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FEDERATION OF AFRICAN SOCITIES OF BIOCHEMISTRY AND MOLECULAR BIOLOGY

NIGERIAN SOCIETY OF BIOCHMEMISTRY AND MOLECULAR BOLOGY (NSBMB)

SHEDA SCIENCE AND TECHNOLOGY COMPLEX, SHESTCO

# BOOK OF ABSTRACTS

## Federation of African Societies of Biochemistry and Molecular Biology (FASBMB)

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**Held at the**

**Sheda Science and Technology Complex (SHESTCO)**

**Hosted by**

**The Nigerian Society of Biochemistry and Molecular Biology (NSBMB)**

**Theme:**

## Redefining the Future of Biochemistry & Molecular Biology Education in Africa Through Advanced Technology and Automation

**24th - 27th November, 2025**

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# SUB-THEME 1

# MOLECULAR BIOLOGY AND BIOTECHNOLOGY [MBB]

FASBMB2025/MBB-001

# Development and Optimization of PCR Protocol for Molecular Characterisation of *Plasmodium falciparum* Trap-Like Protein Gene, a Potential Vaccine Target

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In a 2023 report, malaria affected 263 million people across 83 countries, causing about 597,000 deaths. Parasite drug resistance is increasing, and malaria vaccine development remains difficult. The *Plasmodium falciparum* Trap-Like Protein (*PfTLP*), an uncharacterised TRAP/MIC2 family member, facilitates parasite motility and hepatocyte invasion, making it a promising vaccine target. This study developed sets of PCR protocols for molecular characterisation of the *PfTLP* gene. Ethical approval was obtained from Plateau State Specialist Hospital. Genomic DNA was extracted from malaria-infected human blood samples collected in Jos. Eleven primer sets (JPA–JPK) were designed from the *P. falciparum* reference (XM_001348542.2) to amplify ~1,000 bp overlapping segments covering the 10,632 bp *PfTLP* gene. Multiple gradient PCR optimisations using Q5® High-Fidelity 2X Master Mix were conducted with 3-40 trials per segment. Successfully amplified samples were sequenced and analysed using bioinformatics tools. Results showed a developed and optimised PCR protocol for seven of the eleven target regions, covering approximately 7,000 bp of the *PfTLP* gene. The protocol featured a reaction mix of primers, template DNA, and High-Fidelity DNA polymerase, with a temperature programme of initial denaturation (98°C, 30 sec.), 35 cycles of denaturation (98°C, 30 sec.), annealing (51.2–58.4°C, 30 sec.), and extension (72°C, 2 min.). Gel electrophoresis confirmed successful amplification. Fifty-seven sequences obtained, showed 98-100% similarity to the reference *PfTLP* gene sequence and were deposited in NCBI Genbank database. This study establishes the first optimised PCR protocols, laying the groundwork for subsequent molecular and functional analyses of the *PfTLP* gene.

**Keywords:** *Plasmodium falciparum* TRAP-like protein gene, PCR

FASBMB2025/MBB-002

# Epigenic Effects of Street Food Consumption ON IFN-γ, TNF-α and IL-10 Gene Expression

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Concerns have been raised over the safety of street food consumption due to the possibility of exposure to several environmental pollutants. The present study aimed at determining immune response to street food consumption by evaluating the gene expression of inflammatory IFN-γ, TNF-α and IL-10 in relation to ABO/Rh blood groups, haemoglobin genotypes (Hb) and sociodemographic variables. The prevalence of regular street food consumption among adults in Sagbama LGA, Bayelsa State, Nigeria were also evaluated. A multistage random sampling technique was used to select 200 study participants and they were grouped into two; regular consumers (RC) and non-consumers (NC). RC were regrouped according to their ABO/Rh and Hb. ABO/Rh, Hb, gene expression and sociodemographic variables were determined using cellulose acetate electrophoresis, hemagglutination test kit, real-time PCR technology and a structured questionnaire. The prevalence of regular street food consumption was found to be 90%. More males (60%) than females (30%) consumed roadside food ($p < .05$). Compared with NC a significant increase in IFN-γ and TNF-α followed by a decrease in IL-10 gene expression ($p < .01$) was found among RC (NC: IFN-γ-30±0.15; TNF-α-25±0.11; IL-10-201±0.11 versus RC: IFN-γ-245±.22; TNF-α-350±.22; IL-10-41±.22). RC with blood group $A^+$ and Hb AA had the highest pro-inflammatory gene expression (IFN-γ-257±.02; TNF-α-370±.07) and the lowest anti-inflammatory gene expression (IL-10-29±.22) while those with blood group $O^+$ and Hb AA had the lowest IFN-γ-215±.09, with TNF-α-370±.07 and the highest IL-10-50±.56. Elderly RC had a higher pro-inflammatory gene expression and a lower anti-inflammatory gene expression compared with young RC ($p < .05$). In conclusion, the present study demonstrated that street food consumption has epigenic effects on inflammatory genes in relation to Hb, ABO/Rh blood groups and age. Findings of the present study have implication in health promotional interventions.

**Keywords**: blood group, gene expression, genotype, inflammation, street food

FASBMB2025/MBB-003

# Molecular Studies of Midgut Bacterial Composition of Laboratory-Reared *Aedes aegypti* Revealed Prevalence of Aeromonas species

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Mosquitoes are vectors for diverse medically important pathogens. The gut microbiome influences both mosquito survival and pathogen transmission to mammals. This study investigated the midgut bacterial composition of laboratory-reared *Aedes aegypti* mosquitoes. Immature stages of mosquitoes were collected from natural breeding sites within the University of Jos Main Campus and reared to adulthood under controlled laboratory conditions. Euthanized adults were dissected and mid-guts removed for bacterial culture and isolation. Morphological analysis was performed through Gram-staining and genomic DNA extracted using the Zymo Research Fungal/Bacterial Kit. The 16S rRNA gene was PCR amplified and sequenced and analysed using NCBI BLAST. Phylogenetic relationships among eight sequences were inferred in MEGA 12 using the Maximum Likelihood method with 1000 bootstrap replicates. Isolates were rods (occurred singly, in pairs or clusters) or cocci (in clusters); Gram positive and negative. Sequences of the gram-negative samples ranged from 901-931bp. BLAST analysis showed 100% query coverage and were 99.23–99.89% identical to several *Aeromonas* species. Phylogenetic analysis revealed that isolates were *Aeromonas hydrophila*, *A. encheleia*, *A. lusitana*, *A. crassostreae, A. aquatilis*, and an unclassified *Aeromonas* sp. This implies a diverse *Aedes aegypti* mosquito gut microbiota that can influence the advances in biotechnology for paratransgenesis in vector control.

**Keywords**: *Aedes aegypti*, microbiota, *Aeromonas spp*, 16S rRNA gene, Phylogenetics

FASBMB2025/MBB-004

# Transcriptomic and Histological Effects of *Irvingia gabonensis* Stem Bark Extract on Fructose-Induced Metabolic Syndrome in Rats

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Obesity and metabolic syndrome, once largely confined to high-income countries, are now rising rapidly in low- and middle-income populations, particularly in urban settings. Effective management is hindered by the high cost and side effects of conventional therapies, creating an urgent need for safe, affordable alternatives. Medicinal plants offer promising solutions, not only for weight management but also for mitigating obesity-related complications. *Irvingia gabonensis*, traditionally used in African medicine, has shown anti-obesity and anti-diabetic effects, yet its molecular mechanisms remain underexplored. This study investigated the transcriptomic and histological effects of *Irvingia gabonensis* stem bark extract (IGSBE) in Wistar rats using a well-established fructose-induced model of metabolic syndrome, which recapitulates hypertension, dyslipidemia, hyperinsulinemia, and insulin resistance. IGSBE treatment significantly modulated key metabolic and satiety-related genes, including upregulation of GLUT-4, GIP, and GLP-1, and downregulation of lipase, FTO, and LDL receptor genes. Histological analyses revealed marked reversal of inflammatory and degenerative changes in the pancreas, liver, kidney, and heart. These findings provide novel evidence that IGSBE exerts dual transcriptomic and tissue-protective effects, restoring metabolic gene expression while preventing fructose-induced organ damage. By elucidating its molecular and histological impact, this study highlights *Irvingia gabonensis* as a promising plant-based therapeutic for metabolic syndrome, offering a potential affordable and safe intervention for obesity-related disorders in resource-limited settings.

