BOOK OF ABSTRACTS

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44TH ANNUAL CONFERENCE OF THE NIGERIAN SOCIETY OF MICROBIOLOGY
&
ANNUAL GENERAL MEETING
COVENANT UNIVERSITY
JULY 24-28, 2023

NSM-OTA, 2023

Covenant University, Ota Nigeria
July, 24-28th, 2023

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"Microbial Bio-Heritage and the Post-COVID Dynamics of Global Relevance"

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A Hybrid Conference Held Online and at the CUCRID Conference Hall, Covenant University, Ota Nigeria

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171. Addendum:http://nsm.covenantuniversity.edu.ng/wp-content/uploads/2023/07/NSM-OTA_2023_BOOK_OF_ABSTRACTS_-ADDENDUM.pdf

Paper ID *(HE001)*

Genetic Diversities of Bacterial Resistance Mechanisms to Carbapenems in Enugu State, Nigeria and the Urgent need to Adopt COVID-19 Infection Control Protocol

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Abstract

Background: Carbapenems are β-lactam antibiotics regarded as the most reliable 'last-resort' for the treatment of life-threatening infections caused by Multi-Drug Resistant (MDR) bacterial pathogens. Some bacteria 'species have developed different resistance mechanisms against carbapenems; most worrisome being the acquisition of diverse carbapenem-hydrolysing enzymes (carbapenemases) that vary across regions. The aim of this study was to determine the prevalence and molecular basis of carbapenem resistance in Enugu State, Nigeria and suggest possible solutions. **Materials and Methods**: Isolates of 212 properly characterized *Pseudomonas aeruginosa*, *Escherichia coli* and *Klebsiella pneumoniae* from non-duplicate samples of patients in five secondary and tertiary hospitals within Enugu State were investigated. The susceptibility profiles of the isolates to 16 different antibiotics were investigated and the carbapenem non-susceptible isolates phenotypically and molecularly screened for carbapenemase enzymes production using the modified carbapenem inactivation (mCIM) and the polymerase chain reaction (PCR) respectively. Plasmid profiling and curing were conducted on the carbapenemase enzyme producers to determine the presence and involvement, respectively, of plasmid in their resistance mechanisms. Conjugation experiment was done to confirm the transferability of the resistance genes to other bacteria in an ecosystem. **Results and Conclusion**: Carbapenem resistant bacteria were found to be 38 % prevalent in the State and mediated by 13 different β-lactamase enzymes, including IMI (22 %) and SME (8 %) identified for the very first time in Nigerian hospitals. Plasmid profiling identified three different plasmids. Considering the high level of enzyme-mediated carbapenem resistance in Enugu State, an urgent need for the implementation of good infection control measures (isolation, cohorting and contact precaution) synonymous with that of COVID-19 infection control protocol is recommended.

Keywords: Carbapenem; COVID-19; IMI; Carbapenemases; SME.

Paper ID *(HE002.)*

Isothermal Amplification-based Detection of SARS-CoV-2 using Hydroxynaphthol Blue dye.

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Abstract

Background: The outbreak of Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) in 2019 generated a global panic and enomously strained the health sector globally. Nigeria and many developing countries were affected by shortage of testing kits. We aimed to develop a simple and affordable SARS-CoV-2 detection assay appropriate for developing countries. **Materials and Methods**: Using the SARS-CoV-2 Nucleocapsid (N) gene, six primers were designed for loop-mediated isothermal amplification (LAMP) using PrimerExplorer v. 5. *In silico* analysis of the primers was performed using Mega-X, Bioedit 7.2.5 and NCBI BLAST. Primer efficiency and specificity were determined using synthetic DNA and RNA of SARS-CoV-2 N gene and against related coronaviruses. Hydroxynaphthol blue (HNB) dye was incorporated at 120µM concentration for easy detection of amplified target gene using unaided eyes. The reaction mix contained 1X isothermal buffer, primers (outer, inner and loop), MgSO4, betaine, dNTPs, *Bst* 2.0 DNA polymerase and reverse transcriptase enzyme at optimized concentrations. The assay was performed using a conventional hot water bath at 65°C for 1 hour. Agarose gel electrophoresis was used to confirm amplified products. **Results and Conclusion**: The designed LAMP assay specifically detected SARS-CoV-2 in less than 60 minutes with colour change from purple (negative) to sky blue (positive) at 8 copies/µL concentration of N gene target. Using samples confirmed with real-time reverse transcription PCR, assay sensitivity and specificity for SARS-CoV-2 N gene were 97.53 % (95 % CI:91.36 - 99.70 %) respectively. This simple, affordable assay can provide alternative surveillance option to RT-PCR particularly for developing countries.

Keywords: COVID-19, Coronavirus, SARS-CoV-2, LAMP, RT-LAMP.

Paper ID *(HE003.)*

Candidemia in University Students: Detection, Species Distribution and *In Vitro* Antifungal Susceptibility

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Abstract

Background: Candidemia is a bloodstream infection that poses a significant healthcare challenge and it is associated with high mortality in neonates and healthcare settings. Candidemia is rising globally, and it is underreported wherein it is resistant to antifungals. The primary etiological agent is shifting to non-albicans *Candida* species. This study demonstrated the prevalence, species distribution, and antifungal susceptibility of *Candida* isolates associated with candidemia. **Methodology:** Two hundred and ten (210) volunteer blood samples were obtained and *Candida* was isolated and identified using standard microbiological procedures, under aseptic techniques. The antifungal profile of the Candida species against three antifungal agents was determined using the E-test method. **Results:** About 4.3% (9/210) prevalence of candidemia was observed in this study. Three *Candida* – *C. albicans*, *C. glabrata* and *C. krusei* – species were identified. *C. glabrata* was the most dominant species, accounting for more than half (55.56%; 5/9) of all incidences. Age, gender, underlying disease, and use of antibiotics were significant risk factors contributing to candidemia. All isolates were susceptible to Amphotericin B (with MIC range of 0.09-0.64µg/mL). **Conclusion:** This study showed that non-albicans were the most dominant *Candida* species and emerging antifungal resistance amongst *Candida* species associated with candidemia, underscores the need for routine surveillance to monitor and quickly detect changes in trends, antifungal susceptibility, and resistance patterns. A mass and robust testing of persons with symptoms of bloodstream infection, especially immunocompromised individuals is important for diagnosis and identification of the risk factors that will aid in developing mechanisms to curb incidences of candidemia.

Keywords: Candidemia, Antifungal, *Candida*, Risk factors, Bloodstream infection.

Paper ID (*HE004.)*

Antibacterial Activity of *Acacia nilotica* Leaves Extract against Beta Lactamase producing Bacteria

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Abstract

Background: *Acacia nilotica* has been identified and used as medicinal plant for the treatment of diseases such as diarrhea and dysentery in parts of Northern Nigeria and West Africa. Hence, the phytochemical screening and antibacterial activities of leaves extracts of *Acacia nilotica* were investigated as an attempt to find alternatives to antibiotics due to increasing antimicrobial resistance **Materials and Methods**: The plant leaves were collected from Kalshingi in Akko LGA of Gombe and authenticated at Herbarium of Gombe State University. Phytochemical analyses using standard tests were used to detect tannins, steroids, saponin, flavonoids, glycosides and alkaloids from the leaves. Agar-well diffusion method was employed in testing the sensitivity of the crude leaves extracts on two clinical bacterial isolates, while tube dilution method was used to determine the minimum inhibitory concentration (MIC), and sub-culturing on nutrient agar was used to determine the minimum bactericidal concentration (MBC) **Results and Conclusion**: Phytochemical analyses revealed tannins, steroids, saponin, flavonoid, and glycosides were present in both the methanol and aqueous leaves extracts. The two extracts at concentrations varying from 6.25mg/ml to 50mg/ml exhibited zones of inhibition ranging from 12mm to 20mm against *Escherichia coli* and *Klebsiella pneumoniae*. The MIC test revealed that *E. coli* were inhibited at 1.56mg/ml of aqueous extract and 3.12mg/ml of methanol extract, while *Klebsiella* were inhibited at 3.12mg/ml of both methanol and aqueous extracts. MBC for both bacteria was 6.25mg/ml for each of the extracts. These results suggest that this leaves can be a potential source of alternative to antibiotics.

Keywords: *Acacia nilotica*, Phytochemical, activity, *Escherichia coli, Klebsiella pneumoniae*

Paper ID *(HE005)*

Disinfection potential of locally formulated mix against surface contaminants in Federal University of Lafia

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Abstract

Background: Microbes survive long on frequently used surfaces like doorknobs and computer keyboards. These can become reservoirs of pathogens, requiring efficient disinfection. We aimed to formulate an efficient disinfectant using some readily available local materials. **Materials and Methods**: Sixty swab samples from different computer keyboards and doorknobs from ten locations on campus were serially diluted and aseptically cultured on nutrient agar and sabouraud dextrose agar. Bacteria isolates were identified using Gram staining, cultural characteristics, and biochemical tests. Cultural and microscopic characteristics were used for identification of fungal isolates. Susceptibility of the isolates was tested against different combinations of bleach, alcohol, pine oil and lime. **Results and Conclusion**: The highest and lowest mean bacteria count (± Standard Error logCFU) was from laboratory (7.64 ± 0.13) and office (7.13 ± 0.14) doorknobs respectively. Mean fungal count (± SE logCFU) was highest in classroom (3.29 ± 0.07) and lowest in toilet (3.10 ± 0.07) doorknobs respectively. Differences in counts were not statistically significant. Seven bacteria and four fungal species were identified, with *Staphylococcus aureus* (55.0%) *and* A*spergillus flavus* (46.7%) occuring most. The combination containing bleach, alcohol, pine oil and lime was most inhibitory to the isolates (35 – 40 mm). This formulation could serve as a cheap source of effective disinfectant for frequently used surfaces.

Keywords: Resistance, Disinfection, Bacteria, Fungi, Antimicrobial.

Paper ID *(HE006)*

Isolation and Molecular Characterization of Vancomycin Resistant *Staphylococcus aureus* (VRSA) from Clinical Samples in Various Hospitals in Nsukka and University Teaching Hospital (UNTH), Enugu.

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Abstract

Background: Emergence of vancomycin-intermediate *Staphylococcus aureus* (VISA) and Vancomycin resistant *S. aureus* (VRSA) strains has led to great concern in global public health in both developing and developed countries. This study was performed to isolate, characterize and determine the antimicrobial resistance pattern of VRSA from clinical samples. **Materials and Methods**: A total of one hundred and fifty four (154) clinical samples were collected. Isolates were characterized using conventional techniques and confirmed by PCR detection of the *S. aureus*-specific *nuc* gene. Brain heart infusion agar supplemented with 6 µg/ml was used for phenotypic screening of VRSA. Phenotypic antibiotic resistant profiles of the isolates were determined by disk diffusion method, while screening for vancomycin resistance genes (*VanA and VanB*) was by PCR. The minimum inhibitory concentration (MIC) of the vancomycin resistant isolates were determined using micro broth dilution method. **Results and Conclusion**: A total of 98 isolates were identified as *S. aureus* by conventional methods. Of these, 70 (71.43%) were confirmed by PCR. Of these 70 *S. aureus* strains, 35(47.30%) were detected as VRSA based on antibiotic screening; presence of growth on brain heart infusion agar supplemented with 6 µg/ml of vancomycin. The MIC values ranges from 8µg/ml to 0.5µg/ml. The PCR results revealed that 6 isolates (21.43%; 6/28) and 4 isolates (14.29%; 4/28) of vancomycin resistant isolates carried *Van A* and *Van B* genes respectively. These findings support the need for future surveillance studies on VRSA strains to keep the emergence and transmission of these isolates to a minimum

Keywords VRSA, *Van A* genes, *Van B* genes, Polymerase chain reaction (PCR), Clinical Samples.

Paper ID *(HE007.)*

Prevalence of Bacterial Paediatric Bronchopneumonia Among Children 0-5 Years in Gusau Metropolis, Zamfara State, Nigeria

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Abstract

Background: Bronchopneumonia is the most common type of pneumonia found in children. Among children under five years of age, it is the leading cause of death. Bronchopneumonia accounts for 85% of all respiratory system diseases in children under two years of age. The predisposing factors linked to pneumonia include: malnutrition, absence of exclusive breastfeeding, overcrowding with indoor air pollution, low weight at birth, lack of optimal immunization. **Methods:**Certified structured questionnaire developed by the UNICEF was used to collect demographic and risk factors data from 200 children aged 0-5 years presenting with symptoms of bronchopneumonia, visiting a secondary health care center in the study area. Sterile swab sticks were used to swab the oropharyngeal area of the patients and the swab was immediately placed inside a container with normal saline for storage and transport to the laboratory. Gram stain was performed on each sample to identify the bacteria associated with sample after culturing for 24 hours on MacConkey and Blood agar. Biochemical tests viz catalase, coagulase, citrate utilization test, TSI and VP were carried out for further identification. Antibiotic sensitivity tests were performed using Mueller Hinton agar and incubated for 24 hours. The antibiotic discs used were Amoxilicin (20µg), Augmentin (30µg), Levofloxacin (20µg), Ciprofloxacin (10µg) and Ampiclox (20µg). The results of the zones of inhibition were compared with CLSI standards. **Results:**The overall prevalence of *Klebsiella* spp and *Streptococcus* spp was 80 (40%) and 120 (60%) respectively. The antimicrobial susceptibility pattern showed that *Klebsiella* spp. were highly sensitive to Levofloxacin and Ciprofloxacin while been resistant to Amoxicillin and Ampiclox. *Streptococcus* spp. showed sensitivity to Ciprofloxacin, Levofloxacin and Augmentin.**Conclusion** The results of this study demonstrated that the prevalence of bacterial pneumonitis among children in northern Nigeria is relatively high. The findings of this study suggest that effective prevention and control strategies need to be encouraged in this part of the country to reduce the incidence and mortality associated with this bacterial infection.

Keywords: Prevalence, Bacterial, Paediatric, Bronchopneumonia, Metropolis

Paper ID (*HE008*.)

Isolation and Characterization of Microorganisms from hands of Food Handlers in Yaba College of Technology and its Public Health Effect

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Abstract

Background: Food vending is a crucial public health issue due to the prevalence of foodborne diseases, and food handlers often lack adequate safety measures. This study aimed to examine the potential for food handlers' hands to serve as a vector for foodborne contaminants and to emphasize the importance of personal hygiene and sanitary practices among food vendors. **Materials and Methods**: Ten food vendors were sampled by swabbing their hands, and the swabs were tested for bacterial and fungal contaminants. The types and prevalence of microorganisms present on the food vendors' hands were analyzed using Biochemical and Morphological methods. **Results:** Six types of bacteria and four types of fungi were isolated from the 10 food vendors sampled. The bacteria included *Staphylococcus spp* (25%), *Escherichia spp* (16.7%), *Proteus spp.* (12.5%), *Klebsiella spp.* (12.5%), *Bacillus. spp* (20.8%), and *Enterobacter spp* (12.5%). The fungi were *Aspergillus spp* (50%), *Mucor spp* (10%), *Penicillium spp* (20%), and *Rhizopus spp* (20%). The observational approach revealed poor personal hygiene and sanitary practices among the food vendors.**Conclusion**: The study highlights the importance of personal hygiene and appropriate hand-washing techniques among food handlers. All food handlers should undergo adequate training on personal hygiene practices to prevent the spread of foodborne diseases. The study also suggests the need for better food safety measures in food vending establishments to protect public health. The findings emphasize the significance of food handlers' hands as a potential carrier of foodborne contaminants and a potential source of foodborne disease outbreaks.

Keywords: Food vendors, Hand hygiene, Microorganisms, Food safety, Foodborne diseases.

Paper ID (*HE009*)

Evaluation of the Antifungal Efficacy of Hand Sanitizers on *Candida albicans* Associated with the Hand

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Abstract

Background: The use of hand sanitizers as infection control regimen is essential in breaking the chain of transmission of infections spread in human population.**Materials and Methods:** In this study, a total of Thirty (30) samples made up of ten (10) different brands of hand sanitizers were randomly purchased in triplicates from patent medicine vendors (PMV) and cosmetic shop owners within Sokoto metropolis, Northwest Nigeria. Their efficacies were evaluated against the fungal isolate, *Candida albicans* associated with hands of study participants. The fungal isolate was identified by cultural and microscopic examination as well as biochemical tests. The hand sanitizers selected were coded as: BTG-HS, IMJ-HS, DTM-HS, PAS-HS, LVE-HS, DT-HS, CBC-HS, SPT-HS, ALV-HS and GMB-HS. The efficacy of the test formulations was evaluated using the agar well diffusion test and the zone of inhibition recorded against the fungal isolate. Also the minimum inhibitory concentration (MIC) and minimum fungicidal concentration (MFC) studies of the products was conducted, to determine the fungal load reduction; time kill assay and the inuse potency test.**Results and Conclusion:** The result of the agar well diffusion test indicated that DT-HS showed the widest mean zone of inhibition of 26.4±2.8mm. The MIC and MFC test results indicated that DT-HS and SPT-HS were both fungistatic each at 50% concentration while three (3) products, IMJ-HS, DT-HS and SPT-HS were fungicidal each at 100% concentration. The time kill test result showed that only DT-HS caused the highest logarithmic killing of 2.17 (Log_{10} 2.17) of *Candida albicans* 30 seconds after applying the test formulation. The in-use potency test result further revealed that DT-HS showed the highest fungal load reduction of 99.81% of viable cells of *Candida albicans* 30 seconds after applying the test formulation. None of the products met the ASTM E2315, (2008) and the EN1650, (2013) performance protocol. Regulatory Bodies are therefore encouraged to carry routine inspection of hand sanitizers sold within the study area to intercept and destroy substandard products sold to unsuspecting members of the public.

Key words: Hand sanitizer, Fungi, Efficacy testing, Performance Protocol

Paper ID *(HE010)*

Antimicrobial, Antioxidant, and Phytochemical Constituents of the Fermented Seeds of *Nigella sativa*

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Abstract

Background: *Nigella sativa* commonly called black seed has been used in traditional medicine worldwide to treat a wide range of ailments. **Method:** This study assessed the pH, phytochemical constituents, *in -vitro* antimicrobial screening against *Staphylococcus aureus, Salmonella typhi, and Escherichia coli* using the agar well diffusion method and antioxidant potentials of the 14-day fermented seeds of *N. sativa* by ABTS 2,2'-azinobis-(3-ethylbenzothiazoline-6-sulfonic acid) and DPPH (2,2-diphenyl-1-picrylhydrazyl) methods. **Results and Conclusion:** The acidity of the sample was revealed by the decline in its pH from 5.50 ± 0.01 to 3.52 ± 0.03 during days of fermentation. In addition to the presence of phenols and tannins on days 7 and 14, phytosterols were only present on the 7th day but absent on the 14th day while saponins were detected in the sample only on the 14th day. The antimicrobial analysis was measured by the diameter of the zones of inhibition obtained, which were in accordance with the tested concentrations (100%, 50%, and 25%). The recorded zones of inhibition for 100mg/mL were (10.0 ± 1.2 mm to 24.0 ± 1.4 mm) And the 25mg/mL concentration zones of inhibition obtained were 5.0 ± 0.8 mm to 14.0 ± 1.2 mm against the organisms. There was a direct link between the antioxidant activity of the fermented sample of *N. sativa* and the concentration of the sample tested. Hence, this study suggests that the antioxidant and antimicrobial potentials of the fermented seeds of *N. sativa* convey their therapeutic relevance in herbal medicine against the selected organisms.

Keywords: Antibacterial, Antioxidant, Black seed, Fermentation, *Nigella sativa*.

Paper ID *(HE011.)*

Antibiotic Susceptibility Profiles of Vibrio species Isolated from Dumpsite Soils in Zaria, Kaduna State Northern Nigeria.

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Abstract

Vibrio species infections remain a serious threat to public health and waste management has emerged as one of the greatest challenges facing environmental protection agencies in Nigeria. This study was therefore, designed to assess the prevalence of *Vibrio* species in Zaria Metropolis dumpsite soils, and their antibiotics susceptibility patterns. A total of one hundred and twenty (120) soil samples were collected from sixteen waste dumps in four locations in Zaria Metropolis. The locations were Sabon-Gari, Samaru, Tudun-Wada and Zaria City over a period of twelve months. Vibrio species were isolated after enrichment in alkaline peptone water (pH 8.6) and streak on Thiosulphate-Citrate-Bile-Salt-Sucrose (TCBS) agar. Seven 7(5.83%) isolates were confirmed to be *Vibrio cholerae* non-O1 using *Vibrio cholerae* O1 and *Vibrio cholerae* O139Antisera and were tested for susceptibility against ten commonly used antibiotic which include Streptomycin (10µg), Erythromycin (15µg), Chloramphenicol (30µg), Ciprofloxacin (5µg), Penicillin (10µg), Norfloxacin (10µg), Ampicillin (10µg), Amoxicillin (10µg), Cephalexim (30µg) and Sulphamethoxazole (25µg). Results revealed a higher prevalence 4(57.14%) of isolates in samples taking from Tundun-Wada as compared to 0(0.00%), 2(28.57%) and 1(14.29%) for Samaru, Zaria city and Sabon-Gari respectively. For the antimicrobial susceptibility test, the highest resistance obtained (38.27%) among Vibrio species isolates was observed to Ampicillin and Penicillin. The isolates were Multiple Antibiotic Resistance (MAR) to 4-6 antibiotics and four different phenotypic resistance profiles were observed among them. The origin of this resistance could be trace to the faecal constituent of the waste dumps produced by people or animals that have been treated indiscriminately with various antibiotics or items containing residual antimicrobial agents disposed of in dump sides. There is need for consistent monitoring programme by appropriate regulatory agencies to ensure regular removal and effective management of wastes.

Keywords*:* Waste Management, *Vibrio* species, Prevalence, Antimicrobial Resistance, Multiple Antibiotic Resistance.

Paper ID *(HE012)*

Antibiotic Susceptibility Profile of Isolated Bacteria from Sachet Water Sold on the Streets in Sokoto Metropolis

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Abstract

Background: Sachet water is a major source of drinking water for low- and middle-class Nigerians. Antibiotics resistant bacteria have previously been isolated from drinking water in Nigeria. Antibiotic susceptibility profile of isolated bacteria from sachet water sold on the streets in Sokoto metropolis was therefore investigated. **Materials and Methods**: Twenty-five sachet water samples comprising 5 different brands were randomly purchased on the streets in Sokoto. Isolation and identification of bacteria in the water samples was done by mixing 1ml of water sample with 9ml of buffered peptone water as pre-enrichment and incubated at 35ºC for 24 hours. The 24 hours' culture was then streaked on several selective media namely Mannitol Salt Agar (for *Staphylococcus species*), Cetrimide Agar (for *Pseudomonas species*), MacConkey Agar (for *Shigella species* and *E. coli*) and Salmonella-Shigella Agar (for *Salmonella species*) followed by some biochemical tests. *Bacillus species* were isolated by heterotrophic plate count method followed by Gram staining. Gram-positive spore-bearing isolates were identified as *Bacillus species*. Antibiotic susceptibility test was carried out on the isolated bacteria against four antibiotics namely nitrofurantoin (300µg), ampicillin/sulbactam (30µg), levofloxacin (5µg) and oxacillin (1µg) using the agar disc diffusion method. **Results and Conclusion**: The isolates identified were *Staphylococcus species, Pseudomonas species, Klebsiella species, Bacillus species, and E. coli*. *Staphylococcus species* had the highest percentage occurrence of 40% while *Klebsiella species* had the lowest percentage occurrence of 10%. It was observed that all of the isolates were sensitive to levofloxacin with values ranging from 26 to 40mm; all but *Pseudomonas species* were sensitive to nitrofurantoin with values ranging from 21 to 24mm, while all organisms were resistant to ampicillin/sulbactam and oxacillin with value of 0mm, using CLSI standard. Emergence of resistant bacterial isolates to ampicillin/sulbactam and oxacillin needs to be taken seriously as it may lead to great economic loss as a result of failure in clinical treatments.

Keywords: Antibiotic, Susceptibility profile, Resistant bacteria, Sachet water, Sokoto metropolis.

Paper ID *(HE013.)*

Antimicrobial activities of ethanolic extracts of *Salvia officinalis* leaves on *Proteus mirabillis*

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Abstract
Background: Proteus mirabilis is among the most isolated microorganisms in reported cases of Urinary Tract infection (UTI). It has shown significant resistance to several conventional antibiotics. Alternatively, this research focused on discovering the effectiveness of ethanolic extracts of *Salvia officinalis* leaves on *Proteus mirabilis* isolates. Methods: Sterile containers were used to obtain clean-catch urine samples from 20 hospitalized patients who are between the ages of 18-50. Spread-plate technique was used to culture samples on MacConkey agar for 24 hours at 32^0C. Suspected colonies from a pure culture with a pale-smooth appearance and urease-positive were subjected to molecular identification of the *Ure*R gene using PCR. Following the respective evaporation of the crude ethanolic extracts of the dried and fresh leaves, 2.0mg, 4.0mg, 6.0mg, 8.0mg, and 10.0mg were dissolved into 10ml dimethyl-sulfoxide respectively. Antimicrobial susceptibility test was conducted using the Agar-well diffusion technique. Results: The zones of inhibition (ZIB) measured for the dried leaves ranged from 12-26mm for the various ethanolic concentrations 2.0mg-10ml, 4.0mg-10ml, 6.0mg-10ml, 8.0mg-10ml, 10.0mg-10ml respectively, while the ZIB recorded for the fresh-leaves ranged from 10-24mm. No significant ZIB (≤3mm) was seen on the negative control which was the ethanol without extract. Ciprofloxacin 30µg was used as a positive control (≥29mm) Conclusion: Dried-leaf extracts of *Salvia officinalis* presented better antimicrobial activity on *Proteus mirabilis* compared to fresh-leaf extracts. The moisture content of fresh leaves was observed to favor microbial growth. Ultimately, this research successfully demonstrated the potential of *Salvia officinalis* as a medicinal plant in treating infections caused by *Proteus mirabilis*.

Keywords: Antimicrobial resistance, Plant extract, *Proteus mirabilis*, *Salvia officinalis*, UTI

Paper ID *(HE014.)*

Frequency of Active Cough among Paragonimiasis Patients in Coastal Communities in Calabar, Nigeria

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Abstract

Background: This study was aimed at investigating the epidemiology of paragonimiasis in two communities in Calabar suburb, namely Akpabuyo and Calabar-South. **Materials and Methods**: Seven sputum examinations per person were carried out for the presence of *Paragonimus uterobilateralis* eggs/ova. Frequency of active coughing per 15 minutes by each candidate was recorded. **Results and Conclusion**: The overall prevalence was 28.2% and 15.6% respectively. The Geometric Mean Intensity of Paragonimus eggs/ova was 87 and 63 per $5ml^{-1}$ of sputum respectively, and comparable between the sexes. Prevalence of active cough was 47.6%, and increased with age from those who were 20 years of age and above. Prevalence of reported history of clinical presentations in Akpabuyo and Calabar South were respectively as follows; cough (88.9% and 72.0%), haemoptysis (23.9% and 14.3%), and chest pain (35.6% and 36.5%). Prevalence of active-cough was very high among fishermen/women in both populations (92.8% and 90.9% respectively). Above 90% of fishermen/women, farming and artisans reported a history of cough, haemoptysis and chest pain in this study. Overall, 42.2% and 43.7% in both populations respectively were crab-eaters. Crab-eating was comparable in both sexes, but higher among those in the two oldest age groups. The risk of being infected was highest among fishermen/women in both populations. The overall risk of being infected with paragonimiasis was (675 times and 44 times respectively) higher among crab-eaters than among non-crab-eaters. Metacercariae crab infection was 5.4% and 5.2% in Akpabuyo and Calabar south respectively. In conclusion, paragonimiasis is endemic in the study areas. Urgent steps are needed to curb the scourge.

Keywords: Paragonimiasis, Coughing, Crab-eating, metacercariae-crab-infection, Calabar.

Paper ID *(HE015)*

Molecular Determinants of Virulence in Pathogenic *Stenotrophomonas maltophilia* Strains from Patients Visiting Mararaba Medical Centre, Nasarawa state

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Abstract

Background: *Stenotrophomonas maltophilia*, a Gram-negative bacterium originating from the soil and plant rhizosphere is an emerging multidrug resistant pathogen in nosocomial settings. It was initially not considered highly virulent but in recent times has acquired traits which in addition to its intrinsic resistance determinants have made it a threat to immunocompromised patients. This study investigated molecular virulence determinants of identified *S. maltophilia* strains using shotgun metagenomics.**Methods:** Faecal metagenomic sample of two patients diagnosed of non-typhoidal Salmonella infection in Mararaba Medical centre, Nasarawa state were sequenced with Illumina NovaSeq platform at 30x depth coverage and analysed using VFAnalyser on Virulence factor Database, ResFinderFG, and PathogenFinder on centre for genomic epidemiology web resource.**Results:** Pathogenic *S. maltophilia* were identified in the samples. The strains SM10 and SM27 contained *smeF, emrB, emrA, emrC* genes which code for efflux pumps; *aph(6)llc, aph(3)llc* for aminoglycoside resistance; *blaL1* for cephalosporin resistance and genes to tolerate mercury and copper toxicity. SM10 and SM27 contained 105 and 106 virulence genes respectively. Genes responsible for immune evasion, biofilm formation, antiphagocytosis, LPS O-antigen, host iron uptake, lysing of host's haem, host magnesium uptake, and stress adaptation, notable in *Acinetobacter, Pseudomonas, E. coli, Salmonella, and Mycobacterium* species were identified in both strains. A transposon (Tn501) and insertion sequence (ISpa36) previously reported in *P. aeruginosa* were identified in both strains. **Conclusion**: Presence of these virulence genes, pathogenic protein families, mobile genetic elements and resistance genes increases the pathogenic and virulence profile of SM10 and SM27, making both strains a threat to human health whose spread should be monitored and curtailed.

Keywords: *Stenotrophomonas maltophilia*, Virulence, Resistance, Molecular determinants, Genes, Pathogen

Paper ID *(HE016)*

Screening for Human Papillomavirus among Women in Adamawa and Taraba States North-Eastern, Nigeria

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Abstract

Background: Human Papillomavirus (HPV) is an epitheliotropic and etiological agent of cervical cancer that is responsible for more than 99% of all Cervical Cancer which is the major gynaecological malignancy and the second most common cancer among women worldwide. The objectives of this study was to Screen and determine the Prevalence of HPV using Visual Inspection with Acetic Acid (VIA) and Pap Smear test among Women in Adamawa and Taraba states of Nigeria. **Materials and Methods**: A total of four hundred and thirty-two (432) women who met the inclusion criteria were recruited for the study in Adamawa (210) and Taraba (222) State. The age range for the participants was between 15-55 years. This was a descriptive survey study. The prevalence of HPV infections was determined using visual inspection with 5% diluted acetic (VIA)/and or lugol's iodine (VILI) and Pap test. **Results and Conclusion**: From the 432 women screened, 170 were positive for precancerous lesions using VIA/VILI given a prevalence rate of 39.4%. Taraba State had the highest overall HPV prevalence at 56.5% while Adamawa State had 74 positive cases with a prevalence of 43.5%. However, there was no significant difference between States and HPV infections. (χ^2_{VIA}= 2.898; α=0.05). For Pap smear screening, 195 (45.1%) of the women in both States were positive for abnormal cytology. Taraba State 111(56.9%) had higher cases for abnormal cytology than Adamawa State 84(43.1%). There was no association between HPV infection and State (χ^2_{VIA}=5.453; α=0.05). based on marital status the highest prevalence was observed among married women 94(55.3%). The prevalence of HPV infection based on age group 35-44 years had the highest incidence of 90(46.2%) and 83(48.8%) for both VIA and Pap respectively. The results of this study have provided more detailed information about HPV and may contribute significantly to the prevention of cervical cancer through primary high-risk HPV testing and HPV vaccination against the oncogenic viruses.

Keywords: Cervical cancer, human papillomavirus, precancerous, cytology.

Paper ID *(HE017.)*

Fulfilling *in vitro* Bacterial Cell Surface Properties do not translate to *in vivo* Probiotic Functions

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Abstract

Background: In this study the hypothesis of whether *in vitro* bacterial cell surface properties correlate with *in vivo* probiotic functions was assessed. **Material and Methods:** Two divergent *Bacillus subtilis* strains isolated from *iru*, an indigenous fermented *Parkia biglobosa* (Jacq. Benth) food condiment in West Africa, characterized using phenotypic and polyphasic genomic DNA fingerprinting techniques, in combination with reference *B. clausii* UBB-07 (MTCC 5472) strain, were evaluated for their *in vitro* probiotic properties. **Results and Conclusion** *B. subtilis* U146A possessed the highest hydrophobicity of 44.96%, 44.11% and 61.73% for *n*-hexadecane, toluene and chloroform, respectively. It autoaggregated very rapidly, compared to the other two *Bacillus* strains, and this increased with time, over a period of 4 h. Again, *B. subtilis* U146A formed the strongest coaggregation phenotype with *Salmonella enterica* subsp. *enterica* serovar Typhimurium LT2. On the contrary, *B. clausii* UBB-07 with the least cell surface features significantly adhered to differentiated and undifferentiated HT-29 cell lines (note: HT-29 monolayers mimic the *in vivo* conditions) more than others, while *B. subtilis* U146A with the maximum hydrophobic interactions, autoaggregation and coaggregation was the least adhered strain. *B. clausii* UBB-07 also demonstrated the greatest inhibition of adhesion to HT-29 cells by *S. enterica* serovar Typhimurium MBU 1047 under exclusion, competition and displacement assays. Findings from this study have established that there is no direct relationship or correlation between bacterial cell surface properties and attachment to human epithelial cells, required for gut colonization and expression of probiotic functions. Hence, bacterial cell surface characteristics only may not be adequate in determining the adhesion indices of probiotic strains for *in vivo* applications.

Keywords: *Bacillus subtilis*, food condiments, *in vitro*, probiotic functions, *in vivo*.

Paper ID *(HE018.)*

Knowledge and Attitude towards Human Papilloma Virus Infection, Vaccines, and Cervical Cancer Prevention among Students in Two Universities in South-Eastern, Nigeria

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Abstract

Background: The insurgence of human papillomavirus (HPV) infection and cervical cancer cases in Nigeria are alarming. HPV is the commonest viral sexually transmitted infection in the world and HPV type-16 and 18 are known high risk types that is the leading cause of cervical cancer. Rare studies have been carried out among Nigerian University students (postgraduate or undergraduate students) on understanding of HPV infection and their attitude towards vaccine acceptance. **Materials and Methods**: The study was questionnaire based which involved 800 students from two Universities in South East, Nigeria participated in this survey with the aim of evaluating their level of knowledge and attitudes concerning HPV infection, prevention and cervical cancer preventive measures. The study further sensitized the participants on HPV vaccination, the health effects of HPV infection and its possible cancer outcome.**Results and Conclusion**: The study revealed that only 257 (32.1%) and 300 (37.5%) participants have knowledge about HPV and cervical cancer, respectively. Furthermore, none of the participants have been administered with HPV vaccine, with 93% of them not ready to take the vaccine. It was observed that the majority of the participants (98%) believed that early hospital visits could help in mitigating HPV or cervical cancer infection. The perception of the participants were observed to be significantly ($p < 0.05$) different after the sensitization versus before. Effective awareness creation amongst students, non-students and the general public is necessary in HPV vaccination, and in abating the burden of cervical cancer in southeast Nigeria.

Keywords: Cervical, Cancer, Infection, Vaccination, Papillomavirus

Paper ID *(HE019.)*

Characterisation of Infectious and Inflammatory Markers of Prostate Cancer in Nigerian Men

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Abstract

Background: Prostate cancer is the second most diagnosed cancer in men worldwide. It has been hypothesized that infections leading to inflammation may significantly contribute to prostate cancer development. New findings suggest that bacterial toxins may play a role in the development of prostate cancer. This study was conducted to identify genotoxin-producing *E. coli* and inflammatory markers of prostate cancer in Nigerian men.**Materials and Methods**: This study recruited 70 adult males (47-95 years) attending the Urology Clinics of the Lagos State University Teaching Hospital, Ikeja and the Federal Medical Centre, Abeokuta. Subjects without prostate cancer served as controls. Midstream urine (30ml) and blood (5ml) samples were collected from the study participants. *Escherichia coli* was isolated from urine samples and analyzed for the presence of colibactin (clb) and cytolethal distending toxin (cdt) genes by polymerase chain reaction (PCR). The presence of C-reactive protein was detected in serum samples using human c-reactive protein (CRP) ELISA kit.**Results and Conclusion**: *Escherichia coli* was isolated from 31.4% (22/70) of the study participants. The prevalence of clb and cdt genes in the urine of study participants is 22.7% (5/22) and 0% (0/22), respectively. We found no association between urinary genotoxins and prostate cancer in the present study ($p = 0.63$). A significant difference was observed in serum levels of CRP between prostate cancer patients and controls. CRP levels were associated with prostate cancer development, prostate-specific antigen (PSA), and Gleason score. The association between infection with genotoxic bacteria and prostate cancer in Nigerian men requires additional investigation.

Keywords: *Escherichia coli*, genotoxins, inflammation, prostate cancer, c-reactive protein.

Paper ID *(HE020.)*

Antimicrobial effects of aqueous extract of *Garcinia kola* nuts on *Salmonella* isolates from Chicken droppings

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Abstract

Background: The onerous threat of antimicrobial resistance to public health highlights the need for continuous research that will discover more potential medicinal plants that possess inhibitory potentials on bacteria especially those with multidrug-resistant qualities. Hence, this study investigated the antibacterial effect of hot and cold aqueous extracts of *Garcinia Kola* on *Salmonella* isolates.**Methods**: Sterile universal containers were used to collect one gram each of chicken fecal samples from domestic chicken coops and dissolved in Buffered Peptone Water to recover injured cell. A loop-full of the sample was streaked on prepared Salmonella-Shigella Agar plates. Suspected isolates were confirmed molecularly using PCR to identify the invA virulent gene from the isolate. Hot and cold water served as a menstruum for extracting bioactive contents from Garcinia Kola. Following evaporation of the crude hot and cold-water extracts, 0.25mg, 0.5mg, 1.0mg, and 2.0mg of the extract were respectively dissolved into 10 ml of distilled water. The Agar-well diffusion method was used in conducting the antimicrobial susceptibility tests**. Results**: Significant zone of inhibition (ZIB) of 9mm, 12mm and 17mm was observed for isolates subjected to 0.50mg-10 ml, 1.00mg-10 ml, and 2.00mg-10 ml concentrations of cold-water extracts respectively while No zone of Inhibition (NZI) was observed at 0.25g-10 ml concentrations. For hot water extracts, growth inhibition ranging from 9mm, 11mm, 15mm, and 23mm was respectively noticed for concentrates of 0.25mg-10 ml, 0.50mg-10, 1.00mg-10 ml, and 2.00mg-10 ml. Heavy growth persisted for the negative control plate which contained distilled water without extracts. Augmentin 30µg was used as a positive control (≥31mm) **Conclusion:** This research simply has amplified the medicinal importance of the consumption of *Garcinia Kola* particularly as it relates to the management of gastroenteritis caused by Zoonotic Non-enteric *Salmonella*. However, the clinical toxicity and safety of the plant need more understanding.

Keywords: Antimicrobial resistance, Aqueous, Chicken, *Salmonella*, *Garcinia Kola.*

Paper ID *(HE021.)*

Occurrence of Multi-Drug Resistance and Extended Spectrum β-Lactamases in Meat from Livestock Farms in Aba, Nigeria.

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Abstract

Background: This study was aimed at determining the muti-drug resistance of *Escherichia coli* and *Klebsiella pneumoniae* and ESBLs production in cow, pig and poultry farms in Aba, Nigeria. **Materials and Methods**: A total of 110 rectal swabs and 100 raw meat samples were obtained from cows and pigs while 90 samples each of cloacal swabs, faecal droppings and drinking water were obtained from the poultry farms. The samples obtained were processed following microbiology laboratory standards. The isolates were identified and characterized using their cultural and morphological characteristics and confirmed by subjecting them to biochemical tests and molecular confirmation. Antibacterial susceptibility test was performed with the disc diffusion method according to the procedure of the Clinical and Laboratory Standards Institute. ESBL production was screened and confirmed using a double disc synergy assay. **Results and Conclusion**: Out of 110 rectal swabs and 100 raw meat (beef) samples of cow assessed, 39% and 34% *E. coli* isolates and 32% and 30% *K. pneumoniae* were obtained, respectively. A total of 36% isolates of *E. coli* and 34.6% isolates of *K. pneumoniae* were obtained from 110 samples of rectal swabs of pig. Out of the 100 samples of raw meat (pork), 35% and 61% isolates of *E. coli* and *K. pneumoniae* respectively were obtained and only 55.6% *E. coli* isolates in the faecal swab (FS) were obtained. *E. coli* and *K. pneumoniae* isolates obtained in the three farms were very resistant to ceftazidime (30µg), and amoxicillin-clavulanic acid (20/10 µg). The isolates were very susceptible to colistin(10µg), and amikacin(30 µg). A total of 48.8% and 50.8% strains of *E. coli* and *K. pneumoniae* respectively from the three farms with more than half being resistant to different classes of antibiotics. ESBLs were obtained more from poultry samples (47.3%) while the lowest ESBLs producers were obtained from the cow (24.3%) samples. Livestock farmers should minimize the use of antibiotics.

Keyword: Multi-drug-resistance, *E. coli*, *K. pneumonia*, Livestock, ESBLs

Paper ID *(HE022.)*

Evaluation of the Antimicrobial Activities of *Allium sativum*, *Garcinia kola* extracts and *Persea americana* Essential oils against some Clinical Isolates

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Abstract

Background: The study is aimed at determining the antimicrobial activities of *Allium sativum* extracts, *Persea americana* essential oil and ethanol and aqueous extracts of *Garcinia kola* against some clinical isolates. **Materials and Methods**: Twenty (20) fruits of *P. americana*, 50 cloves of *A. sativum* 300 seeds of *G. Kola* were used in this study. The essential oil (EO) of *P. americana* was obtained by hydrodistillation, while ethanolic and aqueous extracts of *G. kola* were obtained by cold and hot extraction using water and ethanol (70%) as solvents. The *A. sativa* extract was derived directly from its juice. The EO, juice and extracts were dissolved and diluted in 0.05% ethanol and reconstituted in water to give concentrations of 25% (v/v), 50% (v/v), 75% (v/v), and 100% (v/v) while *G. kola* extract was diluted to 250, 125, 62.5 and 31.25 mg/ml. Twenty-five (25) mg/ml of chloramphenicol and 1 ml of distilled water were used as positive and negative controls respectively. Nose, mouth and wound swabs were cultured in different selective media for bacteria and fungi identification following standard microbiology procedures. The antibacterial and antifungal susceptibility assays were performed using agar well diffusion and disc diffusion techniques**. Results and Conclusion**: Fourteen (14) *Staphylococcus* species were obtained. Other isolates include, *Mucor sp, Rhizopus sp, Fusarium* sp, *Aspergillus* sp and *Candida albicans* were isolated from the samples. At 25% (v/v) and 100% (v/v), *A. sativum* extracts produced the highest zones of inhibitions of (23±0.5 -25±0.6 mm) against *S. aureus*. The *P. americana* EO inhibited *S. aureus* at 100% (v/v) with 23±0.7 mm recorded.The zones of inhibition for *S. aureus* from nose and mouth samples was 24±0.7 mm.. At 62.5 mg/ml, *G. kola* hot, aqueous and ethanol extracts zones of inhibition recorded were 18±0.4 and 20±0.3 mm ; 12±0.6 and 16±0.5 mm respectively against *A. niger*, and *A. fumigatus.* Extracts of *A. sativum*, *G. kola* and *P. americana* should be considered good candidates for topical treatment of infections.

