentalis, and Zea mays) polluted before planting (PBP) and polluted 2 weeks after planting (PAP). The comet frequency values obtained were statistically lower ($P<0.05$) in all the control samples (UC = 8.00±3.61bc, OC = 11.67±3.06b and MC = 4.67±2.08c). However, higher but nonsignificant comet values were recorded amongst the polluted samples (UPB = 46.33±2.08a, UPA = 50.00±0.00a, OPB = 49.67±0.58a, OPA = 48.67±1.53a, MPB = 49.33±1.16a and MPA = 50.00±0.00a). The damage scores ascertained were in the range of 9.33±4.93 for UC to 188.33±2.08 for MPA. Furthermore, various levels of DNA damages were revealed through photomicrographs for each test plant. Extreme genetic damages occurred in MPA, UPA, MPB and OPB while OPA had extensive damages. Moreover, medium DNA damages were observed in UPB whereas, mild and zero damages were shown in the leaves of all the controls. Hence, the observed trait in UPB as shown in the present study, could be attributed to the plants' high level of stress tolerance or DNA repair ability.

Keywords: *Comet assay, Crude oil, DNA breaks, Ecosystems, Plants*

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BB_010: Genetic Diversity in Adult Muscovy Duck (Caraina Moschata) of Kwara State Origin using Nuclear CYP2U1 Gene

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Over the past years, different types of molecular markers have been used to advance the study of genetic diversity within and between populations. The domestic Muscovy duck (Cairina moschata) is an economically important species that is known for considerable variation in their phenotypic characteristic; they are raised by duck lovers, and found around the world for their unique meat taste and low-caloric content. In this study, genetic diversity and phylogenetic relationship of 13 Muscovy duck populations raised amongst duck farmers in Kwara State of North Central Nigeria were sequenced using 747-bp long fragment of nuclear spanning the Cytochrome P450 Family 2 Subfamily U polypeptide 1 (CYP2U1) genes. A total of 18 variable sites were reported containing substitutions polymorphic sites with 17 singletons variables. The haplotype diversity of each sampling locations are 0.833, 0.714 and 1.000 for ADE, KEY and IDO, respectively. Close genetic distance existed between ADE and KEY Muscovy duck, whereas IDO genetic distance is far from ADE and KEY counterparts. The populations studied have 8 haplotypes with 0.00388 of nucleotide diversity per site (Pi) and 18 mutations with parsimony informative site of 1 with haplotype (gene) diversity of (71.8%) which indicates high genetic variation and gene polymorphisms between the populations. This study shows the suitability of nuclear CYP2U1 gene in genetic diversity evaluation among Muscovy duck found in the study area.

Keywords: *CYP2U1, Diversity, Muscovy duck, Sequence.*

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