**Keywords:** *Irvingia gabonensis*, metabolic syndrome, gene expression, histology, fructose.

FASBMB2025/MBB-007

# Association of CYP17A1, HSD3B1, and ERCC6 Gene Polymorphisms with Prostate Cancer Susceptibility and PSA Levels in Nigerian Men

Olubanke Olujoke Ogunlana[1,2*], Kaze Niels Nguedia[1,2,3], Christogonus Chichebe Ekenwaneze[1,2], Suleiman Zakari[1,2], Emmanuel Chimuebuka Amadi[1,2], Oluwadamilola Ayeye[1], Stephen Ikuerowo[4], Ajani Olagunju[4], Anthony Idedia Micheal[5] and David Enoma[6]

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Prostate cancer is a leading malignancy among Men of African Origin, with genetic and hormonal factors contributing to its development. Variants in genes regulating androgen biosynthesis and DNA repair, including *CYP17A1*, *HSD3B1*, and *ERCC6*, may influence disease risk. This study examined associations between selected single nucleotide polymorphisms (SNPs) in these genes and prostate cancer susceptibility, prostate-specific antigen (PSA) levels, and family history among Nigerian men. A total of 118 participants (cases and controls) were genotyped for *ERCC6* (rs2228528), *HSD3B1* (rs1047303), and *CYP17A1* (rs4919686, rs743572). Genotype frequencies were analysed using Chi-square and Fisher's tests; logistic regression adjusted for age estimated disease risk. All genotypes were in Hardy-Weinberg equilibrium ($p > 0.7$). Logistic regression showed that CYP17A1 (rs4919686) was significantly associated with prostate cancer ($p = 0.045$); individuals with the AC genotype had increased risk (OR = 46.4; 95% CI: 1.08–1984) after age adjustment. Age remained an independent predictor of both prostate cancer and PSA ($p < 0.004$). Other SNPs showed no significant associations. The CYP17A1 (rs4919686) variant may contribute to prostate cancer susceptibility among Nigerian men through androgen biosynthesis pathways. Findings support the need for larger, population-based studies to validate CYP17A1 polymorphisms as potential biomarkers of prostate cancer risk.

**Keywords:** Prostate cancer, Gene polymorphism, PSA, Men of African Origin, Molecular biomarkers.

FASBMB2025/MBB-008

# Molecular Characterization and Phylogenetic Analysis of Selected Tropical Fruit Species

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Molecular characterization of plants is vital for accurate taxonomic classification, conservation of valuable germplasm, and genetic improvement programs. In this study, tropical fruits were identified, genomic deoxyribonucleic acids characterized and evolutionary history investigated. Genomic DNA was extracted from fruit mesocarps using gDNA extraction kits. Amplification via conventional Polymerase Chain Reaction using universal primers, agarose gel electrophoresis for separation and Sanger DNA sequencer. Phylogenetic analysis was performed by blasting using NCBI GenBank, and trees were built using maximum likelihood method via MEGA 12 software. Extracted DNA fragments had 574, 534, and 576 base pairs for *Adenanthera pavonina*, *Terminalia catappa*, and *Dacryodes edulis*, respectively, with molecular weights of 3.78 Mda, 3.52 Mda and 3.80 Mda. Blast analysis confirmed the species similarities, showing e-value of 0.0, percentage identities of 96.14%, 98.92%, and 98.88% for *A. pavonina*, *T. catappa* and *D. edulis*, respectively. The phylogenetic trees constructed exhibited close genetic relationships with reference sequences previously reported from countries in Austria, China, Belgium, India, and Nigeria, with Bootstrap values ranging between 36-40%, 76-77%, and 62-78% respectively. The bootstrap values obtained for *Terminalia catappa* and *Dacryodes edulis* suggest a moderate level of clustering and a reliable relationship between these species of interest and reported species, suggesting common ancestor. However, for *Adenanthera pavonina*, the value seems unreliable, expressing divergence. The reliable genetic relationships confirm accurate species identification and also provide insight into the evolutionary linkages between species. These findings expand the genomic database of the selected tropical fruits in this study, confirming their species taxonomy and offering valuable genomic information for agricultural studies. This information can be explored as foundation for future research on genetic conservation, plant diversity and breeding of these tropical fruit species.

**Keywords**: deoxyribonucleic acid, molecular data, tropical fruits, taxonomy, evolutionary history.

FASBMB2025/MBB-009

# RT-qPCR-based Gene Expression Profiling of Key Sex-Differentiation Genes Identifies Srd5a2 Downregulation in Familial 46xy Dsd

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Disorders of Sex Development (DSD) arise from abnormalities in chromosomal, gonadal, or hormonal regulation that affect normal sexual differentiation. Understanding the molecular expression patterns of genes involved in sex determination is essential for accurate diagnosis. This case-control study investigated the expression of *SRY*, *WNT4*, *AR*, *SRD5A2*, and *CYP21A2* in 46XY DSD patients, with emphasis on three siblings suspected to have impaired *SRD5A2* function. Twenty-five DSD patients and twenty healthy controls (ten males and ten females) aged 16–45 years were enrolled. Approximately 1 ml of peripheral blood was collected into RNase-free cryovials containing RNAhold at the TETFund Centre of Excellence in Urology and Nephrology, UDUTH Sokoto, and preserved at −80 °C. Total RNA was isolated using the Qiagen nucleic acid extraction kit, quantified with NanoDrop, and reverse-transcribed using EasyScript One-Step SuperMix. Gene expression levels were quantified by real-time PCR on a Rotor-Gene Q 5plex HRM instrument (Qiagen), normalized to RPL32, and analyzed using the 2^−ΔΔCt method. Statistical significance was determined using the Student's t-test at $p < 0.05$. The three siblings exhibited *SRY* and *AR* expression comparable to male controls, markedly reduced *WNT4* expression compared to the female control, and consistently downregulated *SRD5A2* transcripts, whereas *CYP21A2* remained unchanged. These findings suggest that the DSD phenotype in the siblings is associated with impaired androgen metabolism due to reduced *SRD5A2* transcription rather than defects in *SRY* or *AR* pathways, indicating a likely hereditary regulatory alteration affecting *SRD5A2* expression.

**Keywords:** 46XY DSD, SRD5A2, gene expression, qPCR, androgen metabolism

FASBMB2025/MBB-010

# Correlation of Plasma *Plasmodium Falciparum* Histidine-Rich Protein-2 Levels with Disease Severity and Outcome of Malaria Patients in Sokoto Metropolis, Nigeria

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Accurate diagnosis of malaria is key to proper management, control and an ideal diagnostic parameter that correlates with disease outcome is required. Hence, the study aimed to determine if plasma *Plasmodium falciparum* histidine-rich protein-2 (*Pf*HRP$_2$) levels correlate with malaria severity and whether it could be used to predict outcome in children. The study enrolled 250 volunteers, comprising 150 malaria infected, 100 healthy controls, grouped into severe malaria, uncomplicated and non-malaria(control). Clinical assessments, Biochemical and haematological parameters were determined using standard methods. There was no significant difference in the demographic characteristics of the study volunteers. The malaria status of volunteers with severe and uncomplicated malaria was confirmed by both *Pf*HRP$_2$ and microscopy. Levels of Lactate, Creatinine, Bilirubin, *Plasmodium falciparum* parasite count, and *Pf*HRP$_2$ were significantly ($p< 0.05$) higher while levels of Bicarbonate, Glucose, PCV and Haemoglobin were significantly ($p< 0.05$) lower in the severe malaria group compared to the uncomplicated and the control group. A positive correlation was observed between *Pf*HRP$_2$ concentration and parasite count and several outcomes of malaria disease severity. Severe malaria group show a high Area under the Curve (AUC) of 0.99 with high predictive power compared to the uncomplicated malaria group (~0.61) with predictive power and control group (~0.008) with no predictive power. Patients with very high *Pf*HRP$_2$ levels are most likely to manifest one or more clinical signs of severe malaria which would facilitate the identification of patients at greatest risk of progressing to complicated or severe malaria, and their isolation for prompt, effective treatment to avoid death or complications.

**Keywords**: *Plasmodium falciparum, Plasmodium falciparum* histidine-rich protein 2 (*Pf*HRP$_2$), Severe malaria, Uncomplicated malaria, infection.

FASBMB2025/MBB-011

# Association of Adiponectin Gene Polymorphism with Adipokine and Lipid Profile in Breast Cancer Patients from Kano, Nigeria

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Breast cancer constitutes 25% of all cancer cases diagnosed in Kano State, Nigeria. This study investigated the relationship between adiponectin gene polymorphisms (AGP) and adipokine and lipid profile in breast cancer patients in Kano. Methods The study population was composed of 80 randomly consented breast cancer patients from the three major hospitals in Kano State, Nigeria, and 40 age-matched controls across the metropolis. Biochemical assays were analyzed using standard procedures and ELISA. Furthermore, AGP was investigated using PCR—PCR-restriction fragment length polymorphism. The incidence of breast cancer was highest in patients aged 41–50 years (25%), with a high frequency of overweight and obesity. Serum adiponectin and HDL levels were lower ($p<0.05$) in the patients, whereas those of leptin, TC, TG, and LDL were higher ($p<0.05$) relative to control subjects. A positive significant correlation was observed between leptin and adiponectin ($r=0.522$, $p<0.0001$), TG vs TC (0.446, $p=0.001$), LDL vs TG (0.419, $p=0.002$), and TC vs LDL ($r=0.965$, $p<0.0001$) in the patients. No significant association in genotype frequencies for 276G/T ($\chi2=2.70$, $p=0.26$) and 45 T/G ($\chi2=1.126$, $p=0.569$) polymorphisms between patients and controls. Furthermore, BMI was significantly associated with the 276G/T genotype. This study suggests that the adiponectin 45 T/G and 276 G/T gene polymorphisms may not significantly influence the risk of breast cancer among patients attending these hospitals in Kano State. However, the 276 T/G genotype shows a potential association with obesity in this population. Notably, variations in adiponectin and leptin levels appear to be linked to breast cancer risk, highlighting their potential as novel biomarkers for predicting breast cancer prognosis and progression.