Keywords: Antimicrobial, Essential oil, *A. sativum*, *G. kola*, *P. americana*

Paper ID *(HE023)*

Prevalence and Risk Factors of *Mycobacterium tuberculosis* and Human Immunodeficiency Virus Coinfection Among Patients on Antiretroviral Therapy in a Specialist Hospital, Lokoja

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Abstract

Background: Worldwide tuberculosis (TB) prevalence increased as a result of the Human Immunodeficiency Virus (HIV) epidemic. Nevertheless, the widespread use of efficient antiretrovirals has lately reversed the trend. **Material and Methods:** This study was carried out to detect *Mycobacterium tuberculosis* using GeneXpert in HIV seropositive patients attending Kogi State Specialist Hospital, Lokoja. The study was done using 325 confirmed HIV patients (86 males and 239 females). A structured questionnaire was administered and 325 patients who consented were enrolled in the study. Sputum specimen (2 ml) was collected from each patient, processed, and examined using Xpert® MTB/RIF Assay Version 4. **Results and Conclusion**: The prevalence of HIV/TB was found to be 6 (1.85%). Infection was more prevalent in the age group 26-35 years (3.92%) and among the females (83%) than their counterpart males (17%). Co-infection was found only among the married (2.43%). A higher prevalence (1.89%) was found in patients from monogamous families (2.41%) and in patients residing in rural areas compared to urban dwellers (1.65%). Occupation-specific prevalence showed that farmers had the highest prevalence (2.56%) followed by those who identified as traders (2.16%) and civil servants (1.79%). Yet among patients who identified as students, no incident of TB was observed. Patients with secondary education had the highest prevalence (3.08%) followed by patients with tertiary education (1.58%). Patients with no formal education and primary education had no co-infection. Between the sociodemographic factors that were assessed and the HIV patients who had TB infection, there was no statistically significant correlation (P>0.05). The rate of HIV/TB co-infection, though low in this study, could worsen the clinical outcomes in affected patients. Therefore, there should be increased public health awareness of TB and HIV transmission and prevention in the study area.

Keywords: HIV, Tuberculosis, Coinfection, Antiretroviral therapy, Nigeria.

Paper ID *((HE024)*

Antibiotic Sensitivity Pattern of *Salmonella* species Isolated from Street Hawked Porridge Beans sold in Bonny Island.

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ABSTRACT

Background

Antibiotic sensitivity testing is the measurement of the susceptibility of bacteria to antibiotics. It is usually carried out to detect bacteria species resistance to some antibiotics. Antibiotic sensitivity testing gives the clinician a broader view on the choice of antibiotics from empirical treatment assessment. **Methodology** This research was carried out to determine the antibiotic sensitivity pattern of *Salmonella* species isolated from porridge beans hawked in Bonny Island from three food vendors. Microscopic, cultural, biochemical and antibiotics susceptibility test assays were carried out to confirm *Salmonella* isolates. **Result** Antibiotics susceptibility tests were performed for the isolates, which exhibited that all *Salmonella* species were susceptible to Ciprofloxacin (CPR)-5μg, Nitrofurantoin (NIT)-30μg, and Oflotaxin (OFL)-5μg. On the other hand, intermediate resistance of the *Salmonella* species to gentamicin (GEN)-10μg, and Cefuroxime (CXM)-5μg, and finally, resistance to Augmentin (AUG)-30μg, Cefuroxime (CAZ)-30μg, and Cefuroxime (CRX)-30μg was recorded. Therefore, it can be stated that hawked foods are possible route of transmission for *Salmonella* in Bonny Island. **Conclusion** However, due to lack of intense antibiotic resistance among these bacteria, most of them can be treated with the antibiotics available in the market. Nonetheless, strict monitoring and regular surveillance is necessary.

Keywords: Ciprofloxacin, Oflotaxin, Cefuroxime, Porridge beans, Augmentin

Paper ID *(HE025)*

Sensitivity of *Staphylococcus* species from Fresh Raw Milk Samples to Common Antibacterial Agents in Parts of Kaduna State, Nigeria

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Abstract

Background: The global problem of antimicrobial resistance is particularly challenging in developing countries of which Nigeria is not left out. The aim of the study is to test the susceptibility or resistance of *Staphylococcus* species from milk samples to some commonly used antibiotics. **Material and Methods** :A total of 592 quarter milk samples, 30 bulk milk samples and 27 swab samples from hands of men that milk the cow were obtained from 12 dairy farms in Kaduna and Zaria, Nigeria. **Results and Conclusion:** One hundred and three (103) Staphylococcal isolates that were Gram positive and catalase positive were identified biochemically, out of which the identities of 51 different Staphylococcal species were confirmed using the Microbact Microgen kit. From these, 30 selected isolates were tested against 9 commonly used antibiotics. These include: Amoxicillin (30mg), Chloramphenicol (30mg), Gentamycin (10mg), Ciprofloxacin (5mg), Vancomcin(30mg), Erythromycin (15mg), Trimethroprim sulfamethozazole (25mg), Tetracyclin (30mg) and Cefoxintin (30mg). The antibacterial sensitivity pattern of the 30 isolates to common antibiotics showed a complete (100%) resistance to Amoxicillin and a complete (100%) susceptibility to Ciprofloxacin, but the isolates showed varying degrees of resistance & susceptibility to the other antibacterial agents, ranging from 0.33-0. 89mm.All the isolates exhibited multiple antibiotic resistance to 3-6 antibiotics. Methicillin resistance was manifested in the resistance of the organisms to Cefoxintin (a surrogate of Methicillin).

Keywords: *Staphylococcus*, Milk, Antibacterial agent, Susceptibility, Resistance

Paper ID *(HE026.)*

Bacteriological Quality of Fresh Cow Milk from Dairy Farms in Parts of Kaduna State, Nigeria

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Abstract

Background: The study was carried out to determine the bacteriological quality of farm fresh raw cow milk with emphasis on the detection of Staphylococcus species. **Methods**: A total of 592 quarter milk samples, 30 bulk milk samples and 27 swab samples of the hands of men that milk the cow were obtained from 12 dairy farms in Kaduna and Zaria, Nigeria. The bacteriological quality of the milk samples were determined by the California Mastitis Test and the Total Viable Staphylococcal Count. **Results and Conclusion**: The prevalence of subclinical mastitis from positive California Mastitis Test (≥+) was 24.5%. The mean Staphylococcal count was 4.2 $\log_{10}$cfu/ml. The number of suspected Staphyloccocal isolates that were Gram positive and catalase positive were 103(number of isolate), which were then biochemically screened down to 51, with their identities *confirmed* using the Microbact Microgen Kit. Among the Staphylococcal species, *Staphylococcus aureus* showed the highest population of phenotypic identity with 38%. This organism is important from public health point of view as they have been associated with the onset of food poisoning in human beings.

Keywords: Milk, Diary farms, *Staphylococcus* species, Zaria.

Paper ID *(HE027.)*

Electrophysiological Characterization of Antibiotic Resistant *Pseudomonas aeruginosa* for Simple Rapid Bioelectrochemical Detection System

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Abstract

Background: *Pseudomonas species* is a Gram-negative rod with promising research characteristics. This study was carried out to characterize antibiotic resistant *Pseudomonas species* using a simple rapid bio-electrochemical detection system. **Material and Methods**: Two hundred (200) clinical samples including urine, wound swab, sputum, and high vaginal swab were obtained from Federal Medical Centre and Specialist Hospital Yola, Adamawa State, Nigeria and were investigated for the presence of *Pseudomonas species*. Isolation and identification of the organisms were done using cultural and morphological characterization, microscopic examination and biochemical reactions, while antibacterial susceptibility and electrogenicity potentials was done using Kirby Bauer dick diffusion (inoculum were standardized to 0.5 Mc Farland- 1 x 10^8 CFU/mL) and cyclic voltammetric analysis methods,. **Results and Conclusion:** Results obtained showed a 12.33±0.29 % occurrence of *isolates*. Percentage resistance of isolates to Ciprofloxacin (10µg/mL) was 91.0±1.0 %, followed by 80.67±1.15 % resistance to Streptomycin (20µg/mL) and Amoxicillin (10µg/mL). All the isolates elicited voltage greater than 100mV, with urine from federal medical center Yola, sample 14 (UFY14) having the highest voltage of 591.36 ± 1.14mV and the least was obtained for UFY85 with 317.16 ± 3.94 mV. Ciprofloxacin (10µg/mL) at the 5th, 4th and 2th hours generated currents of 1.90E-03, 1.70E-03 and 0.30E-03 respectively; While Amoxillin (10µg/mL) at 4th and 2nd hours generated 1.70E-03 and 0.30E-03 currents respectively. In the same vein, Streptomycin (20µg/mL) at the 4th and 2nd hours generated 1.90E-03 and 1.60E-03 currents respectively compared to the control with a current of 0.10E at the 5th hour. Differences in current elicited and cyclic curves pattern showed that the isolates continues to metabolize in the presence antibiotics, thereby exhibiting resistance detectable in less than 5 hours. Based on these results, species of *Pseudomonas* can be considered as a good electrogenic species while microbial fuel cell and cyclic voltammetric analysis can a profitable tools for rapid detection of antibiotic resistant species of *Pseudomonas.*

Keywords: *Pseudomonas species*, voltammetric, electrogenic, fuel-cell, antibiotic resistance.

Paper ID *(HE028.)*

Incidence and Antifungal Susceptibility Testing of Candida species from Urine of Diabetic Patients in University College Hospital, Ibadan

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Abstract

Background: *Candida* species have been linked with humans as harmless commensals for a long time. However, they become opportunistic pathogen in immunologically weak and immunocompromised people including diabetic people. Therefore, the study aimed to investigate the incidence and antifungal susceptibility testing of *Candida* in urine of Diabetic Patients in University College Hospital, Ibadan. **Materials and Methods**: The study was a hospital–based cross-sectional design. Sample size of 179 mid-stream urine in sterile universal containers from 102 (57%) male and 77 (33%) female, regardless of age, gender,tribe or religious affinity, was calculated using Raosoft formular. *Candida* isolates were identified using Gram staining and biochemical methods. Confirmation and speciation of *Candida* was performed on Candida Chrome agar. Antifungal susceptibility testing of the isolates was performed to determine Minimum inhibitory Concentration (MIC) of Fluconazole against isolates. Data generated was analyzed using diagnostic test calculator software, Chi- square, descriptive and inferential statistics. **Results and Conclusion**: *Candida* species were isolated from 16 (8.9%) of the samples which included 9 (5.0 %) *Candida albican*, 6 (3.3%) *Candida tropicalis*, and 1 (0.6%) *Candida glabrata*. Also, 8.2% co-infection of *Candida* with other *Enterobacteria* was observed. Analysis showed no significant relationship between gender and candida isolates (p-value =0.2). Varying MIC of Fluconazole against *Candida* species was observed with 2 µg/ml of fluconazole being the prevalent MIC. The study revealed that candiduria is not gender biased in as much as predisposing factor is present and can also be eradicated if the right antifungal drug is administered at the right concentration.

Keywords: *Candida* species, Diabetes mellitus, Fluconazole, Fungi, Minimum inhibitory concentration,

Paper ID *(HE029)*

Isolation of Antibiotic Susceptibility Pattern of Methicillin Resistant *Staphylococcus aureus* from Wound Sample of Patients Attending General Hospital Minna Nigeria.

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Abstract

Background: Methicillin-Resistant *Staphylococcus aureus* refers to any strain of *S. aureus* that has developed resistance to methicillin and other beta lactam drugs. It is accountable to variety of difficulty to treat human infections. This study aim was to isolate methicillin resistant *Staphylococcus aureus* from Wound sample of Patients Attending General Hospital Minna Nigeria and test their antibiotic susceptibility patterns. **Materials and Methods**: A total of 100 wound samples were collected using sterile swab sticks. All the collected sampls were inoculated onto mannitol salt Agar (MSA) and incubated for 24 hours at 37^{o}C. Using the conventional bacteriological process, which comprises the Gram reaction, catalase reaction, coagulase test, and mannitol fermentation, the suspected *aureus* isolates. From the wound samples 17.0% (17/100) *Staphylococcus aureus* was isolated. The disc diffusion method was used for antibiotic susceptibility patterns of methicillin resistant *Staphylococcus aureus* and the results interpreted according to Clinical Laboratory Standard Institute Guidelines (CLSI). The isolate were tested for susceptibility to methicillin drugs and considered to be resistant to Methicillin when the zone of inhibition around Oxacillin 1ug, Cefoxitin 30ug and Vancomycin 30ug was < 13 mm. **Results and Conclusion**: The results of antibiotic susceptibility pattern of methicillin resistant *Staphylococcus aureus* tests show that *Staphylococcus aureus* exhibited 76.5% resistant to Oxacillin, 23.5% resistant to Cefoxitin and least resistant was accounted against Vancomycin 11.8%. Methicillin resistance rapid spread *Staphylococcus aureus* is concerning, necessitating the establishment of surveillance studies as well as prudent antibiotic use.

Keywords: *Staphylococcus aureus*, Methicillin, Resistant, antibiotics

Paper ID *(HE030)*

Prevalence, Risk factors and Antifungal Susceptibility of Orofungal infections among HIV Patients in three Senatorial Zone in Anambra State

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Abstract

Background: Fungal diseases are life-threatening and are responsible for a largely silent epidemic, often hidden killers causing substantial morbidity and mortality in susceptible individuals. This study aimed at assessing the prevalence, risk factors and antifungal resistance profiling of oro-fungal infections and their causative organisms among HIV-positive patients in Nnamdi Azikiwe teaching hospital; **Materials and Methods**: A total of 180 patients who gave their consent were used for the study carried out from January 2022 to August 2022. Oral swab samples of the patients were taken with the aid of sterile swab sticks, and cultured on Sabouraud's dextrose agar, Chrome agar and blood agar at 37°C incubation. Fungal organisms isolated were characterized accordingly using biochemical test and also with fungal atlas for mold identification. ITS region molecular typing was also used to identify the top four most frequently occurring isolates. Structured questionnaires were used to obtain demographic details of the participants and for risk factors evaluation. Isolates were also evaluated for pathogenicity using haemolysis and enzyme assays. Antifungal susceptibility testing of the isolates was conducted using the disc diffusion method. Data obtained were statistically analyzed. **Results and Conclusion**: The oro-fungi isolated organisms isolated are *Candida albicans, Candida glabrata, Candida krusei, Candid tropicalis, Candid neoformans, Histoplama capsulatum* and *Aspergillus fumigatus.* Overall prevalence of the isolates in the participants (n=180) showed that *C. albicans* was the most prevalent isolate with an occurrence of 84.78% followed by *C. glabrata* (60.33%). *Cryptococcus neoformans* and *Histoplasma capsulatum* were the least occurring isolates with the occurrence of 6.79% and 2.99% respectively. The overall Gender distribution were: NAUTH 88 male (48.89%) and 92 female (51.11%); Age range 36-45 years had the highest frequency of 37.22% while age range >75 years had the lowest patient frequency of 0.56%, distribution based on marital status, married accounted for 60.56% and single patients were 39.44 % frequency. Distribution based on educational level and profession, it was observed that 32.22% of patients that participated in the study had primary school education as their highest accounted for the most population that took part in the study point while those that had university education had the least participation frequency of 21.12%. Artisans had the highest participation frequency of 62.22% while house wives participated the least with a frequency of 5.56%. 15.56% of the participants had Hepatitis B vaccination while 100% of the participants were already participating in HAART. Their antifungal exposure profiling showed that they were mostly exposed to fluconazole at a median frequency of 70%. The result shows a relatively high prevalence of *Candida* infection among HIV patient.

Keywords: Susceptibility, Oro-fungal, Prevalence, Antifungal, Pathogenicity

Paper ID *(HE031)*

Probiotic Potentials of Lactic Acid Bacteria Isolated from Some Nigerian Indigenous Fermented Foods

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Abstract

Background: Lactic acid bacteria (LAB) are responsible for the fermentation of many indigenous foods in Nigeria and may possess probiotic properties which can attribute to the gastrointestinal health of humans and livestock. This study aimed to characterize LAB from some Nigeria indigenous fermented foods.**Materials and Methods**: LAB isolated from nunu, kunnu zaki, ogi and cassava pulp were assayed for antagonistic activities against *Yersinia enterocolitis, Enterococcus cloacae, Escherichia coli, Salmonella enteritidis, Staphylococcus aureus, Klebsiella oxytoca, Citrobacter freundii* and *Serratia liquefaciens* obtained from the Microbiology laboratory of the University of Ilorin Teaching Hospital. The survivability of the LAB isolates in the gastrointestinal tracts was determined by testing their tolerance in acid, bile, phenol, simulated gastric and intestinal juices. Isolate's hydrophobicity, aggregative abilities and haemolytic activities were also assayed. In vivo antimicrobial activity was also determined using *Salmonella enteritidis*-infected broiler chicks. **Results and Conclusion**: Ten of the LAB isolates had antibacterial activities with highest zone of inhibition (28.00±2.00 mm) produced by *Lactobacillus fermentum* against *Salmonella enteritidis*. Also, *L. fermentum* along with *L. brevis, L. plantarum, L. paracasei* and *Pediococcus pentosaceus*, tolerated pH 1.5 and 0.5% bile salt, simulated gastric and intestinal conditions, 0.4 % phenol, and had percentage hydrophobicity, auto- and co-aggregation that ranged between 38.76 - 58.06 %, 34.38 - 54.05 % and 47.21 - 74.64 % respectively. The LAB were non-haemolytic and demonstrated in-vivo antimicrobial activity against *S. enteritidis* in broiler chicks. *L. fermentum* and four other LAB isolated in this study, possess probiotic properties and can be used as prophylaxis against gastrointestinal diseases.

Keywords: Probiotics, lactic acid bacteria, Fermentation, Nigerian indigenous foods, gastrointestinal diseases.

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Paper ID *(HE032)*

Current Status of Gastro-intestinal Parasites among Pupils in some Selected Schools in Delta State, Nigeria

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Abstract

Background Gastro-intestinal parasites are micro-organisms that live in the intestine, where they may cause problems or can live for long periods in the bowel without causing any symptoms that may require treatment. Intestinal parasitic infections have been reported to have high prevalence among children in Nigeria because of their vulnerability. **Materials and Methods**: Current status of gastro-intestinal parasites among pupils in five secondary schools in Delta State, Nigeria. The study was investigated between October 2017 and February 2018. A total of 244 stool samples (131 males and 113 females) were collected randomly. The stool samples were analyzed using direct wet mount and the formol-ether (10%) concentration technique. **Results** Out of the 244 stool samples examined, 54(22.13%) were positive for gastro-intestinal parasites based on their ova confirmation, viz: *Ascaris lumbricoides* (58.12%), Hookworm (20.27%), *Strongyloides stercoralis* (1.35%), *Taenia* species (5.41%), *Schistosomia mansoni* (2.70%), *Entamoeba histolytica*/ *dispir* (6.76%) and *Giardia lamblia* (5.41%). There was significant difference ($p<0.05$) between infection and the following: type of school, geographical location, source of drinking water at home, and availability of toilet facility at home in relation to the respondents' feedback when questionnaire was issued. **Conclusion:** There is need for collaboration of the school management, health officers and community leaders on gastro-intestinal parasite control.

Key words: Gastro-intestinal parasite, *Schistosomia mansoni*, *Ascaris lumbricoides* and Hookworm, and Pupils.

Paper ID (HE033)

Biogenic Synthesis of Zinc oxide Nanoparticles using *Lactobacillus fermentii* and its Antimicrobial activity against *Pseudomonas aeruginosa* Biofilm

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Abstract

Background: Biofilm infection leads to different disorders for instance possible cancer development and subsequent increases to the global morbidity rate. Evidence suggests that one of the strongest options for fighting pathogenic biofilm could be probiotics. **Material and Methods:** This study explored the biogenic synthesis of Zinc oxide nanoparticles using *Lactobacillus fermentii* which was characterized using Biochemical test's following Bergey's manual and the antimicrobial activities of the nanoparticles against *Pseudomonas aeruginosa* biofilm was determined. Lactobacillus strains were isolated from Fura and Nunu while the Biofilm was grown from a wild-type *Pseudomonas aeruginosa* (isolated from soil obtained from the farm of Fountain University Osogbo) which was incubated for 24hrs and grown overnight in Lysogeny broth which was diluted in a fresh M63 minimal medium to form the Biofilm.The growth of Biofilm was inhibited using the strains of Lactobacillus that were isolated using "Liquid Co-culture Assay in microtiter Plate" method. The antimicrobial compound which was verified using McFarland standard was carried out as well as the Lactic acid content and hydrogen peroxide production was carried out using the process of titration. The inhibitory effect was estimated and *Lactobacillus fermentii* was used in for the synthesis of Zinc Oxide Nanoparticles which was used to inhibit the formation of Biofilm. **Results and Conclusion:** The *Lactobacillus* strains were identified to be *Lactobacillus fermentii* and *Lactobacillus delbrueckii*. The Lactic acid and hydrogen peroxide production was carried out at an interval of 0-72hrs with a pH range from 5.15 - 4.06 by the third day for *Lactobacillus delbrueckii* and a pH ranging from 5.45 4.38 by the third for *Lactobacillus fermentii.* After the three days estimation of the lactic acid content and hydrogen peroxide, the growth of biofilm was inhibited by *Lactobacillus fermentii* and *Lactobacillus delbrueckii* and was confirmed by measuring the absorbance level at 570nm using a spectrometer

Keywords: Probiotics, Biofilm, Zinc Oxide Nanoparticles, Liquid Co-culture Assay, microtiter Plate.

Paper ID *(HE034.)*

Antibiotics Susceptibility Pattern and Molecular Characterization of Enterotoxigenic *Baclllus cereus* strains Isolated from Food Consumed by School Children in Ilorin Metropolis

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Abstract

Background: Food poisoning is caused by toxin produced by pathogenic organisms like bacteria, viruses etc. These toxins are common causes of food borne illness. *Bacillus cereus* is a known agent of food intoxication. This study was carried out to determine antibiotic susceptibility patten and detect enterotoxigenic gene in *Bacillus cereus* strains isolated from food consumed by school children in Ilorin metropolis **Materials and Methods**: Six strains of *Bacillus cereus* identified as *Bacillus cereus* (OQ235070), *Bacillus cereus* (OQ235071), *Bacillus cereus* (OQ235072), *Bacillus cereus* (OQ235073), *Bacillus thuringiensis* (OQ235074), *Bacillus cereus* (OQ235075) and *Bacillus cereus* (OQ235076) were obtained from culture collection of the Microbiology laboratory, Kwara State University, and were used for this research. Antibiotic susceptibility test was carried out on the isolates using standard technique. Detection of resistance gene, plasmid profiling and curing, and detection of enterotoxigenic genes were done using standard microbiological methods. **Results and Conclusion**: All the isolates were resistant to minimum of two antibiotics before and after plasmid curing. The study discovered that 98 % of the isolates were susceptible to Ofloxaxin (5µg), Centamincin (10µg), Pefloxacin (5µg) and Augmentin (30µg), while 90 % of the isolates were resistant to Amoxylin(25µg), Streptomycin (10µg), and Chloramphenicol (30µg), . Plasmid profiling showed that all the *Bacillus cereus* isolated harbored mega plasmid with equal size of 5000 bp. Curing removed all the plasmid, presence of enterotoxin virulence gene nhe A, B, C and hbl C, D were observed but hbl A was not found. In conclusion the *Bacillus cereus* strains studied were found to be multi-drug resistant and carried enterotoxigenic genes.

Keywords: *Bacillus cereus*, Enterotoxigenic, Plasmid profiling, Plasmid curing, Food poisoning, School children

Paper ID *(HE035.)*

Antibacterial Activity and Acute Toxicity of *Tamarindus indica* against Methicillin Resistant *Staphylococcus aureus* Isolated from Hospital Environment.

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Abstract

Background: This study was aimed at providing alternative antimicrobials drugs through the determination of the antibacterial activity and acute toxicity of *Tamarindus indica* (Tamarind) against methicillin resistance *Staphylococcus aureus* (MRSA) isolated from hospital environment, using n-hexane and methanol as extraction solvents. **Material and Methods:** The test organism was isolated using cultural, morphological, biochemical and molecular approach, while Qualitative and quantitative phytochemical analysis technique, agar well diffusion and broth dilution techniques were used to determine the phytochemical constituents and antibacterial potency of the plant extracts. Agar-based test using Oxacillin (5mg/L) was employed to confirm that the isolate is MRSA. Eight (8) phytochemical components namely flavonoids, saponins, tannins, phenols, alkaloids, terpenoids, glycosides and steroids were determined. **Results and Conclusion**: N-hexane (5g each of leave and fruit) and methanol fruit extracts had the highest percentage (11.34±0.32%, 10.13±0.00% and 10.05±0.05%) quantity presence of phenol while 10.13% flavonoid was present in methanol leaf extract. Eighteen (18) species were identified, out of which 1 was confirmed *Staphylococcus aureus and* was resistant to Oxacillin (5mg/L) and was designated as *Staphylococcus aureus* (SaD) or D4 which showed amplification bands corresponding to the expected band size (756bp). Methanol extracts of Tamarind fruit was active at 80 mg/mL, while leaf extracts were active at 50 mg/mL. The highest activity with mean inhibition zones (MIZ) of 26.33 ± 0.47mm and 25.33 ± 1.25mm was obtained at a concentration range of 50 mg/mL to 80mg/mL against SaA. Methanol fruit extract had the lowest (1:10 to 1:0.125 dilution range) minimum inhibitory concentration (MIC) (4.69 mg/mL) and minimum bactericidal concentration (MBC) (9.38mg/mL) against the test organisms. Fraction from methanol fruit extract was the most active at 30 mg/mL (26.33 ± 0.47mm) and 50 mg/mL (26.33 ± 0.94mm) against all the test isolates. Acute oral toxicity studies result reveals a safe dose (LD_{50}) of above 5000mg/mL/kgbw. It can be concluded based on these results that *Tamarindus indica* possesses antibacterial activity against resistant strain of *S. aureus.* Therefore, it can be recommended for further studies towards the development of alternative drug.

Keywords: Medicinal plant, *Tamarindus indica*, methicillin resistance, Tamarind, oxacillin.

Paper ID *(HE036.)*

Antibiogram of fungal and bacteria species Associated with Toilet Door Handles in The Students' Residential Hall at Covenant University

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Abstract

Background: This study investigated the presence of fungal and bacteria species on toilet door handles in male and female residence halls at Covenant University and their antibiotic susceptibility patterns. **Materials and Methods**: Forty-eight (48) swab samples were collected from forty-eight (48) toilet door handles using sterile swab sticks between February 2023 – April 2023. Following the isolation of fungal and bacterial species, cultural and morphological characteristics and biochemical tests were used to identify the 21 isolates. Antibiotic susceptibility tests were carried out using the Kirby Bauer method with the following antibiotics: Cefotaxime 30µg (CTX), Ceftazidime 30 µg (CPZ), Tetracycline 10 µg (TET), Cotrimoxazole 25 µg (COT), Gentamycin 10 µg (GEN), Cefuroxime 30 µg (CRX), Chloramphenicol 10 µg (CHL), Ceftriaxone 30 µg (CTR), Ciprofloxacin 5 µg (CIP), Meropenem 10 µg (MEM), Vancomycin 30 µg (VAN), Amikacin 30 µg (AMK), Ampicillin 10 µg (AMP), Erythromycin 5 µg (ERY), Tetracycline 30 µg (TET), Cefuroxime 10 µg (CRX), Augmentin 30 µg (AUG), Ceftazidime 10 µg (CPZ), Cephalexin 1.5 µg (CP). **Results and Conclusion**: A significantly higher number of isolates were obtained from female toilet door handles (57%) than from male toilet door handles (43%). The isolates include *Citrobacter* spp, *Enterobacter* spp, *Escherichia coli*, *Klebsiella* spp, *Enterococcus* spp, *Bacillus* spp, *Staphylococcus* spp, *Pseudomonas spp*, *Proteus* spp, *Micrococcus* spp, and *Candida* spp. The antibiotic susceptibility test showed that all isolates showed no zone of inhibition to Cefuroxime, Cefotaxime, and Vancomycin (100%) and were highly susceptible to Amikacin (100%), Ciprofloxacin (89%), and Cephalexin (88%). It is important to encourage good personal hygiene among students to prevent infection and create awareness of good antimicrobial stewardship.

Keywords: Toilet, Antibiogram, Door handle, Residential halls, Microorganisms.

Paper ID (HE037)

Inhibitors of Protein Targets of *Plasmodium falciparum*

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Abstract

Background: The World Health Organization records over 247 million cases of malaria worldwide, resulting in 619,000 deaths in 2021. Children under five years of age account for more than 70% of these deaths, and Sub-Saharan Africa is the region in which most fatalities occur. The deadliest malaria parasite is *Plasmodium falciparum* and treatment is becoming problematic as more antimalarials lose their effectiveness owing to spread of drug resistance parasites. Artemisinin combination therapies are currently considered the gold standard, but treatment is under threat as parasite exhibits delayed clearance to artemisinin and resistance to partner drugs like lumefantrine, mefloquine, amodiaquine, sulfadoxine/pyrimethamine, piperaquine. This systematic review evaluated drug targets (receptors, ion channels, enzymes, carrier molecules) in *Plasmodium falciparum* for new drug development. **Materials and Methods:** Eighty-five articles on *Plasmodium falciparum* therapeutic targets and protein inhibitors were compiled from Google Scholar, ProQuest, PubMed, and Science Direct. The range of papers was from 2013-2023. 14 publications with relating keywords on inhibitors of protein targets of *Plasmodium falciparum* were retrieved for the review while articles within that range having no definitive data were excluded. **Result and Conclusion:** Most recently, inhibitors of Dihydroorotate dehydrogenase (DHODH), Artefenomel (OZ439), and Ferroquine which has completed phase I and II clinical trials for drug candidates in treating malaria, has been published and are being tested in combination with other partner drug, to act against different stages of the parasite. In selecting proteins for drug discovery, essentiality and vulnerability across the parasite's life cycle, druggability and availability of target-based assays are paramount. Application of modern proteomics and cellular proteins from database search which aids in parasite multiplication gives ideal information on new generation of lead compounds. Additionally, advancements in *in silico* approaches facilities elucidation of protein targets for drug development.

Keywords: Malaria, Resistance, Drug targets, Drug development, sub-Saharan Africa.

Paper ID *(HE038.)*

Identification of New Drug Resistance Marker Genes in *Plasmodium falciparum*

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Abstract

Background: In sub-Saharan Africa, malaria is the leading cause of infant mortality among children and expectant mothers. The World Health Organization statistics report 239 million cases of malaria globally in 2021 with over 588,000 fatalities. *Plasmodium falciparum* is the most severe cause of malaria in Africa. The severity of *Plasmodium falciparum* is traceable to single nucleotide polymorphisms (SNPs) that confer resistance to antimalarial drugs. This systematic review investigated marker genes for drug resistance in *Plasmodium falciparum* in Africa.**Materials and Methods**: The review was conducted through a literature search using two scientific databases (Google Scholar and Public Library of Medicine) which focused on molecular markers for *Plasmodium falciparum* covering the period 2017 to 2022. A total of 4,205 articles were returned with the inclusion criteria focusing on; *Plasmodium falciparum*, single nucleotide polymorphisms, artemisinin, antifolates, chloroquine, antimalarial drugs. Articles were pre-screened by their title and abstract. Articles on resistance marker genes in *Plasmodium falciparum* were downloaded for this review.**Results and Conclusion**: SNPs detected in the *kelch*-13 propeller genes of *Plasmodium falciparum* (C580Y, R539T, I543T, F446L and N458Y) spurred the detection of molecular markers that were determined by DNA methylation profiling, micro-arrays, DNA and RNA sequencing of infected patients' blood. Variations seen in the molecular markers of different variants of *P. Falciparum* could be a result of mutation or the effect of other factors. Thus, in the management of the malaria crisis, *in-vivo* testing and molecular marker detections can help in the predictive surveillance of *Plasmodium* drug resistance across Africa.

Keywords: Malaria, Molecular markers, Drug resistance, Polymorphisms, Genes.

Paper ID *(HE039.)*

Comparative Study of Ethnobotanical Properties of *Tetrapleura tetraptera* from South-South, Nigeria

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Abstract

Background: *Tetrapleura tetraptera* (Tt) is valued for its culinary usage and in treatment of various ailments in the South-South, Nigeria. This study was aimed at comparing the phytochemicals, mineral content, bioactive compounds, antioxidants and antimicrobial properties. **Materials and Methods**: *Tt* samples were aseptically collected from nine markets in three states; Bayelsa, Edo and Rivers States. Ethanolic and aqueous extracts of Tt were freeze dried and reconstituted. Phytochemicals, mineral concentrations, antioxidants properties (PMcAp) and bioactive compounds (BCs) were determined using standard methods and GC-MS analysis. *Tt* extracts were tested against bacteria; *Bacillus spp, Escherichia coli, Pseudomonas spp, Staphylococcus aureus, Salmonella spp* and *Shigella spp* while fungi; *Candida albican, Aspergillus niger, Apergillus flavus, Penicillum expansum* and *Penicillum notatum* using agar well diffusion method and data obtained were analysed using descriptive statistics. **Results and Conclusion**: PMcAp varied significantly ($P<0.05$) within locations and across samples. Alkaloids, coumarin, glycosides, flavonoids, phenolic, steroid, tanins, terpenoids, saponins and triterpenes detected while anthocyannine, amino acid and philobatannin were absent in all the samples and both extracts. Mineral concentrations ranged; Ca(152.50±0.35-171.75±0.21)> K(79.95±0.21-84.40±0.42)> Na(45.68±0.39-51.60±0.42)> Fe(29.02±0.16-38.65±0.35)> Mg(23.70±0.28-26.75±0.49)> Zn(17.50±0.14-20.20±0.41)> Cu(0.50±0.21-1.07±0.01)> Cr(0.01±0.00-0.03±0.01)> Pb(0.01±0.00-0.02±0.01). Antioxidants; DPPH (ug/100g) 10(83.35±0.04-83.83±0.04); 20(84.28±0.00-90.77±0.04); 30(48.37±0.53-87.60±0.04); 40(79.71±0.04-88.43±0.04) and 50(68.73±0.07-126.51±0.07) while FRAP (0.32±0.00-0.39±0.00). Prominent BCs revealed; d-Threo-O-ethylthreonine, 2-Propanamine, 1H-Imidazole, Cyclotetrasiloxane, 2-Cyclopenten-1-one, 3-Isoxazolamine, Toluene-D8, Tiglic acid, N-formyl-dl-methionine, Diisopropyl. Zones of inhibition varies among *Tt* extracts, solvents, across and within the test organisms; *Tt* extracts ranged (3.00±0.02-25.00±0.05mm), ethanolic (4±0.02-25±0.01mm) and aqueous (3±0.02-17±0.00mm) extract. The presence of PMcAp, BCs and antimicrobial activities has elucidated Tt usefulness and potential to be exploited.

Keywords: *Tetrapleura tetraptera*, Phytochemicals, mineral concentrations, antioxidants properties, bioactive compounds.

Paper ID *(HE040.)*

Exploring Validated *pfkelch13* Markers for Detection of *Plasmodium falciparum* Resistance to Artemisinin in sub-Saharan Africa

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Abstract

Background: Prevalence of resistant artemisinin *Plasmodium falciparum* with genetic mutations of *kelch13* (*Pfkelch13*) gene threatens the malaria control through precise detection and elimination efforts. The present review evaluates the prospect of exploring validated *Pfkelch13* markers for detection of prevalent *Plasmodium falciparum* resistance to artemisinin in sub-Saharan Africa. **Methods:** Reports of *Pfkelch13* genes from published articles related to the molecular markers from thirteen studies in Africa, Asia, America and Europe in the last ten years were selected for the review. PubMed (n=6) and Google Scholar (n=7) were searched for these relevant articles while articles published generally on malaria resistance gene markers other than *Pfkelch13* were excluded from the review. **Result:** Despite the efficacy of artemisinin combinations, *Pfkelch13* resistance gene propeller on chromosome 13 domains reported in Southeast Asia is now emerging in sub-Saharan Africa population. More than 260 non-synonymous *Pfkelch13* gene mutations have been reported with thirteen validated markers (C580Y, F446I, N458Y, C469Y, M476I, Y493H, R539T, I543T, P553L, R561H, P574L, R622I, A675V) and nine associated markers (P441L, G449A, C469F, A481V, R515K, P527H, N537I/D, G538V and V568G) were reported in Asia and European countries. Eight of the validated markers (P553L, M476I, C580Y, A675V, P574L, R561H, R622I and F446I) were previously reported in sub-Saharan Africa. **Conclusion:** The *Pfkelch13* verified markers found among the sub-Saharan Africa population are important for the genotyping artemisinin resistance, predictive diagnosis and molecular surveillance of *Plasmodium falciparum* resistance to artemisinin. Exploring these validated markers will enhance preventive measures and provide valuable diagnostic information for effective malaria control in sub-Saharan Africa.

Keywords: Artemisinin resistance, *Pfkelch13* markers, *Plasmodium falciparum*, Mutation, sub-Saharan Africa.

Paper ID *(HE041.)*

Mosquito Species Distribution and Epidemiological Surveillance of Wolbachia-infection in Ota, Ogun State, Nigeria

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Abstract

Background:
Climate change is anticipated to worsen the spread of mosquito-borne diseases like dengue and malaria. It facilitates the spread of mosquitoes, viruses, and other epidemics. Hence, there is a need to continually innovate and design sustainable solutions to this environmental public health challenges. A search for *wolbachia* in mosquitoes in Ota, Ogun State has been spurred by recent reports of detecting *wolbachia*-strain infections in field mosquito species in certain West African nations and the possibility for developing these as disease vector biocontrol strategies. This study aims to use a comprehensive mosquito larval surveillance system of the study location to assess mosquito species distribution and *Wolbachai*-infection.**Materials and Methods**: A comprehensive mosquito larval survey was conducted in different study sites from November 2022 to March 2023 within Ota. Mosquitoes larvae was reared to adulthood, counted, grouped by species, sex, and locations of capture. Adult mosquitoes were identified using the standard taxonomic keys. Identified specimens were labeled and stored at -20 °C for later use. DNA from the mosquito were extracted individually following the protocol described by Livak (sodium chloride precipitation). One microliters from the extract was used for PCR and double distilled water was used as the negative control. **Results and Conclusion**: Larvae mosquitoes (823) emerged as young adults. Of these, 511 (62.1%) were identified morphologically as females, while 312 (37.1%) were males. *Aedes* species accounted for 183 (22.2%) *Anopheles* 306 (37.2%), while *Culex* species made up the remaining 334 (40.6%) of the total population. In this study, DNA taken from mosquito samples using PCR was used to identify the wsp gene, which encodes for the Wolbachia surface protein. The findings demonstrated that the size of the wsp gene in *Ae. albopictus, Ae. aegypti*, ranged from 590 to 632 bp, indicating that *wolbachia* are in some of the mosquito. The mosquitoes analysed showed presence of *Wolbachia*-infection. Continuous monitoring of mosquito population and their breeding sites for Wolbachia infection is useful as possible biocontrol interventions.

Keywords: Wolbachia, Integrated vector control, Mosquito borne disease, Biocontrol, Mosquito.

Paper ID *(HE042.)*

Propagation and Characterization of Wild-type *Plasmodium falciparum* in Ota, Ogun State, Nigeria

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Abstract

Background: *Plasmodium falciparum* malaria still ravages sub-Saharan Africa despite multiple efforts to see its decline. Several prevalence studies carried out within sub-Saharan Africa have established the rising increase *in Plasmodium falciparum* malaria. *In vitro* culture provides a controlled environment for the growth and development of the parasites. *In vitro*, continuous culture of *Plasmodium falciparum* wild-type isolates is important to understanding the phenotypic and genotypic characteristics of parasites in circulation. **Material and Methods:** Blood samples were collected from confirmed symptomatic malaria patients from the Covenant University Medical Centre, Ota, Ogun State Nigeria, with ethical approval obtained from the Covenant Health Research Ethics Committee (CHREC). A Roswell Park Memorial Institute (RPMI) 1640-based medium was used with supplements of 2 mM L-glutamine, 25 mM N-2-hydroxyethylpiperazine-N-2-ethane sulfonic acid (HEPES), 25mM Sodium Bicarbonate ($NaHCO_3$), 1 mg/L hypoxanthine, 5 g/LAlbumax II, 2.5 mg/L Gentamicin, Penicillin-Streptomycin, 5% hematocrit, and 2 g/L D-Glucose with carbon dioxide (CO_2) at 37 ˚C in a CO_2 incubator. A thin smear was prepared from the cultures, microscopy was carried out and staining was done using 3 % and 10 % Giemsa solution for phenotypic identification. **Results and Conclusion:** The results of genetic diversity using MSP2 markers showed that the 3D7 and FC27 families are prevalent in the study site.

Keywords: *In vitro* culture, *Plasmodium falciparum*, Phenotypic identification, Molecular characterization,

Paper ID *(HE043.)*

Mycosynthesis and Characterization of Silver Nanoparticles using *Penicillium oxalicum* filtrate and its Antimicrobial Activities

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Abstract

Background: Mycosynthesis of nanoparticles using biological processes is a good alternative compared to physical and chemical processes because it can be easily scaled up and is eco-friendly and cost-effective. *Penicillium* spp. are saprophytic fungi, which produce secondary metabolites like antibiotics that inhibit the growth of microorganisms. This study was designed to investigate the mycosynthesis and characterization of silver nanoparticles using *Penicillium oxalicum* filtrate and evaluate its antimicrobial activities. **Materials and Methods**: Silver nanoparticles (SNPs) were mycosynthesized using *Penicillium oxalicum* filtrate. SNPs characterization was done using visual observation, UV–visible spectroscopy, scanning electron microscopy, transmission electron microscopy, energy dispersive x-ray (EDX), Fourier transform infrared spectroscopy and x-ray diffractor. Agar well diffusion method was used for the antimicrobial activity. **Results and Conclusion**: There were changes in colour from yellow to brown indicating the formation of SNPs and a strong plasmon resonance peak at 450 nm with a broad band ranging from 350– 550 nm. The SNPs were spherical with size ranging from 20 -50 nm. The presence of amino acids, alcohol, and hydroxyl group indicated the capping and stabilization of proteins in the nanoparticles. The EDX spectra revealed a strong signal for silver element and the crystallographic SNPs. *S. pneumoniae* and *S. aureus* were highly susceptible with zones of inhibition of 23±0.27 mm and 22± 0.15 mm respectively. Mycosynthesized SNPs by *Penicillium oxalicum* filtrate (PESNPs) exhibited significant antimicrobial activity against the test pathogens.