**Keywords**: Breast cancer, Adiponectin gene polymorphisms, Adipokine, Lipid profile, Obesity.

FASBMB2025/MBB-012

# Characterization of Bacterial Lipase from Palm Oil Mill Effluent and Its Application in Detergency

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Bacteria with the ability to produce lipase occur in different environments, which include agro-industrial palm oil mill, olive oil mill, vegetable oil factory, industrial wastes and many others. Though Palm oil agro-industries play a crucial role in the economic growth of palm oil-producing nations such as Nigeria, it produces a substantial amount of solid and liquid wastes in the process of crude palm oil production (CPO). In this study, palm oil mill effluent (POME) was used as the source of extracellular lipase secreted by bacteria due to the presence of the primary liquid wastes of the industry, which is palm oil mill effluent (POME). Highly lipolytic POME bacteria were chosen and 16S rRNA was used to identify the bacteria as Stenotrophomonas maltophilia strain ANO (NCBI accession: PQ219406). The number of IU/mg purified extracellular lipase was 1428.88 with 11-fold purification. Biochemical characterism revealed pH and temperature optimum of 8.0 and $50^0$C. The lipase was however compatible to commercial detergents particularly at alkaline PH range and consequently enhancing oily/fatty de-staining capability on white cloth with enhancement of oily stain removal detergency. This paper indicates that in Nigeria the local detergents manufacturers might be required to adopt this eco-friendly solution of adding lipase into detergent formulations in order to enhance oily fatty stain bondage-determinacy.

**Keywords**: Bacteria, lipase, lipolytic, alkaline, extracellular, strain.

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# Mitochondrial Bioenergetics as a Predictor of Preeclampsia Susceptibility Among Women in Ogun State

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Preeclampsia (PE) is pregnancy-induced hypertensive disorder and a leading cause of maternal and fetal morbidity and mortality globally. Although, many strategies have been developed to manage. PE, mitochondrial biogenetics may be advocated in predict susceptibility to PE in pregnant women. Venous and umbilical cord blood, urine and placenta samples were obtained from pregnant women at State Hospital Ota, Ogun State on the day of delivery. The samples were collected from preeclampsia (n=11) women and normotensive women (n=31). Level of glycolytic (aldolase) enzyme were determined spectrophotometrically in plasma venous and cord and as well as in heavy and light mitochondria. Tricarboxylic acid cycle (malate dehydrogenase) and electron transport chain enzyme (complex 1-NADH-Dehydrogenase and complex 11- succinate dehydrogenase) were determined spectrophotometrically in heavy and light mitochondria. Date where analyzed using Mann-Whitney u test with $p<0.05$. Systolic, diastolic and mean arterial blood pressures in PE (168.00±8.00, 103.00±3.00 and 124.67±4.67mmHg) were significantly ($p<0.05$) higher than normotensive women (118.73±2.50, 71.00±2.18 and 86.73±2.11mmHg) respectively. Level of aldolase mitochondria (heavy and light) had no significant different, but decreased significantly in aldolase plasma venous and cord in PE with 58% and 48% than NW respectively. Malate and NADH dehydrogenase activities in heavy and light mitochondria had no significant different among the two groups. Succinate dehydrogenase activities in heavy mitochondria were 4 times lesser than that of NW, whereas in light mitochondria no significant different observed. The finding of this study revealed that reduction in Aldolase (plasma venous and cord blood) and succinate dehydrogenase (heavy mitochondria) activities in pregnancy could predisposing factor to preeclampsia.

**Keywords:** Pre-eclampsia, malate dehydrogenase, complex 1-NADH-Dehydrogenase and complex 11- succinate dehydrogenase.

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# Cytogenetic Findings in Ovotesticular Disorder of Sex Development: Evidence of 47, XXY Mosaicism in a Nigerian Cohort

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Disorders of Sex Development (DSD) includes a heterogeneous group of conditions characterized by atypical chromosomal, gonadal, or anatomical differentiation. Ovotesticular DSD, marked by the coexistence of both ovarian and testicular tissues, represents one of the rarest and most complex subtypes. This study aimed to determine the cytogenetic profiles of ovotesticular DSD patients attending Usmanu Danfodiyo University Teaching Hospital (UDUTH), Sokoto. Out of the twenty-four (24) patients with suspected DSD, six (6) were confirmed to have ovotesticular DSD based on clinical and gonadal evaluation. All six patients presented with ambiguous genitalia and histological confirmation of both ovarian and testicular tissues. Cytogenetic analysis through karyotyping revealed chromosomal mosaicism in all six cases, with a consistent 47,XXY pattern. This finding suggests a strong link between ovotesticular DSD and sex chromosome aneuploidy, highlighting the relevance of cytogenetic analysis in the diagnostic process. The predominance of 47,XXY mosaicism further underscores the necessity for early chromosomal characterization to inform gender assignment, guide management, and prevent late presentations commonly observed in Nigerian patients. Integrating cytogenetic evaluation into routine DSD diagnosis could significantly improve outcomes and contribute to more personalized and evidence-based clinical care.

**Keywords:** Ovotesticular DSD, 47,XXY, Chromosomal Mosaicism, Cytogenetic Analysis, Nigeria

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# Development and Optimization of a Loop-Mediated Isothermal Amplification (LAMP) Assay for Rapid Detection of *Mycobacterium leprae*

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*Leprosy*, caused by *Mycobacterium leprae*, remains a major public health concern in endemic regions due to its slow progression, nonspecific early symptoms, and lack of rapid, sensitive diagnostic tools. This study developed and optimized a loop-mediated isothermal amplification (LAMP) assay for the specific detection of *M. leprae* DNA. Primers were designed using Primer Explorer, and assay efficiency was improved by inserting seven thymine bases (TTTTTTT) between the forward and backward inner primers. The modification enhanced amplification rate by 1.5-fold increase and reduced reaction time by approximately 40% (30 min to 20 min). The optimized LAMP reaction performed best at 60 °C, consistent with the optimal temperature (60 °C) range for Bst DNA polymerase. The assay demonstrated a detection limit of $3 \times 10^3$ ηg/μL and showed specificity, with no cross-reactivity to *Mycobacterium tuberculosis*. Furthermore, the lyophilized LAMP mix retained optimal activity of detection time at twenty-five (25) min, optimal temperature at 60 °C after rehydration and room-temperature storage for three (3) months, indicating potential for field deployment. These findings confirm the assay's sensitivity, specificity, and stability, supporting its application as a rapid diagnostic tool for early leprosy detection in resource-limited settings.

**Keywords:** *Mycobacterium leprae*, LAMP assay, molecular diagnostics, primer optimization, leprosy.

FASBMB2025/MBB-016

# Whole Genome Sequencing of Rabies Virus from Slaughtered Dogs in Jama'a and Lere Local Government Areas of Kaduna State, Nigeria

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Rabies is a fatal zoonotic disease caused by the rabies virus and is majorly spread via bites from infected domestic dogs. It remains one of the lethal neglected tropical diseases, with almost 100% fatality once symptoms appear. Every year, about 59,000 people die from rabies worldwide, but the true number maybe higher due to under-reporting, mostly in developing countries. People involved in the slaughtering or processing of dog meat may also be at risk of infection, if exposed to infected tissues. Limited data on complete rabies virus genomes in scientific databases, makes it difficult to understand the virus's evolution and transmission patterns. This study conducted whole-genome sequencing of the rabies virus in dogs slaughtered for meat in Jama'a and Lere Local Government Areas of Kaduna State, Nigeria, between March and July 2023. Brain tissue from 234 slaughtered dogs were screened for rabies antigen using the direct fluorescent antibody test, and 21 samples (8.9%) tested positive. Positive samples were further analyzed using multiplex PCR to amplify overlapping 400 bp fragments covering viral genome, followed by sequencing on the MinION platform. Phylogenetic analysis was performed using the Maximum Likelihood method. The genome characterization confirmed the presence of all five structural proteins: N, P, M, G, and L. Phylogenetic analysis revealed that the isolates belonged to the Africa 2 lineage, indicating active circulation of the variant in the area. The findings show that apparently healthy dogs can harbor the rabies virus, posing a significant occupational and public health risk to dog meat processors.