Keywords: Mycosynthesis, Silver nanoparticles, *Penicillium oxalicum* filtrate, Antimicrobial activity, Scanning Electron Microscopy.

Paper ID *(HE044)*

Bioactive Compound Estimation and Antimicrobial Activity of *Brassica oleracea* (broccoli) Extract against *Candida albicans*

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Abstract

Background: The necessity for natural products that are alternative methods of antimicrobial stewardship has arisen as a result of multidrug resistance to antibiotics. This study aimed at evaluating the inherent bioactive compounds in *Brassica oleracea* (broccoli) and analyzing the extract efficacy against *Candida albicans*, an opportunistic human fungal pathogen that causes candidiasis in about 75% of women at least once in their lifetime. **Materials and Methods**: 100g broccoli powder was dissolved in 1litre of 80% methanol and water, respectively. Extract yield and phytochemical analyses were determined using standard methods. Gas Chromatography-Mass Spectrometry was used to detect inherent bioactive compounds. Antimicrobial assay against *Candida albicans* was done using agar diffusion assay. **Results and Conclusion**: Yield of the extract of broccoli for both methanol and water (solvents) were 12.84±0.08% and 15.89±0.03%, respectively. Saponins, terpenoids, flavonoids, cardiac glycosides and alkaloids were present while phenol, steroids, tannins and anthraquinones were absent in both extracts. Quantitatively, the compounds ranged from 14±0.35%, 75±0.70%, 115±1.41 % to 535±2.00% for flavonoids, terpenoids, saponin and alkaloids, in methanol extract respectively. The aqueous extract had 0.007±0.03% (terpenoids), 0.0087±0.15% (phenol), 0.01±0.01% (alkaloids), 0.0125±0.05% (saponin), 0.0189±0.18% (tannin) and 0.1139±0.10% (flavonoids). 25±0.25mm and 23±0.15mm were inhibition zones against *C. albicans* by the methanol and aqueous extracts, respectively. Fluconazole, showed highest inhibition zone of 26.0±0.18mm. 20% and 30% were the MIC for methanol and aqueous extracts, respectively. n-Hexadecanoic acid, 3-Methyl-4-isopropylphenol, 9-octadecenoic acid methylester, 9-Eicosene,(E), 9,12-Octadecadienoic acid, 1,4-Dihydronaphthalene benzene and 4-Heptafluorobutyryloxyhexadecane accounted for 40.48% of the total bioactive compounds identified in this study. Conclusively, broccoli extract exhibited inhibitory effect against *C. albicans*.

Keywords: Candidiasis, *Brassica oleracea*, Antimicrobial, Natural product, Phytocompound

Paper ID *(HE045)*

Probiotics for the Control of Malaria and other Infectious Diseases

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Abstract

Background: Antimalarial drug resistance poses a challenge to malaria control efforts, leading to the exploration of alternative strategies such as probiotics. The gut microbiota composition is associated with malaria severity, and specific probiotic strains can influence it. Anti-α-Gal antibodies targeting *Plasmodium* sporozoites could offer protection against malaria transmission. **Materials and Methods**: Potential probiotic lactic acid bacteria (LAB) were screened from fermented foods (*kunun-zaki, kindirmo* and *pulque*). Culture-dependent isolation and molecular identification of specific LAB genera using 16S rRNA was done. *In vitro* assessments to detect potential probiotic properties such as tolerance to acid and bile, adhesion and haemolytic property, survival of gastrointestinal juices and antimicrobial potential were studied. Promising LAB were studied *in vivo* using a mouse model to evaluate their impact on gut microbiota and immune responses by analysing the parasitaemia progression, survival rate, and specific immune response (IgM, IgG3, IFN-γ, IL-4). **Results and Conclusion**: Through 16S rRNA molecular identification techniques, specific LAB genera with probiotic potential are identified from the fermented foods with *Limosilactobacillus fermentum* being the most predominant at 68% representation. *In vitro* assessments confirm their probiotic properties, while *in vivo* experiments using a mouse model reveals the impact on gut microbiota composition by changing the LAB population in the gut. Also, progression of parasitaemia was suppressed, survival rate was improved, and modulation of immune response varied. Further, genetically engineered LAB for the expression of antimalarial peptides, paving the way for the development of a probiotic-based vaccine is suggested for future study. The findings contribute knowledge to the development of functional foods, probiotics, and probiotic-based vaccines for malaria prevention and treatment.

Keywords: Alpha gal; Gut microbiota; Lactic acid bacteria; *Plasmodium*; Probiotics

Paper ID *(HE046)*

Antibiotic Susceptibility Profile of *Escherichia Coli* Isolates from Female Urine Samples in Alex-Ekwueme Federal University Ndufu-Alike, Ikwo, Ebonyi State.

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Abstract

Background: *Escherichia coli* is one of the most common causative agents of bacterial infections. Antimicrobial resistance patterns of *Escherichia coli* continue to pose a great threat to public health worldwide and has led to serious health problems such as prolonged hospitalization and treatment failure. This study is aimed at isolating, identifying and elucidating the antibiotic susceptibility profile of *Escherichia coli* from female urine samples in Alex Ekwueme Federal University Ndufu-Alike Ikwo Ebonyi State. **Materials and Methods:** Urine samples were collected from 30 female students of Alex Ekwueme Federal University Ndufu - Alike Ikwo Ebonyi State. The samples were inoculated onto sterile plates of Eosin Methylene Blue agar, and incubated at 37^{o}C for 18-24hr. Pure isolates were identified by cultural characteristics and PCR confirmation. The isolates were tested against some selected antibiotics. The overall prevalence of *Escherichia coli* was high as urine samples of students within the age group of 15-39 years old had *E. coli*. Infections of *Escherichia coli* were found in students who resided within the school hostels and off campus. **Results and Conclusion:** The *Escherichia coli* isolates were equally most susceptible to Meropenem (10µg), Amikacin (30µg), Chloramphenicol (30µg) and Norfloxacin (10µg), Gentamicin (10µg) were effective against *Escherichia coli* and Doripenem (10µg) had little effect on *Escherichia Coli* and It can be inferred that cefuroxime (30µg), Thrimethroprim sulfamethoxazole (25µg), Ciprofloxacin (5µ) and Tetracycline (30µ) did not affect *Escherichia coli.* These results show a high prevalence of antibiotic resistance to *Escherichia coli* in the urine samples from female students in our university. It also highlights the need for surveillance and monitoring of antibiotic resistance in urine samples. The detection of these isolates suggests that they pose a threat to humanity, therefore, proper hygiene practices and alternative antibiotics should be considered to prevent antibiotic-resistant bacteria in female students.

Keywords: *Escherichia coli*, Public Health, Antimicrobial Resistance, Antibiotics, PCR

Paper ID *(HE047.)*

High Colonization of Gastrointestinal Carriage Rates of Clostridioides difficile among different age groups in Four Local Government Area of Lagos State, Nigeria

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Abstract

Background: *Clostridioides difficile* causes *Clostridioides difficile* infection (CDI), a considerable threat to public health globally. In humans it is influenced by a number of factors including age, exposure to antibiotics and the environment to which the subject is exposed. As a consequence, reports on *C. difficile* carriage in humans vary from country to country and hospital to hospital. This study was therefore set out to study the carriage rates of *C. difficile* in four local Government in Lagos. **Materials and Methods**: A total of 763 stool samples were collected by random sampling method from both children and adults of both sex, [from hospitals (males n =150; females n =233) and community (males n =169; females 211)]or age ranged [< 1 (n=167), 1-5 (n=76), 6-9 (n=44), 10-19 (n=94), 20-29 (n=83), 30-39 (n=123), 40-49 (n=102), > 50 n=74)] from private hospitals and health centres of 4 LGAs consisting of Agege (n = 152), Ikeja (n = 223), Mushin (n = 197), Surulere (n = 191). A well structured closed ended questionnaire was used to obtain patients demograph including the use of antibiotics and/or local herbs. Ethnical approval was from LUTH (REF:ADM/DCST/221). The samples were identifed as *C. difficile* using colonial morphology, fluorescence, and standard biochemical anaerobic procedures while definitive identification was performed using API 20A.**Results and Conclusion**: Out of 763 samples, 156 (20.4%) were detected with the highest and lowest carriage rate from Ikeja and Mushin LGAs respectively. Out of the 382 samples from the hospitals, 79 (20.6%) were positive for *C. difficile* while 77 out of 381 (20.3%) were from the communities with females having a higher carriage rate than males at a rate of 21.1% in the hospital and 20.9% in the community but the value was not statistically significant ($p < 1.77$). The use of herbs by patients also was statistically significant ($p < 0.001$).

Keywords: *Clostridioides difficile*, Colonization, Age, Hospital, Community

Paper ID *(HE048)*

Immunogenetic Variation in Humans and Malaria Susceptibility

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Abstract

Background: Globally, malaria is a significant public health burden. Genetic variations have been known to affect the susceptibility of individuals to certain infections. Research has identified several genetic factors that are associated with malaria susceptibility. Certain immunogenetic variations in the hosts affect their immune responses to *Plasmodium*, making some individuals more susceptible than others to malaria infections. Several studies have identified genetic variations in various populations across the globe that contribute to malaria susceptibility and resistance. This review paper aims to identify the known immunogenetic variations in current studies. **Materials and Methods:** Over seventy papers were accessed from **s**cientific databases such as Google Scholar, PubMed, ProQuest and Science Direct to identify the immunogenetic factors. The range of papers was from 2018 – 2023 and was checked to ensure they had the relevant keywords on immunogenetic variation in humans and malaria susceptibility as inclusion criteria. Eventually, twelve publications with definitive information were used. **Results and Conclusion**: Polymorphisms in the human leukocyte antigen (HLA), polymorphisms in toll-like receptors (TLRs) sickle cell anaemia, sickle cell trait, duffy antigen, thassalemias, melanesian ovalocytosis and glucose-6-phosphate dehydrogenase (G6PD) deficiency and the production of certain interleukins are genetic adaptations to malaria. This explains both malaria immunity and susceptibility. Natural selection over time has favoured individuals with genetic variants that provide some degrees of resistance to malaria. Understanding immunogenetic variations and their relationship with malaria susceptibility can aid in the development of more effective strategies for preventing and treating the disease.

Keywords: Immunogenetics, Genetic variation, Malaria susceptibility, Host-parasite interaction, Single-nucleotide polymorphism

Paper ID *(HE049.)*

Antibacterial and Antioxidant Potentials of Root Extract of *Chrysophyllum albidum* (g. don) against Selected Bacterial strains Implicated in Diarrhea and Dysentery

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Abstract

Background: This study assessed the antibacterial and antioxidant properties of root extract of *Chrysophyllum albidum* implicated in diarrhea and dysentery. **Materials and Methods:** The powdered sample (1500 g) was cold extracted in methanol and sterile distilled water (3:2 v/v). The mixture obtained was concentrated *in vacuo* using a rotary evaporator and lyophilized. The root extract was screened for antibacterial and antioxidant activities against bacterial isolates obtained from culture room of Microbiology Laboratory, Aminu Kano Teaching Hospital, Kano, Kano State, Nigeria. The antibacterial and antioxidant activities were determined using standard microbiological techniques. The minimum inhibitory concentration (MBC) and minimum bactericidal concentration (MBC) were determined using agar dilution method. **Results and Conclusion:** The root extract at a concentration of 10 mg/mL exhibited antibacterial activities that ranged from 10±0.82 mm to 24±0.82 mm. The minimum inhibitory concentrations of the root extract ranged between 0.63 mg/mL and 1.25 mg/mL while the lowest MIC was 0.63 mg/mL. The minimum bactericidal concentrations ranged between 0.63 mg/mL and 2.5 mg/mL while the lowest MBC was 0.63 mg/mL. The antioxidant assay of root extract showed significant activities when compared with vitamin C used as control. The root extract exhibited percentage inhibition of 75.76% while the vitamin C used as control had 63.53% percentage inhibition at a concentration of 15.625 µg/mL. The root extract which possessed antioxidant potentials expressed significant antibacterial properties against the bacterial strains associated with diarrhea and dysentery.

Keywords: Antioxidant activities, *Chrysophyllum albidum*, Diarrhea, Dysentery, Vitamin C

Paper ID *(HE050.)*

High Throughput Genomic Sequencing Reveals HIV-1 Diversity, Unique Isolates and Drug Resistance Mutations in Nigeria

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Abstract

Background: Genomic surveillance is critical in the fight against rapidly mutating RNA viruses including HIV-1. We set out to evaluate HIV-1 subtypes, characterise the isolates, determine evolutionary history of variants and evaluate drug resistance mutations in Nigeria. **Materials and Methods**: A total of 559 samples were collected among HIV-1 positive patients across the six geo-political zones of Nigeria after obtaining ethical clearance from the National Health Research Ethics Committee (NHREC), Abuja; and informed consent from each participant. Analysis for HIV-2 infection was performed to detect any coinfections. Samples were sequenced using MiSeq, a next-generation sequencing (NGS) technology, and NGS reads analysed.**Results and Conclusion**: There was 0% HIV-1 co-infection with HIV-2. Of the 559 samples analysed, 122(21.82%) samples had undetectable viral load (VL), 437 (78.12%) had VL > 1000 cp/ml, 175 were <1.60-3.49 Log copies/ml, 186 were 3.51-5.00 Log copies/ml and 7 were 5.01-6.40 Log copies/ml. Higher VLs were observed in drug-naïve patients. HIV-1 subtype distribution and circulating recombinant forms were as follows: 33(35.48%) subtype G, 28(30.11%) CRF0, 16(17.20%) CRF43 basal, 7(7.53%) CRF30, 9(9.62%) non-typable. Phylogenetic analysis reveals HIV-1 diversity in Nigeria with seven unique isolates, suggesting a rapid evolution of the virus in the population. Drug resistance was highest against nevirapine and efavirenz. Continual genomic surveillance of HIV-1 is recommended as this is key in the fight against the virus. Newer regimens that are more efficacious should be introduced in the management of HIV/AIDS patients.

Keywords: HIV-1 Molecular Epidemiology, HIV-1 Diversity, HIV Drug Resistance, Phylogenetic Analysis, HIV-2.

Paper ID *(HE051)*

Prevalence of Non-Tuberculous Mycobacteria (NTM) and *Mycobacterium tuberculosis* complex (MTBC) Among Patients Attending Tuberculosis Referral Centers in Nasarawa State Nigeria

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Abstract

Background Globally, Nontuberculous *Mycobacteria* (NTM) infections are on the rise, and their prevalence is beginning to be surpassed by *Mycobacterium tuberculosis* complex (MTBC). **Materials and Methods**: A total of three hundred and eighty (380) sputum and completed structured questionnaire were collected from consented clients (age ≥15 years) and cultured with Lowenstein Jensen glycerol solid media. The isolates were confirmed as NTM and MTBC using Tuberculosis Antigen Rapid test. **Results and Conclusion** The prevalence rates of NTM and MTBC in connection to demographic characteristics indicated that females had (6.3%) and (17.9%) significant prevalence levels, respectively. Respondents with secondary education had a greater incidence of 7.9% and 13.7%, respectively. Also smokers showed a prevalence rate of 10.2% and 20.5%, respectively. Alcohol users had greater prevalence at 6.8% and 15.5%, respectively. All of the demographic parameters show a statistically significant difference (P 0.05). The age 41–50 group had a greater frequency of NTM and MTBC rates of 3.4% and 10%. Regarding marital status, the frequency of NTM and MTBC was higher for singles with 5.5% and 12.1%, respectively, with P>0.05 and P0.05. NTM and MTBC prevalence were most significant in relation to residency at 8.9% and 21.8%, respectively; P>0.05 and P0.05. Businesspeople had the most prevalence of NTM and MTBC (5.5% and 10.8%, respectively; P>0.05); HIV positive people, had the most prevalence of NTM and MTBC (7.3% and 18.2%, respectively; P>0.05 and P>0.05). These findings suggest that there may be unique risk factors associated with each of these demographic factors that may contribute to the misdiagnosis of NTM and MTBC.

Keywords: Nontuberculous mycobacteria, Prevalence, Sputum, Pulmonary Tuberculosis Complex, *Mycobacterium tuberculosis*

Paper ID *(HE052.)*

Prospects of Volatile Biomarkers for Diagnosis of Malaria

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Abstract

Background: Malaria remains a disease of public health concern in countries like Nigeria with 31.3% of the world's burden. Microscopy remains the gold standard of parasite detection alongside a plethora of Rapid Diagnostic Tools (RDTs). However, recent HRP2-gene deletions in *Plasmodium falciparum* render them undetectable by widely used HRP2 RDTs posing challenges for malaria detection. This review will explore the potential of volatile biomarkers for the identification of malaria asymptomatic cases that currently go undetected using non-invasive methods.**Materials and Methods**: The review was conducted utilizing an extensive search of articles that had been pre-screened for title and abstract using PubMed and Google Scholar for the years 2015–2022. Publications downloaded were those related to using volatile organic compounds (VOCs) for disease diagnosis. **Results and Conclusion**: Studies showed the utility of VOCs in the diagnosis of lung cancer and tuberculosis using E-nose analysis of sweat and exhaled breath. Isoprene and five additional malaria-related VOCs were found in human breath and connected to oxidative stress. Other research identified four thioethers, carbon dioxide, isoprene, acetone, benzene, and cyclohexanone with high specificity for malaria and correlated with parasitaemia levels. The lack of universal VOCs that are specific and sensitive to malaria due to variations of body odour in individuals influenced by genetic and environmental factors was observed. Potentials exist for malaria diagnosis using VOCs biomarkers for next-generation screening methods. However, more research and the development of E-noses devices that could detect these VOCs more specifically and sensitively is needed.

Keywords: Volatile organic compounds, VOCs Biomarkers, Malaria, E-noses

Paper ID (HE053.)

Differential Attraction in Malaria Transmission and Host Microbiota-Vector-Environment Complex: A Review

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Abstract

Background: Mosquito-borne diseases significantly burden human health across the world. Their eradication remains challenging, this therefore necessitates a comprehensive understanding of the intricate interactions between the host, the mosquito vector, and the environment. The complex interplay between them influences human susceptibility to mosquitoes. Identifying the specific microbial factors that influence mosquito attraction and the underlying molecular mechanisms involved will pave the way for novel interventions targeting microbiota-vector interactions. **Materials and Methods**: Two scientific databases (Public Library of Medicine and Google Scholar) were searched, with the year of search specified as 2018 - 2023. A total of 13,923 search results were returned from PubMed and Google Scholar databases. Articles were pre-screened using their title and abstract. Only 52 articles with the interconnection of the differential attraction in humans and the contribution of the environment were downloaded for this review.**Results and Conclusion**: This review provided insights into why mosquitoes showed variation in host preference, both between and within species due to variations in the volatile compounds (VOCs) like CO_2, lactic acid, terpenes produced by hosts. It also highlights role of the environment in the proliferation of mosquitoes due to favorable climatic condition for their breeding and contributory factor for the human skin microbiota based on the mode of delivery, hygiene routine et.c. The VOCs identified should be used in the development of non- invasive diagnostic techniques to reduce the burden of malaria.

Keywords: Differential attraction, Mosquitoes, Skin Microbiota, Environment, Vector control.

Paper ID *(HE054.)*

Phytochemical Analyses and Antibacterial Activities of *Jatropha tanjorensis* j.l. ellis & Saroja Leaves Extract against Selected Clinical Pathogens.

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ABSTRACT

Background: *Jatropha tanjorensis* is an important medicinal plant that has been used to treat different ailments**.** The leaves of *Jatropha tanjorensis* were collected and assessed for their phytochemical compositions and antibacterial activities using methanolic and aqueous extracts to determine their inhibitory effects on selected clinical isolates. **Material and methods:** Fresh *Jatropha tanjorensis* leaves were collected, identified, dried at room temperature and finely ground. Two hundred grams (200g) of the leaves were macerated in 1000ml of solvent to obtain the extracts. Phytochemical analyses of the extracts were done using appropriate standard methods. The leaf extracts and antibiotic sensitivity were evaluated against *Staphylococcus aureus, Bacillus subtilis, Enterococcus faecalis Escherichia coli, Bacillus subtilis* ATCC 6633, *Staphylococcus aureus* ATCC 25923, *Salmonella typhi* and *Pseudomonas aeruginosa* obtained from the Microbiology Laboratory stock culture in LUTH and Bells University of Technology using the agar well diffusion method. **Results and Conclusion:** The results of the qualitative phytochemical analysis revealed the presence of Saponin, Alkaloids, Phenols, Flavonoids, Reducing sugars, Terpernoids, Steroids and Tannins, Phlobatanins were absent. Quantitative phytochemical analysis revealed that flavonoids from hot water extract had the highest quantity of 98.55mg/100g and reducing sugars from methanolic extract had the lowest quantity of 20.39mg/100g. The cold water extract showed the highest inhibitory effect with the zone of inhibition of 19.83mm against *S. aureus,* while methanolic extract showed the lowest zone of inhibition of 13.17mm against *B. subtilis.* The lowest MIC value 10.24mg/ml was obtained against *B. subtilis* while the highest MIC value 20.48mg/ml was observed against other isolates. The GC-MS analysis revealed the presence of 57 bio active components with 1,2,3-Benzenetriol having the highest percentage of 66.38%. From this research, it can be inferred that *Jatropha tanjorensis* has the potential of a prospective antibacterial drug, although there is still need for extensive and synergistic study.

Keywords: Antibacterial, Bioactive compounds, Extraction, *Jatropha tanjorensis*, Phytochemical.

Paper ID(HE055)

Molecular Identification of Antibiotic Resistance genes in *Staphylococcus saprophyticus* Isolated from Patients with Urinary Tract Infections in Lagos State.

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ABSTRACT

Background: *Staphylococcus saprophyticus* is the second most common pathogen after *Escherichia coli* causing urinary tract infections (UTIs) in sexually active young women worldwide. *S. saprophyticus* is often resistant to antibiotics used empirically for the treatment of UTIs. This study was carried out to characterise and investigate the presence of genes encoding antibiotic resistance factors among *S. saprophyticus* isolates from non-pregnant female patients with UTIs in the age group 20 to 50 years in Lagos State, Nigeria. **Methods:** Molecular characterization of 88 *S. saprophyticus* clinical isolates using Sanger sequencing method, antimicrobial susceptibility to 15 antibiotics by a disk diffusion method and antibiotic resistance genes using polymerase chain reaction were done. **Results:** The results of the study showed various degrees of resistance of the isolates to Gentamicin (48 %), Ceftriaxone (58 %), Cefoxitin (66 %), Cefdinir (69 %), Erythromycin (91 %), Oxacillin (97 %) and Amoxycillin/clavulanic acid (99 %). The isolates also showed varying degrees of susceptibility to fluoroquinolones. The isolates were susceptible to ciprofloxacin (81 %), levofloxacin (73 %), ciprofloxacin/tinidazole (61 %), ofloxacin (56 %), and pefloxacin (65 %). The multiplex PCR assays of antibiotic resistance genes of 58 isolates screened showed that 35 of the isolates carried *mecA*, 8 *femB*, 17 *ermA*, 27 *aac* (6')-*aph* (2'') and 4 *blaZ* genes respectively. Thirty-two out of 75 *S. saprophyticus* strains with multiple antibiotic resistance (MAR) index that was higher than 0.2 harboured only one plasmid. **Conclusion:** This study showed that *S. saprophyticus* is widely present in urine samples of sexually active women and adequate measures must be adopted to ensure that it is correctly identified. Appropriate treatment regimens must be adopted to prevent the spread of antibiotic resistance genes especially fluoroquinolones which is the drug of choice for the treatment of urinary tract infections.

Keywords: Antibiotic, Plasmid, Resistance, Urinary tract infections, Isolate.

Paper ID *(HE056.)*

Prevalence of Human Bocavirus and Adenovirus among Children with Respiratory Tract Infections in Ilorin, Nigeria

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Abstract

Background: Human adenovirus type 7 (HAdV7) and human bocavirus (HBoV-1) are associated with mild to severe upper and lower respiratory infections in children. HAdV7 co-infections with HBoV-1 have been implicated in wide-spread morbidity in sub-Saharan Africa. The study aimed to detect these viruses in children under 5-year-old with Respiratory Tract infections attending the University of Ilorin Teaching Hospital Ilorin, Nigeria using polymerase chain reaction (PCR). **Materials and Methods**: Two Hundred (200) children under 5- years old were recruited with confirmed symptoms of respiratory tract infections, nasopharyngeal (NP) and oropharyngeal (OP) samples were collected using sterile flocked swab. The socio-demographic information/ risk factors and clinical presentations were obtained with the aid of well-structured questionnaire. Viral detection was done using real-time polymerase chain reaction; the genes amplified were Hexon for HAdV7 and VP1 for HBoV-1. **Results and Conclusion**: Out of the 200 samples, 35 (17.5%) were positive with 7% (14/200) prevalence recorded for HAdV7 and 10.5% (21/200) for HBoV1 respectively. Of the 35 positive samples, co-infection was observed in 15 (7.5%) of the samples. It was observed that 111 subjects were male, and there was no significance difference in the prevalence of the viruses with respect to gender. The prevalence was significantly higher amongst 0-1year age group. There was statistical significance for some of the socio-demographic and risk factors. According to findings from this study, HAdV7 and HBoV-1 are important cause of infection in the respiratory system of children. It is therefore important to carry out more research on these viruses and highlight the transmission patterns and the severity of the disease in Nigeria among this susceptible age group.

Keywords: Children, Human Adenovirus, Human Bocavirus, Respiratory infection, Co-infection

Paper ID *(HE057)*

Susceptibility of Hospital Isolates to Streptomycin.

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Abstract

Background: Monitoring the antibiotic susceptibility of pathogens in a clinical setting is important as it helps ascertain the potency of the antibiotic substance as well as expose possible antimicrobial drug resistance in the pathogens. With the increasing emergence of antimicrobial drug resistance strains and the challenge it poses for the healthcare system, it is important to determine the local patterns of drug susceptibility/resistance as this data would guide empirical antibiotic use. Hence this study on susceptibility of bacterial species isolated from University of Ilorin Health Services center to streptomycin was carried out.**Materials and Methods**: Settling plate and swabbing methods were used for the isolation of bacteria pathogens from different locations (Laboratory, Laundry, Pharmacy, Dressing room, Injection room, Consulting room, General toilet, doors, wards and benches) in the clinic environment. Nutrient and MacConkey agar were used for the isolation. Identification and characterization of isolates was done using Gram-stain and biochemical tests such as catalase, coagulase, indole production, citrate utilization, triple iron sugar utilization and methyl red-Voges Proskauer as described by (Monica, 2004). Disc diffusion and broth dilution methods were used for antibiotic susceptibility test and determination of minimum inhibiting concentration (MIC) and minimum Bactericidal concentration (MBC) respectively at a concentration of 5 -160 µg/ml. **Results and Conclusion**: A total of eight bacterial species were isolated namely, *Staphylococcus spp, Escherichia spp, Enterobacter spp, Seratia spp, Bacillus spp, Proteus spp, Klebsiella spp* and *Streptococcus spp.* Results of the antibiotic susceptibility test to streptomycin showed that all isolates were sensitive at 5µg/ml except *Streptococus spp, Seratia spp and Klebsiella spp* which were only sensitive at concentrated range of 40-80µg/ml. The MIC of the antibiotic to all isolate ranged from 20-80 µg/ml while the MBC ranged from 20-160 µg/ml. Most of the microbial isolates, demonstrated low sensitivity to Streptomycin and the presence of streptomycin resistant bacterial species in the hospital environment could further worsen the condition of immunocompromised patients, thereby increasing their cost of health care and prolong hospital stay.

Keywords: Susceptibility, Isolates, MIC, MBC, Streptomycin.

Paper ID *(HE058)*

A Comparative Study of Antibiotics Resistance Pattern of some Bacteria Isolated from Car and Office Door Handles

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Abstract

Background: Multidrug-resistant bacteria have over the years posed a public health concern, especially with the difficulty and cost of treatment of infections they cause. Fomites such as door handles are thus potent means through which pathogens are transmitted from one person to another as contact with them is made. This study thus compares the antibiotics resistance pattern of bacteria isolated from car and office door handles.**Materials and Methods**: Using the simple random sampling method, twenty samples(20) from car door handles and twenty samples (20) from office door handles were collected,the isolation of bacteria was done using standard microbiological procedures and identification of the isolates done using cultural, microscopic and biochemical characterization. Determination of the antibiotics sensitivity pattern of the isolates was done using the Kirby-Bauer disc diffusion method on Muller Hinton agar. Antibiotics used included Ofloxacin (5 µg), Gentamicin (10 µg), Ceftriaxone (30 µg), Augmentin (30 µg), Ciprofloxacin (5 µg), ErythromYcin (5 µg), Streptomycin (30 µg) and Cloxacillin (30 µg).**Results and Conclusoion**: The results showed a significant frequency of occurrence of *Staphylococcus aureus* with 35% and *Klebsiella pneumoniae* having the least with 5%. From car door handles, *S. epidermidis* recorded 37% while *K. pneumoniae* recorded the least with 17.4%. The isolates exhibited resistance to antibiotics including Augmentin and Ceftriaxone (≤22 mm) while they were more susceptible to Ofloxacin (≥16 mm). All the *K. pneumoniae* isolated from car door handles exhibited resistance to Augmentin and Ceftriaxone. These results show that these surfaces could be a possible reservoir of infection by these bacteria, leading to difficulty in the treatment of infections caused by them.

Keywords: Multidrug resistance, Car door handles, Office door handles, Public health, Bacteria

Paper ID *(HE059.)*

Bacteriological Evaluation of Ready to Eat Cut Fruits and Carrots from Selected Markets in Lagos.

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Abstract

Background: Ready to eat (RTE) cut fruits are vended on the streets of Lagos, due to their convenience and accessibility. However, the consumption of cut fruits sold in open markets may constitute health risks owing to microbial contamination. **Materials and Methods**: This study aimed at detecting the presence of common food borne pathogens in 35 samples of Pineapple, watermelon and carrots (PWC) using standard bacteriological and molecular methods. The isolates were also subjected to antibiotic susceptibility testing (AST) against 12 commonly administered antibiotics (disk diffusion method). **Results and Conclusion**: The Aerobic Plate Count ranged from 1.0- $2.5x10^2$cfu/ml in all samples, eight species belonging to seven genera; *S. aureus. S.epidermis, Salmonella spp. E.coli, Klebsiella spp.,Shigella spp.,Proteus spp.* and *Vibro cholerae* were isolated from PWC. The results showed that *Escherichia coli* was the most occurred with Watermelon (31%), Pineapple (29%) and Carrots 23.53%. Carrot was the most contaminated having the incidence of *Vibrio cholerae* and *Proteus* spp. which were absent in others. The AST showed that the gram negatives isolates had total resistance (100%) to Ampicillin-Cloxacillin (20/10µg) and Nalidixic Acid (30µg) and to 300µg- Nitrofurantom (77.7%), 30µg-Cefuroxime (88.89%), 30µg-Amoxillin-Clavulnate (83.33%), while maintaining susceptibility to 5µg-Ofloxacin (77.78%) and 5µg-Levofloxacin; (66.67%). The MAR indices ranged from 0.3-0.8 with 94% isolates having MAR indices > 0.4 and thus classified as multi-drug resistant (MDR) strains. The significant presence of these pathogens and MDR strains in the RTE fruits shows that consumers of RTE PWC in Lagos state are prone to food-borne infections. Appropriate food safety measures for handlers and vendors are thus recommended.

Keywords: Bacteria, Ready-to-eat fruits, Lagos, Antibiotic sensitivity, multi-drug resistant

Paper ID *(HE060)*

Risk Factors for Asthma in Children and Assessment of Knowledge of Parents and Caregivers.

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Abstract

Background: Asthma is an immunoglobulin E-mediated chronic inflammatory disease of the airways, affecting 334 million people globally. Understanding the risk factors associated with paediatric asthma is crucial for effective disease control, particularly in developing countries where asthma prevalence is rising. This study investigated the hygiene hypothesis and other early-life-related risk factors associated with paediatric asthma and also assessed the knowledge of parents and caregivers about the disease. **Materials and Methods**: A total of 82 children with asthma attending paediatric respiratory clinics in Lagos, along with 81 healthy controls, were enrolled in this study. Data on asthma risk factors and knowledge were collected using a modified version of the international study of childhood asthma and allergies (ISAAC) questionnaire. Correlational and regressional analyses were used to determine the risk factors for asthma and identify factors influencing changes in asthma knowledge. **Results and Conclusion**: Significant risk factors for childhood asthma included respiratory infections and antibiotic use during infancy (OR=26.6; 95% CI: 6.586-17.431, $p<0.001$), maternal exposures during pregnancy (OR=5; 95% CI: 2.6-11.4, $p<0.001$), breastfeeding duration, and parental history of asthma (OR=21.25; 95% CI: 2.8-16.4, $p=0.003$). Pet ownership was found to be protective against asthma. The mean asthma knowledge score was 3.05 out of 5. Knowledge scores varied across the different ages, educational levels, and marital status of the parents and caregivers. Parents with asthma who regularly visited the doctor exhibited significantly higher levels of asthma knowledge ($p=0.026$). These findings will inform targeted interventions towards asthma control and enhance the clinical management of asthma.

Keywords: Asthma, hygiene hypothesis, risk factors, knowledge, Nigeria

Paper ID *(HE061.)*

Characterization and Molecular Profiling of Selected Multidrug Resistant Bacteria Isolated from Ready-to-Eat Seafoods Sampled from Makoko Market

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Abstract

Background: Seafoods are an important source of proteins, minerals and vitamins in the diet. They could also become a route of contamination leading to foodborne diseases. This study seeks to characterize and analyse the antibiotic resistance patterns and potential virulence factors in selected multidrug resistant bacteria in ready-to-eat seafoods sampled from Makoko community. **Materials and Methods:** Selected (viable) bacteria isolates previously isolated from seafoods (Bonga fish, Herring "shawa" fish, Catfish, Crayfish, Crocker fish, Barracuda fish and Soul fish) sampled from Makoko market were retrieved and sub-cultured. Differential culture media such as Thiosulphate citrate bile salt agar, Mac-Conkey agar, Nutrient agar, Salmonella-Shigella agar and Eosin methylene blue agar were used to sub-culture the bacterial isolates. The isolates were further subjected to Gram staining as well as biochemical tests after which antibiotic sensitivity test was carried out on the isolates using 20/10µg Amoxicillin clavulanate, 5µg each of Levofloxacin, Ofloxacin, and Cefixime, 10µg each of Imipenem and Gentamycin, 30µg each of Cefotaxime and Nalidixic and 300µg of Nitrofurantoin. The multidrug resistant isolates were subsequently profiled genetically, using molecular techniques. **Results:** Thirty-four (34) bacteria isolates were re-cultured, the predominant bacterial species identified included *Staphylococcus spp.*, *Citrobacter spp.*, *Bacilli sp*. and *Proteus spp.* A total of 25 (73.5%) of these isolates displayed multidrug resistance. Furthermore, the molecular analysis revealed the presence of resistance genes such as blaCTX-M, blaTEM and blaOXA related to extended-spectrum beta-lactamase (ESBL) producing bacteria, also IMP and KPC for carbapenem-resistant bacteria. **Conclusion**: These findings underscore the importance of ensuring food safety and the sensitization of Makoko residents on the hazards that could emanate from improper handling of these seafoods. Further studies are required to establish the possible sources of contamination and to also extradite the appropriate measures for suppressing antibiotic resistance in these bacterial pathogens.

Keywords: seafoods, multidrug-resistance, food-borne pathogens, genes, antibiotic resistance

Paper ID (HE062.)

The Role of *Bacillus thuringiensis* var. *israelensis* in Malaria Vector Control

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Abstract

Background: Malaria, caused by *Plasmodium* parasites and primarily transmitted by the female *Anopheles* mosquitoes remains a significant global health burden in tropical regions. Vector control strategies have played a crucial role in reducing malaria transmission and *Bacillus thuringiensis* var. *israelensis* (Bti) has emerged as a promising biological agent for malaria vector control because it produces toxins (crystal and cytolytic) that specifically target mosquito larvae making it an environmentally friendly and effective tool for malaria vector control. This review evaluates the role of *Bacillus thuringiensis* var. *israelensis* (Bti) in malaria vector control.
Methods: Fifty-five relevant review articles between 2016-2023 were sourced from scientific databases; PubMed and Google Scholar to evaluate the role of *Bacillus thuringiensis* var. *israelensis* in malaria vector control. Fifteen publications with relating keywords on Bti in malaria vector control were retrieved while articles within that range lacking conclusive data were excluded.
Result and Conclusion: Studies have shown Bti application in Brazil, Kenyan and Nigeria significantly reduced larval populations of Anopheles mosquitoes with larval mortality rates of 90% in treated breeding sites and entomological surveys reveals substantial decline in adult mosquito abundance in Bti-treated areas, resulting in a subsequent reduction in malaria cases. This underscores the potential of Bti effectivity in malaria vector control and highlights its ability to selectively target mosquito larvae. Integrating Bti into malaria control programs can enhance effectiveness of vector control strategies. Further research and implementation efforts are warranted to optimize Bti application and maximize its impact on malaria burden reduction.

Keywords: Malaria, vector control, *Bacillus thuringiensis* var. *israelensis*, mosquito larvae, Anopheles mosquitoes.

Paper ID *(HE063.)*

Prevalence and Associated Risk Factors of *Staphylococcus aureus* among a Cohort of Immunocompromised Individuals in Lagos, Nigeria

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Abstract

Background: Immunocompromised individuals are susceptible to opportunistic infections, including those caused by *Staphylococcus aureus*. The aim of this study was to determine the prevalence, virulence, and associated risk factors of *S. aureus* among a cohort of immunocompromised individuals in Lagos, Nigeria. **Materials and Methods**: A total of 300 participants, including 150 HIV/AIDS cases, 100 diabetes cases, and 50 HIV/Tuberculosis co-infection cases, were recruited. Nasal swab samples were cultured, and standard microbiological techniques were used for *S. aureus* identification. The isolates were characterized for antibiotic resistance, the presence of the *mecA* gene for methicillin resistance and the Panton-Valentine leucocidin *(lukf-PV*) gene using the *MecA* and *Pvl* primers respectively. A modified questionnaire was also administered to investigate the risk factors associated with *S. aureus* nasal carriage. **Results and Conclusion**: The overall prevalence of *S. aureus* was 17% (51/300). Prevalence was highest among HIV/AIDS cases (16.7%, 25/150), followed by co-infection cases (14%, 7/50), and diabetes cases (5%, 5/100). Antibiotic resistance was observed, with zones of inhibition that ranged from 0 mm - 40 mm. Ampicillin showed 100% resistance, penicillin 90.2%, and erythromycin 19.6%. Methicillin-resistant *S. aureus* (MRSA) prevalence was 78.4% (40/51), with the highest occurrence among HIV/AIDS patients (52.5%, 21/40). Recent antibiotic use, regular contact with animals, and household member contact with animals were associated with *S. aureus* nasal carriage. Variations in hand hygiene practices, including regular hand washing and hand washing after nose picking, were also observed. This study reveals a considerable prevalence of *S. aureus*, particularly MRSA, among the immunocompromised individuals studied. The findings emphasize the need for improved antibiotic stewardship practice in this vulnerable population.

Keywords: *Staphylococcus aureus*, Risk factors, Immunocompromised individuals, Antibiotic resistance, MRSA

Paper ID *(HE064.)*

Antimalarial Drug Resistance: Insights from the Application of Quantum Approaches to Antimalarial Drug Assays and Discovery

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Abstract

Background: Malaria continues to be a public health crisis. Underscoring this persistence is the ability of the disease parasites to develop resistance to existing antimalarials designed to treat them. While new drugs are urgently needed, the drug development process as is currently known is tedious and time-consuming, necessitating novel approaches to drug discovery and development. Quantum approaches are one of such approaches predicted in literature to aid better and faster screening techniques for drugs discovery and design. Studying the different quantum approaches reported by previous researchers, we explored these approaches with respect to antimalarial drug assays and discovery. **Materials and Methods:** This study is a systematic review of the application of quantum approaches to antimalarial drug assays and discovery. The sources of information for this review were PubMed database, Google, and Future Learn websites. Only articles focusing on quantum computing or quantum approaches as applied to antimalaria drug assays, and articles written in English were considered. 66 records were initially retrieved from all sources; following title, abstract and full-text screening, 20 articles were included in the study. **Results and Conclusion**: This study revealed that quantum approaches have served to uncover novel residues and mechanisms of antimalarial drug target inhibition, improved the understanding of mechanisms of antimalarial drug action, aided in developing rapid and sensitive diagnostic assays, and facilitated *in-silico* identification of active antimalarial compounds. Specific quantum approaches used included quantum dots, quantum similarity studies, quantum chemical analysis, and molecular dynamics simulation. While quantum approaches show promise to accelerate antimalarial drug discovery, there remain opportunities for further applications.

Keywords: Antimicrobial Resistance, Antimalarials, Drug discovery, Quantum, Malaria

Paper ID *(HE065.)*

Characterization and Molecular Profiling of Selected Multidrug-resistant Bacterial Pathogens from Water and Sediments Sampled from Makoko

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Abstract

Background: Water is highly essential for life; however, it serves as the route of transmission for many infectious pathogens. The increasing prevalence of multidrug-resistant (MDR) bacteria in water samples poses a significant public health risk. This study aimed to characterize and analyse the molecular profile of selected MDR bacteria isolated from water and sediment samples collected from Makoko community. **Materials and Methods**: Sample collection and isolation of bacterial species from the samples was previously done. The water samples were purposively collected into 1-litre sterile plastic bottles while a Van Veen grab sampler was used for collection of the sediment samples into sterile zip-lock bags, as reported. The viable bacteria species previously isolated were then subjected to culturing on various selective media which included Thiosulphate citrate bile salt agar, Mac-Conkey agar, Nutrient agar, Salmonella-Shigella agar and Eosin methylene blue agar. The isolates were thereafter subjected to biochemical characterization after which, test for antibiotic susceptibility was done using 5µg each of Levofloxacin, Ofloxacin, and Cefixime, 10µg each of Imipenem and Gentamycin, 30µg each of Cefotaxime and Nalidixic and 300µg of Nitrofurantoin. The multidrug resistant isolates were further profiled genetically using molecular techniques. **Results:** A total of forty-one (41) bacteria species previously isolated were re-cultured, predominantly *Enterobacter spp., Bacillus spp., Salmonella spp., Proteus spp., Klebsiella spp.*, and *Staphylococcus spp.* 96% of the selected Gram-negative isolates were glucose positive and scarcely produced Hydrogen sulphide. Multidrug resistance was recorded in 97% of the isolates. The molecular analysis of the MDR bacteria isolates, demonstrated the presence of genes associated with different antibiotics. These genes include blaTEM, blaCTX-M, and blaOXA for beta-lactam resistance, as well as KPC and IMP for carbapenem resistance.**Conclusion**: The findings of this study contribute to existing knowledge on antibiotic resistance. The urgent need for improved water quality alongside infection-control measures to combat the spread of MDR bacteria is also highlighted by these findings. Further studies are required to investigate the contamination pathways, potential risks associated with MDR bacterial infections in Makoko community and to explore strategies for mitigating its negative impact on human health.

Keywords: Water quality, multidrug resistance, Makoko community, Bacteria, antibiotic resistance

Paper ID *(HE066)*

Determination of Nutracetical (antioxidant, antitumor and Immunomodulatory) Potential of EPS by some *Rhizobium* sp.

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Abstract

Background: (Extracellularly biosynthesised high molecular weight polymers have diverse industrial applications. This study investigated the *in-vitro* antioxidant, cytotoxic activities, antitumor and Immunomodulatory potential of some purified Rhizobial- exopolysaccharides (EPS). **Materials and Methods**: (The Total Antioxidant Activity (TAA) was evaluated using dot-blot,1,1-Diphemy 1-2-picryl-hydrazyl (DPPH) staining and phosphomolybdenum assay, Total Phenolic Content (TPC) via Folin-Ciocalteu's assay, Ferric Reducing Antioxidant Power (FRAP) and cytotoxicity via Brine Shrimp Lethality Test (BSLT). Immunoglobulin level, Carcino Embryonic Antigen (CEA), antitumor activity and haematological analysis were assessed on albino mice.) **Results and Conclusion**: (The scavenging assay for the antioxidant increased in a dose dependent manner across the EPS samples tested. Rhizobial-EPS had the highest DPPH (96.69%), TPC (1.588µm/mL), TAA (1.895µm/mL) and FRAP (2.137µm/mL) compared to the standard which was lower than the EPS produced by all Rhizobia with *Rhizobium leguminosarum*S2 having the highest values. The cytotoxicity showed no mortality rate of the brine shrimp tested. The mice injected peritorially with EPS produced from USDA 110 had the highest production of immunoglobulin (IgA, IgG and IgM) intensity. The mice administered with Rhizobial-EPS prior to tumor induction had the maximum IgA, IgG and IgM (98±0.36, 128±0.08, 85±0.03Mg/dl) intensity while the slightest IgA, IgG and IgM (62±0.21,69±0.02 and 60±0.05) was obtained in tumor induced mice without treatment. The Lymphocyte (79 cells/µL), Neutropile (73cells/µL) and packed cell volume (43.0%) of tumor induced mice administered with Rhizobia-EPS were significantly higher than the mice induced with tumor and were left untreated. EPS from *Rhizobium* sp. had antioxidant and immunomodulatory activity on the treated mice and had no lethal effects on brine shrimps.)

Keywords: Exopolysaccharides (EPS), Rhizobia-EPS, *Rhizobium leguminosarum*S2, antioxidant, immunomodulatory.

Paper ID *(HE067.)*

Assessment of Antimicrobial Potential of Endophytic *Bipolaris yamadae* uilrz3

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Abstract

Background: The incessant resistance of pathogenic microorganisms to existing antibiotics has informed the exploration of alternative sources of production of antimicrobial agents. This study aimed to explore endophytic *Bipolaris yamadae* UILRZ3 against selected pathogenic microorganisms. **Materials and Methods**: The endophyte was fermented in potato dextrose broth for 7 days following standard procedures and extracted using ethanol to allow evaluation of the antibacterial potential. The crude extract was screened using agar well diffusion method and the disc diffusion method to screen the standard antibiotic. Minimum inhibitory concentration (MIC) was determined using the broth microdilution technique. Column and thin-layer chromatography are used for the fractionation of extract. Bioautography was adopted for screening the fractions while Gas chromatography-Mass spectrophotometry was used to identify the bioactive compounds. **Results and Conclusion**: The bacteria were susceptible to the extract with zone of inhibitions ranging from 4.50 ±0.43-15.00±1.89mm at 512µg/ml. *Staphylococcus aureus* was resistant to all the standard antibiotics but susceptible to the four fractions of endophyte. The GC-MS analysis detected and identified ten bioactive compounds that could be responsible for the antibacterial activity of the extract. Therefore, this study recommends further work on the partially purified fractions for harnessing them as antimicrobial agent.

Keywords: Endophytic fungi, Antibiotic resistance, *Bipolaris yamadae*, GCMS, *Staphylococcus aureus*

Paper ID (HE068.)

In Silico and *In vivo* Evaluation of The Effects of Silymarin on Testosterone-Induced Benign Prostate Hyperplasia in Male Wistar Rats

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Abstract

Background: Benign prostate hyperplasia (BPH) is a condition where the prostate grows and develops non-cancerously. Silymarin is well-known for its potential medicinal properties and has undergone thorough investigation regarding its capacity to stimulate liver cell regeneration and alleviate inflammation. The current study, therefore, sought to evaluate the anti-hyperplasia efficacy of silymarin on testosterone-induced benign prostate hyperplasia rats.**Materials and Methods**: Thirty male Wistar rats were randomized into five groups (n = 6). Twenty-four rats were castrated using an anaesthetic agent (ketamine,2.5 mg/kg) in order to eliminate the influence of endogenous testosterone during the study. The castrated rats were allowed to recover for four weeks before the commencement of the study. Testosterone propionate was administered subcutaneously, at 2.5 mg/kg body weight every day for thirty days to induce benign prostate hyperplasia (BPH). The rats' groups were designated A-E. The groupings were as follows: non-castrated control, castrated control, castrated control + Testosterone propionate (BPH), BPH + 50 mg/kg silymarin, BPH + 0.5 mg/kg Dutasteride (standard drug). At the end of 10 weeks, the rats were fasted overnight, blood samples were collected *via* ocular puncture, and tissues were harvested for biochemical and morphological analyses.**Results and Conclusion**: Increase in prostate size in BPH rats was decreased when treated with silymarin. Also, silymarin markedly caused a decrease in malondialdehyde concentration in serum and prostate compared to untreated BPH rats ($p < 0.05$). Silymarin markedly ($p < 0.05$) increased the activities of antioxidant enzymes in the prostate and liver compared to untreated BPH Conclusively, oral administration of silymarin lowered BPH abnormalities in male Wistar rats.

Keywords: Benign prostate hyperplasia, silymarin, 5α-reductase, antioxidant, Testosterone.

Paper ID *(HE 069)*

The Role of Infection and Inflammation in Prostate Cancer Development

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Abstract

Background

Prostate cancer (PCa) is a prevalent disease among black men and is recognized as the second most frequently diagnosed cancer. PCa is described by the abnormal proliferation of cells within the prostate gland, which can be further compounded by inflammation leading to various complications. Modifiable and non-modifiable factors have been associated with PCa that include infections [caused by bacterial, viral, and protozoan pathogens, including sexually transmitted infections (STIs)], age, family history, and ethnicity. The process of inflammation is a vital defence mechanism against invasive infections. However, persistent chronic inflammation can exacerbate existing tissue damage. **Materials and Methods** Extensive search was done using scientific databases such as Pubmed, ScienceDirect and Google Scholar. Articles were pre-screened using abstracts and titles from 2017-2022. A total of 64 articles related to the literature on infections, inflammation and prostate cancer were downloaded. **Results** Researchers have found evidence suggesting that inflammation contributes to the aetiology of PCa. Studies have indicated that men with a history of STIs caused by *Neisseria gonorrheae*, *Trichomonas vaginalis*, *Ureaplasma urealyticum*, and *Treponema pallidium* are more prone to developing PCa. Chronic inflammation resulting from infections is a major risk factor for PCa. **Conclusion** Understanding the intricate relationship between inflammatory processes in the tumour microenvironment is crucial for preventing the progression of PCa and optimizing targeted treatments. By comprehending the mechanisms behind inflammatory signatures, researchers aim to reduce PCa mortality rates and enhance the effectiveness of treatment strategies.

Keywords: Infection, acute inflammation, chronic inflammation, prostatitis, prostate cancer,

Paper ID *(HE070.)*

Antibiogram characteristic of PCR-confirmed *Escherichia coli* isolates from cloaca of chickens in poultry farms in Abakaliki Metropolis, Ebonyi State

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Abstract

Background: The demand for poultry products has increased in recent years especially as more people realize the nutritional and economic value of chicken and their products. However, bacterial diseases associated with the consumption of poultry products remain a public health threat to the poultry industry. This study elucidates the antibiotics susceptibility profiles of *Escherichia coli* isolated from chicken cloacal swabs in poultry farms in Abakaliki metropolis.**Materials and Methods**: A total of nine (9) samples were collected over a 3-month period using the random sampling technique, and investigated for the presence of *E. coli* using the streak plate method on Eosine Methylene Blue (EMB) Agar. Polymerase chain reaction (PCR) technique was used to confirm the identity of the isolates. The susceptibility profile of the isolates was determined using the Kirby-Bauer disc diffusion assay containing varying concentrations (5 µg - 30µg) of selected antibiotics. **Results and Conclusion**: Twenty-six (26) *E. coli* isolates were selected for the antibiotic susceptibility testing, from which the Multiple Antibiotic resistance profile (MARP) and Multiple Antibiotic resistance index (MARI) were determined. Counts of *E. coli* obtained across the sampling locations ranged from 150-517 CFU/g. The findings of this study showed that all 26 isolates were resistant to Cefuroxime and Doripenem. The isolates also exhibited resistance to other antibiotics in the order: 97% for Chloramphenicol, 96% each for Sulfamethoxazole-Trimethoprim and Tetracycline, and 73% each for Ciprofloxacin and Gentamycin. MARP ranged from 10 drugs (CXM/MRP/AK/SXT/CIP/C/CN/TE/DOR/NOR) to 4 drugs (CXM/MRP/TE/NOR). All *E. coli* isolates had MARI from 0.4-1.0. The findings indicate a high prevalence of multiple drug-resistant *E. coli* in the cloacae of chickens, necessitating the need for better surveillance, improved hygiene practices, alternative therapy and monitoring of antibiotic resistance patterns in animal husbandry.

Keywords: Poultry; *Escherichia coli*; Antibiotics; Multidrug resistance; Public health.

Paper ID *(HE071)*

Prevalence and Antibiogram of Healthcare-Associated Methicillin-Resistant *Staphylococcus aureus* (HA-MRSA) in a Public Tertiary Healthcare Facility (NH) in Enugu, Enugu State, Nigeria.

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Abstract

Background: Methicillin resistant *Staphylococcus aureus* (MRSA) remains a major cause of both community and healthcare-associated infections. This study was designed to determine the prevalence and antibiogram of healthcare-associated MRSA (HA-MRSA) in a public tertiary healthcare facility (NH) in Enugu, Enugu State, Nigeria. **Materials and Methods**: A total of 62 {(male-33; female- 29; urine-47, wound swabs-10, sputum- 1, urethral swab (U/S)-1, bone tissue aspirate- 3)} clinical samples were obtained from NH in Enugu State (Ethical clearance No, IRB/HEC No- S.313/IV). *S. aureus* were isolated, characterized and identified based on standard microbiological procedures. Antibiogram of MRSA isolates using cefoxitin 30µg (MRSA screening), oxacillin 1µg (MRSA screening), ceftazidime 30µg, ciprofloxacin 5µg, clindamycin 2µg, penicillin 10µg, erythromycin 15µg, nitrofurantoin 300µg, gentamicin 5µg, sulphamethaxazole 25µg, vancomycin 20µg and tetracyline 30µg was determined by disc diffusion method. **Results and Conclusion**: Prevalence of MRSA was significant amongst the isolates obtained from males (48.5%) than females (41.4%). The highest prevalence of MRSA in relation to age and sample source were obtained from {(31-45) and (46-60)} years and urine as (66.7%) and (42.6%) respectively. HA-MRSA were highly resistant to penicillin (100%), tetracycline (95.6%), and erythromycin (95.6%), but moderately susceptible to gentamycin and ciprofloxacin. A mean multiple antibiotic resistance index (MARI) of 0.8 was observed in this study with 96% > 0.2. In conclusion, prevalence of HA-MRSA was high in our study area. Therefore, more proactive measures must be taken to curb this public health menace before it escalates beyond control.

Keywords: MRSA, HA-MRSA, Antibiotic resistance, Antibiotics, Clinical samples

Paper ID *(HE072.)*

Antibiogram of Methicillin-Resistant *Staphylococcus aureus* Strains from Dairy Product in Nasarawa, Nasarawa State, Nigeria

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Abstract

Background: Dairy products have been found to be a major vehicle for the transmission of multidrug-resistant MRSA strains to man. This study determined the antibiogram of methicillin-resistant *Staphylococcus aureus (*MRSA) strains from traditionally-pasteurized dairy product (*Kindirmo*) in parts of Nasarawa, Nasarawa State, Nigeria. **Methods:** One hundred and sixty samples were collected from vendors using random sampling from the areas selected for the study. The samples collected from January 2021 to April 2021. Each sample was collected into sterile screwed-capped plastic bottle and labeled appropriately. Standard microbiological procedures were used in isolating and identifying MRSA strains from the samples. Characterization of the MRSA strains was carried out using Microgen® kits. The MRSA strains were evaluated for their susceptibility to Cefoxitin (30µg), Clindamycin (2µg), Chloramphenicol (30µg), Doxycycline (30µg), Gentamicin (10µg), Sulphamethoxazole/trimethoprim (25µg), Tobramycin (30µg), and Vancomycin (30µg), using the Kirby-Bauer technique. **Results:** Of the 160 samples examined, eight MRSA strains (NWT8, NWT12, GNK3, MRU7, MRU9, ARB8, ARB14, and ARB18) were obtained, giving a prevalence of 5.0%. All of the MRSA strains were resistant to Cefoxitin (0-1mm); 62.5% were resistant to Tobramycin (7-11mm); and 25.0% were resistant to Chloramphenicol (4-10mm). Five (5) antibiotic resistant phenotypes were recorded among the MRSA strains. **Conclusion:** The occurrence of MRSA in *Kindirmo* as recorded in this study, suggest that, the consumption of the product constitute a hazard to consumers. Basic hygiene requirements during production and selling of the product should be imposed by relevant authorities. This will go a long way in ensuring the safety of the product.

Keywords: Antibiogram, MRSA, Dairy Product, Nasarawa, Nigeria

Paper ID *(HE073)*

Detection of Extended Spectrum β-lactamase (ESBL)-Resistant gene in *Salmonella* species and *Escherichia coli* Isolated from Drinking Water in some Selected locations in Southwestern Nigeria.

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Abstract

Background: The quality of water available for households use were investigated in some selected locations in Nigeria. **Methods:**A total of 180 water samples were collected and 100 ml of the each water sample were analyzed using membrane filtration technique. The antimicrobial susceptibility testing of the *E. coli* from the water samples were determined using standard microbiological protocols and detection of ESBL resistance genes.**Results:** Microbiological mean total coliform count (TC) values obtained in both stored and source water in sampling locations were high ranging from (3.10 cfu/100ml ± 1.46 cfu/100l to 156.80 ± 42.9 for stored water) and (0.50 cfu/100 ml ± 0.31 to 90.60 ± 38.05 for source water). Also, the source waters were devoid of faecal coliform whereas stored water had mean count values between 0.80 cfu/100ml ±0.70 and 64.30 cfu/100ml ±14.15. Twenty-five *E. coli* isolates and twenty *Salmonella* species obtained from the water samples were resistant to most antibacterial used. However, four of the *E. coli* isolates were sensitive to cefotaxime (30µg) and four of the *Salmonella* species were sensitive to gentamicin (10µg) and cefuroxime (30µg). Thermocyler PCR with TEM F-CCCCAAGAACGTTTC, TEM R-ATCAGC AATAAACCAG C and SHV F- AGGATTGACTGCTTTTG, SHV R-ATTTGCTGATTTCGCTCG revealed that eleven out of the twenty-five *E. coli* isolates (44%) screened for ESBL resistance genes had TEM genes while four of the isolates (16%) had SHV gene. Although, none of the *Salmonella* sp. screened for ESBL resistant genes (Bla $_{TEM}$, Bla $_{SHV}$ and Bla $_{CTX-M}$) were positive for the genes but there could be other factors responsible for presence of multiple resistant genes in them. **Conclusion**: This study concluded that drinking water could be a source of exposure to antibiotic - resistant *E. coli and Salmonella* species which may pose a threat to human populations and their health in the study area.

Keywords: Water, *E. coli, Salmonella species,* Antibiotic resistance, ESBL**.**

Paper ID *(HE074.)*

Phytochemicals and *in silico* Antibacterial Studies on Fruitskin Ethanol Extract of *Annona muricata* Linnaeus

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Abstract

Background: Research has shown that, antibiotic resistance is projected to be the most dangerous form of antimicrobial resistance (AMR) in the current trend. It is estimated to cause around 10 million deaths annually, including other forms of AMR, by 2050. **Materials and methods** In this study, The Annona muricata plant was sourced from Covenant University premises and identified. Fresh and frozen fruit skin ethanol extracts were then prepared from the plant. The resulting filtrate was concentrated using a rotary evaporator at a temperature of 45 degrees Celsius. The fresh extract was labelled ESA F2 while the frozen extract was labelled ESA F1. Phytochemical screening was carried out on ESA F1 and ESA F2 and in silico antibacterial studies on ESA F2 only. Since there is no standard drug for antibiotic resistance, therefore no known binding site on the marker enzyme has been discovered; a binding site was predicted to accommodate our novel drug candidate. The binding interaction of the 14 hit compounds from the GC-MS output of ESA F2 was determined by docking the resultant compounds into the predicted active site of subunits A and B of DNA gyrase and topoisomerase IV, using PyRx AutoDock vina to establish their binding affinity and interaction profile. **Results:** Phytochemical screening showed Saponins, alkaloids, and steroids were found to be present in ESA F2 only while terpenoids, cardiac glycosides and quinones were found present in both ESA F1 and ESA F2. The GC-MS carried out on ESA F1 and ESA F2 indicated 36 and 17 peaks respectively. Major compounds such as Ethanediamide, N,N'-bis(1-phenylethyl)- , 2-Carboxycinnamic acid, and 9-Eicosene, (E)- were found to be present in ESA F2 but absent in ESA F1 which could be as a result of the breakdown of these compounds during the process of freezing. Compounds such as Benzaldehyde, Benzofuran, and Benzofuran, 2-methyl, were present in both ESA F2 and ESA F2. **Conclusion**: Ethanediamide,N,N’-bis(1-phenylethyl)-[AKOS000448688] showed the highest binding affinity for GyrA and GyrB as well as Topoisomerase IV while 2-carboxycinnamic acid out of all the 14 hit compounds screened for bound to the predicted site on all polypeptides studied which infers that this hit compound might likely be the active principle responsible for the reversal of fluoroquinolone resistance in gram negative bacteria.

Keywords: *Annona muricata*, antimicrobial resistance, cardiac glycosides, phytochemicals, Ethanediamide,N,N’-bis(1-phenylethyl).

Paper ID *(HE075.)*

Antibiogram Profile of Bacteria Isolated from WUPA Sewage Treatment Plant, Abuja

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Abstract

Background:The presence of antimicrobial-resistant bacteria in municipal sewage treatment plants (STPs) has raised concerns regarding the potential dissemination of resistant strains into the environment. This study aimed to characterize the antibiogram of bacteria isolated from Wupa sewage treatment plant. Thus providing insights into the prevalence and resistance patterns of these bacteria species.**Materials and Methods**: Physicochemical and Microbiological properties of the homogenized activated sludge were determined by qualitative techniques and subsequent biochemical tests were used to identify the isolates. The antibiotic susceptibility profiles of the isolates were determined using Modified Kirby-Bauer disc diffusion technique. **Results and Conclusion**: The physicochemical analyses of the sludge sample revealed characteristics typical of organic waste material as it showed high moisture content (88.7±2.3%), slightly basic pH (6.86±0.22), and a significant presence of organic matter (37.48±4.2%). The total heterotrophic bacterial counts and coliform counts of the sludge sample were $6.08\pm2.2x10^6$cfu/g and $1.76\pm0.2x10^6$cfu/g respectively, the total *Salmonella-Shigella* counts and total *Staphylococcus* counts were $3.2\pm0.4x10^5$cfu/g and $4.3\pm0.3x10^5$cfu/g respectively, while the total *Pseudomonas* count and total fungal counts were $1.4\pm0.1x10^5$cfu/g and $1.3\pm0.1x10^5$cfu/g respectively. Fourteen (14) bacterial and five (5) fungi genera comprising majorly, *Staphylococcus, Enterobacter, Bacillus, Streptococcus, Escherichia, Shigella, Pseudomonas, Salmonella, Aspergillus, Mucors, Penicillum, Rhizopus,* and *Candida* were isolated. The bacterial isolates were highly resistant (<14mm) to Amoxicillin-Clavulanic and Cefuroxime, while susceptibilities (≥20mm) to Ofloxacin and Gentamicin were observed among the isolates. The results revealed a diverse array of bacterial species with varying degrees of susceptibility to antimicrobial agents, highlighting the need for effective wastewater management strategies to mitigate potential public health and environmental risks.

Keywords: Public health, Antimicrobial, Environment, Wastewater, Organic matter.

Paper ID (HE076)

Human Papillomavirus Genotypes and Risk Determinants Among Nigerian Women with Lesions

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Abstract

Background: The second most common infection-related cancers worldwide are those associated with human papillomavirus (HPV). HPV is a leading cause of cancer deaths in Nigerian women with over 7,000 deaths annually. However, very little is known about the molecular epidemiology of HPV in Nigeria in spite of its significance in evidence-based policy and prevention. We, therefore, set out to evaluate the circulating genotypes of HPV in women who had abnormal cervical cells and determine the association. **Materials and Methods**: Cervical swab samples were collected from 250 consenting women accessing cervical cancer test facilities at JUTH, Jos, FMC, Keffi and the National Hospital, Abuja, after ethical approval and informed consent. Structured questionnaires were also administered to obtain socio-demographic information. Samples were analysed for atypical squamous cells of undetermined significance (ASCUS), low and high squamous cell intraepithelial lesions (LSIL and HSIL) using Papanicolaou stains (Pap smear), and HPV DNA using type-specific primers that targeted E6 and E7 oncogenes of the virus. **Results and Conclusion:** A total of 89 (35.6%) had HPV infection while 39 (15.6%) had abnormal cervical cells, out of which 19 (48.7%) were ASCUS, 12 (30.8%) were LSIL and 8 (20.5%) were HSIL. Women aged 40 - 49 years were more likely (4.4%) to have abnormal cervical cells. In addition, we found that 13 HPV genotypes namely; HPV- 6/11, 16, 18, 33, 35, 39, 42, 43, 45, 51, 58, 59 and 66 were responsible for the abnormal cervical cells with HPV-18 predominating. Identification of genotypes in each type of lesion showed that HPV-18 and 16 predominated in HSIL (100.0% and 45.5%) respectively. The HPV-16, 31 and 58 predominated in LSIL (36.4%, 33.3% and 30.0%) respectively, while HPV-33 and 35 were the most predominant in ASCUS (50.0% and 33.3%) respectively (P=0.001). Moreover, our findings revealed that HPV-18, 16, 33 and 59 were the most circulating genotypes in the population. These findings provide strong molecular evidence on the circulating genotypes of HPV in patients with abnormal cervical cells in Nigeria with critical implications for prevention, control and policy.

Keywords: Human papillomavirus, HPV genotypes, Cervical cancer, Cervical cells, Nigeria

Paper ID *(HE077.)*

Recent Advances in Immunotherapy for Prostate Cancer Treatment

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Abstract

Background: According to Global Cancer Observatory's (GLOBOCAN) estimates of 2020, prostate cancer (PCa) is a major global public health concern affecting men over 40 years. PCa is one of the most commonly diagnosed cancers and the 5th leading cause of death linked to cancer. **Materials and Methods**: This review utilized various scientific databases, including PubMed, Scopus, and Google Scholar. The search targeted relevant articles published between 2019 and 2023, focusing on prostate cancer, immunotherapy, metastatic castration-resistant prostate cancer, and combination therapy. A total of 210 articles were returned. After screening, 71% of the studies had titles and abstracts related to the study focus prioritizing immunotherapeutic approaches like ADT/PI3K inhibitors, PARP inhibitors, and precision medicine to target mCRPC.**Results and Conclusion**: From various studies reviewed, cancer treatment options such as chemotherapy and radiotherapy pose many challenges because of their lack of specificity for cancer cells, as normal cells are often destroyed. To overcome the non-specific limitation of cancer cells, immunotherapy has emerged. It involves making use of the immune system cell-mediated surveillance to find and eliminate cancer cells in the body possibly through the program death ligand-1 pathway blockage. Combinational therapy is an effective strategy to counteract immunosuppression in PCa patients. Recently, the Food and Drug Administration approved the PARP inhibitor such as talazoparib in combination with enzalutamide for the treatment of HRR gene-mutated metastatic CRPC. These recent findings provide more innovative and effective approaches to treating mCRPC. This review looked at the most recent immunotherapy treatments for mCRCP and the future hope towards countering immunosuppression in PCa.

Keywords: Prostate Cancer, Immunotherapy, metastatic castration-resistant prostate cancer (mCRPC), poly-ADP ribose polymerase (PARP) inhibitors, combination therapy.

Paper ID *(HE078.)*

Possible Transmission of Antibiotic and Heat Resistant *Salmonella typhimurium* and *Listeria monocytogenes* in Raw Chicken Sold in Abuja, Nigeria.

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Abstract

Background: Widespread use of antibiotics in livestock production in large-scale across the globe has become of public and veterinary health importance because of its implication in antibiotic resistance. Adequate data in this area of research is not readily available in Nigeria; this study was undertaken in view of the possible link between antimicrobial resistance in farm animals and humans. **Methods:** Fifty samples of raw beef were collected from different vendors by simple random sampling and slaughterhouses within Abuja and screened for the presence of *Listeria monocytogenes* and *Salmonella typhimurium* using standard microbiological methods. The total bacterial and fungal counts, antibiotic susceptibility to Ampicillin (10ug), Erythromycin (15ug), Chloramphenicol (30ug), Streptomycin (10ug), Gentamicin (10ug), Amoxicillin (10ug), Ciprofloxacin (5ug), Cefuroxime (30ug) by disc diffusion method and heat sensitivity at 55, 60 and 65 ^{o}C for 15 minutes were determined. **Results:** The results show that ten isolates of *Listeria monocytogenes* and eighteen isolates of *Salmonella typhimurium* were isolated from the samples. The total viable bacterial count ranged from 1x 10^9 - 8x 10^9cfu/g while the fungal count ranged from 1x 10^3 - 9x 10^9cfu/g. One (10 %) of the *Listeria monocytogenes* isolates was resistant to all antibiotics tested while all the *Listeria monocytogenes* isolates were resistant to Cefuroxime. Eight (44.4%) of the *Salmonella typhi* isolates were resistant to at least three antibiotics. All the *Listeria monocytogenes* and *Salmonella typhi* isolates did not survive beyond 60 ^{o}C upon heat treatment.**Conclusions:** The results of this study indicated a high prevalence of *Salmonella typhi* and *Listeria monocytogenes* in selected beef in Abuja. Beef therefore may represent a large reservoir for antimicrobial-resistant *Salmonella typhi* and *Listeria monocytogenes*.

Key Words: Infectious disease, raw beef, antibiotic susceptibility, heat treatment.

Paper ID *(HE079.)*

Phytochemical, Antioxidant, and *in silico* Antiviral Study of *Cassia fistula* against Selected Biomarkers of Covid-19

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Abstract

Background: The severe acute respiratory syndrome Coronavirus-2 (SARS-CoV-2) is a single-stranded RNA virus from the family of Coronaviruses that causes the coronavirus disease (COVID-19). As of March 2023, there had been 761,402,282 confirmed cases and 6,887,000 fatalities from the infection worldwide. This study investigated the phytochemical constituents, antioxidant capacity, and *in silico* antiviral effect of *Cassia fistula* pod extract on selected biomarkers of COVID-19.**Materials and Methods**: *Cassia fistula* pods were plucked from the orchards of Covenant University. The phytochemical constituents of fresh (CFE1) and freeze-dried (CFE2) aqueous extracts of *Cassia fistula* were ascertained using phytochemical screening assays and gas chromatography-mass spectrometry (GC-MS). The antioxidant activity was investigated using 2,2-diphenyl-1-1-picrylhydrazyl (DPPH) and ferric-reducing antioxidant power (FRAP) assays. Molecular docking was carried out to compare binding affinities of standard inhibitors and phytochemical constituents of CFE1 against selected biomarkers.**Results and Conclusion**: Qualitative phytochemical analysis showed that *Cassia fistula* extract contains tannins, saponins, flavonoids, quinones, phenols, terpenoids, cardiac glycosides and anthocyanins. The values for total phenols is 0.697 ± 0.22 mgGAE/ml, total flavonoids 1.425 ± 0.03 µgQE/ml, and total tannins is 1.930 ± 0.56 mgGAE/ml for CFE1, The values for total phenols is 0.333 ± 0.09 mgGAE/ml, total flavonoids 1.391 ± 0.01 µgQE/ml, and total tannins is 1.77 ± 0.39 mgGAE/ml for CFE2. The most abundant compounds for CFE1 and CFE2 are hexamethyl-cyclotrisiloxane (59.18%) and 4-methyl-3-penten-2-one (59.18%) respectively. Oxalic acid, allyl tridecyl ester and methyl 4-{5-[n-(4-chlorophenyl) iminomethyl]-2-furyl}benzoate had higher binding affinities for spike protein than the standard inhibitor, calpeptin. In conclusion, certain phytochemicals present in *Cassia fistula* are likely to be potential drug candidates in combatting COVID-19.

Keywords: COVID-19, *Cassia fistula*, Molecular docking, GC-MS, Phytochemicals.

Paper ID *(HE080)*

Antibiogram of Multi-drug Resistance Bacteria from the Hands of Primary School Children in Ebonyi State, Nigeria.

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Abstract

Background: This study was carried out to isolate, identify and characterize multi-drug resistant bacteria from primary school children within Ebonyi North Senatorial District, Nigeria. **Material and Methods**: In total, 384 swabs were obtained from the hands of pupils in 10 primary schools over a period of ten (10) months using standard microbiological techniques. The isolates obtained were examined and identified by colonial morphology, Gram reaction and biochemical tests. Antimicrobial susceptibility was performed on the isolates by Kirby-Bauer paper disc diffusion method. The pathogenicity test was carried out using albino rats which were injected Intraperitoneally with some of the potential multidrug resistant bacteria. **Results and Conclusion:** *Staphylococcus*, were more prevalent 150(46.1%) than other bacteria in these order *Escherichia* 60(18.5%), *Shigella* 36(11.1%), *Klebsiella* 33(10.2%), *Salmonella* 28(8.6%) and *Pseudomonas* 18(5.5%).Generally, most of the bacterial isolates were highly susceptible to Ciprofloxacin (30µg) (87.9%) and Gentamicin (10µg) (83%) but highly resistant to Tetracycline (30µg) (100%) and Nalidixic acid (30µg) (97.6%). The multiple antibiotics resistance (MAR) index showed that 98.2 % of the bacterial isolates were multi-drug resistant. Pathogenicity test showed that organs of the animals used manifested various damages ranging from lymphocytic infiltration around the portal tract (acute hepatitis**),** mild periportal chronic inflammatory infiltration (mild hepatitis) and necrosis of renal tubules. Mortality rate of 50 % was observed in albino rats infected with *Pseudomonas* while 25 % was observed in albino rats infected with other bacteria isolates. Hands can act as carriers for multidrug resistant bacteria, suggesting the need for proper hand hygiene, disinfection of school environment and surfaces.

Keywords: Antibiogram, Multi-drug Resistance, Hands, Primary Schools, Pathogenicity.

Paper ID *(HE081)*

Occurrence of biofilm-producing antibiotic resistant Enterobacteriaceae in locally prepared Soy-Milk beverage sold within Abakaliki metropolis

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Abstract:
Background: The occurrence of enteric bacteria in street-vended beverages is a serious public health threat. This present study investigated the bacteriological quality, incidence, and antibiotics resistance profile of biofilm-producing Enterobacteriaceae isolated from soy-milk beverages sold in selected six locations within the Abakaliki metropolis in Ebonyi State.**Materials And Methods:** Eighteen (18) samples were randomly obtained from Ishieke, Romchi Park, International Market, Spera'n'Deo Park, Ogoja Road, and Meat Market. The samples were subjected to culture-based and biochemical methods to ascertain their bacteriological quality. Tube binding assay and the disk diffusion method were used to determine the biofilm-producing ability of the isolates and the antibiotic-resistant profile respectively. **Results and Conclusion**: The total aerobic count ranges from 5.7± 0.45 x 10^7 to 6.6±0.84 x 10^6 cfu/ml while coliform count ranged from 2.6±0.14 x 10^3 to 8.4±0.98 x 10^4 cfu/ml. Of the 25 distinct colonies that were selected for further analysis, 8% (2) of the isolates were non-biofilm producers while 92% (23) of the isolates were biofilm producers based on the formation of visible rings on the tubes. All the isolates exhibited multidrug resistance, with a mean Multiple Antibiotics Resistance Index (MARI) of 0.6 and resistance to erythromycin (100%), Ceftazidime (96%), Gentamycin (56%), Ceftriaxone (40%) having the highest frequency among the biofilm-producing bacterial isolates. The enteric bacteria identified in this study were of the genus *Klebsiella (*28%), *Enterobacte*r (28%), *Salmonella* (12%), Proteus (12%), *Shigella* (8%), *Escherichia* (8%) and *Serratia* (4%). This study raises concerns about the contamination of street-vended beverages in Abakaliki and the need for constant surveillance to ensure food safety.

Keywords: Biofilms, Antimicrobial resistance, Soy-milk, Enteric bacteria, Food safety

Paper ID *(HE082.)*

Comparative Evaluation of GenoType MTBDRplus Line Probe Assay with Solid Culture Method for Early Diagnosis of Multidrug Resistant Tuberculosis (MDR-TB) in North Central Nigeria

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Abstract

Background: Multi-drugs resistant Tuberculosis (MDR-TB) poses a great threat to the TB control programs worldwide. Early diagnosis of rifampicin (RIF) and isoniazid (INH) drug resistant *Mycobacterium tuberculosis* is essential for effective treatment and control of MDR-TB. This study evaluated the performance of GenoType MTBDRplus Line Probe Assay with solid culture method for early diagnosis of MDR-TB. **Materials and Methods**: A total of 112 consented and confirmed MDR-TB participants were enrolled from January to December 2022 into the study. All sputum samples were subjected to AFB microscopy, solid culture, DST and LPA methods and the results were compared. **Results and Conclusion**: Of the 122 samples, 95.5% were positive, 1.7% were negative, 1.7% were contaminated, and 1.1% were non-tuberculosis mycobacteria (NTM) on solid culture. On LPA, 96.4% of the samples were positive, 3.6% were negative, and 1.1% were NTM. The sensitivity for Rifampicin and Isoniazid monoresistance and that of MDR were 95.7%, 72.9%, and 97.1%, respectively. The specificity for Rifampicin and Isoniazid monoresistance and that of MDR were 88.4%, 88.7%, and 100%, respectively. The most frequent occurring mutation among the MDR strains were rpoB MUT2 and katG MUT2. The LPA test gave a timely diagnosis of monoresistance to rifampicin and isoniazid and proved highly sensitive and specific for an early diagnosis of MDR-TB. This makes it a valuable tool for early diagnosis of MDR-TB.

Keywords: *Mycobacterium tuberculosis*, Multi-drugs resistant, Rifampicin, Isoniazid, Line Probe Assay

Paper ID *(HE083.)*

Antimicrobial Activity of Some Common Antiseptic on Bacteria and Fungi from the Surface of Human Skin

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ABSTRACT

Background: From birth to dead, the normal human skin is colonized by huge numbers of organisms that live as parasites or commensals on its surface. This study assessed bacteria and fungi that are found colonizing the skin of human body and the effectiveness of some common antiseptics on the isolates.**Methods:** The surface of human skin was scrubbed with moistened swab sticks; the samples were inoculated on appropriate culture media (Nutrient, MacConkey, Potatoes Dextrose and Manitol salt agar) for the growth and identification of the organisms following standard procedures. The isolates were also subjected to the action of some antiseptics (A=Chloroxylenol, B=Chlorhexidine and C= Trichlorophenol) using agar diffusion method. **Results:** Some bacteria and fungi isolated were; *Klebsiella pneumonia, Staphylococcus epidermidis and Escherichia coli*; *Aspergillus flavus*, *Candida albicans*, and *Trichophyton rubrum*. The zones of inhibition in millimetres (mm) of antiseptic A against *klebsiella pneumonia, Staphylococcus epidermidis,* and *Escherichia coli* are (15.71, 48.12, 5.36), antiseptic B against *klebsiella pneumonia, Staphylococcus epidermidis,* and *Escherichia coli* are (32.09, 33.71, 45.91), antiseptic C against *klebsiella pneumonia, Staphylococcus epidermidis,* and *Escherichia coli* are (0.00, 18.77, 8.27) Antiseptic A against *Aspergillus flavus, Candida albicans,* and *Trichophyton rubrum* are (14.87, 25.97, 0.00), antiseptic B against *Aspergillus flavus, candida albicans,* and *Trichophyton rubrum* are (8.32, 19.41, 3.91), antiseptic C against *Aspergillus flavus, candida albicans,* and *Trichophyton rubrum* are (33.83, 23.97, 0.00).**Conclusion:** High load of organisms are found on human skin. The use of antiseptics to clean the skin can help to reduce their effects.

Keywords: Skin, Antiseptic, Colonized, *Aspergillus flavus*, *Candida albicans*

Paper ID (HE084.)

Antibiogram of Bacteria and Fungi from Cowhide (Ponmo*)* Wastewater

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ABSTRACT

Background: "Ponmo" is obtained from roasted cowhide, commonly consumed by the Yoruba(s) in the South western part of Nigeria, but now it is consumed by almost all ethnic groups in Nigeria. This work assessed the bacteria and fungi associated with vended cowhide "Ponmo" wastewaters in Nasarawa Market, Nasarawa State Nigeria.**Methods:** Three samples of the waste water of 200ml each were collected at different sites in Nasarawa Market with sterile containers. The water samples were inoculated in appropriate culture media for growth and identification of the bacteria and fungi species using standard procedures. The antimicrobial sensitivity patterns of the isolates were tested with some common antibiotics using GBMTS discs: Streptomycin (30µg), Ampicillin (30µg), Ceporex (10µg), Tarivid (10µg, Reflacine (10µg), Gentamycin (10µg), Augmentin (30µg), Ciprofloxacin (10µg), Septrin (30µg).**Result:** The total bacterial and fungal count of the samples ranged from 2.1×10^4 to 3×10^4 cfu/ml respectively. Some of the bacteria and fungi isolated include; *Staphylococcus aureus*, *Escherichia coli*, *Klebsiella pneumonia*, *Salmonella tryhimorium; Aspergillus niger*, *Fusarium oxysporium* and *Rhizoctonia solani*. *Staphylococcus aureus* was susceptible to Tarivid (18mm) and Ceporex(15mm), *Escherichia coli* was susceptible to Augmentine (18mm), Gentamycin (17mm) and Reflacine (15mm). *Klebsiella pneumonia* was susceptible to Gentamycin (17mm); *Salmonella typhimorium* was susceptible to Reflacine (20mm) and Ciprofloxacin (23mm). **Conclusion:** In these findings "Ponmo" waste water harboured microorganisms of which some are pathogenic and these can be detrimental to human health.

Keyword: Ponmo, wastewater, pathogenic, *Salmonella tryhimorium*, Ceporex

Paper ID *(HE085.)*

The Prevalence of Pulmonary Tuberculosis in HIV-Infected Patients: A Comparative Study of Microscopy and Mgit Culture

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Abstract
Background: Tuberculosis (TB) is a major opportunistic infection in Human Immunodeficiency Virus (HIV) infected persons and the association of TB with HIV infection has continued to threaten the global control of both diseases. Evaluating the effectiveness and accuracy of both Fluorescent Microscopy (FM)and Mycobacreia growth indicator (MGIT) culture, will contribute to the improvement of diagnostic protocols and ultimately provide better healthcare outcomes for individuals co-infected with HIV and tuberculosis. **Materials and Methods**: Between September 2018 and February 2019, a total of 370 sputum samples were collected from HIV positive patients of different age groups, ranging from less than 10 years old to 60 years and above to determine the prevalence of pulmonary tuberculosis (PTB). These samples were then sent to Zankli TB reference Laboratory at Bingham University Karu in Nasarawa State for analysis. A total of 370 sputum samples were analyzed using fluorescent microscopy (FM) and Macrobacterium Growth Indicator Tube (MGIT) culture methods. **Results and Conclusion**: The prevalence of TB/HIV co-infection was 32.4% for MGIT culture and 22.4% for FM. The majority of the patients (37%) were in the age group 21-30 years, and the majority (63%) were residing in northern Nigeria. There were more females (59.7%) than males (40.3%). The results of this study suggest that FM is not a sensitive method for diagnosing TB in HIV-infected patients. The sensitivity of FM was determined to be 8.3%, which means that 91.7% of the patients with TB were missed by FM. The specificity of FM was 66.8%, which means that 33.2% of the patients who did not have TB were falsely positive for TB by FM.

Keywords: Pulmonary Tuberculosis, HIV, FM, MGIT culture, Nigeria

Paper ID *(HE086.)*

In vivo Antiplasmodial Activities of *Vernonia amygdalina, Cymbopogon citratus*, and *Annona muricata*

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Abstract

The emergence of artemisinin-based drug resistance threatens the elimination of malaria in Sub-saharan Africa and necessitates increased efforts toward the discovery of alternative therapies. This study aimed to determine the *in-vivo* antiplasmodial activities of the ethanolic leaf extracts of *Vernonia amygdalina* (bitter leaf), *Cymbopogon citratus* (lemon grass), and *Annona muricata* (soursop) on chloroquine-sensitive *Plasmodium berghei* in Swiss albino mice (*Mus musculus)*. Phytochemical analysis and acute toxicity testing were carried out on the ethanolic extract of the plants. Ethanolic plant extracts were obtained using cold maceration. Mice were divided into 3 treatment groups of the plant extracts, one negative (10%DMSO), one positive (Chloroquine) control group, and passaged with chloroquine-sensitive *Plasmodium berghei* NK65 strain. The chemo-suppressive activity was carried out using Peter's 4-day test on infected mice at concentrations of 100 mg/kg, 200 mg/kg, and 400 mg/kg bw for all plant extracts. All ethanolic plant extracts had no toxic effects at all dosage concentrations. The anti-plasmodial investigation revealed a dose-dependent reduction in parasitemia for all three plants. *V. amygdalina* revealed chemo-suppression percentages of 48.10 ± 4.32 %, 35.31 ± 4.07 %, and 45.83 ± 3.45 %, respectively while *C. citratus*, showed dosage reduction at 49.66 ± 11.82 %, 20.36 ± 18.07 %, and 30.65 ± 2.62 % respectively. The chemo-suppressive activity of *A. muricata* was also dose-dependent at 25.67 ± 2.99 %, 77.83 ± 2.12 %, and 83.03 ± 3.29 % at 100, 200, and 400 mg/kg bw respectively. *A. muricata* showed the most significant anti-plasmodial activity of the three plants screened in this study compared to the 97.05% inhibition of chloroquine. This study presents the plants' chemosuppressive activities and further studies are recommended for the development.