**Keywords**: Rabies, rabies virus, Whole genome sequencing, MinION, Slaughtered Dogs

FASBMB2025/MBB-017

# Stigmasterol Isolated from *Piptadeniastrum africanum* (HOOK.f.) Attenuates Liver and Colon damage via Modulation of Mitochondrial-Mediated Apoptosis

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Hepatocellular and colonic damage are pathological outcomes from liver and colon toxicity. Modulating mitochondrial-mediated cell death represents a strategic approach in disease management. Although, the use of synthetic drugs for managing disorders is often associated with adverse side effects. In traditional medicine, *Piptadeniastrum africanum* (PA) is reputed for treating disorders, yet its mechanism of action remains largely unexplored. This study investigated the potential of bioactive compound(s) from PA mitigating liver and colon damage through modulation of mitochondrial-mediated cell death. The stem bark of PA was authenticated (UIH- 22562), extracted, fractionated, ethyl acetate fraction (EFPA) was then subjected to column chromatography, yielding a pure compound, *Stigmasterol* through spectroscopic characterization techniques. Forty-two mice (n=7) were exposed to toxicants Dextran Sulphate Sodium (DSS) and Benzo[a]Pyren (BaP) for 10 days to induce colon damage and then treated with *Stigmasterol* at two different doses. Groups-1(vehicle), group-2(oral 4% DSS), group-3(125mg/kg BaP), group- 4(DSS+BaP), group-5(DSS+BaP and 200mg/kg *Stigmasterol*) and group-6(DSS+BaP and 400mg/kg *Stigmasterol*). Immunohistochemical analysis was performed on colon samples to assess expression of inflammatory cytokines, Tumour Necrosis Factor (TNF-α), interleukin (IL-6), apoptotic markers (p53, Caspase-9, Bax), and anti-apoptotic protein Bcl-2. All data were analyzed using descriptive statistics and ANOVA at $\alpha_{0.05}$. The exposure to toxicants, DSS and BaP elevated levels of pro-inflammatory cytokines and pro-apoptotic proteins, alongside a decrease in anti-apoptotic markers. Treatment with *Stigmasterol* effectively reversed these effects, suggesting its role in suppressing inflammation and apoptosis via mitochondrial pathways. Conclusively, *Stigmasterol* demonstrates protective effects against colon toxicity by modulating mitochondrial- mediated cell death, highlighting its potential as a natural therapeutic agent.

**Keywords:** Benzo[a]Pyrene, Colon damage, Cytokines, *P. africanum*, Stigmasterol

FASBMB2025/MBB-18

# Stability Enhancement of Novel Catalytically Active Inclusion Bodies from Recombinant AMS8 Lipase via Immobilization onto Adsorption Material

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The application and use of enzymes solely depend on their stability upon being subjected to the harsh conditions of temperature, pH, and organic solvents, which are ubiquitous in most industrial settings. This is normally achieved by immobilizing the enzyme onto a suitable support material. This research aimed at immobilizing the inclusion bodies of recombinant LipAMS8 lipase (LipAMS8 CatIBs) onto seplite (LX 120) nonionic hydrophobic, cross-linked polymeric adsorption material to improve its stability. So far as we know, this is the first naturally occurring lipase of CatIBs to immobilize and characterize. The emergence of catalytically active inclusion bodies (CatIBs) has completely changed people's perception of heterologous aggregation of protein. LipAMS8 lipase was originally isolated from cold-active bacteria and when overexpressed in *E. coli.* BL21(De3)/pET32b formed an active enzyme (non-classical). It was isolated and separated using simple solubilization with moderate centrifugation. Scanning Electron Microscopy (SEM)analysis of the isolated inclusion bodies revealed them as proteinaceous particles with a rod-like cylindrical shape. LipAMS8 CatIBs were immobilized onto 1 g of seplite LX 120 at an agitation of 200 rpm for 2 hours. SEM and F-TIR were used to ascertain immobilization. Characterization of the immobilized LipAMS8 CatIBs revealed its optimum temperature at $20^0$C, pH 9.0, and retained up to 55% residual activity when treated with various buffers. Treatment with organic solvents and metal ions indicated its higher stability. LipAMS8 CatIBS immobilization may improve its stability and hence pave away to the source of potent lipase which is highly demanded in many processes.

**Keywords**: Immobilization, catalytically active inclusion bodies (CatIBs), Recombinant, Seplite.

FASBMB2025/MBB-19

# Integrative Toxicological and Proteomic Evaluation of Venoms from Nigerian Viperidae and Elapidae Snakes

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Envenoming by snakebite is a serious health problem that maims and kills a large number of people, primarily in rural areas of developing African countries. A combination of mass spectrometric analyses and the WHO guideline for venom toxicity studies were adopted for this study. Viper venoms contained cytotoxic-inducing proteins such as SVMPs, SVSPs, and cytotoxins, whereas elapid snake venoms contained neurotoxic proteins such as $PLA_2$, 3-FTx, and neurotoxins. The PDQuest annotated protein spots on the 2-DE gels showed that the proteins in these snakes' venoms were differentially expressed between snake families and species. Compared to the crude venom, the SVMP fraction induced hemorrhagic effects with a diameter of $26.00 \pm 1.00$ mm in *E. ocellatus* and $21.33 \pm 1.52$ mm in *B. arietans*. Both SVSP and SVMP had anticoagulant effects; however, the SVSP fraction had a stronger effect, with a longer anticoagulation time of $30.00 \pm 3.00$ min in *E. ocellatus* and $26.00 \pm 2.00$ min in *B. arietans*. Our findings show that there is significant variation in the toxin profiles of these snakes, both at the species and family levels. This has an impact on the clinical manifestations of envenomation. Given the importance of SVMPs in altering the integrity of the membrane structure and impairing the blood coagulation system, an antivenom that can specifically neutralize its activity could inhibit the hemorrhage effects of the venoms.

**Keywords**: Neglected tropical disease, snakebite envenoming, snake venom, toxicological assay, proteomics.

## SUB-THEME 2

## DRUG AND VACCINE DEVELOPMENT (DVD)

FASBMB2025/DVD-004

# Expression of *Plasmodium falciparum* autophagy-related protein 12 and the identification of a novel binder from MayBridge rule of 3 diversity fragment library using WaterLOGSY NMR method

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Malaria remains a global health threat largely because of parasite resistance to currently available drugs. This underscores the dire need for identifying novel targets for antimalarial drugs and fortunately, *Plasmodium falciparum* Atg12 (*Pf*Atg12) has been identified to play a vital role in the survival of malaria parasites. Therefore, the present research aims to discover a novel *Pf*Atg12 inhibitor from MayBridge Ro3 diversity fragment library. The *Pf*Atg12 gene was amplified, and agarose gel electrophoresis analysis revealed the *Pf*Atg12 gene had the expected molecular size of 358 bp. The gene was then cloned into pET-15b expression vector and the recombinant plasmid was then transformed into *E. coli* BL21 (DE3) cells for expression of the recombinant *Pf*Atg12 protein, which was affinity-purified using nickel resin. SDS-PAGE analysis of the expressed and purified r*Pf*Atg12 revealed the anticipated molecular weight of 14 kDa. Subsequently, 885 compound fragments from MayBridge Ro3 diversity fragment library were subjected to WaterLOGSY NMR-based method to identify hit fragment(s) that bind to the r*Pf*Atg12. We observed that one compound was the only fragment that truly binds to r*Pf*Atg12 which led to the conclusion that it is the primary hit fragment and binder to the purified r*Pf*Atg12 that can be considered for further fragment-based drug discovery targeted towards developing novel antimalarial drug.

**Keywords**: Malaria, *Plasmodium*, autophagy, antimalarial drug, *Pf*Atg12

FASBMB2025/DVD-005

# Effect of Quercetin Silver Nanoparticle and Vitamin A on Pro and Anti-Inflammatory Markers in Dengue-Stimulated Peripheral Blood Mononuclear Cells

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Dengue virus (DENV) infection is associated with severe immune dysregulation, characterized by cytokine storms and activation of the NLRP3 inflammasome. This study explored the immunomodulatory potential of quercetin-mediated silver nanoparticles (QAgNPs), alone and in combination with Vitamin A in peripheral blood mononuclear cells (PBMCs) stimulated with dengue virus antigens. QAgNPs were synthesized using standard protocol. The nanoparticles were characterized via Dynamic Light Scattering (DLS), Scanning Electron Microscopy (SEM), and Energy Dispersive X-ray Spectroscopy (EDX). PBMCs from healthy mice were stimulated with DENV antigen and treated with QAgNPs, Vitamin A, or a combination of both (NPsA) at concentrations ranging from 12.5 to 100 µg/mL. Gene expression levels of pro-inflammatory (IFN-γ, IL-21, IL-15, NLRP3) and anti-inflammatory (IL-10) cytokines were quantified using RT-qPCR. QAgNPs displayed a hydrodynamic diameter of approximately 45 nm and contained 46.8% elemental silver. Upon DENV stimulation, IFN-γ expression reached 1.87±0.32-fold higher than the negative control. IL-21 peaked at 2.839±0.243-fold higher, and IL-15 expression was elevated to 1.524±0.256-fold higher, NLRP3 at 2.890±0.838-fold higher and IL-10 reached a consistently high level of 2.84±0.347-folds. With the best treatments at 12.5µg/mL, NPsA reduced IFN-γ to 0.220±0.005-folds, IL-21 to 0.764±0.185-folds, IL-15 to 0.003±0.004-fold, and NLRP3 to 0.013±0.001-folds. Concurrently, IL-10 was significantly upregulated to 13.584 ± 0.832-fold higher than the positive control. This suggests that QAgNPs alone and in combination with Vitamin A has potential as novel adjunct therapeutic strategy in managing dengue-induced immune dysregulation.