Keywords: Medicinal Plant, Antiplasmodial, *In vivo*, Chemo-suppression

Paper ID *(HE087.)*

Plasmid profile of bacteria isolated from mint leaves and lettuce grown in Lagos Metropolis

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Abstract

Background: Misuse of antibiotics in agriculture has resulted in the emergence of antibiotics resistance among bacterial population. This study evaluated antibiotics resistance profile of bacteria isolated from mint leaves and lettuce (MLL) grown in Lagos Metropolis. **Materials and Methods**: Ten- fold serial dilutions were carried out on each sample, while bacteria were isolated and identified using Bergey's Manual of Determinative Bacteriology. Antibiotics susceptibility screening of bacteria using Kirby-bauer disc diffusion method with single-disc (30µg); Amoxicillin, Azithromycin, Cefotaxime, Cefpodoxime, Chloramphenicol, Tetracycline, Erythromycin, Linezolid, Vancomycin, Cefepime, Ciprofloxacin and Gentamicin while Multiple Antibiotics Resistance index (MI), plasmid DNA profile and curing were done using standard methods and acridine orange. **Results and Conclusion**: Bacterial identified; *Enterobacter aerogenes, Proteus mirabilis, Bacillus* sp, *Pseudomonas aeruginosa*, *Escherichia coli*, *Shigella* sp *Salmonella* sp, *Enterobacter faecalis*, and *Klebsiella* sp. The highest percentage resistance to nine antibiotics and MI were recorded for *Pseudomonas aeruginosa* and *Proteus* sp (88.9; 88.8%); and *Pseudomonas aeruginosa* (0.89; 0.88) while *Escherichia coli*, *Enterobacter faecalis* and *Klebsiella* sp; and *Salmonella* sp (55.6; 11%); and *Bacillus sp*, *Escherichia coli*, *Enterobacter faecalis* and *Klebsiella* sp; and *Salmonella* sp (0.56; 0.11) recorded the least for MLL. Multiple copies of plasmid DNA with 2023-23130 Kbp were observed in *Pseudomonas aeruginosa* and *Salmonella* sp. antimicrobial resistance profile of plasmid DNA cured bacteria depicted *Pseudomonas aeruginosa* recorded the highest percentage resistance (71.4%) while *Enterobacter faecalis*, *Escherichia coli* and *Bacillus* sp; and *Klebsiella* sp recorded the least (42.9; 43%). The presence of antibiotics resistance bacteria in MLL poses potential health risks to consumers. Cultivation, transportation, handling of MLL should be done with safety measures.

Keywords: Plasmid profile, Antibiotic resistance, mint leaves, lettuce, Lagos metropolis.

Paper ID *(HE088)*

Comparison of the Prevalence and Antibiotic Resistance Patterns of Multidrug-resistant (MDR) *S. aureus* isolates obtained from Poultry Birds in South-south, Nigeria

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Abstract

Background: *Staphylococcus aureus* is associated with food poisoning, human and animal diseases. The misuse of antibiotics in poultry farms leads to the development of multidrug resistant (MDR) *S. aureus* strains globally. This study compared the prevalence rates and antibiograms of *S. aureus* isolated from poultry birds in South-south, Nigeria. **Materials and Methods:** A total of 586 swab samples were randomly collected from apparently healthy birds from poultry farms. *S. aureus* isolates were identified by Gram staining and biochemical tests and Methicillin-resistant *S. aureus* (MRSA) by Cefoxitin test. Ampicillin/Sulbactam(20µg), Co-trimoxazole(25µg), Erythromycin(15µg), Tetracycline(30µg), Cefotaxime(30µg), Ciprofloxacin(30µg), Roxithromycin(30µg), Cloxacillin(5µg), Gentamicin(15µg) and Levofloxacin(5µg) were also tested using Kirby-Bauer disk-diffusion method. **Results:** At Eku community, total prevalence rates for *S. aureus* and MRSA were 33.0% and 21.5% respectively. Asaba, 44.4% and 43.4% while Okada, 56.1% and 27.7% respectively. The overall prevalence rates were 45.2% and 31.4 % respectively. Antibiograms of the isolates showed significant resistant to Cloxacillin (100%), Tetracycline (93.9%), Ciprofloxacin (78.8%). Gentamicin had the most significant susceptibility rate (53.0%) at Eku. At Asaba, resistance was 100% to Cloxacillin, Ciprofloxacin and Co-trimoxazole; Erythromycin and Roxithromycin were 98.9%. Levofloxacin (63.6%) and Gentamicin (61.4%) had the most significant susceptibility rates. At Okada, highest resistant rates were Erythromycin (94.6%), Co-trimoxazole (92.8%) and highest susceptibility rates were Gentamicin (79.3%) and Levofloxacin (78.4%). Most isolates in this study had Multiple Antibiotic Resistance indices of 1.0, 0.83 and 0.5 i.e. multi-resistance to 3-6 classes of antibiotics. **Conclusion:** This calls for caution in using antibiotics in animals indiscriminately and urgent need for surveillance to mitigate the spread of these pathogens in poultry farms and humans in Nigeria.

Keywords: Prevalence, Antibiotics, Poultry birds, Multidrug resistant (MDR) *S. aureus*, Multiple Antibiotic Resistance (MAR) indices,

Paper ID *(HE089.)*

Phytochemical, Antioxidant, and *in silico* Antibacterial studies of *Syzygium malaccense* against fluoroquinolone resistance

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Abstract

Background: According to the Centre for Disease Control in 2019, antibiotic resistance results in 2.8 million infections each year. Fluoroquinolone resistance by bacteria species causes community acquired or healthcare-associated urinary tract infections and intra-abdominal infections, with over 50% of infections in some parts of the world, particularly in Asia. This study assessed the phytochemical, *in vitro* antioxidant and *in silico* antibacterial properties of fresh (AAJ1) and fermented (AAJ2) aqueous extracts of *Syzygium malaccense* on selected biomarkers in fluoroquinolone resistance. **Materials and Methods**: Fruits of *Syzygium malaccense* were plucked from the orchards of Covenant University. The phytochemical constituents of AAJ1 and AAJ2 were assessed using phytochemical screening assays and gas chromatography-mass spectrometry (GC-MS). The antioxidant activity was investigated using 2,2-diphenyl-1-1-picrylhydrazyl radical (DPPH) and ferric reducing antioxidant power assays (FRAP). Molecular docking was carried out to compare binding affinities of standard inhibitors and phytochemical constituents of AAJ1 against selected biomarkers. **Results and Conclusion**: Qualitative phytochemical screening showed that *Syzygium malaccense* extract contains flavonoids, phenols, and anthocyanins. The total phenolic content for AAJ1 and AAJ2 was 0.750 ± 0.12 mgGAE/ml and 1.005 ± 0.31 mgGAE/ml respectively. The total flavonoids content for AAJ1 and AAJ2 was 1.037 ± 0.09 µgQE/ml and 1.092 ± 0.06 µgQE/ml respectively. GC-MS chromatogram revealed the presence of 12 compounds. The most abundant phytochemicals were 2-butoxy-ethanol (54%), Hexamethyl-cyclotrisiloxane (17%) and octamethyl-cyclotetrasiloxane (6%). Oleonitrile and 3-methyl-5-phenyl-1H-1,3,4-benzotriazepin-2(3H)-one exhibited higher binding affinity for DNA gyrase and topoisomerse IV than the standard inhibitors. In conclusion, certain phytochemicals present in *Syzygium* malaccense are likely to be potential therapeutic candidates for fluoroquinolone-resistant infections.

Keywords: Fluoroquinolone resistance, *Syzygium malaccense*, Molecular docking, GC-MS, antioxidant assays.

Paper ID *(HE090.)*

Phenotypic Vancomycin Resistant *Enterococcus faecalis* Isolated from Chicken Meat Sold in Local Markets in Lagos and Abeokuta, Nigeria

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Abstract

Background: The abuse of vancomycin in livestock farming as growth promoters have encouraged the emergence of vancomycin resistant *Enterococcus faecalis* (VRE) in food chains. This study detected the presence of VRE in chicken meat bought from markets across 22 local government areas in Lagos and Abeokuta, Nigeria. **Materials and Methods:** A total of 123 chicken meat samples were macerated, pre-enriched and subjected to standard microbiological isolation techniques. Identification was by Gram staining and matrix assisted laser desorption ionization time of flight mass spectrometry. Kirby-Bauer method was used to determine antibiotic susceptibility using 10 panels of single disc antibiotics (Oxoid;5-30µg). **Results and Conclusion:** Thirty isolates were confirmed as *Enterococcus faecalis.* Frozen chicken meat were frequently contaminated with *Enterococcus faecalis* than freshly dressed chicken meat. The study showed that 3(10%) were phenotypically resistant to vancomycin, two of the vancomycin resistant *Enterococcus faecalis* isolates were obtained from frozen chicken meat while the third isolate was detected in freshly dressed chicken meat. Results of antibiotic susceptibility showed that 21(70%) of the isolates were resistant to tetracycline, 16(53.3%) to streptomycin, 8(26%) rifampin and (23.3%) erythromycin. The isolates were most susceptible to gentamicin 27(90%), ciprofloxacin and ampicillin 25(83.3%) and 24 24(80%) to penicillin. The 3 phenotypically resistant VRE isolates were found to be multidrug resistant to between three and five antibiotic classes. The study revealed that freshly dressed chicken meat and commercially retailed raw frozen chicken meat harbour multidrug vancomycin resistant *Enterococcus faecalis.* Appropriate use of antibiotics in animal feeds will reduce the potential public health risks of having these strains in the food chain.

Keywords: Multidrug resistance, Vancomycin resistant *Enterococcus faecalis*, Chicken meat

Paper ID *(HE091.)*

Molecular Characterization of Gram-positive Bacteria Isolated from Non-Dairy Products within the Lagos Metropolis

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Abstract

Background: With antimicrobial resistance emerging as a global health concern, there is need to investigate the microbial quality of various foods and their association with antimicrobial resistance. This study was aimed to determine the prevalence of antibiotic-resistant genes in Gram positive bacteria isolated from ice-lolly, a water-based/non-dairy frozen snack, sold to school children in Lagos, Nigeria. **Materials and Methods**: Gram-positive organisms were isolated from 100 ice-lolly samples via plate count technique and identified by gram staining and other conventional biochemical tests. Antibiotic susceptibility testing, Kirby Bauer disc diffusion method, with 8 antibiotics including Imipenem (10µg), Erythromycin (15µg), Linezolid (30µg), Vancomycin (5µg), Ciprofloxacin (5µg), Gentamicin (10µg), Piperacillin Tazobactam (100µg/10µg), and Trimethoprim-sulfamethoxazole (1.25µg/23.75µg) on the isolates. Genes implicated in antibiotic resistance were amplified using multiplex PCR method. **Results and Conclusion**: A total of 67 (67%) isolates were obtained from 100 ice lollies collected. Results show that Bacillus spp. were the most prevalent (40 = 59.7%) Gram-positive bacteria found in the ice lollies followed by Corynebacterium (20=29.9%) and Coagulase-negative Staphylococcus, CoNS (7=10.4%). All species showed significant levels of resistance to vancomycin with all 7 (100%) Staphylococcus species, 15 (75%) Corynebacterium species and 17 (44.7%) Bacillus species resistant to the antibiotic. While all the Staphylococcus spp. possessed, at least, one gene (mecA), no gene was detected in 11 (55%) of Corynebacterium spp., and in 22 (57.9%) of Bacillus spp. The presence of antibiotic-resistance genes in these isolates could signal a significant clinical danger in a seemingly harmless snack consumed by a large population of school children in Nigeria.

Keywords: Food safety, antimicrobial resistance, multiplex PCR.

Paper ID *(HE092.)*

Bacterial Pathogens Isolated from Surgical Wound and their Antimicrobial Resistance Pattern in a Mission Hospital in Anambra, Nigeria

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Background: Surgical wound infections are among the most common healthcare-associated infections with complications that can have significant long-term effect on the morbidity, mortality, and quality of life for patients. Knowledge on local pathogens and sensitivity to antimicrobial agents are crucial for successful treatment and management of surgical wound infection. **Methods**: A total of 200 wound swabs from 112 male and 88 female patients of ages from 10 – 70 years with surgical wound infection were collected using sterile swabs and analyzed using standard microbiological methods. Antibiotic disk diffusion method was used to determine the antibiotic resistance profile.**Results:** Result showed that 142(71%) wound specimens were culture positive while 58(29%) showed no growth on culture media. The majority of the culture-positive wounds (90.1%) showed single bacterial growth while the remaining (9.9%) revealed poly-microbial growth. The most predominant isolate from the infected surgical wound was Gram-positive *Staphylococcus aureus* 53 (37.3%), followed by Gram-negative *Pseudomonas aeruginosa* 45(31.7%), *Escherichia coli* 32 (22.5%) and *Klebsiella pneumoniae* 12 (8.5%). The result of their antibiotic sensitivity test showed that the majority of the wound isolates were highly resistant to Ampicillin 126(88.7 %), followed by Erythromycin 114(80.3%), Gentamicin 109(76.7%) and Trimetoprim-sulphametoxazole 103(72.5%). **Conclusion:** The overall findings on the antimicrobial profile revealed high level of antimicrobial resistance from microorganisms isolated from surgical wound infections to commonly prescribed antibiotics. Therefore, there is a need for adequate intervention to control the spread of antimicrobial resistance.

Keywords: Surgical wound, Wound infection, Antimicrobial resistance, Surgical wound infection, Wound pathogenic bacteria

Paper ID *(HE093.)*

Drug Resistance Pattern of *Mycobacterium Turberculosis* in North central Nigeria

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Abstract

Background: Tuberculosis resistance is a major contributor to the global health burden from anti-microbial resistance. In Nigeria, resistant TB (DR-TB) accounts for significant cost to the healthcare system, people affected by DR-TB, and their families. While standard surveillance on the treatment focuses on Rifampicin (RIF) and/or Isoniazid (INH) resistance, an understanding of the complete pattern of resistance is crucial for allocating health resources. This study aim to described predominant drug resistance patterns in North Central Nigeria.**Materials and Methods**: Between January to December 2021, 112 sputum samples were obtained from consented confirmed positive DR-TB clients in North Central Nigeria. About 2-5 ml of the samples were decontaminated using the standard N-Acetyl L-cysteine (NALC)/4% Sodium Hydroxide (NaOH) method. About 0.5ml bacterial suspension was inoculated into Lowenstein Jensen (LJ) slant comprised of 1.2ml of 40.0ug/ml, 0.6ml of 0.2ug/ml and 0.6ml of 2.0ug/ml RIF, INH and Ethanbutol (EMB) anti TB drugs respectively using drug susceptibility testing (DST) proportional method **Results and Conclusion**: Resistances were detected in 85 samples, and the resistance pattern showed that 36.6% was mono-resistance, 33.9% multi-drug resistance, and 8.0% were poly-resistance. No pre-extensively drug resistant or Extensively-drug resistant strain was identified. Though the majority of resistance were RIF and INH, EMB showed a significant resistance. We recommend continued Multi-drugs resistant TB (MDR-TB) surveillance in the region.

Keywords: Tuberculosis, Drug-resistance, Rifampicin, Isoniazid, ethambutol

Paper ID *(HE094)*

Seroprevalence of Cytomegalovirus Infection among Pregnant Women Attending some Hospitals in Kaduna State, Nigeria

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Abstract

Background: Cytomegalovirus (CMV) infection especially in pregnancy may cause complications such as congenital infections leading to neurological disabilities in children that result in blindness, neuro-developmental delay and sensory neural hearing loss. This study was carried out to determine the seroprevalence of human cytomegalovirus infection among pregnant women attending antenatal clinics in Yusuf Dantsoho and 44 Nigerian Army Reference Hospitals in Kaduna metropolis. **Materials and Methods:** Blood samples (5ml each) were collected from ninety-two pregnant women and screened for CMV IgM antibodies using Enzyme Linked Immunosorbent Assay (ELISA). Structured questionnaire was used to obtain data on socio-demographic and risk factors associated with the CMV infection. **Results:** Out of the 92 pregnant women examined, 30 (32.6%) tested positive to CMV IgM antibodies. There was statistically significant association between CMV infection and age, previous pregnancy ($p< 0.00001$) and sharing of cups or utensils ($p=0.0190$). There was no significant association between CMV infection and marital status ($p=0.0856$), gestation age ($p=0.6970$), history of blood transfusion ($p=0.7919$), occupation ($p=0.0221$) and educational level ($p=0.1375$). **Conclusion:** The high prevalence of CMV infection observed in this study indicates that the virus is prevalent in the study area, and it is therefore advisable that routine screening of CMV infection be implemented for all pregnant women in the State.

Keywords: Seroprevalence, Cytomegalovirus, IgM, Pregnant women, Kaduna

Paper ID *(HE095)*

Antimycobacterial Assessment of *Annona muricata* Fruit-Skin Extract: Phytochemical Analysis, Antioxidant Properties, and Molecular Docking

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Abstract

Background: Tuberculosis remains a major global health concern, claiming around 1.6 million lives in 2021, according to the World Health Organization's 2022 Global TB report. However, limited research has been conducted on the antimycobacterial properties of *Annona muricata* fruit-skin extract. This study aimed to investigate the phytochemical composition, antioxidant activity, and *in silico* antibacterial assessment of ethanol extracts from fresh (ESA1) and frozen (ESA2) fruit-skin of *Annona muricata*, on selected biomarkers of tuberculosis infection. **Materials and Methods**: Annona muricata Linn plant samples were obtained from fresh and frozen fruit skins. For antioxidant screening, 200 grams of the sample was collected and homogenized. The fresh fruit skin was extracted with 95% ethanol for 24 hours, while the frozen sample was thawed and then subjected to the same ethanol extraction process. The antioxidant activity of the extracts was evaluated using 2,2-diphenyl-1-picrylhydrazyl (DPPH) and ferric-reducing antioxidant power (FRAP) assays. Molecular docking was done to assess the binding affinities of phytochemical components in ESA1 to selected biomarkers and comparing them to standard inhibitors. Phytochemical screening using qualitative and quantitative analysis was conducted to identify the presence of specific compounds, such as flavonoids, total phenolics, and total tannins. **Results and Conclusion**: Phytochemical analysis revealed the presence of tannins, flavonoids, and phenols in both ESA1 and ESA2 extracts. The quantitative phytochemical analysis showed that the total phenol content in ESA1 was 0.254±0.042 mg GAE/ml, and in ESA2, it was 3.10 ± 0.47 mg GAE/ml. The total flavonoid content in ESA1 was 1.45 ± 0.016 µg QE/ml, whereas in ESA2, it was 1.21 ± 0.093 µg QE/ml. Additionally, the total tannin content in ESA1 was 1.26 ± 0.168 mg GAE/ml, and in ESA2, it was 4.71 ± 1.77 mg GAE/ml. The most abundant compound for ESA1 and ESA2 is hexamethyl- Cyclotrisiloxane with percentages of 34.06% and 33.04% respectively. The antioxidant capacity, as measured by ferric radical antioxidant capacity, was determined, along with the corresponding IC50 values for ESA1 and ESA2. Molecular docking analysis highlighted naphthalene and 2-(4-methylphenyl) isoindole-1,3-dione as exhibiting high binding affinities to specific biomarkers associated with *Mycobacterium tuberculosis*. These compounds showed potential interactions with cysteine synthase, enoyl acyl protein reductase, RNA polymerase, and tryptophan synthase. The findings suggest that certain phytochemicals present in *Annona muricata* fruit-skin ethanol extract have promising antimycobacterial properties. These compounds demonstrate potential as candidates for the treatment of tuberculosis. Further research is warranted to explore their therapeutic applications.

Keywords: *Annona muricata*, Tuberculosis, Phytochemical screening, GC-MS, Molecular docking, Antioxidant assay.

Paper ID *(HE096.)*

Thin layer Chromatography, Antimicrobial activities and Phytochemical screening of *Phyllantus amarus* (schum and thom) on Selected Bacterial and Fungal species

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Abstract

Background: Medicinal plants have become part of health care delivery systems and have been used for the treatment of microbial infections. **Materials and Methods**: Two hundred and fifty grammes (250 g) dry powder of the whole plant of *P. amarus* was sequentially extracted with 750ml each of dichloromethane and methanol using the Soxhlet apparatus. The antimicrobial activities of the *Phyllanthus amarus* (Schum and Thonn) methanol and dichloromethane extracts was accessed by the disc diffusion method at 100mg/ml, 50mg/ml and 25mg/ml on clinical isolates of *S. aureus*, *S. pyogenes*, *P. aeroginosa*, *P. mirabilis* and *T. Mentagrophytes*. Minimum Inhibitory Concentration (MIC) of the extracts was determined by the agar dilution method. 20µl *P. amarus* methanol and dichloromethane extracts were applied as small spots seperately on 10cm x 10cm aluminum sheets silica gel 60 F_{254} (Merck) and developed with hexane/ethylacetate 1:1; hexane / ethylacetate, 4:1 and hexane / ethylacetate / chloroform / acetic acid, 2:1:1:1 solvent systems. **Results and Conclusion**: Most significant antimicrobial activity was on *S. aureus* by the Methanol extract at 100mg/ml with the zone of 17.83±0.29mm. The least activity was on *T. mentagrophytes* by the Methanol extract at 50 mg/ml (6.53±0.75mm). The Gram-positive strains were most susceptible to the extracts forming inhibition zones ranging from 12.55±0.85mm to 17.83±0.29mm (methanol extract) and 10.00±0.85mm to 14.60±0.99mm (dichloromethane extract). The antimicrobial activity of the extracts was minimal on the fungal strain with inhibition zones of between 6.53±0.75mm to 7.50±0.85mm. MIC obtained for the methanol extract ranged from 6.25mg/ml to 50mg/ml and 12.5mg/ml to 50mg/ml for the dichloromethane extracts. Alkaloids, tannins, flavonoids and saponins were found to be present in the methanol extract, dichloromethane extract was positive for alkaloids and flavonoids. Thin Layer chromatography profiling of the extracts revealed the presence of bioactive constituents with different R_f values.

Keywords: Thin Layer chromatography, antimicrobial activity, *Phyllanthus amarus*, MIC, Phytochemical screening.

Paper ID *(HE097.)*

Prevalence of *Candidiasis* Among Pregnant Women in their 2nd and 3rd Trimester Pregnancy Attending Antenatal Care at the General Hospital Nasarawa.

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Abstract

Background: Prevalence of Vaginal *Candidiasis* (VC) is on the rise with an estimated 70 to 75 % of healthy adult women having at least one-episode during their lifetimes**. Materials and Methods**: Seventy-nine (79) High Vaginal Swab (HVS) specimens were collected from 2nd and 3rd trimesters pregnant women of ages of 20-49 years attending antenatal care at the General hospital, Nasarawa. Ethical approval was obtained, consent forms and questionnaires were given to all respondents before sample collection. All collected samples were examined microscopically and processed for fungal cultures. The identification of *Candida* species was done by morphological and physiological methods (culture on CHROMagar, Germ Tube Test (GTT), Lactophenol Blue staining and Carbohydrate Fermentation tests. **Results and Conclusion**: Thirty-two (32) respondents were positive for Vaginal *Candidiasis* indicating a prevalence rate of 41%. The prevalence rate for positive cases were found in the 3rd trimester respondents of ages 20-29 years i.e. Eight 8 (25%) and Least number of negative cases were found in the 2nd trimester respondents of ages 20-29 years i.e. 5 (11%). Sixty- eight (68) respondents are married (86% of the study population), 5 are single (6% of the study population) and 6 are co-inhibiting (8% of the study population) respectively Out of the 79 samples collected, 26 (33%) were symptomatic while 53 (67%) asymptomatic. From the 2nd trimester respondents, 12 (46%) were symptomatic and in the 3rd trimester respondents, 14 (54%) were also symptomatic. Thirty-one 31 (59%) from the 2nd trimester respondents were asymptomatic and another 22 (42%) from the 3rd trimester were asymptomatic. Carbohydrate assimilation test was positive for glucose, galactose and sucrose. There was appearance of small sprouting tube-link out growths or filaments projecting from the cell surface, there was production of germ tubes in all the test tubes tested indicating the presence of *C. albicans* as compared with previous similar findings.

Keywords: Prevalence, Vaginal *Candidiasis*, Pregnant women, Antenatal care, Nasarawa.

Paper ID *(HE098.)*

Prevalence and Antibiogram of *Salmonella enterica* Isolated from Seafood Sold in Rivers State

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Abstract

Background: The consumption of seafood contaminated with *Salmonella enterica* can lead to life threatening illnesses and its multidrug resistant profile could be of public health concerns. This study was aimed to assess the prevalence and antibiogram of *Salmonella enterica* isolated from seafoods sold in Rivers State, Nigeria. **Materials and Methods:** A total of 126 raw and parboiled samples of *Crassostrea gasar* (Oyster) (42), *Panaeus monodon* (Prawn) (42) and *Buccinum undatum* (Whelks) (42) were collected from different markets (Bakana, Creek road and Kaa) and subjected to bacteriological and biochemical analyses using standard conventional methods such as production of hydrogen sulphide for specific identification of *Salmonella enterica***.** The antibiogram of *S. enterica* was determined using Kirby-Bauer disc diffusion technique. **Results and Conclusion:** *Salmonella enterica* (31.75%) were isolated from the seafoods and *Panaeus monodon* (Prawn) (40%) had the highest prevalence. *Salmonella enterica* were resistant to Impenem/Cilastatin (45µg) (97.5%) Augmentin (30µg) (95%), Cefotaxime (25µg) (92.5%) and Nitrofurantoin (300µg) (90%) and sensitive to Ofloxacin (5µg) (65%) and 100% of the isolates had a MAR index ≥0.2. The high prevalence and resistance rate observed in this study indicates the potential risk of transmission of *S. enterica* to humans through seafood consumption, which can have serious implications for public health. It is thus essential that more effective control strategies be put in place to reduce the prevalence of *S. enterica* in seafoods sold in Rivers State, Nigeria

Keywords: Antibiogram, Prevalence, Seafoods, *Salmonella enterica*, Rivers State.

Paper ID *(HE99)*

Prevalence of Bacteriuria amongst Pregnant Women Attending Primary Health Care Centers in Rivers State

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ABSTRACT

The presence of bacteria in urine is known as bacteriuria. Bacteriuria could be asymptomatic or symptomatic and could cause urinary tract infections. The prevalence of bacteriuria amongst pregnant attending primary health care was investigated. About 200 urine specimens were collected from pregnant women in Bundu, Churchill and Potts Johnson health centres. **Material and Methods**: The urine specimens 0.1ml were cultured on McConkey, Eosin Methylene Blue, and Mannitol salt agar plates for isolation of total coliform, faecal coliform, and *Staphylococcal* population. Socio-demographic information were obtained using structured questionnaire. **Results and Conclusion:** Results showed that the minimum age group reported was 0-20 years while the maximum age group was 35-40 years. Percentage of married pregnant women in the locations ranged from 60-78% while percentage of those cohabiting and unmarried ranged from 18.8- 30%. There was a significant difference between marital status and location ($P \leq 0.05$). Data on the level of education amongst pregnant women ranged from 11.3- 55%. Churchill had the highest prevalence of bacteriuria 37.5%, while Potts Johnson had the least 23.5%. There was no significant difference in bacteriuria amongst the location ($p \leq 0.05$), more so, data showed that bacteriuria was highest in pregnant women within the age of 26-30 years while 0-20 years had the least bacteriuria. Data revealed that bacteriuria amongst pregnant women was influenced by the sources of water used in cleaning after urination as well as the number of persons sharing similar toilet. Despite the observed differences in bacteriuria based on toilet types used by pregnant women, there was no significant difference ($P>0.05$) between the kind of toilet facility used. Prevalence of bacteriuria amongst pregnant women aware of UTI was 42% while those unaware was 50.5%. However, there was no significant difference between awareness of UTI and bacteriuria ($P>0.05$). Prevalence of bacteriuria was also high in the second trimester and low in the third trimester. Generally, prevalence of bacteriuria in pregnant women who attended this health care was high and investigation of risk factors associated with such occurrences is recommended.

Keywords*:* Bacteriuria, second trimester, third trimester, Rivers State

Paper ID *(HE100.)*

Molecular Detection and Prevalence of Urogenital Schistosomiasis Infection among School children in Sabon-Gari Local Government Area, Kaduna State, Nigeria

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Abstract

Background: Urogenital 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.**Materials and Methods**: 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 5-14 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.**Results and Conclusion**: *Schistosoma haematobium* was the leading cause of urogenital 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 11-14 years were more susceptible to the infection than those between 5-10 years. There was a significant association between the age, sex of the children and the infection ($P < 0.05$). 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 African countries.

Keywords: Urogenital schistosomiasis, Haematuria, Prevalence, Sequencing, *Schistosoma haematobium*

Paper ID *(HE101.)*

Prevalence and Risk factors Associated with *Cryptosporidium* oocysts in Chickens Slaughtered in Live birds Markets in Zaria Metropolis Nigeria

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Background: Cryptosporidiosis, a zoonotic disease caused by *Cryptosporidium* spp. Cryptosporidiosis occurs in animals and man with a rapidly expanding host range. **Objectives*:*** This study was carried out to determine the prevalence and risk factors associated with *Cryptosporidium* oocyst in chickens slaughtered in Live Bird Markets (LBM) in Zaria metropolis, Kaduna State, Nigeria.**Materials and Methods:** The study was cross-sectional in design, where 384 fecal samples from chickens from 4 LBM were collected. All the samples were concentrated using the Formal Ether Concentration method; where 1g of the fecal sample was homogenized in 10ml of 10% formalin. The mixture was sieved. 3ml of diethyl-ether added to the filtrate and centrifuged for 10 minutes at 2000rpm. The supernatant was decanted and a thin smear was prepared and stained using the Ziehl Neelsen; where the thin smear was air dried and fixed with absolute methanol for 3-5 minutes and then flooded with Ziehl Neelsen carbol fusin for 20min, rinsed with water and decolorized with 5% hydrochloric acid for 30 sec., then counter stained for 60 secs, using methylene blue, rinsed and air dried. The slide was was then examined using ×10 objective lens. A nested PCR was used to detect the subunit ribosomal RNA (SSU rRNA) gene *Cryptosporidium* spp**.** in 10 pooled samples. **Results and Conclusion:** Of the 384 fecal samples, 47(12.2%) were positive for *Cryptosporidium* oocyst. Daily cleaning of cages was also associated with lower risk of *Cryptosporidium* oocyst. Presence of chicken of different breeds (OR =1.93 95% CI=1.0407-3.5617: p=0.0369), large flock size (OR=0.55 95% CI=0.2961-1.0249; p= 0.0598) and presence of other birds in the same cage (OR=1.53 95% CI =0.7349-3.1719; p = 0.2567) were all associated with higher risk of *Cryptosporidium* oocyst. The SSU rRNA gene of *Cryptosporidium* was detected in 6 of the 10 samples screened using PCR. Sequence analysis in three samples revealed 82.74% to 90.35% identity with Cryptosporidium species sequences in the gene bank. Our result revealed that samples from poultry are a potential source of *Cryptosporidium* infections to humans.

Keywords: Cryptosporidium, Oocysts, Poultry Faces, Prevalence, Risk factors,

Paper ID (HE102)

Efficacy of Probiotic *Lactobacillus* species for the Treatment of Type 2 Diabetes in Mice

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Abstract

Background: Probiotics are live microorganisms which when consumed provide health benefits to the consumer. This study aimed to evaluate the efficacy of probiotic *Lactobacillus* species for type 2 diabetes (T2D) treatment in mice. **Materials and Methods:** Streptozotocin-induced diabetic male mice (40 mg/kg) were treated with probiotic *Lactobacillus* species (*L. casei, L. delbrueckii, L. fermentum* & *L. plantarum* - 10^8 CFU/mL) isolated from cabbage, ogi, tiger nuts and palm wine. The diabetic control group was given placebo for the treatment period. The *Lactobacillus* species were established as probiotics due to their antimicrobial activity & tolerance to bile salts and low pH. Fasting blood glucose (FBG), fasting serum insulin (FSI) and insulin resistance (HOMA-IR), were measured using a glucometer and an enzyme-linked immunoassay (ELISA) kit, after four weeks of treatment. **Results and Conclusion:** Mice treated with *L. casei* had FBG of 105.50±2.6mg/dL, FSI of 6.45±0.1µu/ml, and HOMA-IR of 1.68±0.1. Mice treated with *L. delbrueckii* had FBG of 106.75±2.5mg/dL, FSI of 6.40±0.4µu/ml, and HOMA-IR of 1.70±0.1. Mice treated with *L. plantarum* had FBG of 93.50±2.6mg/dL, FSI of 6.48±0.2µu/ml, and HOMA-IR of 1.48±0.1. Mice treated with *L. fermentum* had FBG of 107.00±3.7mg/dL, FSI of 6.58±0.1µu/ml, and HOMA-IR of 1.75±0.1. The diabetic control group that had FBG of 368.50±13.5mg/dL, FSI of 3.45±0.2µu/ml, and HOMA-IR of 3.13±0.1. The results showed that the probiotic treatment was effective in significantly ($p < 0.05$) reducing FBG, increasing FSI and improving HOMA-IR. Furthermore, *L. plantarum* was more effective than the other *Lactobacillus* species in the treatment of T2D.

Keywords: Type 2 Diabetes, *Lactobacillus casei, Lactobacillus delbrueckii, Lactobacillus fermentum, Lactobacillus plantarum*

Paper ID *(HE103.)*

Antibacterial Activities of Aqueous and Ethanolic Extracts of *Averrhoa Carambola* Leaves against Urinary Tract Infection Pathogens

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Abstract

Background: Millions of people worldwide suffer from urinary tract infections (UTIs), a common bacterial infection. The investigation of alternate therapy options is necessary due to the rise in antibiotic-resistance by UTI bacteria. Tropical fruit trees like *Averrhoa carambola*, also referred to as star fruit, have long been used for therapeutic purposes. This study investigated the antibacterial activites of aqueous and ethanolic extracts of *A. carambola* leaves against selected UTI-causing bacterial strains. **Materials and Methods:** A total of 16 bacterial isolates of *Escherichia coli, Salmonella typhi, Proteus mirabilis, Proteus vulgaris, Staphylococcus aureus, Klebsiella pneumoniae and Pseudomonas aeruginosa* were recovered from clinical isolates and tested against ciprofloxacin (10µg) and ampicillin (10µg) positive controls antibiotics. Aqueous and ethanolic extracts of *A. carambola* leaves were prepared using standard extraction techniques. The antibacterial potential was evaluated using the agar well diffusion method, measuring the inhibition zones against common UTI pathogens. The MIC was determined using the broth dilution technique. **Results and Conclusion:** Both aqueous and ethanolic extracts of *A. carambola* leaves exhibited significant antibacterial activities against the tested UTI *Salmonella typhi* (27.23±0.02 mm) followed by *Proteus vulgaris* (20.18±0.03 mm), *Klebsiella pneumonia* (17.2±0.02 mm), *Escherichia coli* (17.2±0.02mm), *Staphylococcus aureus* (18.03±0.06 mm), *Pseudomonas aeruginosa* (17.26±0.02 mm),The ethanolic extracts showed antimicrobial activities against the test bacteria at varying range with minimum inhibitory concentration (MIC) value, 21-28mg/ml and 15-20mm inhibition zones (IZ) in diameter.*Escherichia coli* and *Salmonella paratyphi* had zones of inhibition of 15mm each at the concentration of 50 mg/ml. Aqueous extract of *A. carambola* exhibits highest antibacterial activity against *Klebsiella pneumoniae* (15.19 ± 0.02 mm) at the same concentration. Phytochemical analysis of the plant's extracts showed the presence of anthroquinone, flavonoids, glycosides, terpenes, tannins and reducing sugar. The observed antibacterial activities of *A. carambola* leaf extracts against UTI pathogens suggests their potential as alternative treatment options. The phytochemical analyses of the plant extracts showed the presence of bioactive compounds like flavonoids, glycoside, terpenes, tannins alkaloids, proteins and amino acids, carbohydrates which contribute to their antibacterial properties.To combat the growing problem of antibiotic resistance, the use of *A. carambola l*eaf extracts as natural antibacterial agents against UTIs shows potential.

Keywords: Urinary tract infection, plant extracts, antibacterial activities, phytochemical constituents, disc diffusion.

Paper ID *(HE104.)*

Phytochemical Analyses and Antifungal Activities of *Curcuma Longa* and Ketoconazole on some Non-Dermatophytic Fungal Isolates from Prison Inmates in Owerri, Imo State, Southeast Nigeria.

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Abstract

Background: Non-dermatophytes have been proved to cause cutaneous infection and have been treated using herbal remedies. The study determined the comparative antifungal activities of *Curcuma longa* and ketoconazole against some non-dermatophytic fungi isolated from prison inmates in Owerri Correctional center. In addition, phytochemical screening was done on *Curcuma longa*.**Materials and Methods**: The antifungal susceptibility tests of *Curcuma longa* and ketoconazole against A*spergillus flavus, A. sydowii, A. tamari, Candida tropicalis, C. parasilosis, C. orthopsilosis, C. haemulonis, Fusarium solani, Paecilomyces dacthylethromorp, Pseudallescheria boydii, Purpureocilium lilacinum, Trichoderma harzianum* and *T. lixii* were carried out using the Kirby Bauer disc diffusion method on Muller-Hinton agar supplemented with 2% glucose and 0.5µg/ml methylene blue dye. Fluconazole 25µg(0.025mg) discs of the oxoid brand produced in the United Kingdom were used for the antifungal susceptibility test. The phytochemical composition of *Curcuma longa* was also carried out using methanol to determine the bioactive compounds. The susceptibility test results were obtained by measuring the inhibition zone diameter in millimeters. **Results and Conclusion**: The antifungal susceptibility test for *Curcuma longa* showed zones of inhibition ranging from 5-14mm at different concentrations. Ketoconazole was the more effective against the dermatophytes with zone of inhibition ranging from 7 - 45mm and this could be attributed to the composition of the drug. *Curcuma longa* rhizome showed the presence of steroid (1.733mg/100g) as the most abundant active compound followed by tannin (0.662mg/100g), glycosides and phenolic compound (0.389mg/100g) each, saponin (0.321mg/100g), alkaloids (0.210mg/100g) while flavonoid is the least with (0.100mg/100g). Ketoconazole was seen as a drug of choice for the treatment of the cutaneous infections caused by the non-dermatophytes while *Curcuma longa* is a promising herb that can be applied for the treatment. Further study is suggested with *Curcuma longa* using other solvents to harness its antifungal potentials.

Keywords: Non-dermatophytes, Cutaneous infection, Correctional Center, *Curcuma longa*, Ketoconazole.

Paper ID *(HE105.)*

Mycobacteriophage annotation: From FASTA file to assigning functions to genes

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Abstract

Background: According to UN projections, superbugs and associated forms of antibiotic resistance might cause up to 10 million deaths by 2050. While microbes have been good sources of antibiotics, there is an increased research focus on bacteriophage (phage) therapy to curb the menace of multidrug resistance. Phages are viruses that produce lysins which breakdown bacteria cell walls. To understand phage diversity and evolution, sequencing and annotation of the genomes are required. Annotation comprises of auto-annotation using bioinformatic tools, databases and validation by curators. **Materials and Methods**: For the Howard Hughes Medical Institute Science Education Alliance-Phage Hunters Advancing Genomics and Evolutionary Science (HHMI SEA-PHAGES) program, the FASTA files of sequenced phage genomes can be downloaded from its actinobacteriophage database (phagesdb.org). and imported to DNA Master for auto-annotation. DNA master runs with BLAST, Glimmer, Genemark which help in gene evaluation – gene identification, start site prediction. Protein functions are called using BLASTp the Phamerator (Phamerator.org), and HHPred. ARAGORN and tRNA-scan-SE identify tRNA and tmRNA, while transmembrane domains are detected using SOSUI. Gene Content Similarity (GCS) tool on the (phagesdb.org) is used for genome comparison. **Results and Conclusion**: Phages belonging to Clusters A, C, F, Q and N were annotated using different bioinformatic tools and databases. The ratio of predicted functions to hypothetical proteins vary. The genes could be either in the forward or reverse orientation. The assigned functions of the phages broadly belong to structural proteins, lysis, DNA replication and Integration. Annotated genomes are published in GenBank and as ASM Microbiology Resource Announcements.

Keywords: Phage, Genome annotation, Bacteriophage, Phage therapy

Paper ID (*HE106.*)

Molecular Identification and Antibotic Susceptibility of Microbes Isolated from Watermelon (*Citrulus lanatus*)

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Abstract

Fruits like watermelon are to be handled hygienically. Through the exploration of microbial composition of watermelon, there could be better understanding of the microbiological quality and safety of fruits and vegetables for human consumption. Microbial diversity in watermelon is a crucial aspect of food safety which can provide insight into antimicrobial resistance pattern. This study identified bacteria species isolated from watermelon from Oru and Iseyin using biochemical and molecular techniques (polymerase chain reaction). Also their antimicrobial susceptibility patterns were determined following assay to commonly used antibiotics. The Sample were purchased by the farm express way in each town and 2 g of fruit samples were cut and mashed for isolation. The preliminary biochemical tests revealed the presence of twenty three organisms. The antimicrobial susceptibility revealed that most isolates were sensitive to Perfloxacin 13 (100 %), the isolates that were sensitive to Gentamicin 12 (92.3 %), Ciprofloxacin 9 (69.23 %), Amoxicilin and Septrin 8 (61.5 %), Streptomycin and Erythromycin 7 (53.8 %), Oflaxacin 6 (46.15%), Chloramphenicol and Spiramycin 5(30.08%), Ampiclox and Zinnacef 4 (30.07 %)., Rocephin 2 (16.92%). The thirteen isolates were further subjected to molecular characterization by using 16S rRNA molecular markers. The result shows that the isolates were *Lactobacillus reuteri (CP084584.1), Bacillus mendelii (CP104930.1), Curtobacterium flaccumfaciens (NR043690.1), Lactobacillus helveticus (CP031016.1), Acinetobacter lwoffii (CP054803.1), Lactobacillus casei (AP012544.1) and Lactobacillus vaccinostercus* (AB218800.1:13-1548) with respective homology to available sequences. The findings from this study reveal the safety of watermelon for consumption and help in developing appropriate strategies for harvesting, storage, preventing or reducing microbial contamination of watermelon.

Keywords: Molecular technuques, Antimicrobial-susceptibility, Bacteria, *Citrulus lanatus,* Antibiotics.

Paper ID *(HE107.)*

Antibiogram of *Klebsiella Pneumoniae* isolates from Urine Samples of patients attending secondary health care facilities in Wukari, North-East Nigeria.