**Keywords**: Dengue, Cytokines, Vitamin A, Quercetin, Nanomedicine

FASBMB2025/DVD-006

# Immuno-Haematological Profiles and Cytokine Expression Modulation as Therapeutic Targets for Enhancing Treatment Outcomes and Supporting Elimination Efforts in Chronic Lymphatic Filariasis

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Lymphatic filariasis (LF) remains a significant neglected tropical disease despite decades of global control efforts. Although transmission has been substantially reduced in many endemic regions, little is known about the persistent immuno-haematological and cytokine imbalances among individuals with chronic manifestations. This research explored immune cell dynamics and blood profile variations in LF-affected patients from Osun State, Nigeria, to identify potential biomarkers relevant for improved therapy and sustained elimination monitoring. A total of 7,388 participants from 12 Local Government Areas (LGAs) were examined for circulating filarial antigens using Abbott Filarial Test Strips. Blood specimens from five individuals with chronic LF complications were analyzed with a fully automated haematology system. In addition, expression levels of cytokine genes, IL-10, IL-1β, IL-12, TNF-α, IFN-γ, TGF-β, and IL-6, were quantified from matched blood and lymphatic fluid samples through quantitative real-time PCR to evaluate immune modulation patterns. In the results obtained, no circulating antigen was detected in any LGA, suggesting probable interruption of LF transmission. Haematological evaluation showed anaemia, lowered haemoglobin concentration, and altered red cell indices, coupled with diverse leukocyte responses. Cytokines analyses revealed increased IL-10 expression and suppression of key pro-inflammatory mediators, indicating a dominant regulatory immune state that could delay parasite clearance. These findings suggest that Osun State has entered a post-transmission phase of LF elimination. However, ongoing cytokine dysregulation and blood profile anomalies emphasize the need for continued immune surveillance and host-directed therapeutic approaches to optimize antifilarial treatment and maintain elimination success.

**Keywords:** Lymphatic filariasis, Immuno-haematological profiles, Cytokine modulation, Gene expression, Therapeutic targets

FASBMB2025/DVD-007

# Assessment of Pro-Inflammatory Cytokines, G6PDH and LDH Levels in Subjects Treating Diabetes with Metformin and Glibenclamide Drugs

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Diabetes mellitus is a metabolic disorder which presents as elevated blood glucose concentration. Hypoglycemic drugs such as metformin and glibenclamide have been used in lowering blood glucose concentrations. Prolonged use of some drugs can result in drug resistance. Little data exist on drug resistance with metformin and glibenclamide drugs as it relates with the biochemical changes seen with the prolonged usage of these drugs. The aim of the study was to determine the expression of pro-inflammatory cytokines (IL-1 and IL-6) using Standard ELISA readers and the determination of G6PDH and LDH levels in the blood of subjects. The results of this study show that the expression of pro-inflammatory cytokines was significantly different ($P<0.05$) with higher expression of IL-1 in male subjects on metformin (10.94 pg/mL) and glibenclamide (7.60 pg/mL). Lower levels of G6PDH (0.860 µgHb and 1.111 µgHb) and high levels of LDH (277.9 µL and 275.8 µL) were seen in both male and female subjects on metformin and glibenclamide. Findings from this study shows that prolonged use of metformin and glibenclamide drugs results in notable changes in the interleukins and glucose markers of diabetic subjects, which suggests the effects of drug resistance experienced by diabetic patients on metformin and glibenclamide drugs.

**Keywords:** Diabetes, Metformin, Glibenclamide, pro-inflammatory cytokines, G6PDH, LDH.

FASBMB2025/DVD-008

# Green Synthesis and Characterization of Silver Nanoparticles Using *Pisum sativum* Seed Extract and Evaluation of Their Antimicrobial Properties

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Nanoparticles have gained significant attention in modern medicine due to their diverse applications in antimicrobial therapy and drug delivery. This study aimed to synthesize and characterize silver nanoparticles (AgNPs) using *Pisum sativum* (pea) seed extract through an eco-friendly green synthesis approach. The synthesis was achieved by mixing the seed extract with $AgNO_3$ solution, and the formation of AgNPs was confirmed by a color change attributed to surface plasmon resonance. The nanoparticles were characterized using Fourier Transform Infrared Spectroscopy (FTIR) to identify functional groups responsible for reduction and stabilization, while Scanning Electron Microscopy (SEM) revealed distinct morphology of the nanoparticles. The biosynthesized AgNPs demonstrated strong antimicrobial activity against *Staphylococcus aureus*, *Escherichia coli*, *Candida albicans*, and *Aspergillus fumigatus*. The presence of bioactive compounds in *Pisum sativum*, such as lutein, zeaxanthin, vitamins C and E, and zinc, likely enhanced the reducing and capping efficiency during synthesis, contributing to the nanoparticle's biological activity. These findings suggest that *Pisum sativum*-derived AgNPs can potentially serve as effective, natural antimicrobial agents with various applications in biomedicine and pharmaceuticals. Future work should focus on mechanistic studies and cytotoxicity evaluation to support their safe therapeutic use.

**Keywords:** *Pisum sativum*, green-synthesized silver nanoparticles, antimicrobial activity, FTIR, SEM

FASBMB2025/DVD-009

# Phytocompound-Based Enhancement of Oral Glucose Tolerance in Experimental Diabetes: Evidence from Succinic Acid & Hexamethylcyclotrisiloxane

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This study assessed the *in vivo* antihyperglycemic effects of plant-derived Succinic acid and Hexamethylcyclotrisiloxane in alloxan-induced diabetic Wistar rats. The experiment was carried out at the standard animal research facility of the Faculty of Pharmaceutical Sciences, Enugu State University of Science and Technology (ESUTH), Agbani, Enugu State, under the Department of Pharmacology. The rats were randomly grouped into seven categories, and oral glucose tolerance was measured to evaluate the hypoglycemic impact of the phytochemical treatments. After four weeks of administration, findings revealed that rats treated with 100 mg/kg body weight (b.w) of Succinic acid alone and 200 mg/kg b.w of 1:1 Succinic acid and Hexamethylcyclotrisiloxane showed greater glycemic recovery compared to those administered 100 mg/kg b.w of Hexamethylcyclotrisiloxane alone or 1:1 100 mg/kg b.w of the combined extract. Results also indicated a statistically significant improvement ($P < 0.05$) in oral glucose tolerance and regulation. These outcomes highlight that both Succinic acid and Hexamethylcyclotrisiloxane, whether administered independently or in combination, may promote dose-dependent oral blood glucose tolerance and support body weight stabilization in diabetic conditions.

**Keywords:** Antihyperglycaemic effect, Succinic acid, Hexamethylcyclotrisiloxane, Diabetes, Oral Blood Glucose Tolerance.

## SUB-THEME 3

## BIOINFORMATICS AND DATA DRIVEN RESEARCH (BDR)

FASBMB2025/BDR-001

# A Comprehensive *In Silico* Approach to Investigate the Anti-Diabetes Potential of Natural Compounds against Diabetes Protein Targets

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Diabetes mellitus is a complex metabolic disorder requiring multi-target therapeutic strategies. This study computationally evaluated phytochemicals from medicinal plants like *Zingiber officinale* and *Azadirachta indica* as potential multi-target antidiabetic agents. We screened these natural compounds against five key protein targets: Glucose Transporter 1 (GLUT1), Peroxisome Proliferator-Activated Receptor Alpha (PPAR-α), Heat Shock Protein (HSP), Sirtuin 6 (SIRT6), and Progesterone Receptor (PR). Molecular docking was used to determine binding affinities, while drug-likeness and oral bioavailability were assessed using Lipinski's, Veber's, and Ghose's rules. The majority of compounds demonstrated favorable physicochemical and ADMET profiles. Key findings revealed strong interactions across multiple targets. For instance, quercetin and calcitriol showed high affinity for GLUT1, suggesting a role in glucose transport modulation. Terpenoids like hinesol and viridiflorol displayed profiles suitable for activating PPAR-α to regulate lipid metabolism. For HSP, compounds such as carotol and arachidonic acid showed potential for mitigating oxidative stress. Gingerol and fatty acids exhibited optimal properties for binding to SIRT6, impacting glucose homeostasis. Overall, flavonoids (quercetin), terpenoids (gingerol, carotol), and fatty acids (arachidonic acid) emerged as the most promising candidates, combining strong binding, excellent drug-likeness, and multi-target potential. These findings strongly support their progression to molecular dynamics simulations and in vitro validation as lead scaffolds for developing novel, multi-target antidiabetic drugs.

**Keywords**: Diabetes Mellitus, Phytochemicals, Molecular Docking, Multi-target, Drug-likeness.

FASBMB2025/BDR-002

# A Comprehensive *In Silico* Approach to Investigate the Anti Typhoid Potential of Natural Compounds against Typhoid Protein Targets

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Typhoid fever, caused primarily by *Salmonella enterica* serovar Typhi, remains a global health burden, particularly in developing countries where inadequate sanitation and rising antimicrobial resistance (AMR) exacerbate morbidity and mortality rates. Natural compounds are a promising reservoir of bioactive molecules with potential to overcome resistance mechanisms. In this study, an in-silico approach was employed to evaluate phytochemicals and natural derivatives against key typhoid-associated bacterial proteins, including Acetate kinase (AckA, PDB: 2OUR), DNA Gyrase subunit B (GyrB, PDB: 1VSC), and β-Lactamases (PDB: 2YK9), which are critical for bacterial energy metabolism, DNA replication, and antibiotic degradation, respectively. Molecular docking revealed that *Carpaine* (-9.5 kcal/mol), *β-Amyrin* (-8.6 kcal/mol), and *Stigmasterol* (-8.4 kcal/mol) exhibited strong inhibitory potential against AckA. For GyrB, *Vicenin* (-9.0 kcal/mol) and *Rutin* (-8.6 kcal/mol) demonstrated stable binding interactions, while *Rutin* (-11.0 kcal/mol), *Basic Blue 47* (-10.3 kcal/mol), and *1-Amino-2,4-dihydroxyanthraquinone* (-10.0 kcal/mol) showed pronounced affinity against β-Lactamases, suggesting a capacity to block resistance pathways. Drug-likeness assessments indicated that compounds such as *Resveratrol*, *Apigenin*, and *Quercetin* complied with Lipinski's, Veber's, and Ghose's rules, reflecting good oral bioavailability. ADMET analysis further confirmed that candidates including *γ-Sitosterol* and *Cinnamic Acid* displayed favorable absorption, blood–brain barrier penetration, and minimal cytochrome P450 inhibition, with low predicted toxicity. These findings provide a strong basis for further in vitro and in vivo validation and highlight natural compounds as viable alternatives in the fight against anti-bacterial resistance.

**Keywords**: Typhoid, in-silico, proteins, Drug-likeness, ADMET

FASBMB2025/BDR-003

# A Comprehensive *In-Silico* Approach to Investigate the Anti-Cancer Potential of Natural Compounds against Lung Cancer Protein Targets

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Lung cancer is a cancer that originates from epithelial cells. The most common (about 85% of all diagnoses) are non-small cell lung cancers (NSCLCs) by multidrug resistance strains. This study computationally evaluated phytochemicals from medicinal plants like turmeric, green tea, onions, soybeans and parsley as potential multi-target anti-cancer agents. We screened these natural compounds against five key protein targets; Epidermal Growth Factor Receptor, Anaplastic Lymphoma Kinases, ERBB Family Receptor, Receptor Tyrosine Kinases, Kristren Rat Sarcoma Protein. Molecular docking was used to determine binding affinities, while drug likeness and oral bioavailability were assessed using Lipinski's Veber's and Ghose's rules. The majority of compounds demonstrated favourable physiochemical and ADMET profiles. Key findings revealed strong interactions across multiple targets. For instance, withaferin A and tetrandrine showed high affinity for EGFR. Rutin and Ursolic Acid displayed profiles suitable for activating ALK. For ERBB, compounds such as Ellagitannin and Rutin showed potentials. Tetrandrine and Beta-boswellic exhibited optimal properties for binding ROS1. Overall, withaferin A, Rutin, Ellagitannin and Beta boswellic emerged as most promising candidates, combining strong binding, excellent drug-likeness, and multi-target potential. These findings strongly support their progression to molecular dynamics simulations and in-vitro validation as lead scaffolds for developing novel, multi-target anti-cancer drugs.

**Keywords**: Lung Cancer, Phytochemicals, Molecular Docking, Multi-target, Drug-likeness

FASBMB2025/BDR-005

# Host Blood Transcriptional Signature Enables Accurate Diagnosis of *Plasmodium falciparum* Malaria in Children

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Malaria remains a major global health challenge with 247 million cases annually. Current diagnostic methods, including microscopy and rapid diagnostic tests, have significant limitations in sensitivity (60-95%) and specificity, particularly at low parasite densities. Host transcriptional responses to infection may provide more sensitive and specific diagnostic biomarkers than direct parasite detection methods. We analyzed whole blood gene expression profiles from 155 children (93 symptomatic *Plasmodium falciparum* malaria cases, 62 healthy controls) using microarray data (GEO accession GSE34404). Differential expression analysis was performed using the limma package with stringent criteria (FDR <0.05, $|\log_2 FC| > 1$). We developed a 16-gene diagnostic signature comprising the 11 most strongly up-regulated and 5 most strongly down-regulated genes. Signature scores were calculated as the difference between geometric mean expression of up- regulated and down-regulated genes. Diagnostic performance was evaluated using receiver operating characteristic curve analysis. We identified 195 significantly differentially expressed genes (162 up-regulated, 33 down-regulated), reflecting robust immune activation responses. The 16-gene signature achieved exceptional diagnostic performance with area under the curve 0.9953 (95% CI: 0.9893-1.0000), sensitivity 97.85%, and specificity 98.39%, correctly classifying 152 of 155 samples (98.06% accuracy). The signature showed profound separation between groups (Cohen's d=3.37, $p<2.22\times10^{-16}$), indicating minimal distributional overlap. Individual signature genes demonstrated strong discrimination, suggesting biological robustness. These findings establish proof-of-concept that host transcriptional profiling can provide highly accurate malaria diagnostics. External validation in diverse cohorts and translation to clinically feasible platforms such as quantitative RT-PCR could enable improved case detection, enhanced surveillance, and better antimalarial stewardship in endemic regions.

**Keywords:** Malaria, Plasmodium falciparum, transcriptional biomarkers, diagnostic accuracy, host response

FASBMB2025/BDR-006

# A Comprehensive *In Silico* Approach to Investigate the Anti-Ulcer Potential of Natural Compounds against Ulcer Protein Targets

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Peptic ulcer disease (PUD) continues to be a significant global health concern, especially in developing regions where *Helicobacter pylori* infection, poor dietary habits, and excessive use of non-steroidal anti-inflammatory drugs (NSAIDs) remain prevalent. To identify safer and more effective treatment alternatives, this study employed an in-silico molecular docking approach to evaluate bioactive compounds from natural and synthetic sources against key ulcer-related protein targets Cyclooxygenase (COX) (PDB: 401Z), Muscarinic M1 receptor (PDB: 3EOU), E-Cadherin extracellular domain (PDB: 4ZT1), $H^+/K^+$ ATPase (gastric proton pump) (PDB: 2XZB), and Histamine H2 receptor (PDB: 2BU1). The docking results revealed strong binding affinities, with Beta-Amyrin (-12.1 kcal/mol) exhibiting the highest interaction against COX, followed by Simiarenol (-9.9 kcal/mol) for the E-Cadherin receptor, Lapatinib (-8.9 kcal/mol) for the $H^+/K^+$ ATPase, Ptupb (-11.4 kcal/mol) for the Histamine H2 receptor, and Celecoxib (-8.0 kcal/mol) for the Muscarinic receptor. Drug-likeness and ADMET analyses indicated that these compounds possess good oral bioavailability, low toxicity, and minimal cytochrome P450 inhibition. Overall, the study suggests that these ligands have promising gastroprotective potential and could serve as lead compounds for future anti-ulcer drug development.

**Keywords**: Peptic ulcer, in-silico, molecular docking, Cyclooxygenase, Muscarinic receptor, ATPase, Histamine H2 receptor, E-Cadherin.

FASBMB2025/BDR-007

# Molecular Insights into Polycystic Ovary Syndrome Identify miR-93-5p as a Key Player in Disease Pathogenesis

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Polycystic Ovary Syndrome (PCOS) is a common and multifaceted endocrinopathy that affects at least 5% of women of reproductive age. It is characterized by an increased luteinizing hormone (LH) to follicle-stimulating hormone (FSH) ratio, leading to hyperandrogenism and abnormal folliculogenesis. MicroRNAs (miRNAs) have recently gained significant attention for their roles in the diagnosis, treatment, and prognosis of various disorders. This study aims to investigate miRNAs involved in the onset and progression of PCOS. Gene expression profiles derived from multiple datasets deposited in the NCBI database were analyzed. Bioinformatics and evolutionary genomic tools were employed to identify overlapping dysregulated genes among selected experiments. Dysregulated miRNAs implicated in PCOS were identified through a comprehensive literature review, and their corresponding target genes were retrieved using the miRDB database. To uncover the potential biological functions of these miRNAs, the identified miRNA–target differentially expressed genes (miR-DEGs) underwent downstream functional characterization. Gene Ontology and pathway enrichment analyses were performed using the DAVID bioinformatics platform, while miRNA–mRNA sequence homology assessments were conducted with BiBiServ2. Analysis of three independent datasets identified 326 overlapping differentially expressed genes (DEGs). Among the dysregulated miRNAs, miR-93-5p, miR-145-5p, miR-21-5p, miR-223-3p, and miR-342-3p emerged as key regulators targeting these DEGs in PCOS. Functional enrichment analysis revealed significant involvement of these miRNAs in transcription factor regulation, apoptosis, and some signaling cascades such as the FoxO, PI3K-Akt, MAPK, and insulin signaling pathways. Notably, miR-93-5p demonstrated unique associations with ovarian follicle development and luteinizing hormone secretion, suggesting its central role in the hormonal and metabolic dysregulation characteristic of PCOS. Collectively, these findings underscore the crucial involvement of the identified miRNAs in PCOS pathogenesis, with miR-93-5p standing out as the most promising candidate due to its multifaceted regulatory functions. This highlights miR-93-5p as a potential key diagnostic biomarker and therapeutic target for PCOS.