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Abstract

Background: The increasing frequency of *Klebsiella pneumonia* isolates from reoccurring clinical cases of urinary tract infection (UTI) has instigated investigating its trends in relation to antimicrobial resistance patterns. This research examined urine samples of hospitalized and non-hospitalized patients for the presence of *Klebsiella pneumoniae,* and established its antibiogram. **Methods:** Sterile container with boric acid was used to collect mid-stream urine samples from 20 hospitalised and 20 non-hospitalised patients that are within the ages of 18-50. Using streak-plate technique, samples were cultured in MacConkey agar at 37°C for 24 hours. Suspected colonies presenting with pinkish colouration and mucoid on the line of streaking resulting from fermentation and gas production was sub-cultured to get pure isolates. Isolates were indole negative. PCR was used to identify the *Khe* genes from isolates. Also, isolates were subjected to antimicrobial sensitivity test using agar disk diffusion method. **Results:** *Klebsiella pneumoniae* was not isolated from any of the non-hospitalised patients' samples but was isolated from 25% of hospitalised patients' samples, which indicated that *Klebsiella pneumoniae* could be a Hospital Acquired Infection (HIA). All isolates were sensitive to Chloramphenicol 30µg (≥21mm), Gentamycin 30µg (≥22mm), Streptomycin 30µg (≥22mm), and Ciprofloxacin. 30µg (≥24mm), Also, isolates shown multi-drug resistance to Augmentin 30µg (≤13mm) and Amoxicillin 30µg (≤11mm). **Conclusion:** *Klebsiella pneumoniae* has shown to be prevalent in hospital environment. Consequently, hospital equipment and environments should be kept clean always. Resistance of isolates to Augmentin and Amoxicillin could have resulted from prolong use of the antibiotics due to extended hospital stay.

Keywords: Antibiogram, Nosocomial, *Klebsiella pneumoniae*, Urine samples, UTI.

SUBTHEME: CLIMATE CHANGE TRANSITIONS AND EVOLUTION OF MICROORGANISMS (ENVIRONMENT)

Paper ID *(CCE001.)*

Physicochemical and Bacteriological Quality Assessment of Selected Tap Water from Male and Female Hostels within Nile University of Nigeria, Abuja

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Abstract

Background: Water is a resource that all living things require to survive. Water should have good physical, chemical and microbiological quality. The present study aimed to assess the quality of drinking water in Nile University male and female hostels which was determined by; examining the physicochemical parameters with reference to the standards set by the World Health organization (WHO) and Standard Organization of Nigeria (SON). Isolation and conventional identification of bacterial isolates using biochemical tests, the molecular identification and the antibiogram of bacteria isolates were carried out. **Material and Methods:** A total of ten (10) water samples, five (5) samples each from the male and female hostels were aseptically collected in sterile sample bottles. Physicochemical parameters (colour, odour, taste, temperature, turbidity, pH, hardness, conductivity, resistivity, salinity, total dissolved solids, atmospheric pressure, dissolved oxygen, biological oxygen demand) examined in each water sample were within the limits recommended with the exception of Total hardness in water samples (F1, F2, F3, F4, M1, M2, M5) and color in the water samples (F1, F2, F3, F5, M1, M2, M4, M5). **Results and Conclusion**: Total bacterial counts in water samples ranged from (1.03×10^6 - 2.78×10^6 CFU/mL) in the female hostel water samples and ranged from 1.40×10^6 - 2.24×10^6 CFU/mL in the male hostel water samples. The total coliform counts in water samples ranged from 3.2 - 5.0×10^5 CFU/mL in the female hostel and 3.2×10^5 - 5.5×10^5 CFU/mL in the male hostel respectively. The probable organisms identified were various groups of microorganisms which included: *Bacillus species, Staphylococcus species, Listeria species, Aeromonas species, Proteus species* and *Alcaligenes faecalis* (with code FA1, FA2, MA1 and MA3 had the accession numbers: MT180585.1, KT254063.1, KF712271.1 and JN374993.1 for each strain respectively). However, the molecular identification of some of the bacterial isolates confirmed the presence of *Alcaligenes faecalis* in the sample F1, F2, M1 and M3. The most sensitive antibiotics against each bacterial isolates in water samples were Gentamicin (range Zone of Inhibition (ZOI) of 15-19mm) at concentration of 10µg/mL, ciprofloxacin (range ZOI of 14-17mm) at concentration of 5µg/mL and nitrofurantoin (range ZOI of 24-29mm) at concentration of 10µg/mL. This study shows that ,although the organisms identified and confirmed are usually opportunistic and don't necessarily cause major health hazards, the quality of the drinking water in the male and female hostels at Nile University of Nigeria needs to be managed better and treated more often to prevent the presence of any opportunistic microorganisms.

Keywords: Water, physical parameters, bacteria, WHO, SON

Paper ID *(CCE002)*

Bacterial Quality of Air, Water, Soil, Hand Swabs, and Feeds, from Livestock Farms in the Southeast

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Abstract

Background: The study evaluated the bacterial quality of air, water, soil, feed samples and hand swabs in four cities in Abia State(Aba and Umuahia) and Imo state (Mbaise and Okigwe). **Materials and Methods**: Air was sampled with passive sedimentation technique, water (2.5 liters) and soil (50g) samples, were collected randomly from the water sources and surrounding soil in the farms respectively; while hand swabs from the farmers and feeds (20g) were collected with sterile swab sticks and containers respectively. Total heterotrophic bacterial count (THBC), total coliform count (TCC) and total potential pathogenic bacterial count were all analysed by growing the samples on general purpose, differential and selective media after serial dilution respectively. All the bacterial isolates were identified using their cultural characteristics, including elevation, margin, colour, size and surface texture. The Gram stain was conducted on all the bacteria and microscopically examined to differentiate between Gram-positive and Gram-negative bacteria. Furthermore, the isolates were confirmed by subjecting them to biochemical tests and molecular characterization. **Results and Conclusion**: The highest THBC ($28.43\pm0.3\times10^5$, $26.70\pm0.7\times10^5$, $26.26\pm0.5\times10^5$ CFU/ml), TPPBC ($17.47\pm0.5\times10^5$ CFU/ml and $20.02\pm0.5\times10^5$ CFU/ml) and TCC ($24.06\pm0.4\times10^5$, $17.93\pm0.6\times10^5$ and $22.36\pm0.4\times10^5$ CFU/ml) for pig, cow and poultry farms respectively were obtained in Aba pig farm, cow abattoir, and poultry farms respectively while Mbaise recorded the lowest values for THBC, TPPBC and TCC. A total of 10 bacterial isolates were obtained. Three (3) Gram-positive (*S. aureus* ,*Streptococcus pyogenes*, *Bacillus subtilis*) and seven (7) Gram-negative (*Escherichia coli, K. Pneumoniae, S. Enterica, Vibrio* cholerae, *Pseudomonas aerogenes, E. Aerogenes, Shigella* sp) *Escherichia coli* had the highest total percentage distribution (n=259) in all four cities and *Shigella* sp (n=74) was the least distributed. Of the four cities (Aba, Umuahia, Mbaise and Okigwe) studied, Aba farm had the highest percentages of *E. coli* (31.67%; 82/259), *K. pneumoniae* (33.67%;68/218), *P. aeruginosa* (30.28%; 43/31.85%), *E. aerogenes* (31.85%; 43/135) and *S. pyogenes* (36.57%; 49/134). Among the bacterial isolates, *S enterica* had the highest percentage values (42.38%; 64/151) while *Shigella* sp had the least percentage values (12.16%; 9/74). Overall, of all the cities, Aba had the highest bacterial burdens. Livestock farmers should therefore maintain appropriate hygienic measures to reduce bacterial spread.

Keywords: Bacteria, Count, Hygienic, Livestock, Southeast

Paper ID *(CCE003)*

Impact of Pesticides residues on Soil Bacterial Populations in selected Communities of Ondo South, Nigeria

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Abstract

Background:

Farmers use natural and synthetic pesticides to protect crops against rodents, insects, and disease-causing microbes. With an increasing human population, large quantities of pesticides are used to control pests and increase food yields. Pesticides have been linked to numerous environmental problems, including water, soil and air contaminations, biodiversity loss, and pest resistance. Despite the known risks, farmers in most nations are increasing their pesticide use. This study aims to evaluate the amount of pesticides in selected soil samples and its impact on the microbial population of the soil. **Materials and Methods**: Soil samples from ten communities designated A to J were collected with soil auger from tillage and rooting depth of plants (0 – 21cm) into sterile polytene bags in triplicates. Cultural, morphological and biochemical reactions were used for bacterial identification, while Gas Chromatography - Mass Spectrometry (GC-MS) was used in the pesticide analysis.**Results and Conclusion**: In the control community (OAUSTECH), bacterial population range from 90.00±0.00 x 10^5cfu/g to 92.67±0.58 x 10^5cfu/g across the eight locations while the population ranged from 16.67±1.16 x$10^5$to 71.33±1.16 x 10^5 cfu/gin the treatment communities. The bacterial number in the treatment communities differ significantly ($P < 0.005$) compared to the control. For pesticide analysis, Endosulfan ether range from 0.01 ± 0.006 - 0.04 ±0.006ppm; Dieldrin from 0.03±0.0012- 0.05 ±0.0010 ppm; Dichlorodiphenyltrichloroethane (DDT) from 0.03 ±0.0012-0.06±0.0025 ppm and Endrin ketone from 1.20 ± 0.0037-2.06 ±0.015ppm. The results of this study, showed that pesticides residues negatively affected soil microbial populations, validating and supporting the current views about the environmental concerns.

Keywords: Crops, Pesticides, Agricultural loss, Pollution, Bacteria

Paper ID *(CCE004)*

Bacteriological and Physico-chemical Quality of Borehole Water in Masaka, Community, Nasarawa State, Nigeria.

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Abstract

Background: Borehole water is generally considered a safe source of drinking water because it is abstracted with low microbial load with little need for treatment before drinking. However, borehole water resources are commonly vulnerable to pollution, which may degrade their quality. An assessment of microbial and physicochemical qualities of borehole water in the rural environs of Masaka Community, Nasarawa state, Nigeria was carried out. **Methods:** Two hundred and fifty millilitres (250ml) of five water samples were collected randomly from different boreholes within the community. The total bacterial and coliform counts and the identification of isolates were carried out using standard microbiological methods. Physicochemical parameters were analyzed using standard methods which includes Total Dissolved Solids (TDS), turbidity, odor, color, nitrate, nitrite, sodium fluoride, chloride, pH and hardness. **Results:** Heterotrophic total bacterial count in the water sample ranged from 2.01 x 10^{-2} - 5.02 x10^{-2} cfu/ml. The fecal coliform count of the water analyzed ranged from 4x10^2 - 8x10^2 cfu/ml. The total coliform count of the borehole water analysed ranged from 14/100 - 25/100 ml. The following genera of bacteria species which include *Escherichia, Klebsiella, Proteus, Shigella, Pseudomonas, Staphylococcus, Salmonella* and protozoan *Giardia intestinalis* were identified. The physicochemical parameters of the water sample accessed revealed that the quantity of nitrate (23-35 mg/L), sodium (100-177 mg/L), fluoride (0.1-1.2mg/L), nitrite 0.1, TDS (258-359 mg/L) and turbidity (1-3 NTU) accessed in the water samples were consistent with the permissible limits allowed by WHO and the Nigerian standard for drinking water of 50, 200,1.5, 250, 0.1,600 mg/L. However, the results obtained for the pH 6.9-8.9mg/L , water hardness 105-115mg/L and chloride 252-259mg/L and 5 NTU exceeded the acceptable limits of pH (6.5-8.5), water hardness(100); chloride (250mg/L). The water had foul smell. **Conclusion:** This study revealed that water from the Masaka community sources could pose severe health risks to consumers and is unsuitable for direct human consumption without treatment.

Keywords: Borehole, Water, Physicochemical, Bacteriological, Coliform

Paper ID *(CCE005).*

Monitoring the Biodegradation of Drilling fluids by Bacteria from Freshwater Habitat

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Abstract

Background: Artificial and natural release of petroleum and related products into the environments endanger life forms. This leads to de-vegetation, contamination of potable water sources, fall in reproduction of organisms due to disruption in food chain, and death of organisms inhabiting the polluted environments. Biodegradation by natural populations of microorganisms represents one of the primary mechanisms by which petroleum and other hydrocarbon pollutants can be removed from the environment, is cheaper and the most efficient for environment-safe depollution. This study aimed at monitoring the biodegradation of drilling fluids by bacteria in freshwater. **Materials and Methods**: The biodegradation flasks, one containing the water sample and the toxicants- water-based drilling fluid (WBDF) and oil- based drilling fluid (OBDF) separately at 1 % (v/v) and a control without the toxicants were set up and monitored for 20 days at room temperature. At day 0- and 5-days intervals, samples from the biodegradation flasks, were taken to isolate the drilling fluid utilizing bacteria using mineral salt medium by the vapor phase method and identify the isolates by morphological and biochemical characteristics, also, to determine the pH using the pH meter, Dissolved oxygen (DO) using DO meter, Biological Oxygen Demand (BOD) 5- day method and the Chemical Oxygen Demand (COD) by the titrimetric method. **Results and Conclusion**: The drilling fluids utilizing bacteria isolated included species of; *Micrococcus*, *Pseudomonas*, *Bacillus*, *Corynebacterium*, *Proteus.* The COD was found to range from 79.4 - 193.1 mg/L ± 20.46 (SE) and 78.1- 298.5 mg/L ± 40.46 (SE) for the OBDF and WBDF respectively while the BOD ranged from 16.1 - 65.7 mg/L ± 8.78 (SE) and 11.7 - 68.8 mg/L ± 10.27 (SE) for OBDF and WBDF respectively. The percentage ultimate biodegradation of the drilling fluids at day 20 was observed to be 60.3 % and 79.9 % for OBDF and WBDF respectively. The result of the findings showed WBDF to be easily biodegradable than OBDF. The difference in their levels of biodegradation could be due to the differences in their compositions.

Keywords: Biodegradation, drilling fluids, bacteria, freshwater, COD.

Paper ID *(CCE006.)*

Polystyrene degrading bacteria isolated from the larvae of *Rhyncophorus phoenicis*

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Abstract

Background: Biodegradation of polystyrene (PS) by insect larvae with chewing mouthparts has been confirmed in different insect species, and have been linked to the activities of intestinal microorganisms. **Materials and Methods**: In this study, larvae of the African palm weevil (*Rhyncophorus phoenicis*) were fed with PS foam for 21 days, and the gut microbiota was investigated afterward by dissecting and plating out in minineral salt medium. Bacteria isolated from the gut were screened for PS biodegradation in Erlenmeyer flask using PS film incubated in MSM at 30ºC and pH of 7, for 28 days. PS degradation was confirmed by weight loss and Fourier Transform Infrared (FTIR) spectroscopy. **Results and Conclusion**: Two bacterial species capable of PS degradation were isolated from the gut of the *R. phoenicis* and were identified on the basis of their 16S rRNA sequences as *Pantoea dispersa* and *Lysinibacillus macriodes*, with accession numbers OQ652023 and OQ652017 respectively. After incubation for 28 days, the isolates caused 8.8% reduction in weight of PS film from its initial mass of 3 g. FTIR spectroscopy results confirmed the formation of groups suggestive of degradation products. The presence of carbonyl group shows up as absorption peaks in the range of 1640-1760 cm^{-1} and hydroxylic group at 3000-3700 cm^{-1}. The isolates were able to accumulate polyhydroxyalkanoate (using sodium hypochlorite-chloroform method) equivalent to 44% of their dry cell weight. Coupling biodegration of PS with PHA production shows promise for PS waste management and product recovery.

Keywords: Polystyrene, polyhydroxyalkanoate, *Pantoea dispersa, Lysinibacillus macriodes*

Paper ID *(CCE007)*

Response of a Marine Microalgae and Copepod to the Toxicity of an Effluent

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Abstract

Background: Discharges of treated effluents from producing industries is a continuous source of pollutants to the marine ecosystems. Typically, effluents comprise of one or more pollutants such as hydrocarbons, heavy metal rinses and detergents of which after treatment, the pollutants may be at a level that could affect the marine ecosystem. This study aimed to determine the acute toxicity of the treated effluent and the response of Microalgae-*Skeletonema costatum* and Copepod-*Acartia tonsa* when exposed to the treated effluent in a marine system. **Materials and Methods**: The microalgae and copepod which are standard test organisms for acute toxicity testing as selected by Nigerian Upstream Petroleum Regulatory Commission were sourced from Nigerian Institute for Oceanography and Marine Research, Buguma in Rivers State, acclimatized to laboratory conditions and utilized in whole effluent acute toxicity test of the effluent. Utilizing different concentrations of the treated effluent, growth inhibition test (for microalgae) and mortality test (for copepod) was performed using static without renewal option at 22^{o}C under continuous white light for 72hours. Thereafter, median inhibition/lethal concentration (IC_{50}/LC_{50}) were calculated. **Results and Conclusion**: The treated effluent was more toxic to *Acartia tonsa* (72hours-LC_{50} 473.19mg/l) when compared to *Skeletonema costatum* which had 72hours-IC_{50} >100,000mg/l. The study revealed that the treated effluent displayed moderate toxicity to the copepod and was non-toxic to the microalgae. Hence, more efforts should be put in place by the regulatory agencies in ensuring that operators adhere strictly to effective guidelines of wastewater treatment to avoid extinction of sensitive species.

Keywords: Treated Effluent, Microalgae, Copepod, Toxicity, Toxicity Index.

Paper ID *(CCE008)*

Anthracene degradation and Polyhydroxyalkanoate Production by Hydrocarbon Degrading Bacteria Isolated from Municipal Dumpsite

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Abstract

Background: Anthracene is one of the sixteen (16) priority polycyclic aromatic hydrocarbons with three closed benzene rings. The degradation of this toxic pollutant and the simultaneous synthesis of polyhydroxyalkanoate (PHA) is of significant importance, as it would improve the essence of bioremediation by reducing the PHA production cost. **Materials and Methods**: Two hydrocarbonoclastic strains capable of degrading anthracene were isolated from Abule-Egba municipal dumpsite in Lagos State and identified using biochemical tests and 16S rRNA ribotyping. The isolates are *Bacillus cereus* AAR-1 (OQ999178) and *Enterobacter* sp. AAR-3 (OQ999355). Optimization procedure to enhance anthracene degradation was carried out using Taguchi L16 (4*3) array, where 16 experimental runs was designed. **Results**: Ten percent (10%) seed inoculum grown for 8 days on a minimal salt medium containing anthracene (400 ppm) and 2 g/L NH_4Cl as carbon and nitrogen sources respectively, were observed to be the optimized conditions that enhanced anthracene degradation with concomitant PHA accumulation by *Bacillus cereus*. This bacterial biomass had 1 x 10^6cfu/ml colony count and yielded a 286 mg/L PHA following the hypochlorite-chloroform solvent extraction protocol. The *Enterobacter* sp. bacterial count of 8 x 10^6 cfu/ml maximally accumulated 71mg/L PHA from its biomass when cultured on a 100 ppm anthracene and 0.5g/l NH_4Cl. The Fourier transform infrared (FTIR) functional analysis confirmed the polymer extracted from the two bacteria to be PHA based on the peaks generated at typical PHA spectral regions between 3321-3384cm^{-1} and 1730-1788 cm^{-1}, corresponding to OH and C=O functional groups, respectively.**Conclusion:** This study reports of the presence of hydrocarbon degrading bacteria in municipal dumpsite with dual capacity that could degrade recalcitrant pollutant while accumulating industrially important biopolymer.

Keywords: Biodegradation, polyhydroxyalkanoate, polycyclic aromatic hydrocarbon, dumpsite.

Paper ID: (CCE009)

Effect of Storage Containers on the Bacteriological Quality of Water

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Abstract

Background: Water is life and access to good quality water cannot be overemphasized. This study was carried out to determine the effect of storage containers on the bacteriological quality of water. **Materials and Methods:** Water sample was collected from three bore holes sited in Owerri municipal. A 10 litre water sample was collected in 3 sterile storage containers (clay, plastic and metal containers) from each bore hole and stored for 21 days under aseptic conditions. One 1ml of each water sample were inoculated on Nutrient agar, MacConkey agar, eosin Methylene blue agar and Salmonella-Shigella agar plates using spread plate count method and incubated at 37ºC for 18 hours. **Results and Conclusion:** The mean total heterotrophic bacteria count from the bore hole water stored in clay, plastic and metal containers was 83.3±4.0 CFU/100ml, 36.4±8.5 CFU/100ml and 52±2.8 CFU/100ml respectively while the mean coliform count for clay and plastic containers was 6.9±1.5 CFU/100ml and 1.0±3.2 CFU/100ml respectively. The bacteria isolated from the 3 water storage containers used in this study were characterized using standard microbiological and biochemical methods. *Staphylococcus* species, *Shigella* species, *Escherichia coli* and *Salmonella* species were isolated from the 3 water storage containers. *E. coli*, *Staphylococcus* species and *Salmonella* species were isolated from the clay containers; *Staphylococcus* species and *E. coli* were isolated from the plastic containers while *Shigella*, *Salmonella and Staphylococcus* species were isolated from the metal containers. It was observed that *Staphylococcus* species was isolated from all the storage containers examined. The usefulness of water as a drink and use for domestic activities underlines it portability. Results also showed that no particular container was the best for storage of water over time. Therefore, it is recommended that water stored in clay, metal and plastic containers should be treated before drinking.

Keywords: Clay containers, Plastic containers, Metal containers, Storage, Bacteriological quality

Paper ID: (CCE010)

Molecular and Biochemical Characterization of Autochthonous Cellulolytic Microorganisms from three Waste Dump Sites in Lagos, Southwest Nigeria.

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Abstract

Background: This study was conducted to evaluate and identify cellulolytic microorganisms associated with landfill dumpsites in Lagos, Southwest Nigeria, and to provide insights into the potential use of these microorganisms in solid waste management.**Materials & Methods**: Soil and leachate samples were obtained simultaneously (0 – 30 cm depth) at intervals from three dumpsites in Lagos, using aseptic procedures. Thereafter, composite samples of soil and leachates were generated independently and transported to the laboratory for analysis. Microorganisms were isolated from both soil and leachate samples using the serial dilution technique on sterile nutrient agar (NA) and potato dextrose agar (PDA). Subsequently, cellulase-producing microbial species were identified using conventional and standard microbiological techniques, and also by cultivation on starch–casein agar. Pure cultures of isolates were inoculated on sterile filter paper placed on Starch - casein agar plate. Isolates were selected based on their abilities to break down the filter paper. Screening for utilization of aromatic acids was carried out in 250 ml conical flasks containing minimal agar medium with composition: minimal agar medium (pH 7.2),1.0 g/L aromatic acids (vanillic), trace elements (1.0 mL), phosphate buffer and pH indicator bromothymol blue. The DNA of some selected isolates with cellulolytic activity were extracted and sequenced using phylogenetic 16S rRNA sequences, ITS, and bioinformatics tools. **Results & Conclusion**: Among the bacterial species, *Bacillus* sp. had the highest cellulose degradative ability and was the most prevalent (50%) in occurrence among bacterial species while *Aspergillus* sp. emerged as the most commonly occurring fungal isolate (35.7%). Data of selected sequenced cellulolytic isolates were deposited at NCBI GeneBank with Accession numbers; KP843680.1 (*Vibrio tubiashii*), MK748310.1 (*Aspergillus aculeatinus*), LC496490.1 (*Aspergillus aculeatus*), CP029751.1 (*Staphylococcus aureus*) and JX144699.1 (*Bacillus mycoides*) strain JP44SK9. Environmental surveillance for these microorganisms with microbial synergistic capabilities, could transform solid waste management into a highly efficient biotechnological process that facilitates volume reduction, waste recycling and Bioenergy production.

Keywords: Biodegradation, cellulose, genomics, landfills, lignocellulose, solid, waste, sustainable development

Paper ID *(CCE011).*

Plant Growth-Promoting Potentials and Molecular Identification of Three Fungal Species Isolated from Rhizospheric Soil

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Abstract

Background: Extensive use of agrochemicals for crop improvement and production is becoming worrisome because of their increasing price and environmental implications. Plant growth promoting fungi are free living soil microorganisms that directly or indirectly exert beneficial effects on plants when applied as biofertilizers. Hence, the overall objective of this study was to isolate fungi from rhizospheric soil, screen them for plant growth promoting activities and identify the fungal isolates using molecular approach. **Materials and Methods:** Rhizospheric soil samples collected around nine randomly selected plantain suckers obtained from Obasanjo farm, Ota, were investigated for the presence of plant growth promoting fungi by assaying for phosphate solubilisation and indole acetic acid (IAA) production. Phosphate solubilisation assay was carried out by culturing the fungal isolates on Pikovskaya's agar medium while IAA produced was quantified spectrophotometrically after growth on potato dextrose broth supplemented with L-trptophan. Identification of the fungal isolates was based on morphological characteristics and sequencing of the genes within the internally transcribed spacer (ITS) of the isolated fungi.**Results:** Of the ten (10) fungi isolated, three (3) isolates (30%) solubilized insoluble phosphate with solubilisation index (SI) ranging from 1.95 to 3.00. These fungi were identified as *Diplodia cajani* strain UOI01 (MZ948826), *Lasiodiplodia brasiliensis* strain UOI02 (MZ948827) and *Fusarium luffae* strain UOI03 (MZ948828). All phosphate solubilizing fungal isolates produced indole acetic acid of varying concentrations ranging from 0.59±0.02 -1.65±0.01 mg/ml.**Conclusion:** Rhizospheric fungi isolated from this study have the potential to improve plant growth and development, and can therefore serve as biofertilizers for sustainable agriculture.

Keywords: Fungi, plant-growth promotion, Rhizospheric soil, Biofertilizers, Phosphate solubilization

Paper ID *(CCE012.)*

Polyhydroxyalkanoate (PHA) Production Potentials of Bacteria Isolated from Waste Dump Sites

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Abstract

Background: Polyhydroxyalkanoates (PHAs) are naturally occurring polyesters synthesized by bacteria as intracellular carbon and energy storage compound under nutrient-limiting conditions with excess carbon source. They are biodegradable, thermoprocessable, biocompatible and piezoelectricable, making them attractive as biomaterials. The overall objective of this study was to isolate bacteria from waste dump sites, screen them for PHA production potentials and identify the isolates using molecular approach. **Materials and Methods:** Soil samples were randomly collected at the depth of 0-20 cm from waste dump sites located at Iju, Bells University of Technology and Sango Ota using hand auger. Bacteria were isolated by spread plate technique and PHA production assay was carried out using Sudan black B stain test and spectrophotometer. The effects of different carbon (glucose, lactose, sucrose, maltose, mannitol, starch, ethanol and fructose) and nitrogen (yeast extract, urea, ammonium chloride and ammonium sulphate) sources on PHA production were also investigated and the PHAs accumulated were quantified spectrophotometrically. Identification of the bacterial isolates was based on biochemical characterization, amplification and sequencing of the 16S rRNA gene loci. **Results:** Of the 64 bacteria isolated, 44 were positive for PHA accumulation. However, only the best 6 bacteria namely *Alcaligenes faecalis* strain UMAGOD12 (MH091063) and five strains of *Serratia nematodiphila* (MH091061, MH091064, MH091066, MH091065 and MH091062) which accumulated 0.064±0.02, 0.079±0.01, 0.074±0.03, 0.055±0.01, 0.054±0.01 and 0.053±0.02 mg/ml PHA respectively were selected for further studies. Growth of the selected isolates in minimal salt medium containing different carbon sources showed that PHA accumulation was higher in the presence of starch and maltose, while yeast extract and ammonium chloride were the best among the nitrogen sources used. **Conclusion:** Results obtained from this study showed that these organisms with PHA production potentials can serve as promising candidates for industrial production of biomaterials that are environment friendly and medically useful.

Keywords: Bacteria, Polyhydroxyalkanoate production, Waste dump sites, Carbon and nitrogen sources, Biomaterials

Paper ID *(CCE013)*

Microbial Response of Indigenous Species from Stone Mining Sites to Antibiotics and Heavy Metals

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Abstract

Background: Biological technologies are cost-effective green eco-friendly options in curbing dire environmental pollution impacts. This study investigated exposures of indigenous microorganisms from two quarries in Ibadan to environmental pollutants. **Materials and Methods**: Microorganisms were isolated from environmental samples using Nutrient agar and Potato Dextrose Agar. Microbial identifications employed macroscopic, microscopic morphology and biochemical characteristics. **Results and Conclusion:** Forty-six bacterial genera -*Bacillus* Spp. (29), *Staphylococcus* Spp. (7), *Pseudomonas* Spp. (5), *Corynebacterium* Spp. (3) *Paenibacillus* Sp. (1) and *Clostridium* Sp. (1) were exposed to 8 antibiotics- Ceftazidime-30 µg, Cefuroxime-30 µg, Gentamycin-10 µg, Ceftriaxone-30 µg, Erythromycin-5 µg, Cloxacillin-5 µg, Ofloxacin-5 µg and Augmentin-30 µg. While fungi *Aspergillus* and *Penicillium* spp. were tested with 9 heavy metals- silver (Ag)(25-100 mgl^{-1}), aluminium(Al)(100-600 mgl^{-1}), cobalt(Co)(50-300 mgl^{-1}), iron(Fe)(1-600 mgl^{-1}), manganese(Mn)(100-600 mgl^{-1}), nickel(Ni)(25-300 mgl^{-1}), lead(Pb)(100-600 mgl^{-1}), tin(Sn)(25-300 mgl^{-1}) and zinc(Zn)(100-600 mgl^{-1}) at varied concentrations above permissible levels. From both sites, bacterial isolates expressed 100% sensitivity to Gentamycin and Ofloxacin with Zones of Inhibition (ZOI) 16-32.1 mm and 20-29.1 mm diameter respectively. Though multiple resistance to Ceftazidime and Cefuroxime (100%), Cloxacillin (95-100%), Ceftriaxone (90-96.15%), Augmentin (50-96.15%) and Erythromycin (20-42.31%). All 46 bacteria revealed multi-antibiotic resistance (MAR) index >0.2. Overall, MAR index for site 2 (0.755) was > site 1 (0.599). All *Aspergillus* strains exhibited 100% tolerance to the 9 tested heavy metals- Ag (100 mgl^{-1}), Sn, Co and Ni (300 mgl^{-1}) and Fe, Al, Pb, Mn and Zn (600 mgl^{-1}) with no statistical difference (p>.05) to controls. This microbial resistance and tolerance traits to antibiotics and elevated heavy metals concentrations may indicate their bioremediative capability for polluted environments.

Keywords: Antimicrobial resistance, *Aspergillus* strains, Bacterial species, heavy metals, mining site

Paper ID (*CCE013*)

Removal of Selected Heavy Metals by *Bacillus velezensis* AAK1 Strain (OK625530.1)

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Abstract

Background: Biocorrosion is a metal deterioration influenced by microbes such as sulphate-reducing bacteria. Due to illegal mining activities in various North Western states, heavy metal contamination of water bodies is a growing environmental issue in Nigeria. **Materials and Methods**: This study was carried out to screen and characterize biosurfactants produced by *Bacillus velezensis* AAK1 strain (OK625530.1). The biosurfactant was assayed for inhibitory activities against (*Desulfovibrio piger*) and test for the bioremoval of heavy metal from metal-contaminated water. The bacteria was isolated from soil samples obtained from mechanic workshop in Malumfashi town of Katsina state, Nigeria, identified through morphological, biochemical characteristics and confirmed through molecular techniques. Biosurfactant producing capability of the isolate was conducted using standard procedure. The bioremoval efficiency of some heavy metals from contaminated water was determined using inductively coupled plasma optical emission spectrophotometer (ICP-OES). **Results and Conclusion:** The bacterium was gram positive rod and identified as *Bacillus velezensis* AAK1 strain (Accession number OK625530.1). The isolate was positive for blood haemolysis, drop collapse, oil displacement, and emulsification index tests. The chromatogram revealed the characterized biosurfactant as Rhamnolipid with biocidal effect on *Desulfovibrio piger* at concentration of 500mg/ml with mean zone of inhibition of 23±0.5mm while the minimum zone of inhibition of 9±0.2mm was recorded at the concentration of 62.5mg/ml. The ability of rhamnolipid to remove heavy metals that include Copper (Cu^{2+}), Lead (Pb^{2+}), Nickel (Ni^{2+}), and Cadmium (Cd^{2+}) proved effective. Heavy metals were removed within the least and highest range of 557±5.00-176.73±05.09 (62%) Cadmium and 502.7±3.51-208.52±06.34 (69%) Nickel respectively. The use of rhamnolipid in the remediation of heavy metal contaminated water bodies can serve as the best option for metal remediation; and an excellent pollution control strategy that is very effective and eco-friendly.

Keywords: Biocorrosion, Heavy metal, Biosurfactant, Rhamnolipid, *Bacillus velezensis* AAK1

Paper ID *(CCE014)*

Assessment of Heavy Metals Around Cassava Processing Mills in Aba, Abia State

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Abstract

Backgroud: Cassava (*Manihot esculenta*), is a major staple crop cultivated by most peasants farmers within Nigeria and other tropical African countries. The cassava milling engines contribute adversely to the environmental pollution due to release of heavy metals from dewatering machines, grates and grease use in lubricating parts of the grinding machine. **Materials & Methods:** Fifteen samples comprising of cassava effluent, effluent-polluted soil and unpolluted soil were collected from five different locations in Aba, Abia State. The soil samples were randomly collected using a sterile soil auger at a depth of 15cm. The unpolluted soil were collected at a dustance of 100m away from the milling sites. The presence of heavy metals such as iron, lead, cadmium, arsenic, zinc, copper, nickel were determined using Atomic Absorption Spectrophotometer (ASS). The concentration of metal in the raw cassava effluents ranged from: Fe (151.8 - 245.8 mg/l), Pb (11.23 - 48.45 mg/l), Cd (10.11 - 31.06 mg/l), As (17.77 - 61.08 mg/l), Zn (41.33 - 72.88 mg/l), Cu (45.12 - 73.67 mg/l), Ni (66.22 - 93.67 mg/l) and Mn (80.09 - 140.7 mg/l). The concentrations of metals in the effluent was in the order: Fe > Mn > Ni > Cu > Zn > As > Pb > Cd. The metal range for the effluent-polluted soil are: Fe (28.19 - 44.2 mg/g), Pb (3.01 - 11.13 mg/g), Cd (2.23 - 3.25 mg/g), As (6.23 - 10.26 mg/g), Zn (8.23 - 23.11 mg/g), Cu (6.23 - 18.42 mg/g), Ni (4.01 - 8.45 mg/g) and Mn (9.11 - 28.06 mg/g). The order of accumulation of heavy metals in the polluted soil was Fe > Mn > Zn > Cu > Pb > As > Ni > Cd. The concentrations of heavy metals in the unpolluted soils are in the following ranges: Fe (18.56 - 37.15 mg/g), Pb (1.05 - 4.89 mg/g), Cd (0.92 - 2.34 mg/g), As (1.05 - 7.58 mg/g), Zn (11.11 -20.41 mg/g), Cu (1.49 - 3.01 mg/g), Ni (3.45 - 6.05 mg/g) and Mn (4.25 - 11.23 mg/g). The concentrations of metals in the unpolluted soil was in the order: Fe > Zn >Mn > As > Ni > Pb > Cu > Cd. Iron was identified to be higher in all the sampled locations at the range of (151.8 – 245.8 mg/l) for effluent, (28.19 – 44.2 mg/g) for polluted soil and (18.56 – 37.15 mg/g) for unpolluted soil, while manganese, nickel, copper, zinc, arsenic, lead were at a minute level with cadmium being the least. The level of heavy metals in all the sites were significantly higher at ($P < 0.05$) than the level observed in the unpolluted soil. This implies that the pollution level of the polluted soil was anthropogenic. This accumulation of heavy metals should be of concern due to their negative impact on environment and human health.

Keywords: Cassava, Effluent, Heavy metals, polluted soil, unpolluted soil.

Paper ID *(CCE015.)*

Production of Biosurfactants from Bacteria Isolated from Waste oil Contaminated Soil in Afikpo North Local Government Area, Ebonyi State Nigeria

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Abstract

Background Biosurfactants are surface active compounds produced by certain microorganisms which have the ability to reduce surface and interfacial tension at the oil - water interface. This study was designed to produce biosurfactants from bacteria isolated from waste oil contaminated soil samples collected within Afikpo metropolis. **Materials and Methods:** Twelve soil samples were collected from waste oil contaminated soil at a depth of 20 cm using a sterile auger. Standard microbiological procedures and biochemical tests were used to identify the organisms which were then subjected to biosurfactant production using spent oil and vegetable oil as substrates at room temperature and tested using different techniques which included oil spread test expressed as oil displacement activity (ODA), emulsification activity expressed as emulsification index (E_{24}) and haemolysis test.**Results and Conclusion:** Six bacterial isolates (designated A_1, A_2, P_1, P_2, B_1 and B_2) were obtained and were suspected to be *Azotobacter* spp., *Pseudomonas* spp, and *Bacillus* spp. From the results obtained, it was observed that P_1 had the highest ODA of 28.3 ± 0.29 cm, while A_2 showed the least clearance zone of 20.7± 0.26 cm. For emulsification activity, P_1, P_2 and B_1 had emulsification index of 65.3 ± 2.53 %, 61.5 ± 9.27 % and 60. 6 ± 5.83 % respectively on vegetable oil and 56.2 ± 1.70 %, 57.1 1.60 % and 50 ± 1.70 % respectively on spent oil. All the isolates showed clearance zones on blood agar, further revealing their biosurfactants producing ability. This shows that surface active substances produced by these organisms will be effective in the degradation of oil contaminated environment, hence the technology should be harnessed and produced on a large scale and used in the bioremediation of oil contaminated sites.

Key words: Biosurfactants**,** *Azotobacter***,** *Pseudomonas***,** *Bacillus***,** Oil contamination

Paper ID (*CCE016*.)

Influence of Seasonal Variation on the Microbiology and Physicochemistry of Crude Oil Polluted Wetlands

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Abstract

Background: Pollutant such as crude oil spills on an environment affects the physical, chemical and biological properties of that environment. This study was conducted to determine the effect of seasonal variations on the microbiological and physicochemical characteristics of crude oil polluted wetlands in Rivers State, Nigeria. **Materials and Methods:** Soil samples were collected at 3 depths (0-15cm, 15-30cm and 30-45cm) with the aid of a hand auger. Sampling was done for a period of twelve months covering the rainy and dry seasons. Samples were analyzed for physicochemical characteristics, using standard analytical and microbiological methods. The data obtained was analyzed using statistical package for social science (SPSS) version 22 and Duncan multiple range test was used to separate means were differences occurred. **Results and Conclusion:** Higher temperature ranges were observed in the dry season than in the rainy season as seen in Iwofe temperature which ranged from 26.500C (0-15cm) to 28.500C (30-45cm) in the rainy season while in the dry season it ranged from 31.500C (0-15cm) to 33.500C (30-45cm) which was above FEPA permissible limit of 300C for soil temperature. Microbiological analyses showed significantly higher microbial counts in dry season than in rainy season in the wetlands. Total heterotrophic bacterial count in the wet season ranged from 1.09x107-1.05x108cfu/g and from 2.43x107-1.86x108fu/g in dry season. The wetland soils under study revealed total heterotrophic bacteria as having the highest population in all soil depths in both seasons. Hydrocarbon utilizing bacteria such as Bacillus subtilllis JQ433975, B. rigui EU939689, B. flexus FTML01000052 and Lysinibacillus macrolides OM301590 were genetically identified in this study. The study showed that seasonal variation has significant effects on the microbiology and physicochemical characteristics of wetlands and therefore, contribute to wetland degradation.

Keywords: Pollutant, Wetland, Physicochemical, Permissible, Anthropogenic.

Paper ID *(CCE017.)*

Phosphate Solubilizing Bacteria Isolated from the Soil and Aquatic Ecosystems

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Abstract

Phosphate solubilizing bacteria help in making phosphorus available for plant uptake through the production of some organic acids which solubilize insoluble phosphate mineral compounds. This study was aimed at isolation and characterization of phosphate solubilizing bacteria from soil and aquatic ecosystems.Soil samples from around leguminous plant roots were collected at a depth of 5 – 15cm using composite hand sampling technique and three different water samples from fresh, brackish and marine ecosystems were collected using hand sink sampler technique at 5cm below the water surface at constant rate. The samples were cultured on Nutrient agar and Pikoskaya's (PVK) medium using standard microbiological techniques. Biochemical and molecular characteristics were used in the identification of the isolates. Molecular characterization was done based on sequencing of the 16S rRNA. The isolates were screened for the potential to solubilize phosphate using Phosphate Solubilizing Index (PSI). The Total Heterotrophic Bacterial Counts (THBC) of the three aquatic and soil samples ranged from 3.8×10^5 CFU/ml - 1.2×10^9 CFU/g with the Freshwater samples having the least THBC ($1.2 \times 10^4 – 3.8 \times 10^5$ CFU/ml) and the soil samples having the most significant THBC ($2.2 \times 10^7 – 1.2 \times 10^9$ CFU/ml). The total phosphate solubilizing bacterial counts in the water samples ranged from 3.6×10^3 - 4.8×10^5 CFU/ml as the freshwater recorded the least counts($2.7 \times 10^2 – 3.6 \times 10^3$ CFU/ml) while the highest counts were recorded in the soil samples($3.3 \times 10^4 – 4.8 \times 10^5$ CFU/ml). The following organisms: *Pseudomonas xiamenensis* strain PX1, *Bacillus flexus* strain DTFG12, *Bacillus infantis* strain B864/17, *Pantoea dispersa* strain ABRL084 and *Chryseobacterium aquifrigidense* strain CW9 were identified as phosphate solubilizing bacteria and their population was observed to be more in the soil compared to the three water samples. *Pseudomonas xiamenensis* was observed to have more phosphate solubilizing potential when compared to the other isolates.

Keywords: Phosphate Solubilizing Bacteria, soil, fresh, brackish, ecosystem

Paper ID *(CCE018.)*

Effect of Paraquat on Soil Microorganisms

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Abstract

Background: Pesticides are widely used in agriculture for pest control but inadvertently affect soil microbial communities. This study was purposed to determine the effect of Paraquat on soil microorganisms, and to ascertain the pesticide microorganisms present in the soil. **Materials and Methods**: A microcosm study was conducted to investigate the effect of the pesticide on soil microorganism, over a 7-day period, with monitoring at day 1, 3, 5 and 7 respectively. Five different treatments were set up: T1 (control), T2, 10kg of soil + 50 ml of pesticide, T3; 10kg of soil + 100ml of pesticide, T4; 10kg of soil + 150 ml of pesticide, T5; 10kg of soil + 200 ml of pesticide. Microbial population was determined by standard plate count. Bacterial and fungal isolates were characterised based on their cultural characteristics and biochemical tests. **Results and Conclusion**: The results show that the bacterial population in T2 decreased from 2.49 x 10^3 CFU/g on day 0 to 2.25 x 10^3 CFU/g on day 7; in T3, it decreased from 2.5 x 10^3 CFU/g to 2.18 x 10^3 CFU/g; in T4, it decreased from 2.4 x 10^3 CFU/g to 1.96 x 10^3 CFU/g and in T5, it decreased from 2.43 x 10^3 CFU/g to 1.83 x 10^3 CFU/g. In the control (unpolluted soil), the population ranged from 2.24 x 10^3 CFU/g to 2.33 x 10^3 CFU/g. A similar decline was observed in the fungal populations in T2-T5 relative to the control. The pesticide-utilising bacteria isolated were *Pseudomonas* sp., *Micrococcus* sp., *Bacillus* sp., *Staphylococcus* sp. and *Arthrobacter* sp, while the pesticide-utilizing fungi detected include *Penicillium* sp., *Aspergillus* sp., *Trichoderma* sp., and *Fusarium* sp. This study suggests that the exposure to pesticides negatively impacts the survival and proliferation of soil bacteria and fungi. The effect of the pesticide on the soil microorganisms was observed to be dependent on both the duration of exposure and the concentration of the pesticide pollutant. The use of pesticides should be avoided or in unavoidable cases reduced to the minimum to protect soil microorganisms.