**Keywords:** Polycystic Ovary Syndrome; miRNA; Gene Expression, Folliculogenesis

FASBMB2025/BDR-008

# Diagnostic Potential of miR-130a-3P and miR-204-5P in Primary Hypertension: from Computational Predictions to Experimental Validation

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Hypertension remains a major global health challenge, affecting more than 1.4 billion individuals worldwide and constituting a leading risk factor for cardiovascular disease, stroke, and renal complications. Its development is influenced by both genetic predisposition and epigenetic regulation. Among emerging epigenetic regulators, microRNAs (miRNAs) have been recognized as key modulators of disease onset and progression. This study aimed to validate our previous report implicating miR-29a-3p, miR-204-5p, miR-130a-3p, and miR-145-5p in the pathophysiology of hypertension. Blood samples from hypertensive patients attending Specialist Hospital, Sokoto, were analyzed to validate the *in silico* predictions. Oxidative stress markers and lipid profiles were assessed spectrophotometrically, and atherogenic indices were derived from the lipid profile data. In addition, C-reactive protein (CRP) levels were quantified using ELISA. Relative expression of miR-204-5p and miR-130a-3p and their target genes in the aldosterone synthesis and secretion pathway were evaluated using qPCR, and their diagnostic potential was assessed with the easyROC tool. Biochemical analyses revealed significantly reduced levels of endogenous antioxidants (vitamin C, catalase, and glutathione), alongside elevated malondialdehyde (MDA) and CRP, indicating increased oxidative stress and systemic inflammation. Expression profiling showed downregulation of miR-204-5p with a corresponding upregulation of its target ATP2B4, and upregulation of miR-130a-3p accompanied by suppression of LDLR, consistent with post-transcriptional regulation. ROC curve analysis confirmed strong diagnostic potential for both miRNAs, with miR-130a-3p demonstrating the highest predictive accuracy (AUC = 0.853) compared to miR-204-5p (AUC = 0.730). Collectively, these findings identify miRNAs, particularly miR-130a-3p, as pivotal regulators in hypertension, underscoring their potential as diagnostic biomarkers and therapeutic targets. Future studies should validate these candidates in larger cohorts and explore miRNA-based strategies to restore vascular and systemic homeostasis in hypertensive patients.

**Keywords:** miRNA, Genes, Hypertension, oxidative stress, C-reactive protein

FASBMB2025/BDR-009

# *In Silico* Repositioning of Antiviral Compounds Targeting Cell Division Components in Lung Cancer

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Lung cancer is one of the most common malignant cancers and a leading cause of death among cancer patients. Despite tremendous progress in diagnosis, survival rates of individuals diagnosed with lung cancer remain unsatisfying especially in less developed nations. Considering the promising potentials of drug repositioning in shortening the length and financial burden associated with drug discovery, we screened two hundred (200) FDA-approved antiviral compounds for anti-cancer potential. We employed computational prediction to evaluate the pharmacokinetics, drug-likeness, toxicity and medicinal properties using various filters. We further identified hub genes among the most differentially expressed genes in lung cancer (213 cohort data sourced from The Cancer Genome Atlas (TCGA)). Our findings revealed four (4s) antiviral compounds to exhibit excellent drug-likeness characters with little or no toxicity. The compounds were predicted to cross human intestinal cell membrane, distributed through systemic circulation and metabolized by CYP450 monooxygenases. Molecular interaction studies indicated that the compounds strongly bind to major proteins (MELK, NUF2 and CDKN3) implicated in lung cancer initiation and progression. Protein interaction and pathway analysis shows that the proteins were involved at various stages of cell division including formation of stable kinetochore-microtubule attachments and mitotic chromosome alignment. Our findings underscore the latent role of the selected antiviral compounds in targeting key proteins implicated in lung cancer pathophysiology.

**Keywords**: Lung cancer, *In silico*, virus, antiviral compounds

## SUB-THEME 4

## MEDICINAL BIOCHEMISTRY (MB)

FASBMB2025/MB-002

# Effects of *Telfairia Occidentalis* Ethanol Leaf Extract on Atrazine-Induced Ovarian and Uterine Toxicity in Female Wistar Rats

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Atrazine (ATZ), a widely used herbicide, induces reproductive toxicity via endocrine disruption and oxidative stress. *Telfairia occidentalis* (fluted pumpkin), rich in antioxidant phytochemicals, is traditionally valued for fertility-enhancing properties. This study investigated the protective role of *T. occidentalis* ethanol leaf extract against ATZ-induced ovarian and uterine toxicity in female Wistar rats using *in silico* and *in vivo* approaches. Thirty-six rats were divided into six groups (n=6): control, ATZ-only (200 mg/kg), ATZ + *T.O* (200 or 400 mg/kg), *T.O* only (400 mg/kg), and ATZ + melatonin (10 mg/kg). Treatments lasted 14 days with estrous cycle monitoring. Serum reproductive hormones, oxidative stress biomarkers, and histopathology of ovarian and uterine tissues were assessed. ATZ disrupted estrous cycles, reduced weight (142.67 → 130.40 g), suppressed antioxidant defenses; ovary - SOD: 1.39 ± 0.04; CAT: 0.38 ± 0.05; GSH: 0.31 ± 0.03 compared to control - SOD: 6.24 ± 0.32; CAT: 3.85 ± 0.18; GSH: 1.93 ± 0.12, and elevated MDA ovary: 936.55 ± 1.77 compared to control: 96.82 ± 2.07. Serum LH, progesterone, and estradiol were significantly decreased. Co-treatment with *T.O* (400 mg/kg) markedly restored antioxidant activities, ovary SOD: 6.76 ± 0.19; GSH: 1.79 ± 0.03, reduced MDA (440.64 ± 10.53), and normalized the hormones. Histology confirmed preservation of ovarian and uterine architecture. *In silico* docking revealed kaempferol and quercetin strongly bound to ERα and CYP19A1, supporting their estrogenic and aromatase-modulatory activities. *T. occidentalis* extract demonstrated significant protection against ATZ-induced reproductive toxicity, highlighting its potential as a natural therapeutic for herbicide-induced dysfunction.

**Keywords:** Atrazine, *Telfairia occidentalis*, ovarian toxicity, uterine toxicity, estrous cycle.

FASBMB2025/MB-003

# Mechanistic Investigation of Antibacterial activities of Endophytic Fungus SDA12-S21 Against Multidrug-Resistant *Pseudomonas aeruginosa*

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Multidrug-resistant (MDR) Gram-negative bacteria are a major worldwide health concern due to limited treatment choices and associated morbidity and mortality. Endophytic fungi have been reported as prolific sources of bioactive secondary metabolites with pharmaceutical potential. This study evaluated antibacterial activities of endophytic fungus strain SDA12-S21 against multidrug-resistant *Pseudomonas aeruginosa*. The endophytic fungus strain SDA12-S21 was isolated from a surface sterilized stem of *Neocarya macrophylla*. The antibacterial activity of the fungus extract was tested using the agar plug method against clinical MDR *P. aeruginosa.* GC-MS analysis of the extracts revealed various bioactive compounds, including fatty acids and ester ((6Z)-6-Octadecenoic acid, n-hexadecanoic acid, E-8-Methyl-9-tetradecen-1-ol acetate, and oleic acid), as major constituent. The mode of action of the extract was further investigated using time-kill assay and DNA leakage assay. The extract of SDA12-S21 displayed pronounced antibacterial activity against the test *P. aeruginosa,* producing a clear growth inhibition zone measuring 25 mm. The Time-kill-assay demonstrated rapid bactericidal activities, with extract SDA12-R21 attaining a three-log reduction in viable cell counts within 12 hours. DNA leakage assays are consistent with membrane-disrupting actions of the extracts. These findings showed that endophytic fungus associated with *N. macrophylla* possess a potent antibacterial activity against MDR *P. aeruginosa*.