Keywords: Paraquat, microbial communities, pesticide-utilising microorganisms

Paper ID *(CCE019.)*

Fungal Community Structure During Bioremediation of Crude Oil Polluted Soil using Cow Dung and Unperturbed Soil.

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Abstract : The bioremediation of a crude-oil-contaminated agricultural environment was done by measuring the initial hydrocarbon content of the soil before adding cow dung as a stimulant and unpolluted soil. The unpolluted soil addition along with the cow dung treatment improved the removal of hydrocarbon pollution by favouring the growth of indigenous microorganisms, improving their microbial diversity, and the ecosystem function of the soil over time. **Materials and Methods**: One thousand grammes (1000g) of soil was collected from a depth of 0-30cm using an auger, 10g of cow dung manure, and 250g of unpolluted soil was mixed thoroughly. The setup was monitored for physicochemical parameters like total petroleum hydrocarbon, polyaromatic hydrocarbon, temperature, pH, total organic nitrogen, total organic carbon, and electrical conductivity. The culturable fungi were analysed for hydrocarbon-utilizing fungi and total heterotrophic fungi using Sabroud Dextrose Agar, and the non-culturable fungi were analysed using metagenomic-shotgun analysis to compare the community structure before, during, and after bioremediation. **Results and Conclusion** The species abundance and richness were analysed using the Shannon Diversity Index. The dominant phyla obtained for the uncontaminated and contaminated soil were Ascomycota (100% and 94.5%), Basidiomycota (0.0% and 0.4%), and Disosea (0.0% and 5.1%) respectively. The dominant genus of the Ascomycota observed with treatment post-remediation (3 months and 6 months) in the study was *Aspergillus, Candida, Cladosphialophora Exophiala, Fusarium, Ochroconis, Penicillium, Purpureocillium, Scedodosporium, Scytalidium, and Talaromyces. B. moniliell*a was only observed in contaminated soil at 0.4% while *D. acanthamoeba* was only observed in polluted soil and polluted soil with unperturbed soil addition at 5.1% and 4.6%. The structured unperturbed soil addition was able to assist the organic nutrients in removing the hydrocarbon pollution, improving the proliferation of diverse microorganisms during and after the bioremediation protocol and it improved the soil structure and ecosystem function which will improve farmer's yield.

Keywords: Bioremediation, Cow dung, Ecosystem-function, Diversity, Biostimulation.

Paper ID *(CCE020.)*

Unraveling the Public Health Implications of Betaproteobacteria in Bonny Drinking Water: Insights from Metagenomic Profiling.

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Abstract

Betaproteobacteria, is a diverse group of gram-negative bacteria with the potential to act as opportunistic pathogens, that can significantly impact water quality and public health when present in drinking water. A comprehensive study was undertaken to assess the potential impact of Betaproteobacteria on the Bonny drinking water supply. The study employed metagenomic profiling, utilizing Next Generation Sequencing (NGS) and advanced bioinformatics analysis using PATRIC and ABRICATE. The study unveiled a wide range of Betaproteobacteria taxa, providing valuable insights into their abundance and distribution in the water system. Functional annotations shed light on the potential pathogenic and beneficial traits associated with these bacteria. The study area exhibited high species richness, with a total of 318 species identified. Nine potentially pathogenic species; *Oligella ureolytica*, *Pandoraea thiooxydans*, *Burkholderia stabilis*, *Ralstonia pickettii*, *Pandoraea pulmonicola*, *Chromobacterium haemolyticum*, *Cupriavidus metallidurans*, *Burkholderia oklahomensis*, and *Paraburkholderia caballeronis*, with resistant genes, including tetM, ant3-dprime, ceoB, OXA-60, OXA-22, CRH, acrR, OXA-59, and norM, were detected raising concerns about the water quality. Conversely, certain Betaproteobacteria species, such as *Thauera humireducens*, *Burkholderia thailandensis*, and *Nitrosomonas stercoris*, contribute to nitrogen cycling, organic matter degradation, and nutrient cycling, vital for ecosystem stability and water quality. Exploring the functional potential of these bacteria offers opportunities for innovative water treatment and resource management. This study highlights the importance of ensuring safe drinking water and implementing sustainable environmental practices.

Keywords: Betaproteobacteria, Metagenomics, Resistant gene, Public health.

Paper ID (*CCE021*.)

Microbial Deterioration of Reinforced Concrete in Residential and Industrial Buildings Around Lagos and Ogun States, Nigeria

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Abstract
Background: Concrete and buildings, despite high compressive, thermal and acoustic strengths have witnessed deterioration and alarming rates of collapse in recent times. This has been blamed solely on structural defects. But it is becoming clear that biodeterioration, which is an undesirable change in the properties of materials as a result of the activities of microorganisms, is playing a contributory role in building deterioration and eventual collapse.This study determined the role of microorganisms in the deterioration of concrete structures in residential and industrial buildings in Lagos and Ogun states. Materials and Methods: Samples from 50 buildings were collected from selected locations in Lagos and Ogun States. X Ray fluorescence (XRF) and Scanning Electron Microscopy (SEM) were used to determine the level of structural defects and biodeterioration. Molecular identification of the bacterial community DNA was done using 16S rRNA gene amplicons of the composite concrete samples were carried out. Results: Community DNA showed diversity of bacteria and percentage abundance of these phyla: Actinobacteria (27.52%), Firmicutes (23.42%), Proteobacteria (13.49%), Cyanobacteria (13.39%), Gemmatimonadota (8.01%), Chloroflexi (5.29%) and others. Genus Bacillus had the highest percentage occurrence of 18.059 % while Longimicrobiaceae had the lowest incidence of 3.81%. SEM results showed several cracked areas and loosely held particles which are as a result of microbial activities. This is due to ability to utilize the contents of concrete as carbon and energy sources.Conclusion: It was established that microorganisms play a major role in the deterioration of reinforced concrete buildings around Lagos and Ogun States, Nigeria

Keywords: Biodeterioration, Proteobacteria, Structural defects, Buildings, Concretes, Scanning Electron Microscope

Paper ID *(CCE021)*

Screening of Bacteria from Animal Waste with Ability to Degraded Lignin

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Abstract

Background: Animals intestinal wastes were screened for candidate organisms with ability to utilize lignin. **Materials and Methods**: Isolation and identification of the candidate organism was conducted by collecting the animal intestinal waste in sokoto abatoir from 20 slaughtered cows, the sample was serially diluted and then 4th and 5th dilution factors were plated on the plates of nutrient agar and then incubated at 37^0C for 24 hrs. The isolates were gram stained to determine their cell wall architectures, and the other morphological characteristics and then finally identified by the organisms biochemical characterization. The lignin used for the determination of the organisms' degradation ability was extracted from the dried bark of Fig Tree using 1% Sulfuric acid and 4% sodium hydroxide. Isolated organisms were inoculated on a minimal salt medium containing only lignin as carbon source and then finally tested with a methylene blue dye. **Results and Conclusion**: The isolates identified from animal intestinal waste are *Escherichia spp, Bacillu spp, Salmonella, Klebsella* and *Lactobacillus*. The organisms isolated from animal intestinal waste indicate the ability to degrade lignin on methylene blue indicator agar plates with different degradation ability (lysing-showing zones of clearance) ranging from 2mm as lowest within 24 hrs to 38 mm as the highest within 72 hrs. Among the isolated organism, *B. subtilis* show the highest lignolytic activity on methylene blue indicator plate agar with 38 mm zone in 72 hrs. This study concludes that bacteria are a good source of lignin degradation with no environmental implication and within a shorter time frame when compared with other group of microorganisms such as fungi.

Keywords: Lignin, Bacterial, Animal waste, Degradation.

Paper ID *(CCE022.)*

Isolation and Identification of Non-Dermatophytic Molds from Different Air and Soil Samples from Cattle Markets in Abia and Imo States Nigeria.

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Abstract

Background: Soil is defined as a mantle of weathered rock which contains minerals and nutrients. It supports a wide range of microorganisms of which fungi is one of them. It is one of the most complex microbial habitats. Most moulds grow in soil and from there they infect cattle and other animals. The study aimed at investigating the prevalence of non-dermatophytic molds from different air and soil samples from six different cattle markets in Abia and Imo states Nigeria. **Materials and Methods:** Sixty (60) samples of air and soil samples of soil were collected and analysis was done using the settlement plate technique while soil samples were analyzed using tube dilution method and hair baiting technique method for evaluating presence of keratinophilic fungi. **Results and Conclusion:** A total of 13 different species of non-dermatophytic molds were identified and they all occurred at different points of collection from the markets. The most frequently isolated species from air samples were *Aspergillus welwitschiae*, *Absidia corymbifera* (20%) respectively in Abia State and *Fusarium linchenicola, Absidia corymbifera* (20.6%) respectively in Imo State. For soil samples, *Absidia corymbifera* (29%) and *Aspergillus flavus* (21%) were frequently isolated in Abia and Imo States respectively while for hair bait, *Aspergillus flavus, Absidia corymbifera* (26%) respectively were found in Abia State and *Aspergillus welwitschiae* (20%) in Imo State. The least isolated species from air samples were *Aspergillus sydowii* (3.3%) and *Cladosporium tenuissinum* (3.0%). For soil samples, *Aspergillus sydowii* (3.0%) were found while for hair bait; *Penicillum citrinum, Aspergillus aculeatus* (6.0%) were found respectively and *Penicillum citrinum, Cladosporium tenuissinum* (2.2%) occurred each in Abia and Imo States respectively. This study revealed that due to heavy deposition of organic materials in cattle markets, it encourages proliferation of keratinous fungi within the soil. This releases spores that are suspended in the atmosphere and contribute to major health challenge.

Keywords: Air, soil, Cattle market, non-dermatophytic molds, hair bait technique.

Paper ID *(CCE023.)*

Microbiological Monitoring Of The Air In a Research Laboratory by Conventional Techniques And Partial Genome Sequencing.

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Abstract

Background: Microbial air monitoring is the process of sampling and analyzing microbial contamination in the air. The ubiquitous nature of microorganisms makes them a major component of the air microbiome, of which laboratory air is not exempted. Such suspended microbes are implicated in contamination of pure culture plates and sterile broths in the laboratory. **Materials and Methods**: To identify contaminants that had been observed on plates, laboratory air and the incubators were monitored. Microorganisms in the air were sampled for identification by passive sampling methods. Nutrient Agar and Potato Dextrose Agar-Ampicillin plates were exposed at different locations in the Microbiology lab and in the incubator at 5 minutes, 10 minutes, 15 minutes and 20 minutes intervals. Plates were incubated at 28^0C and 37^0C, and subjected to daily monitoring and several rounds of purification to obtain individual bacterial and fungal isolates. The isolates were subjected to conventional and molecular identification methods. Bacteria colonies were identified by morphological characteristics, Gram staining and 16S rRNA gene sequencing. **Results and Conclusion**: Yellow and cream pigmented bacteria were the principal colonizers of the Nutrient agar plates from which seven isolates were selected. Fungal filaments grew on Potato Dextrose Agar plates, as either black mycelia or dirty white mycelia that changed to a brown coloration as culture plates grew older. The fungi were identified by microscopy and by characterization by ITS 1F and ITS 4R primers. The combination of conventional methods and partial genome sequencing with Basic Local Alignment Search Tool (BLAST), were used to identify bacteria and fungi isolates to species level. *Proteus mirabilis* (Accession number OR326677) was identified as the dominant bacterial contaminant and *Aspergillus ochraceus* (Accession number OR298111) *Aspergillus niger* (OR 298112), and *Penicillium singorense* (OR298113) were the most frequently encountered fungal contaminants in the laboratory.

Keywords: Sampling, Microbiological monitoring

SUBTHEME: POST-COVID DYNAMICS OF AGRICULTURAL SUFFICIENCY AND FOOD SECURITY (AGRICULTURE)

Paper ID *(PAFF 001)*

Microbial Evaluation and Nutritional Quality Assessment of 'Daddawa' made from *Parkia biglobosa* in Funakaye L.G.A. Gombe State, Nigeria.

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Abstract

Background: The study was conducted to evaluate microbial and nutritional quality of "Daddawa" made from African locust bean. **Materials and Methods**: A completely randomized block sampling method was used to collect the three samples of "Daddawa" that were analyzed microbiologically for the isolation, total viable count and identification of bacteria using standard microbiological techniques and biochemical tests. Antibiotic susceptibility testing of bacterial isolates was performed using the agar disc diffusion method and proximate analysis following standard methods of AOAC.**Results and Conclusion**: The result showed that the total viable count is within the range of 1.29 x 10^5 to 2.17 x 10^5 CFU/g; The *Salmonella* spp, *Shigella* spp, *Pseudomonas* spp and *Escherichia coli* were identified. The isolates from this study showed multiple antibiotic resistance however, only Gentamicin (30ug) and Ofloxacin (30ug) were susceptible with highest zones of inhibition at 24mm and 20mm respectively. The proximate composition were as follows: moisture content of 11.45 – 14.17%, protein 42.50 – 56.15%, fat 23.94 – 33.02%, ash 3.00 – 12.97% and carbohydrate 38.71 – 46.88%. This research finding indicates the presence of a high microbial load in all the 3 samples of "Daddawa" analyzed, which is above the standard established of 10^3 - 10^4 CFU/g allowed for a number of organisms associated with good manufacturing practices. It is therefore, recommended that hygienic practices should be used on the way and manner by which processing procedures take place.

Keywords: Microbial, Nutritional, Food condiment, *Parkia biglobosa* , Nigeria.

Paper ID *(PAFF002.)*

Movement of the A-Strain *Maize streak virus* In and Out of Madagascar

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Abstract

Background: The A-strain Maize streak virus (MSV-A) is the only known cause of maize streak disease (MSD). This disease remains a persistent constraint on maize production throughout sub-Saharan Africa and its adjacent Indian Ocean islands. MSV-A movements across its geographical range can be inferred by using MSV genome sequence data and the times when and places where sequences were sampled. **Materials and Methods**: Here, we use MSV genome sequence data to determine when, and from where MSV-A arrived on the island of Madagascar. Specifically, we use model-based phylogeographic analyses of 524 full MSV-A genome sequences, including 56 newly determined genomes from Madagascar, to reconstruct the most plausible movements of MSV-A to Madagascar.**Results and Conclusion**: We found substantial support for at least eight independent movements of MSV-A variants from East Africa to Madagascar that occurred between approximately 1990 (95% highest probability density interval [HPD], 1986 to 1995) and 2003 (95% HPD, 2000 to 2005). Conversely, we found only marginal evidence of a single instance of MSV-A movement out of Madagascar to the Comoros Islands (95% HPD between 2003 and 2006). Whereas we inferred that across their geographical range MSV-A variants are disseminating at a median rate of 38.9km/year (95% HPD 34.0 to 44.4), following their arrival on Madagascar, MSV-A variants have been moving at a median rate of 47.6km/year (95% HPD 36.05 to 61.70). Human mediated factors are likely major facilitators of both sporadic long-range MSV-A movements between mainland-Africa and Madagascar and, perhaps also, short to medium range movements on the island.

Keywords: Maize streak virus, geminiviruses, maize streak disease, mastrevirus, Madagascar

Paper ID *(PAFF003.)*

Biocontrol of Fusarium wilt of Tomato using Biochar amended with *Bacillus mycoides*

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Abstract

Background: The frequent use of agrochemicals to control plant diseases has detrimental effects on human health and the environment. This study investigated the prospect of soil bacterium *Bacillus mycoides* ANP (MG598443.1) in combination with plant biochar to control fusarium wilt of tomato. **Materials and methods:** The bacterium was used as a single inoculant and in-association with biochar in a greenhouse to screen its ability to control fusarium wilt caused by *Fusarium oxysporum*. Treatments were replicated three times in a completely randomized design. **Results and Conclusion:** Data obtained were subjected to analysis of variance at $\alpha < 0.05$. *Bacillus mycoides* ANP inhibited *Fusarium oxysporum* by 72% during *in-vitro* assay. Greenhouse germination experiment showed that the control seedlings exposed to *Fusarium oxysporum* but not inoculated with *Bacillus mycoides* ANP and/or biochar expressed severe leaf wilting, leaf curl and root rot when harvested. However, Biochar + *Bacillus mycoides* ANP significantly reduced the incidence of *Fusarium oxysporum* by 68% than when only Biochar (42%) and only *Bacillus mycoides* ANP (33%) were used. Similarly, Biochar + *Bacillus mycoides* ANP significantly enhanced the number of leaves, shoot height, stem girth, number of fruit and fruit weight (203±6.3, 82±2.1 cm, 2.21±0.2 cm, 18±1.0, 306±8.5 g) when compared to Biochar only (117±5.6, 62±2.3 cm, 2.13±0.1 cm, 15±1.6, 197±4.3 g), *Bacillus mycoides* ANP only (81±2.1, 55±1.6 cm, 1.63±0.3 cm, 12±0.6, 108±3.7 g) and the control (45±0.6, 48±1.2 cm, 1.10±0.2 cm, 0, 0) respectively. Therefore, biochar in combination with *Bacillus mycoides* ANP is an effective biocontrol agent against fusarium wilt of tomato.

Keywords: Biochar, *Fusarium oxysporum*, Bacteria, Biocontrol. Bacillus

Paper ID (PAFF004)

Occurrence of *Aspergillus* Species from Food Grains and Opened Poultry Feeds Sold in a Local Market

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Abstract

Background: Food and grains are very vital for human and animal consumption and the mycological contamination of food and grains has a detrimental effect on human and poultry health. This study was designed to isolate and identify Aspergillus species from food grains and poultry feeds sold in Mararaba market. **Methods**: Ten feed and grain samples were randomly collected from retailers and used for this study. Phenotypic identification of the isolates was carried out on Sabouroud Dextrose Agar (SDA) in duplicates. A comparative study on the growth rate of the fungal cells were carried out by placing one group of plates in the incubator at 37oC, while the other group of plates were placed on a sterile surface at room temperature (27±2oC) and the plates were observed macroscopically daily for seven days. For molecular identification, Polymerase Chain Reaction was conducted on the Internal transcribed spaces ITS 1 and 4 of the 18SrRNA for the identification of the fungal species. **Results**: From the feed and grain samples assayed, *Aspergillus niger* (20%) and *Aspergillus tamarii* (30%) were predominant and *Aspergillus flavus* had the lowest prevalence (20%). The comparative study of *Aspergillus* growth revealed that both methods were favorable for the growth of *Aspergillus* species. However, the growth of *Aspergillus* species at room temperature revealed more visible growth when compared to the growth of the isolates in the incubator. Results of the molecular analysis confirmed the isolates to be *Aspergillus niger*, *Aspergillus flavus*, and *Aspergillus tamarii*. **Conclusion**: The detection of *Aspergillus* species in poultry feeds and food grains sold in opened sacs is a public health concern and such purchase should be highly avoided.

Keywords : *Aspergillus* species, Food and grains, Poultry feeds, Fungal cells, Identification

Paper ID *(PAFF005)*

Microbial Examination of spoilt Avocado fruit (*Persea americana*)

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Abstract

Background: This study investigated the microorganisms associated with the spoilage of Avocado pear (*Persea americana*) fruits purchased fresh from four markets. The aim was to determine the microbial load and compare the physicochemical properties of the samples. **Materials and Methods**: The pour plate method was employed to isolate microorganisms from the samples. Physicochemical analysis, bacterial count, and fungal count were conducted using standard techniques to assess the contents and microbial load, respectively. The isolates were identified using cultural characteristics, morphological identification and biochemical test. The pH of the samples was measured, and moisture, ash, and total titratable acid content were determined. **Results:** The pH of the samples ranged from 4.08±0.025 to 4.88±0.025. The moisture content of most samples was 70±0%, except for samples from location C, which had 80±0%. The ash content of all samples was 10±0%. The total titratable acid content ranged from 0.40±0.01 to 0.96±0.01 mol/L. The bacterial counts on Nutrient Agar ranged from $1.1x10^5$cfu/ml to $6.7x10^5$cfu/ml, on MacConkey Agar from $1.0x10^5$cfu/ml to $6.0x10^5$cfu/ml, and on De Man, Rogosa, and Sharpe Agar from $2.0x10^5$cfu/ml to $9.6x10^5$cfu/ml. The fungal count ranged from $1.0x10^5$cfu/ml to $6.0x10^5$cfu/ml. Eight species of microorganisms were isolated and identified, including four bacterial species (*Staphylococcus spp*, *Bacillus spp*, *Klebsiella spp*, *Escherichia spp*) and four fungal species (*Aspergillus spp*, *Mucor spp*, *Saccharomyces spp*, *Geotrichum spp*). **Conclusion**: The findings reveal the presence of various microorganisms associated with the spoilage of Avocado pear fruits. The physicochemical analysis and microbial counts provide insights into the quality and microbial load of the samples. Proper handling methods of Avocado fruits are essential to ensure food safety.

Keywords: Avocado pear, Spoilage, Microorganisms, Physicochemical analysis, Bacterial and Fungal count.

Paper ID *(PAFF006.)*

Microbiological Assessment of Groundnut paste sold in Jimeta Markets, Yola, Adamawa State Nigeria

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Abstracts

Background: Groundnut paste is frequently associated with food-borne illness due to contamination traceable to food handlers, processing materials as well as environmental conditions and this therefore necessitated the microbiological quality examination of groundnut paste. **Materials and Methods** Traditionally processed and packaged groundnut pastes with addictive as well as those without addictive (500g each) were purchased and aseptically transported using sterile container to the Microbiology laboratory of the Modibbo Adama University, Yola for analysis. One gram aliquot was analysed for bacteria and fungi occurrence using morphological characteristics, grams reactions and microscopic examination while identification of bacterial spp. were carried out using biochemical reaction. The moisture content of the paste was determined using loss on drying and Karl Fischer titration techniques. **Results:** The percentage moisture content of the groundnut pastes was between the range of 0.77±0.06% and 4.72±0.08%. Total bacteria count fell between 1.8×10^{14} and 12.4×10^{14}cfu/ml with organisms such as species *of Proteus*, *Pseudomonas*, *Bacillus*, *Salmonella*, *Klebsiella*, *Staphylococcus*, *Escherichia*, *Shigella*, *Alcaligenes* and *Enterobacter* were isolated. Total fungal count ranges between 2×10^{7} and 4×10^{7}cfu/ml with identified species of *Aspergillus*, *Rhizopus* and *Penicillium. Proteus* spp. was the most prevalent with a percentage occurrence of 19.23 % while *Escherichia* spp., *Alcaligenes* spp. and *Enterobacter* spp. showed the least prevalence of 3.85%. The results also show that fungi species spread across all the samples with *Aspergillus* spp. obtained in two of the samples, *Rhizopus* spp. in three other samples while *Penicillum* spp. were obtained in four samples. **Conclusion**: It is apparent from the result of this study that the groundnut paste examined were highly contaminated with microbial isolates sufficient enough to be a public health hazard in Jimeta markets and Adamawa State at large, therefore caution must be applied in its uses and consumption.

Keywords: Groundnut paste, Food, Contamination, Bacteria, Fungi, Percentage occurrence.

Paper ID (*PAFF007.)*

Farmers' Perception on Herbicide Usage and Impact on health: An Overview of Status quo in Benue State, Nigeria.

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Background
Herbicide usage has increased significantly. The side effects caused by its irrational use threaten the environment and human health. This study aimed to evaluate farmer's knowledge and perception on health effects of herbicide usage in some parts of Benue State. **Method** Quantitative and qualitative data was collected through cluster sampling technique and face to face interview using validated structured questionnaires. A total of 252 farmers were interviewed from three selected local government areas (Agatu, Okpokwu and Otukpo) in Benue State. Epi Data info version 3.1. was used for data entry and analysed using IBM SPSS version 20.1.**Results** Amongst farmer's interviewed; 56% were males and 44% females and all between 20-50 years. On education level of the farmers;37.7% had secondary education, 30.6% tertiary education, 12.3% primary and 17.9% informal education, while, 1.6% were illiterates. All respondents reported non-use of personal protective equipment during applications. Names of commonly used herbicides were; Paraforce, Sarosate, Force-off, Fitscosate, Actraforce, Dsitop and Weed off. Paraforce and force off were the most commonly used. Some of the farmers reported that they read and adhered to application instructions on the herbicide pack, some, as suggested by their co-farmers. On ill herbicide related ill health; 38.1% of the respondents reported different symptoms of ill-health after application. **Conclusion:** Inappropriate herbicide application has great side effects on health. Farmers had high level of ignorance of the impact of inappropriate herbicide usage and biosafety. We recommend training programs on herbicide usage and urge strict regulation and control of herbicide availability in the country.

Key words: Herbicide, health, environment, biosafety, .farmers.

Paper ID *(PAFF008)*

Cultivation of *Pleurotus ostreatus* (oyster mushroom) using Sawdust supplemented with Waste Human Hair

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Abstract

Background: Waste human hair (WHH) is a part of municipal solid waste generated from salons that may lead to clogging of drainage pipes ensued with flooding. *Pleurotus ostreatus* (mushroom) is capable of utilizing several organic substrate types due to its enzyme secretions. This study determined the potential of WHH in cultivating edible mushrooms *P. ostreatus* (Oyster mushroom). **Materials and Methods**: WHH was collected from two (2) male barbing salons in Benin, Edo state. *P. ostreatus* grain spawn was obtained from Mycofarms and Allied Synergy Limited, Benin City. Microbial analysis of WHH was based on standard methods while pulverised WHH samples (pasteurised and unpasteurised) were mixed with sawdust in varying concentrations (5, 10, 15 and 20% WHH) and used in monitoring the growth of *P. ostreatus* at 25^{o}C and pH of 7.1 for 100 days. Growth of *P. ostreatus* in sawdust and rice bran was used as control. Solid state fermentation was used in this study. **Results and Conclusion**: The total bacterial and fungal counts obtained from WHH samples were $4.50 \pm 1.00x10^2$ cfu/g and $0.61 \pm 0.05\ x10^2$ cfu/g respectively. Among identified bacteria and fungi were *Bacillus* sp, *Citrobacter* sp. *Penicillium* sp. and *Alternaria* sp. Mycelium complete run observed in the pasteurised samples gave rise to mushrooms with the exception of the 20 % WHH sample. However, the control had the largest total yield (355 ± 05 g) and Biological Efficiency (51 ± 01%). Mycelium complete run and produced mushrooms in pasteurised samples could be attributed to lack of competing microorganisms. The yield and efficiency observed in the control could be because of established mycelium-substrate relationship spanning several generations. The potential for recycling WHH provides an avenue for the promotion of the circular economy in Nigeria.

Keywords: Waste human hair, *Pleurotus ostreatus*, Bacteria, Fungi, Mycelium.

Paper ID (PAFF009.)

Incidence of *Baclllus cereus* strains in Food Consumed by School Children in Ilorin Metropolis and Hazard analysis

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Abstract

Background: Food is a crucial aspect of an individual because it nourishes the body. Foodborne diseases are cause by eating contaminated food. This study investigated the incidence of Bacillus cereus in food consumed by school children within Ilorin metropolis and its hazard critical point analysis. **Materials and Methods:** Isolation of Bacillus cereus was done from food samples (rice, sphaghetii, puff-puff, bean, fried meat) collected from some selected school within four Local Government Areas in Ilorin metropolis using Bacara agar. Characterization and identification of isolates were done using conventional colonial morphology and biochemical tests. Molecular identification of isolates was done by extracting DNA that wa use for PCR (Polymarase chain reaction). PCR amplification with Gene Amp(R) PCR system Effect of physiochemical parameters (such as incubation period, temperature, pH, UV-light, salt and monosodium glutamate concentration used in cooking) on the growth of the isolates was carried out. Identification of hazard critical points was done at production and selling point using questionnaire. **Results and Conclusion**: The highest total Bacillus count of 4.75 ± 0.87 ($x10^3$cfu/g) in rice and the lowest total Bacillus count of 1.67 ± 0.49 ($x10^3$cfu/g) in beans sold in all the Local Government Areas were significantly different from each food samples. Isolates were confirmed to be *Bacillus cereus* OQ235070, OQ235071, OQ235072, OQ235073, OQ235075 and OQ235076 except one confirmed to be B. thuringiensis OQ235074. The isolates have optimum growth at 35 0C, pH 3 to 7, incubation period of 12 to 24 hours and 1.0 % monosodium glutamate concentration. Hazard point analysis reveals poor sources of water, illiteracy, and poor hygienic practices among handlers. In conclusion food samples sold to school children examined were found to be contaminated with Bacillus cereus.

Keywords: *Bacillus cereus*, Foodborne diseases, School Children, Ilorin metropolis, Rice and Spaghetti

Paper ID *(PAFF010.)*

Assessment of the Multi-mycotoxins Profile of Tiger nuts and Dates from selected markets in Lagos

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Abstract

Background: Microbial contamination of food is one of the most important public health problems, especially in children, where it can be fatal. Tiger nuts (*Cyperus esculentus)* and dates (*Phoenix dactylifera)* are foods that are usually eaten raw, so there is a high risk of consumers ingesting pathogenic microorganisms through their consumption. This study investigated the incidence of mycotoxins and other fungal metabolites in tiger nuts and dates sold in selected markets within Lagos state.**Methods**: A total of 36 composite samples of tiger nuts and dates purchased randomly from five vendors within each of the 9 selected markets (Agege, Kosofe, Amuwo-Odofin, Ojo, Ikorodu, Apapa, Lagos Mainland, Ibeju-Lekki and Epe) in Lagos State were screened for the presence of fungal metabolites using LCMS/MS analytical method.**Results and Conclusions**: An aggregate of 26 fungal metabolites; Aflatoxins (AFB1, AFB2, AFG1, AFG2; <0.4-2. 05µg/kg ±0.1 SEM), Zearalanone (ZAN; <10 µg/kg), Zearalenol (α-ZEL, β-ZEA;<10 µg/kg), Zearalenone (ZEN <5µg/kg), Diacetoxyscirpenol (DAS <3µg/kg), Trichothecenes (H-T2, T2; <9.6 µg/kg), Acetyl Deoxynivalenol (3-AD, 15-AD; <20µg/kg), Deoxynivalenol (DON; <20µg/kg), Nivalenol (NIV; <20µg/kg), Fuminosins (FB1, FB2, FB3; <40 µg/kg), Fusaric Acid (FSA; <3-81.5µg/kg), Moniliformin (MON; <3 µg/kg), Ochratoxin (OTA; <1.6 µg/kg)), Beauvericin (BEA; <1 µg/kg), Enniatin (ENN A, ENN A1, ENN B, and ENN B1; <1µg/kg) were detected in the nuts and dates, with Fusaric acid recording the highest concentration (81.5µg/kg ±2.4) while other metabolites were present in concentration below the detection limits. The Aflatoxin B1 and B2 concentrations ranged between <LOD-2.05µg/kg ±0.1, which is above the EU recommended limit. The copious amount of Fusaric acid in some of the samples calls for concern, as the acid is a moderately toxic but non-carcinogenic mycotoxin. The results of this findings revealed that tiger nuts and dates could be generally regarded as safe ready- to- eat snacks in terms of mycotoxins level. Bacteriological analysis of the nuts is recommended to predict the actual safety level of the consumers.

Keywords: Tiger nuts, dates, LCMS/MS, Lagos State, multi-mycotoxins.

Paper ID *(PAFF011)*

Fermentation as a Biocontrol Strategy to Mitigate Mycotoxins present in *Sorghum bicolor* l. moench from Selected Markets in Abeokuta Metropolis, Ogun State, Nigeria

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Abstract

Background: *Sorghum bicolor* is a cereal that is widely planted and consumed in Nigeria. Mycotoxin contamination of this grain can present public health concerns to consumers especially children, where it can be fatal. This study investigated the use of fermentation as a biocontrol strategy to mitigate mycotoxins present in *Sorghum bicolor* sold in selected markets in Abeokuta metropolis. **Methods**: A total of 30 samples of sorghum were purchased from 3 selected markets in Abeokuta metropolis and pooled into 3 composites per market. One hundred grammes (100g) of each pooled sample was divided into 2 parts. One part (50g) was allowed to ferment in distilled water spontaneously for 96 hours while the other part was left unfermented. These were screened for the presence of fungal metabolites using LC-MS/MS analytical method. **Results and Conclusions**: Two regulated mycotoxins, Aflatoxin B1 and B2 were detected in high concentrations in the non-fermented grains. AFB1 recorded the mean concentration of 41.6µg/kg +/-0.02 (SE), followed by Aflatoxin B2 (5.77µg/kg +/-0.01 (SE), both above EU recommended limits. Other metabolites were present in concentrations below the detection levels. In the fermented grains, the concentrations of AFB1 and AFB2 were drastically reduced to 5.77-1.54ug/kg respectively, though high amounts of fusaric acids (421ug/kg) were recorded. Fusaric acid is a moderately toxic but non-carcinogenic mycotoxin. Its presence in the fermented grains in high amounts could be of public health concerns. Based on this study, the reduction in AFB1 and AFB2 content in the fermented samples indicate that fermentation can be employed as a biocontrol strategy for the mitigation of mycotoxins in cereal-based foods.

Keywords: Fermentation, *Soghum bicolor*, LCMS/MS, Abeokuta metropolis, mycotoxins.

Paper ID *(PAFF012)*

Fungicidal Potential of Some Microbial Biocontrol Agents against Leaf Blight Disease of Egusi Melon (*Citrullus lanatus*)

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Abstract

Background: Egusi melon (*Citrullus lanatus* (Thumb Mansf.)) is an important vegetable in West Africa grown for its edible seeds and oil. Leaf blight disease (LBD) significantly limits its productivity in Nigeria. Management of LBD with synthetic fungicides has negative consequences on human and environment, necessitating the need to explore natural disease control mechanism. **Materials and Methods**: This study investigated the antifungal potential of four microbial biocontrol agents (BCA) (*Trichoderma harzianum (Th), T. pseudokoningii (Tp), Pseudomonas fluorescens (Pf) and Bacillus subtilis (Bs)*) in the control of three fungal pathogens (*Colletotrichum truncatum (Ct), Colletotrichum gloeosporioides(Cg)* and *Lasiodiplodia theobromae (Lt))* causing LBD of Egusi melon *in vitro* using dual culture procedure and as seed treatment (1g mycelial mat of *Trichoderma* spp and 1mL of *Pf* and *Bs* at 10^8cfu/mL/50 seeds) under screen-house conditions. BCA biotoxins heat stability was investigated using autoclaved BCA impregnated in agar. Mycelial growth was measured and disease incidence (DI) was calculated.**Results and Conclusion**: *Trichoderma pseudokoningii* significantly ($p<0.05$) produced lowest mycelial growth of 0.77±0.10, 0.90±0.05 and 1.65±0.12cm of *Ct*, *Cg* and *Lt* respectively, followed by *Th* whereas, the highest mycelial growth (2.25±0.09-4.60±0.11cm) was recorded from *Pf* on the three test pathogens. *Lasiodiplodia theobromae* inoculated seeds treated with Pf showed significantly higher DI (83.3±16.7%) than those with Ct (0.0±0.0%), Cg (16.7±6.7%) and *Lt* (16.7±0.0%) treated with *Tp*. The bioactive toxins produced by the BCA are thermostable. This study showed that the four BCAs produced antifungal property against LBD of *Egusi* melon, while *Tp* (at 1g/50seeds) is the most effective, producing highest pathogen inhibition and plant growth parameters.

Keywords: *Colletotrichum truncatum*, Egusi melon, *Pseudomonas fluorescens,* Seed treatment, *Trichoderma pseudokoningii·*

Paper ID *(PAFF012)*

Survey Data for Cassava Begomoviruses (2015-2022) reveals Reduced Prevalence of ACMV and EACMV across South-west Nigeria

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Abstract

Background: Cassava mosaic disease (CMD) is implicated in the low cassava tuber yield in Africa and has led to concerted effort by stakeholders to introduce interventions such as trainings and the distribution of clean planting materials. There is however a dearth of data to measure the effectiveness of these interventions. This study seeks to bridge this gap by presenting findings from four surveys conducted to assess the dynamics of CMD in South-West Nigeria.

Materials and Methods: A total of 699 cassava farms were surveyed in 2015, 2017, 2020 and 2022 across South-West states (Oyo, Ogun, Ondo, Lagos, Ekiti and Osun States) in Nigeria.

Results and Conclusion: CMD incidence decreased from 45.1% in 2015 to 14.01% in 2022. Similar patterns were seen for CMD symptom severity which was highest in 2015 (2.7) but significantly reduced in 2022 (2.32). CMD incidence averaged across all survey years ranged from 15.4% - 33.7% with the highest CMD incidence observed in Ogun (33.7%) while the lowest incidence rates were observed in Osun State (15.4%). Other southwest states also had moderate CMD incidence rates – Ekiti (23.4%), Lagos (26.4%) Ondo (19.6%) and Oyo (17.8%). Cutting infections (84.1-94.9%) accounted for most infections in all survey years with the proportion of whitefly infections reducing from 28.9% prevalence level in 2017 to 5.1% in 2022. A total of 2462 cassava foliar samples were collected across the four survey years. *African cassava mosaic virus* (ACMV) was the most predominant virus having been detected in 43.43% of all samples collected. *East African cassava mosaic virus* (EACMV) was detected in significantly lesser proportions (5.56%) and mostly as a mixed infection with ACMV (4.67%). This study showed increased progress towards CMD management and calls for intensified efforts by stakeholder in a bid to prevent rollbacks.

Keywords: Cassava, Cassava mosaic disease (CMD), *African cassava mosaic virus* (ACMV), *East African cassava mosaic virus* (EACMV), Nigeria

Paper ID *(PAFF013)*

Presence of *Listeria* species in Selected Seafood Samples from some Retail Outlets in Lagos State, Nigeria.

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Abstract

Listeria is a bacterial genus that is widely distributed in our environment. Listeriosis caused by *Listeria* species is recognized as an emerging foodborne disease. The aim of the study was to ascertain the presence of *Listeria* in some samples of fresh seafood. Ninety (90) samples comprising five samples each of croaker (*Pseudotolithus elongatus)*, blue whiting (*Micromesistus poutasou)* and shrimp (*Penaeus notialis*) were procured randomly from six retail outlets in Lagos State. The isolation of *Listeria* species was carried out using the Oxoid Listeria Précis method and full identification was carried out using MICROBACT 12L system. Of the 90 seafood samples surveyed, the presence of *Listeria* spp. was noted in 8 samples (8.8%). *Listeria monocytogenes* was found in 3.3% of the samples (3 isolates), which makes up 37.5% of the total Listeria that were isolated from the tested seafood. Other isolated *Listeria* species were *L. innocua* (50%) and *L. grayi* (12. 5%). The study has shown that *Listeria* is present in different kinds of seafood. Thus, there is a need to maintain a high standard of hygiene during the handling and processing of seafood so as to protect the health of consumers.

Keywords: Listeriosis, handling, seafood samples, Microbact, hygiene.

Paper ID (PAFF014)

Aflatoxin Production and Molecular Identification of Fungi isolated from Staples obtained from Central Market, O.A.U., Ile-Ife

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Abstract

Background: Staple foods are important sources of nutrition and commonly available commodities for consumption especially in African countries including Nigeria. Problems associated with their consumption is aflatoxins contamination by fungi which can be accompanied by health implications. **Materials and Methods**: About 500g melon, 750g maize and 560g groundnuts were purchased from three stalls in the Obafemi Awolowo University, Ile-Ife, Nigeria for fungal and toxin screening. Selected seeds were surface sterilized in 1% hypochlorite and rinsed several times with distilled water. The organisms associated with the samples were isolated using Direct plating method. **Result and Conclusion**: Various *Aspergillus* genera, *Rhizomucor*, *Fusarium* were isolated amongst others. Samples were further subjected to aflatoxin analysis to quantify AFB1, AFB2, AFG1 and AFG2 contents using the EEC method for aflatoxin extraction, TLC for aflatoxin detection, densitometry for aflatoxin quantification. From data obtained, no detectable toxins were found in the melon seeds, but detected in maize (25ppb of AFB1, 17ppb of AFB2) and in the groundnut seeds (233ppb of AFB1, 51ppb of AFB2). The sequencing of the ITS 1 and 4 regions of representative strains and results revealed >90% homology with *A. flavus* MT645322.1 with accession numbers MaF (OR250427), Ma6 (OR250428), GrL (OR250429) and GrM (OR250430). Phylogenetic analysis of these fungi with similar sequences obtained from GenBank also showed that Ma6 and GrM clustered with *A. flavus* DQ399307.1 which is an aflatoxigenic fungi and GrL and MaF clustered with clinical isolate *A. flavus* AY677676.1. This study has highlighted the importance of continual surveillance of food staples sold in major markets.

Keywords: Food Safety, Aflatoxins, ITS sequencing, Aflatoxigenic Fungi, Staples.

Paper ID *(PAFF015)*

Bacterial Quality of Locally Branded Commercial Fish Feeds in Lagos and Oyo State Nigeria

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Abstract

Contamination by bacteria and fungi is common to feeds and food not properly stored or handled, consequently affecting the health of animals and humans. The study aimed to evaluate and monitor bacterial quality in five (5) commercial brands of fish feed randomly sampled and subjected to bacterial examination. **Materials and methods**: Dilution factor 1:10 of 1g of powdered fish feeds in 100ml of sterile distilled water were plated on Nutrient agar (NA), MacConkey agar (MCA), and Mannitol salt agar (MSA) and incubated at 27 and 35^{o}C ± 2^{o}C for 24h to 48h. Growth was observed distinct colonies were selected and subcultured till pure cultures obtained. Isolates identified by biochemical method and subjected to antibiotic sensitivity test (Oxoid, UK). **Results** A total of 58 bacteria were isolated, identified and incidence of occurrence include *Staphylococcus* (43.1%), *Corynebacteria* (31.0%), *Klebsiella* (19.0%), *Enterobacter* (1.7%), *Proteus* (3.5%) *and Citrobacter* (1.7%). Frequency of occurrence showed *Staphylococcus sp*. was predominant, occurring at the highest. The antibiotic susceptibility profile showed that all bacteria isolates were susceptible to Ciprofloxacin (5mcg) and Enrofloxacin(5mcg). **Conclusion:** The microbial quality of the feed brands analysed may not necessarily threaten the cultured fish but might be detrimental to the consumer's health if not properly handled. Thus, concerned regulatory bodies should ensure fish feed production is monitored periodically to meet set standards.

Keywords: Commercial Fish Feed, Bacterial quality, Antibiotic Susceptibility Profile, Consumer Health

Paper ID *(PAFF016.)*

Microbial Synthesis of Homofermentative Lactic Acid by *Lactobacillus* sp. Isolated from processed Liquid Milk

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Abstract

Background: Lactic acid, a valuable weak natural organic acid extensively utilized in various industries has been conventionally synthesized through chemical processes. However, the growing demand for sustainable and eco-friendly production methods has stimulated interest in microbial synthesis. This study explored the potential of multi-strain lactic acid bacteria isolated from processed liquid milk to enhance lactic acid synthesis. **Materials and Methods:** Microorganisms were isolated by pour plate technique and screened on deMan Rogosa Sharpe (MRS) agar and were identified according to morphological and biochemical characteristics. Mutagenesis of positive using ethidium bromide (EB) concentration (0.25, 0.5, and 0.75 mg/ml) and 280 nm UV (exposed 30, 60, and 90 s) and quantitative and qualitative analyses using High-Performance Liquid Chromatography (HPLC) were investigated. **Results and Conclusion:** It was found that the isolate exhibited a clear zone on MRS agar, identified as *Lactobacillus* sp., and was selected for mutagenesis. A total of thirteen mutants were isolated out of which three were investigated for their ability to produce lactic acid from substrates. HPLC confirmed parent strain and mutants to produce significant homo-fermentative lactic acid in cheese whey substrate. The parent strain gave a significant mean yield of 2004.87ug/ml as compared to UV and EB mutant strains with 1457.67ug/ml and 239.10ug/ml respectively. Optimum lactic acid yields were produced at 37 °C, pH 4.5, and 150 rpm 16 h fermentation period. This study showed that mutagenesis did not influence optimum lactic acid production. The yield improvement that occurred via mutations might have diverted the metabolism from lactic acid production towards mixed acid fermentation, hence producing reduced levels of lactic acid.

Keywords: *Lactobacillus* sp.; Processed Liquid Milk; Mutagenesis; Fermentation; HPLC

Paper ID *(PAFF017.)*

Lactic Acid in the Food Industry: Current Trends and Future Perspectives

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Abstract

Background: The multifunctional properties of lactic acid present numerous benefits to the food industry by improving product quality and consumer health. Lactic acid is a versatile additive produced by LAB that regulates pH, enhances flavor, and preserves food by inhibiting pathogenic and spoilage microorganisms. The global lactic acid market size currently valued at USD3.1B is projected to grow at a CAGR of 8.0% from 2023-2030; due to its various end-use industries applications in developing and developed countries. This review was designed to synthesize data on the current trends and future perspectives of lactic acid use in the food industry.**Materials and method**: Secondary data were obtained from 157 articles indexed in Elsevier (n=47), PubMed (n=35), Web of Science (n=33), and Google Scholar databases (n=42). Inclusion criteria were articles containing relevant information on strain improvement, genome editing, fermentation approaches, and functional formulations of lactic acid in the food industry. Exclusion criteria were non-English articles and those published outside the last 3 years. Data extraction and statistical standardization with PRISMA were done for consistency and accuracy.**Results:** Literature search identified 15,783 articles, among which 157 were considered based on strain improvement (33.12%), genome editing(18.47%), fermentation approaches (21.02%), and functional formulations of lactic acid in the food industry (27.39%). Currently, the incorporation of lactic acid in cleaning and disinfection solutions, personal care products, calcium lactate in treating calcium deficiency diseases, and as an anti-caries agent has been reported. **Conclusion:** Genome editing of lactic acid-producing bacteria, optimization of production conditions, and the integration of lactic acid in other functional fiber- and protein-containing formulations remain the future perspectives.

Keywords: Lactic acid bacteria, Strain Improvement, Genome editing, Functional formulations, Food Industry.

Paper ID *(PAFF018)*

Biosensors Applications in the Food Industry: A Review

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ABSTRACT

Background: Challenges of specificity, sensitivity and detection limits associated with conventional methods of testing in food processing necessitate biosensor applications. Biosensors are bioanalytical systems that identify and transform biomolecules into readable optical, electrochemical, nano-mechanical, and mass-sensitive signals. Thus, aiding the identification of such biomolecules as DNA/RNA, antigen, protein, or enzyme. The global biosensors market size currently valued at USD26.8B is expected to grow at a CAGR of 7.9% to USD52.93B in 2030. This review was designed to synthesize data on the current trends and future perspectives of biosensor applications in the food industry. **Materials and Methods:** Secondary data were obtained from 149 articles indexed in Elsevier(n=64), Google Scholar(n=41), PubMed(n=25), and Web-of-Science(n=19) databases. Inclusion criteria were articles containing relevant information on mycotoxins, antibiotics, and the use of nanotechnology for developing biosensors. Exclusion criteria were non-English articles and those published outside the last 5 years. Data extraction and statistical standardization with PRISMA were done for consistency and accuracy. **Results:** Literature search identified 873 articles, among which 149 were considered based on mycotoxins(58.19%), antibiotics(62.31%), and nanotechnological use of biosensors(39.18%) in the food industry. Biosensors detection of mycotoxins, residual antibiotics, and food pathogens contribute immensely to safeguarding consumer safety and mitigating the risks associated with foodborne illnesses. Other applications include real-time hygiene monitoring of surfaces, fermentation processes, food quality and freshness. **Conclusion:** Reported limitations include molecular instability, loss of viability due to prolonged use, interferences from complex food matrices, complexity of design/operation, and lack of standardization. As such, leveraging nanotechnology, microfluidics, blockchain and artificial intelligence would enhance biosensor design and development for food industry applications.

Keywords: Biosensors, Antibiotics, Mycotoxins, Nanotechnology, Microfluidics.

Paper ID *(PAFF019.)*

Strain Improvement, Artificial Intelligence Optimization, and Sensitivity Analysis of Asparaginase-mediated Acrylamide Reduction in Sweet Potato Chips

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Abstract

Background: In recent times, L-asparaginase has emerged as a potential anti-carcinogen through hydrolysis of L-asparagine in the blood for anti-leukemic application, as well as that in carbohydrate-based foods, for acrylamide reduction applications in the food industry. **Materials and Methods**: In this study, *Aspergillus sydowii* strain UCCM 00124, isolated from the mesotidal waters of Ikang River, Cross River State, Nigeria, produced an L-asparaginase with a baseline acrylamide reduction potential of 64.5% in sweet potato chips. Plasma mutagenesis with atmospheric pressure and room temperature (ARTP) at a radio frequency of 120 W, was employed to improve L-asparaginase production while artificial neural network embedded with genetic algorithm (ANN-GA) and global sensitivity analysis were used to identify and optimize process conditions for improved acrylamide reduction in sweet potato chips. **Results and Conclusion**: The ARTP mutagenesis generated a valine-deficient mutant, Val$^-$Asp-S-180-L with 2.5-fold L-asparaginase improvement. The ANN-GA hybrid evolutionary intelligence significantly improved process efficiency to 98.18% under optimized conditions set as 118.6ºC, 726.37 g/L asparagine content, 9.92 µg/mL L-asparaginase, 4.54% NaCl, and soaking time of 15 h without significant changes in sensory properties like appearance, texture, flavor, and taste. The sensitivity index revealed initial asparagine content as the parameter to which the bioprocess was most sensitive. The enzyme demonstrated significant thermo-stability with Arrhenius deactivation rate constant, K_d, of 0.00562 min^{-1} and half-life, $t_{1/2}$, of 123.35 min at 338 K. These conditions are recommended for sustainable healthier, and safer sweet potato chips processing in the food industry.

Keywords: ARTP mutagenesis; ANN-GA optimization; Sensitivity analysis; L-asparaginase; Acrylamide mitigation; Sweet potato chips.

Paper ID *(PAFF020.)*

Reducing Trend and Regional Differences in the Incidence and Symptom Severity of Cassava Mosaic Disease (CMD): A Systematic Review and Meta-Analysis of CMD Field Surveys from 2001 - 2022

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Abstract

Background: Cassava mosaic disease (CMD) is a major constraint to cassava productivity and food security in Sub-Saharan Africa (SSA). Over the past two decades, SSA has undergone substantial changes in cropping systems and climate conditions, both of which have the potential to impact the incidence and severity of CMD. This systematic review assessed the variations in CMD incidence and severity in SSA over the last two decades. **Methods**: A comprehensive search strategy identified 2111 unique studies published between 2003 and 2023 from PubMed, Scopus, Africa Journal Online, and Google Scholar. Studies were included if they reported survey data on CMD incidence and severity and/or cassava mosaic begomoviruses detection in SSA. A total of 30 studies reporting surveys conducted from 2001-2022 across 18 countries met our inclusion criteria. A subset of 17 studies were eligible for meta-analysis. Pooled incidence and severity rates were then calculated using a random-effect meta-analysis. **Results and Conclusion**: Our findings indicated a pooled CMD incidence of 53.5% (95% CI: 42.0 - 64.6%) and a pooled mean CMD symptom severity of 2.87 (95% CI: 2.70 - 3.03) in SSA. Cutting infections were the predominant infection type accounting for 84.3% (95% CI: 76.9 - 89.7%) of CMD infections in SSA, while whitefly accounted for only 15.68% (95% CI: 10.33 - 23.09%). Subgroup analysis revealed regional differences in CMD incidence and severity with the highest CMD incidence rates reported in surveys conducted across Central African countries (76.5 - 95% CI: 67.49 – 83.59%) as compared to West African countries where significantly lower incidence (28.01 – 95% CI: 14.17-47.83%) rates were reported. Similar patterns were observed for CMD symptom severity where the most significant severity was observed in Southern African countries (3.23) and the lowest severity in West African countries (2.62). Overall, our study observed a declining trend in CMD incidence and severity over time, suggesting the potential effectiveness of control measures implemented in recent years. This study contributes to the understanding of CMD dynamics in SSA and provides evidence-based guidance for policymakers, researchers, and farmers.

Keywords: Cassava, Cassava mosaic disease (CMD), Sub-Saharan Africa (SSA), Incidence, Severity

Paper ID *(PAFF021)*

Studies on the Physicochemical properties and Mycoflora Composition of Rhizosphere of *Saccharrum officinarum* (sugar cane) plants in Bida Niger State , Nigeria

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Abstract

Background: Sugarcane (*Saccharum officinarum*) is one of the most important species of plant cultivated in tropical and subtropical regions of Africa. An attempt was made to determine some physicochemical and mycological properties of the rhizosphere of sugarcane plants in selected areas of Bida Local Government Area of Niger State. **Materials and Methods:** Rhizosphere samples were randomly collected from sugarcane farmlands in Bangaie and Darachita Wards, Bida, Niger State. Physicochemical parameters such as pH, Electrical Conductivity (EC), Total Organic Matter (TOM), Total Organic Nitrogen (TON), Total Organic Carbon (TOC), Magnesium (Mg), Potassium, Calcium, Phosphates and Sodium were determined as described by American Public Health Association (APHA). Fungal species associated with rhizoplane of sugarcane plant were enumerated, isolated and characterized using standard mycological techniques.**Results and Conclusion:** Physicochemical characteristics of the rhizosphere soil from the sample sites include pH (7.88±0.13 - 8.61±0.24), EC (84±0.31 - 218µS/cm ±1.41), Calcium (880±60 - 3880mg/kg ±100), TOC (1.53±0.13 - 2.34%±0.27), TOM (2.63±0.32 - 4.02% ±0.40), TON (0.24±0.01 - 0.38%±0.04), Sodium (59.3±1.10 - 81.3mg/kg±0.95), Phosphorus (3.12±0.09 - 4.84mg/kg±0.10), Magnesium (196±3.48 - 610mg/kg±2.89) and Potassium (176.2±1.16 -268.4mg/kg±9.41). The Total Fungal Count of the rhizoplane samples ranged from $1.1x10^2$±1.52 to $1.7x10^2$cfu/g. A total of nine (9) fungal species were isolated from the samples. Cultural and microscopic characteristics identified the fungal isolates as *Trichophyton asahii* (19%), *Aspergillus flavus (18%), Penicillium sp. (9%), Malassezia furfur* (9%), *Macroconidia* (9%), *Cunnighamella bertholletiae* (9%), *Pichia* sp. (9%), *Saccharomyces cerevisiae* (9%), and *Microsporum ferrugineum* (9%). Physicochemical parameters of this study can be exploited by farmers, private sector and government institutions while fungal species can be exploited for important agricultural and biotechnological applications.

Keywords: Rhizosphere, Rhizoplane, Sugarcane, Fungi, Physicochemical Properties

Paper ID (PAFF022.)

Nutritional and Phytochemical Compositions of 'Aju Mbaise' used in Postnatal Care among the Igbo Tribe of Nigeria

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Abstract

Background: 'Aju Mbaise' is a polyherbal formulation widely used among women of the Igbo tribe of Nigeria for its beneficial effects on postpartum recovery and the overall well-being of nursing mothers. In this study, we investigated the nutritional and phytochemical compositions of 'Aju Mbaise'. **Materials and Methods**: The 'Aju Mbaise' plants were cleaned, air-dried, and blended into fine powder. Proximate, mineral, and phytochemical analyses were carried out on the powdered sample using gravimetric and spectrophotometric methods. **Results and Conclusion**: The results showed that 'Aju Mbaise' contains appreciable amounts of crude fibre (51.93 ± 0.26 %), ash (9.22 ± 0.21 %), moisture (9.23 ± 0.28 %), carbohydrate (31.48 ± 0.53 %), and energy (623.06 KJ/100 g). It is also rich in macro and micro minerals such as potassium (76.237 ± 0.12 ppm), sodium (48.789 ± 0.22 ppm), magnesium (24.371 ± 0.02 ppm), phosphorus (121.639 ± 0.61 ppm), iron (4.154 ± 0.02 ppm), and zinc (2.023 ± 0.02) ppm. The phytochemical analysis revealed the presence of several secondary metabolites. The total phenols, tannins, and alkaloids content were found to be 0.337 ± 0.19 mg GAE/g, 0.430 ± 0.02 mg TAE/g, and 3.876 ± 0.08 % respectively. These results indicate that 'Aju Mbaise' is a rich source of carbohydrates and crude fibre as well as a good source of phytochemicals that could possess antioxidants and other essential activities. Therefore, these findings can serve as foundational data for both the nutraceutical industry and nutrition practitioners working within the local community settings.

Keywords: Aju Mbaise, Proximate analysis, Mineral analysis, Phytochemicals, Polyherbal formulation.

Paper ID *(PAFF023.)*

Lipase Production Using Yeast Isolates

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Abstract

Yeasts have scarcely been reported as lipase producers compared to bacteria and filamentous fungi. Lipases are versatile enzyme that catalyse the hydrolysis of long chain triglyceride into free fatty acids (FFA) diacylglycerol, monoacylglycerol and glycerol. Lipases are relatively stable and are able to catalyse various reactions, they are of potential importance for diverse industrial application. Yeasts were isolated from wastewater, shea butter, and onions using Yeast Extract Peptone Dextrose Agar. Primary and secondary screening were carried out with phenol red olive oil and tween-80. A total 28 isolates were obtained from the samples, 17 isolates were obtained from wastewater, 8 from shea butter and 3 from onion. Colonial and biochemical tests were used for characterization of the isolates. Highest clear zone from primary screening on phenol-red olive oil and tween-80 agar was 0. 2±0.0mm and 3.0±0.0 mm in diameter respectively. Lipase activity in each fermentation medium was confirmed by measuring the amount of fatty acid liberated from the medium by titrimetric method using enzyme crude extract. *Saccharomyces cerevisiae* from wastewater had the highest lipase enzyme activity of 49.38±1.15 µ/mL followed by *Lipomyces, sp* which had 33.33±1.15 µ/mL and the least was obtained from *Saccharomyces cerevisiae* from shea butter (22.22±1.15 µ/mL). This study suggests *Saccharomyces cerevisiae* and *Lipomyces sp* for lipase production.

Keywords: Lipase, Lipolytic yeast, Olive oil, Lipid, *Saccharomyces cerevisiae*

Paper ID *(PAFF024.)*

Comparative Study of the Probiotic Potentials of Lactic Acid Bacteria (LAB) Isolated from Fermented Maize and Sorghum sold in Abakaliki Metropolis, Ebonyi State.

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Abstract

Background: One of the ways of discovering novel bacteriocins is by isolating microorganisms (Lactic acid bacteria) especially from foods that are fermented locally. This is because all locally fermented foods are predominantly fermented by LAB which exert preservative properties on the foods. Traditional fermented food is considered to be a promising source for useful LAB and various end products including bacteriocins. **Materials and Methods**: Four samples comprising of ten grams(10g) each of Maize (*Zea mays*) and Sorghum (*Sorghum bicolor*) were obtained from International market, Abakaliki were ground in a sterile waring blender. Aliquot samples were inoculated on De Man Rogossa Sharpe agar and incubated at 37^{o}C for 48 hours.The isolates were identified and characterized by physiological and biochemical tests such as catalase ,oxidase, methyl red and indole tests. Six (6) bacteria isolates were isolated and characterized. Species identification was based on the sequence analysis of 16S rRNA genes.The probiotic potentials such as cholesterol assimilation, bile salt assimilation, acid tolerance and cell surface hydrophobicity were determined using standard laboratory procedures.**Results and Conclusion**: The cholesterol and bile salt assimilation ability was 0.02±0.001 - 0.12±0.012 for maize and 0.05±0.001-0.12±0.003 for sorghum with *L. plantarum* and *L. pentosus* , 0.02±0.012 – 0.04±0.015 for maize and 0.035±0.015- 0.039±0.001 for sorghum with *L. fermentum* and *L. paracasei*. The acid tolerance showed a more tolerance to a low pH of 3.0 by the isolates from sorghum. The cell surface hydrophobicity was from 38 - 68% and 56- 65 % for isolates of maize and sorghum on *L. paracasei* and *L. plantarum* respectively. These results offer insightful information and provides a baseline knowledge of the potential sources of probiotics and relative application in functional foods.

Keywords: Fermented foods, maize, lactic acid bacteria, sorghum, probiotic.

SUBTHEME: SUSTAINABILITY AND MICROBES IN BIOECONOMY (INDUSTRY)

Paper ID *(SMB 001)*

Effect of different rates of Single Super Phosphate and Frequency of Megagreen on Nodulation, Nitrogen fixation and yield of Cowpea

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Abstract

Background: Cowpea is a grain crop cultivated in a range of ecologies. To increase yield of cowpea additional soil enhancer must be used. Megagreen contains calcium, silicon, magnesium and trace elements.Megagreen is a bio-stimulant, containing micronized calcite whose particles act quickly on the vegetal metabolism via foliar surface. Experiments were carried out to investigate the effect of different rates of single super phosphate (SSP) and frequency of megagreen on nodulation, nitrogen fixation and yield of cowpea (*Vigna unguiculata*). **Materials and Methods**: The experiment was arranged in split-split plot with application of megagreen at the rates of 1.5 and 3 (kg/ha per 500 litres of water). The application of Megagreen at rates of 1.5 kg/ha per 500 litres of water used were applied at two frequencies: 2 and 3; 2, 3 and 4 (WAP).**Results and Conclusion**: The application of SSP and megagreen at the rate of 3 kg/ha per 500 litres of water at 2, and 3 WAP (S1 M2 R1) recorded more than 200 % increase in yield. The results indicate that application of SSP and megagreen at the rate of 3 kg/ha are the preferred option to improve soil fertility and quality, and increase cowpea yield.

Keywords: Cowpea yield, Megagreen, Mitrogen fixation, Nodulation, Single superphosphate

Paper ID (*SMB 002)*

Investigating the Bioflocculant Production Potential of Microorganisms Isolated From Earthen Pond Sludge

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Abstract

Background: Bioflocculants are biodegradable polymers produced by microorganisms and have gained applications in aggregating dissolved and suspended substances in water. This study aimed to screen, isolate and identify microorganisms from earthen pond sludge for flocculant production. **Materials and Methods**: Samples were collected from earthen pond sludge in *Lapai Gwari* in Bosso Local Government Area of Minna, Nigeria located at longitude 6.5052°E and latitude 9.5246°N, and screened for microorganisms with bioflocculating ability using kaolin suspension and selective medium containing (per liter) NaCl 0.1 g, $MgSO_47H_2O$ 0.2 g, K_2HPO_4 5 g, agar 5.5 g, yeast extract 0.5 g, urea 0.5 g, KH_2PO_4 2 g, and glucose 10 g for bacteria, and $MgSO_47H_2O$ 0.2 g, K_2HPO_4 5 g, agar 5.5 g, yeast extract 0.5 g, urea 0.5 g, KH_2PO_4 2 g, glucose 10 g for fungi. The lyophilized bioflocculant produced by the bacterium was characterized using thermogravimetric property analysis (TGA), Fourier-transform infrared (FTIR) spectroscopy and scanning electron microscopy (SEM) **Results and Conclusion**: Of the twelve (12) microorganisms isolated, *Prestia megaterium* (accession number ON184360) gave the highest potential (30 %) for flocculant production. Tyrosine-protein kinase gene was detected to be responsible for the bioflocculant production. A total of 10.67 g of bioflocculant was produced from 500 mL of the medium. The TGA, FTIR spectra and scanning electron micrograph exhibited typical characteristics of flocculant. The findings of this investigation indicated that *Priestia megaterium* isolated from earthen pond sludge is a suitable substitute for flocculant production.

Keywords: Bioflocculant, Sludge, *Prestia megaterium*, Water, Microorganisms

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Paper ID *(SMB 003)*

Production of Citric Acid using *Aspergillus niger* Isolated from Agrowastes Dumpsite

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Abstract

Background: Citric acid (2-hydroxy-propane-1,2,3-tricarboxylic acid, $C_6H_8O_7.H_2O$) is a weak organic acid and has wide applications in chemical, cosmetic, pharmaceutical, food and beverage industries. The aim of this study was to isolate and screen *Aspergillus niger* from agrowastes (plantain trunk, groundnut shell, sugarcane bagasse and corncob) dumpsites for citric acid production using the agrowastes as a source of reducing sugar. **Materials and Methods**: *A. niger* was isolated from agrowastes dumpsite using potatoes dextrose agar and screened for the potential to produce citric acid using Czapeck dox agar. The agrowastes were pretreated and hydrolyzed. The reducing sugar was determined using spectrophotometry at 540 nm. The hydrolysates were used to compound Czapeck dox broth for citric acid production in submerged fermentation and incubated for 72 h. The citric acid produced was monitored using spectrophotometry at 420 nm and the wavelength was converted to standard measurement using a standing curve. **Results and Conclusion**: *A niger* (accession number OM510398) was identified on the basis of cultural, microscopic and molecular characteristics. The reducing sugar concentration of the hydrolyzate were 21.45, 22.96, 21.86 and 11.52 mg/mL for sugarcane bagasse, corncob, plantain trunk and groundnut shell respectively. The citric acid concentration of the substrates varied considerably with the plantain trunk having the highest absorbance value of 3.8030 (2.7630 g/L of citric acid) while 1.1536 (1.6202 g/L), 0.9392 (1.4672 g/L) and 1.9023(0.3726 g/L) were obtained from corncob, sugarcane bagasse and groundnut shell respectively. The results of this study showed that plantain trunk was the best substrate for citric acid production and can be developed for industrial citric acid production.

Keywords: Citric acid, *Aspergillus niger,* Spectrophotometry, Agrowaste, Dumpsite

FUNDING: TETFUND GRANT NUMBER: TETF/ES/DR&D-CE/NRF2021/SETI/III/00008/VOL.1

Paper ID (*SMB 004)*

A Glance at the Potentials of Keratinases in the Biotechnology Industry

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Abstract

Keratins are fibrous, structural and insoluble proteins that constitute the epidermis and epidermal appendages, such as skin, hair, nails, hooves, horns, scales, claws, and feathers. They are valuable protein sources for animal. However, keratins are insoluble proteins and cannot be digested by common proteases. The structure of keratin is rich in disulfide bridges and sulfur compounds that make it insoluble and resistant to proteases lysis. Keratinases, a kind of metal or serine proteases, is used to designate the subset of proteases with keratinolytic activities. They are mainly produced by fungi, actinomycetes and bacteria, and decompose keratins into available amino acids and peptides. The agro-industrial wastes, especially those emanating from leather and poultry processing industries are considered to have little or no economic relevance due to their structural stability, which makes valorisation difficult. Nonetheless, several strategies have been employed to harness the locked up potentials from keratinous wastes, and these strategies have included thermoenergetic processing, acid or alkaline hydrolysis. Valorisation with the above has yielded products which have not been suitable for industrial applications. Keratinases which can bio-convert keratin to peptides and amino acids, on the other hand, has not been a front runner in the valorisation of keratinous waste biomass; So, it would be prudent to state that keratinases shall enjoy extreme importance soon. The bioconversion of keratinous wastes into amino acids or peptides with functional values would be an attractive endeavour for several applications including animal feed formulations, bioremediation, Textile and leather industries, cosmetics and pharmaceutical industries. The valorisation approach would represent a potentially sustainable strategy for the proper management of keratin-rich agro wastes and keratinolytic microorganisms and enzymes would be beneficial from the biotechnological and industrial viewpoint. This study is a systematic review of the potentials of keratinases in the biotechnology industry.

Keywords: Keratins, Keratinases, valorisation, proteins, agro-industrial waste.

Paper ID *(PAF 005.)*

Crude Oil Biodegradation Potential of Lipase Produced by *Bacillus subtilis* and *Pseudomonas aeruginosa* Isolated from Hydrocarbon Contaminated Soil

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Abstract

Background: Biodegradation of oil pollutants and their derivatives has become the most environmental-friendly method in the developing world. This study was aimed at assessing crude oil biodegradation potential of lipase produced by indigenous bacteria (*Bacillus subtilis* and *Pseudomonas aeruginosa)* isolated from oil contaminated soil. **Materials and Methods**: The bacterial were identified using biochemical tests. plate count method was carried out for the isolation of lipolytic bacteria from the contaminated soil sample. The bacteria colonies were streaked on Tween 80 agar plate and incubated at 37˚C for 48 hours, the possible lipase producing bacteria were screened using agar well diffusion method. Isolates with wider zone on phenol red agar were selected for lipase production. Titrimetric method was used to determine the lipase activity at various pH of 4, 6, 8 and 10 and the biodegradation of the crude oil was determined by gas chromatography mass spectroscopy. **Results and Conclusion**: Lipase produced by *P. aeruginosa* showed maximal lipase activity (U/mL) at pH 8 and 50 ℃ while that of *B. subtilis* showed maximal lipase activity at pH 8 and 40 ℃ when subjected to various pH and temperature. From the initial concentration of 2 g crude oil (w/v), lipase produced by *B. subtilis* recorded 8.11±0.70% of degradation in mineral salt medium within 28 days, while that of *P. aeruginosa* recorded 15.6±0.03% of biodegradation of the crude oil. The GC-MS analysis of the crude oil treatment showed complete mineralization of several compounds and peak reduction, indicating lipase efficiency in hydrocarbon degradation. As revealed by GC-MS analysis, out of the 8 hydrocarbons identified in an undegraded oil, 5 (2-Buten-1-ol, Formaldehyde, dimethylhydrazone, Pentane, n-hexane,) were completely degraded by the enzyme activities while 2 (toluene and methyl, cyclopentane) were identified with hydrocarbons treated with lipase. The lipase enzymes produced by *B. subtilis* and *P. aeruginosa* can serve as useful products for bioremediation of crude oil contaminated soil.

Keywords: Crude oil, enzyme, bacteria, biodegradation, pollution

Paper ID *(SMB 006.)*

Optimization of Beta-galactosidase Production by a Locally Isolated Strain of *Aspergillus niger* using Box Behnken Experimental Design

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Abstract

Background: Beta-galactosidase (EC 3.2.1.2.3) is a glycoside hydrolase enzyme that cleaves lactose into its resulting monosaccharides, glucose and galactose. Beta-galactosidase from microbial sources especially fungi have food, biotechnological, industrial, medical and environmental applications. However, the production of this important enzyme is influenced by a variety of fermentation parameters. An attempt was made to optimize beta-galactosidase production using locally isolated strain of *Aspergillus niger* FGMTF01. **Materials and Methods:** *Aspergillus niger* FGMTF01 was isolated from fermented goat milk using standard mycological techniques. Cultural, microscopic and molecular methods were used to identify the organism. Box Behnken Experimental Design was used to determine the effects of lactose concentration, pH and incubation period on optimum beta-galactosidase activity, specific activity and fungal biomass (wet and dry weight). Optimization for beta-galactosidase production was carried out in shake flasks containing Yeast Peptone Lactose Broth (YPLB) medium with lactose concentrations (20, 40 and 60%), initial pH (5, 7 and 9) and incubation period (3, 5 and 7days).

Results and Conclusion: The optimum fermentation conditions for highest beta-galactosidase activity, specific activity and fungal biomass were observed in design containing lactose concentration = 30%, pH = 7 and incubation time = 7 days which generated an enzyme activity of 71.19U/ml ±1.33, specific activity of 0.2363 mg/ml ±0.05 and biomass (3.80g ±0.5 wet weight and 0.35g ±0.15 dry weight). *Aspergillus niger* FGMTF01 is a promising fungal strain for industrial production of beta-galactosidase using above fermentation parameters. The experimental design can also be used for production optimization of various important industrial metabolites.

Keywords: Beta-galactosidase, *Aspergillus niger*, Optimization, Production, Box Behnken.

Paper ID *(SMB 007.)*

Quality improvement of watermelon-*Clerodendrum volubile* extract wine produced via sequential malolactic fermentation by *Saccharomyces cerevisiae* and *Lactobacillus delbrueckii*

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Abstract

Background: Herbal infusions medicinal benefits in wine and the impact of malolactic fermentation on wine quality is of high significance. The study aimed at improving the quality of watermelon wine with *Clerodendrum volubile* extract using *Saccharomyces cerevisiae* and *Lactobacillus delbrueckii* subsp *bulgaricus.***Materials and Methods**: *S. cerevisiae* and *L. delbrueckii* isolated from palm wine and yoghurt, respectively were identified through morphological and biochemical characterization. Fermentation must was prepared in various dilution ratio ranging from 95:5, 90:10 and 85:15 (watermelon to *C. volubile).* Static fermentation was carried out for 5 days with *S. cerevisiae* followed by malolactic fermentation with *L. delbrueckii* and then fermentation with *S. cerevisiae* for 23 days at room temperature. **Results and Conclusion**: Physicochemical properties, phytochemicals, mineral, and sensory properties were observed. Noticeable was pH decrease (5.21 -.3.33), increased titratable acidity (0.051-0.16 g/l), decreasing reducing sugar (0.59-0.11mg/ml), temperature (30.5-24℃) and increasing total dissolved solids (19.7-48.9^{o}B). Wine fermented with *S. cerevisiae* (D) had the highest phenolic content (481.68 ± 0.37mg/100ml), while flavonoids (48.49±0.3mg/100ml) and vitamin C (29.28±0.7mg/100ml) increased with increase in *C. volubile* concentration. There was abundance of Na^{+} (51.71±55.21mg/100ml), wine G produced highest Mg^{2+} (6.07±0.01mg/100ml) and Fe^{2+} (0.23±0.1mg/100ml) while wine C and F revealed highest K^{+} (4.7mg/100ml) and Ca^{2+}(5.23mg/100ml), respectively. Sample D and H showed the least value of alcohol (1.38±0.5%). Generally, wines were rated above average for the overall acceptability. However, wine E has the highest preference rating. Watermelon-*C. volubile* wine produced with sequential malolactic fermentation can help in the improvement of the nutritional and sensorial properties of wine.

Keywords: Watermelon-*Clerodendrum volubile*, Wine, Malolactic fermentation, *S. cerevisiae*, *L. delbruekii*

Paper ID (*SMB 008)*

Determination of Cellulolytic Potentials of *Aspergillus* species Isolated from Central Waste Dump Site of Nile University of Nigeria.

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Abstract

Background: A large number of microorganisms are capable of degrading cellulose but only a few of these microorganisms produce significant quantities of enzymes capable of completely hydrolysing cellulose. Fungi are the main cellulase-producing microorganisms. This study was aimed to determine the cellulolytic potentials of *Aspergillus* species isolated from the central waste dump site of Nile University of Nigeria. **Materials and Methods**: In this purposed study, three *Aspergillus species* were isolated and characterized using cultural and morphological features as well as microscopic examination (i.e. *Aspergillus flavus, Aspergillus niger,* and *Aspergillus terreus*) from one gram of soil sample (obtained from 5 cm depth) of the waste dump, using pour plate technique, screened on carboxymethylcellulose agar and compared for their ability to degrade cellulose. Screening of fungal isolates was performed by plate method. Cellulolytic fungi were evaluated after 3-7 days for the production of cellulolytic enzymes by staining with 1% Congo red. The diameter of clear zone on fungal plates, gave an approximate indication of cellulase activities. Fungal species were grouped as high and low celluloytic isolates on the basis of cellulase activity using Index of Relative Enzyme Activity (ICMC). **Results and Conclusion**: *Aspergillus niger* produced the most significant cellulolytic activity with Enzymatic Activity of 1.75±0.0 µ/mL followed by *Aspergillus flavus* with Enzymatic Activity of 1.12±0.0 µ/mL while *Aspergillus terreus* did not show any cellulytic activity with 0.00±0.0 µ/mL. *Aspergillus niger* has the highest occurrence which takes (50%), followed by *Aspergillus flavus* with (25%) and *Aspergillus terreus with* (25%).

Keywords: Cellulose, *Aspergillus terreus*, Congo red, enzymes, hydrolysis.

Paper ID *(SMB 009.)*

Assessment of the Potentials of Autochthonous Lipase-Producing Bacteria in the Bioremediation of Palm Oil Mill Effluent

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Abstract

Background: Pollution of the environment caused by the release of untreated palm oil mill effluent (POME) is a major environmental concern. This research aimed to assess the potentials of autochthonous lipase-producing bacteria as a non-invasive procedure in the bioremediation of POME. **Materials and Methods:** The identity of lipase-producing bacteria in POME were determined using morphological and biochemical techniques. Identified isolates were monitored for POME utilization potentials by measurement of optical density at 600 nm in 25 ml Bushnell Haas broth supplemented with 0.25 ml sterilized POME. Individual isolate and consortium were then used for the bioremediation of POME. Total suspended solid (TSS), pH, oil and grease, total organic carbon (TOC), total organic matter (TOM) and total nitrogen (TN) of the raw and treated effluents were evaluated. **Results and Conclusion**: The population (CFU/ml) of total heterotrophic, POME - utilizing and lipolytic bacteria were 3.9 x 10^6, 2.8 x 10^6 and 3.5 x 10^5 respectively. The lipolytic bacterial isolates include *Brenneria nigrifluens*, *Bacillus circulans* and *Paenibacillus pectinilyticus*. Results revealed varying pH of 5.03 and 6.81 - 7.26. The lipolytic bacteria from POME caused reduction efficiency of 100% in TSS and oil and grease contents of the treated effluents relative to the raw samples. The TOC, TOM and TN reduction ranged 16.43-59.79%, 6.18-80.70% and 11.71-93.66% respectively**.** This research indicated that POME indigenous lipase-producing bacteria improved POME quality parameters and therefore suggestive of their potentials in the bioremediation of the effluent with the consortium being most promising.

Keywords: Autochthonous, Bioremediation, Lipase-producing bacteria, Microbial consortium, Palm Oil Mill Effluent.

Paper ID *(SMB 010.)*

Effect of Maturity on the Nutritive value of, *Pleurotus pulmonarius* and *Pleurotus ostreatus*

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Abstract

Background: Different kinds of agricultural wastes have been used for growing various species of edible mushrooms in the world. This research is aimed at the effect of maturity on the nutritive value of *Pleurotus pulmonarius* (*P. pulmonarius)* and *Pleurotus ostreatus* (*P. osreatus*). **Materials and Methods:** Agro-wastes plantain leaves, saw dust and grass straw were collected, sorted, shredded, pasteurized and inoculated with *P. pulmonarius* and *P. osreatus* for a period of four weeks. Percentage proximate content and the percentage mineral content of the two mushrooms harvested separated into pileus and stipe were analyzed using AOAC. **Results and conclusion**: The moisture content was 11.00 -11.12% at the juvenile stage of the species, ash 7.66 -10.85% in an opposite trend, fat content was 3.46% and increased from juvenile to the mature stages of pilei while steady increase in protein 12.00 – 14.82% and crude fibre 17.29 – 25.96%, from juvenile to mature stages of pilei and stipes. For mineral contents, matured and young fruit-bodies of *P.ostreatus* contained more potassium 152.34% than *P.pulmonarius* while Sodium 142.10% was the major element in *P.pulmonarius* increasing as the mushroom matures, Phophorus 4.81-12.53% increase in both mushroom, no significant differences in Calcium <0.16%, Copper <0.06% and Zinc <0.07% of pilei and stipes of both mushroom in all maturity stages, Iron was highest 6.91% in the stipe of *P.pulmonarius* increasing from the juvenile to mature, the trend was also recorded for *P.ostreatus* but at minimal level 1.23%. The finding shows that the pilei of the two mushrooms were where the concentration of the nutritive and mineral elements values was higher than the stipes.

Keywords: *Pleurotus pulmonarius, Pleurotus ostreatus,* pileus, stipe, Agro-wastes

Paper ID *(SMB 011)*

Physicochemical Properties of Intracellular Cellulase extracted from *Hebaloma crustuliforme*

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Abstract

Background: Pollution from agro-industrial waste is becoming a very big ecological problem in Nigeria. A typical example of such pollutant lignocellulosic waste (rice, corn, bagasse waste), which can be degraded into a Glucose by some microorganisms. **Material and Methods**: This study was carried out to determine the physicochemical properties of intracellular cellulase extracted from *Hebaloma crustuliforme* **.** The mushroom were harvested from a farm in Okenugbo via Ago-Iwoye. The crude enzyme was crushing the mushroom in a blender and centrifuge, thereafter, it was precipitated at 80% ammonium sulphate, followed by ion-exchange chromatography and gel-filtration on Sephacryl-200. The peak of the elution profile with the highest activity was pooled from latter chromatographic step and characterized afterwards. **Results and Conclusion:**The specific activity of the enzyme rose from 0.55 to 2.07 U/mg with a yield of 64.88% and 3.76 purification fold. The optimal pH and temperature of the enzyme were 6.0and 50^0C respectively. The enzyme was observed to be thermo-stable at the 40^0C for 30 minutes. The kinetics revealed that the V_{max} was 0.281U/min while K_m 66.67mg/ml. The effect of selected cations and chemical compounds at varying concentrations revealed the activating effect of Mn^{2+} while Hg^{2+}, K^+, Zn^{2+}, EDTA, Mercaptoethanol and Urea inhibit the enzyme's activity. The apparent molecular weight of the enzyme as determined by gel filtration on sephacryl S-200 was 28000 Dalton while the subunit molecular weight (native molecular weight) as determined on SDS PAGE and was found to be 18.5KDa. The results revealed that the isolated enzyme from *Hebaloma crustuliforme* exhibited the properties of cellulase.

Keywords: Cellulase, *Hebaloma crustuliforme*, Ion-exchange Chromatography, Gel Filtration, Kinetics.

Paper ID *(SMB 012)*

Digital Microbiology: Prospect & Challenges of *AI* and *IoT* inRepositioning Microbiologyin Nigeria

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Abstract

Background: In the 21st century microbiology is fast moving towards full laboratory automation and digitalization. The compulsive need of computational biology in the digital dispensation of *Artificial Intelligence* (*AI*) and *Internet of Things* (*IoT*) subjects microbiological workflow to the prospects and challenges of digitalization especially in the post COVID-19 era.**Objective**: This article reviews importance and efficient use of big data, machine learning, and artificial intelligence in the field of microbiology and its challenges in developing countries. **Methods:** A total of 127 literatures published between 2014 and 2023 were gathered from search engines. After analyzing the titles and abstracts, 76 were rejected. The full text versions of 52 papers were analyzed and selected. These papers were divided into four areas; *AI* in microbiology and health systems (15), *IOT* in microbiology (10), digital microbiology (5) and machine learning applications in microbiology (12)..**Results:** It was found that *AI* approaches is gaining significant ground towards investigatory, predictive and diagnostic microbiology. Machine learning (ML) and deep learning (DL) algorithms widely applied in studies on *AI* and *IoT* applications in microbiological investigations lead to novel discoveries. **Conclusion:** We suggest key approaches to maximize the prospect and mitigate the challenges that come with the concept in modern microbiology workspace. We project that the digital era and the use of machine learning and algorithms will impact significantly on the day-to-day activities of the laboratory personnel. There is a need to identify the key stages alongside the analytical process where ICT, *AI* and *IoT* can be applied to provide a benefit.

Keywords: Artificial intelligence, Economy, IoT, Digitalization, Microbiology.

Paper ID *(SMB013.)*

Isolation of Phosphate Solubilizing Bacteria and their ability to Solubilize Inorganic Phosphate forms from Soils in Nasararwa State

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Abstract

Background: Phosphate solubilizing bacteria are a group of bacteria that have the ability to convert insoluble phosphate to bioavailable orthophosphate form for plants in soil ecosystems. The study was aimed at the isolation of phosphate solubilizing bacteria and their ability to solubilize tricalcium phosphate ($Ca_3(PO_4)_2$) and aluminum phosphate ($AlPO_4$) invitro. **Materials and Methods**: Soil samples were collected from maize rhizosphere and isolation was done using spread plate method on Pikovskaya agar. Eight strains of phosphate solubilizing bacteria based on 16S rRNA sequences were identified and they include members of the genera *Acinetobacter, Ochrobactrum, Brucella, Curtobacterium, Leifsonia* and *Microbacterium* with accession numbers OP159676, OP159677, OP159679, OP159680, OP159681 and OP159682 respectively. **Results and Conclusion**: All strains were selected and evaluated for their ability to dissolve inorganic phosphate in the Pikovskaya broth. Phosphate solubilizing activity of all isolates was assessed by the vanadate-molybdate method. All the strains tested showed significantly ($p \leq 0.05$) the ability to solubilize the two different forms of phosphates with ability to solubilize $Ca_3(PO_4)_2$ more than $AlPO_4$ at a concentration of 2500µg/mL for eleven days of incubation. Maximum solubilization of $Ca_3(PO_4)_2$ in Pikovskaya broth medium was observed with *Brucella haematophilia* (420.3 ± 0.28 µg/mL), followed by *Ochrabactrum soli* (400.3 ± 0.06 µg/mL), while for $AlPO_4$, the maximum solubilization was observed in *Brucella haematophilia* (79.0 ± 0.08 µg/mL), followed by *Ochrabactrum soli* (72.8 ± 0.08). The results from these findings could suggest the potential use of these phosphate solubilizing bacteria as biofertilizers which is cheap and ecofreindly.

Keywords: Phosphorus solubilizing bacteria, Inorganic phosphate, Phosphorus, Solubilization, Orthosphosphate

Addendum : http://nsm.covenantuniversity.edu.ng/wp-content/uploads/2023/07/NSM-OTA_2023_BOOK_OF_ABSTRACTS_-ADDENDUM.pdf

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