**Keywords:** Endophytic fungi, *Neocarya macrophylla*, Antibacterial activity, Multidrug resistance, Secondary metabolites

FASBMB2025/MB-004

# Antioxidant Defense and Oxidative Stress Modulation in Hormone-Induced BPH Using Phytochemicals from *Vernonia amygdalina* and Corn Silk

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Benign prostatic hyperplasia pathophysiology is characterized by dysregulated redox balance. Oxidative stress plays a central role in the progression of benign prostatic hyperplasia (BPH). This research investigated the antioxidant potential of *Vernonia amygdalina* (VAE) and *Stigma maydis* (CSE) methanolic extracts in testosterone-propionate-induced BPH rats. Phytochemical HPLC profiling revealed high gallic acid and saponin concentrations, particularly in VAE. Induction resulted in elevated lipid peroxidation (MDA) and reduced antioxidant enzymes (SOD, catalase, glutathione). Both extracts improved oxidative balance, but the combined therapy (50 mg/kg VAE + 100 mg/kg CSE) produced the strongest recovery, marked by enhanced catalase and glutathione and lowest MDA levels, indicating attenuated lipid peroxidation. These results indicate synergistic antioxidant activity that mitigates BPH-driven oxidative stress. The findings suggest that polyphenolic compounds in the extracts may protect prostate tissues by restoring redox balance, improved oxidative biomarker status, and restoration of homeostasis providing a potential plant-based therapeutic approach.

**Keywords:** oxidative stress, antioxidants, *Vernonia amygdalina*, *Stigma maydis*, lipid peroxidation, prostate protection

FASBMB2025/MB-005

# Phytochemical and Biochemical Evidence of Synergy of *Vernonia amygdalina* and *Stigma maydis* on hormonally induced benign prostatic hyperplasia (BPH) in Wistar rats

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This study evaluated the synergistic effects of methanolic extracts of *Vernonia amygdalina* (VAE) and *Stigma maydis* (CSE) on biochemical indices on hormonally induced benign prostatic hyperplasia (BPH) in Wistar rats. The biochemical indices associated with BPH were comprehensively evaluated following administration of methanolic extracts of VAE and CSE in a hormonally induced Wistar rat BPH model. 66 animals were grouped into 11 comprising of 6 animals per group and underwent distinct cohorts for single and combination extract treatments, (with a positive control group treated with a standard drug, Finasteride) with comparative assays on liver (ALT, AST, ALP) and kidney (creatinine, total protein) function biomarkers. The BPH-untreated group showed pronounced biochemical derangements, evidenced by elevated liver enzymes and kidney markers, reflecting systemic toxicity secondary to hormone induction. HPLC analysis revealed VAE as rich in gallic acid and polyphenols, while CSE contained unique compounds such as maleic acid. Testosterone-induced BPH led to elevated prostate index, prostate weight, and hormonal markers (PSA, testosterone, DHT, prolactin, and 5α-reductase). Treatment with combined extracts produced significant reductions in these markers, surpassing effects observed with individual extracts and standard drug (finasteride). The best response was at asymmetric dosing (50 mg/kg VAE + 100 mg/kg CSE), which normalized biochemical indices and restored prostate weight close to baseline. Our findings demonstrate that bitter leaf and corn silk possess protective efficacy beyond prostate tissue, remedying systemic oxidative stress and organ dysfunction associated with BPH and these phytochemicals inherent in them exert additive and synergistic effects in BPH management. These support the promise of combined phytotherapy as a safe, potent, and cost-effective strategy for mitigating not just prostatic but systemic complications of BPH.

**Keywords:** *Vernonia amygdalina, Stigma maydis*, phytochemicals, synergy, benign prostatic hyperplasia, biochemical markers

FASBMB2025/MB-006

# Phytochemical Screening and Biochemical Assessment of the Safety Profile of *Catunaregam nilotica* Methanol Leaf Extract in Albino Rats

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The study aimed to evaluate the phytochemical constituents and assess the biochemical safety profile of the methanol leaf extract of *Catunaregam nilotica* in albino rats. Phytochemical screening was conducted using standard qualitative and quantitative analytical techniques to determine the presence and concentration of major secondary metabolites. Acute oral toxicity was assessed according to Lorke's method, using graded doses up to 500 mg/kg to establish the $LD_{50}$ value. Biochemical parameters for liver (AST, ALT, ALP, albumin, and total protein) and kidney (urea and creatinine) functions were measured using standard spectrophotometric methods. Hematological parameters, including WBC, RBC, hemoglobin, and platelet counts, were analyzed to evaluate hematopoietic effects. Phytochemical analysis revealed abundant alkaloids (12.4 ± 0.85 mg/100 g) and saponins (10.7 ± 0.95 mg/100 g), along with the presence of tannins, flavonoids, phenols, terpenoids, steroids, and glycosides. The extract exhibited no mortality or visible toxicity at 500 mg/kg, indicating an $LD_{50}$ value above this level. Biochemical analysis showed a dose-dependent reduction in liver enzyme activities and increases in albumin and total protein, suggesting hepatoprotection. Renal markers remained within normal ranges except for mild elevations at 1000 mg/kg. Hematological indices were not significantly affected ($p > 0.05$).
The methanol leaf extract of *Catunaregam nilotica* is rich in bioactive phytochemicals and demonstrates no acute toxicity or hematological disturbances at therapeutic doses. Its hepatoprotective and nephroprotective tendencies support its traditional medicinal applications and warrant further pharmacological and toxicological evaluation.

**Keywords:** *Catunaregam nilotica*, phytochemical screening, biochemical assessment, toxicity study, albino rats.

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# Phytochemical Analysis, Antimicrobial Activity, and In vitro Antioxidant Properties of Some Medicinal Plants in Northern Nigeria

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Antimicrobial resistance motivates the search for new therapeutic agents from plant sources. This study evaluated the phytochemical composition, antibacterial activity against *Staphylococcus aureus*, and in vitro antioxidant potential of methanolic leaf extracts of *H. indicum*, *T. terrestris*, *P. olaracea*, and *T. bagwensis*. Extracts were tested at three concentrations (500, 1000, and 2000 µg/mL) using agar well diffusion (vancomycin as standard). Antioxidant activity was measured by the DPPH radical-scavenging assay (ascorbic acid standard). Qualitative and quantitative phytochemical assays revealed significant differences in secondary-metabolite content ($p < 0.05$); *H. indicum* had the highest levels (e.g., total phenols: 548.00 ± 0.41 mg/g). Correspondingly, *H. indicum* exhibited the strongest antibacterial activity (zone of inhibition up to 20.60 ± 0.84 mm), closely followed by *T. bagwensis* (20.60 ± 0.14 mm), while *P. olaracea* produced the least inhibition (15.50 ± 0.03 mm). Vancomycin showed no inhibitory activity against the test strain, indicating resistance. In the DPPH assay, *H. indicum* had the lowest $IC_{50}$ (3.43 ± 0.05 µg/mL), followed by *T. bagwensis* (7.83 ± 0.06 µg/mL) and *T. terrestris* (8.28 ± 0.16 µg/mL); ascorbic acid $IC_{50}$ was 0.001 ± 0.00 µg/mL. These results suggest that the bioactive phytochemicals in these species contribute to their antibacterial and antioxidant effects and warrant further isolation and structural characterization as potential natural therapeutic agents.

**Keywords:** Phytochemicals, Antimicrobial activity, DPPH, Antioxidant, *H. indicum*, *T. bagwensis*, drug resistance

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# Antidiabetic Properties of *Medicago Sativa* (Alfalfa) Aqueous Leaf Extract on Alloxan-Induced Diabetes in Albino Rats

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The study investigated the antidiabetic property of *Medicago sativa* (Alfalfa) aqueous leaf extract on alloxan-induced diabetes in Wistar Albino Rats. A total of 37 rats weighing 120-150g were used for the study. Twelve (12) rats were acclimatized for five days and used for acute toxicity study. Twenty-five (25) rats were acclimatized for seven days and separated into five (5) groups of five (5) rats each; the normal control (NC) group, the diabetic control (DC) group, two (2) test groups and a standard group. All groups, except Normal control, were induced with diabetes intraperitoneally using 150mg/kgb.wt of alloxan monohydrate. The two test groups were respectively treated orally with 250mg/kg and 500mg/kg.bwt of aqueous leaf extract of *Medicago sativa* (Alfalfa) daily for 21 days. The standard group was treated with 7.14mg/kg.bwt of Glucophage (Metformin) daily for 21 days. Blood sugar levels, Aspartate Aminotransferase (ALT), Alanine Aminotransferase (AST), Alkaline Phosphatase, Urea, Creatinine, Total Billirubin and electrolytes (Potassium, Sodium, Chloride and Bicarbonate) were measured at the end of the experiment. The result revealed that the blood glucose levels of the treated rats were significantly ($P<0.05$) reduced by the extract, with 500mg/kg.bwt of the extract showing a higher efficacy than 250mg/kg and metformin. The result also revealed that the *Medicago sativa* leaf possesses organo-protective properties by normalizing the level of the liver enzymes and the kidney biomarkers evaluated. Histological examination showed that the aqueous alfalfa extract caused reconstruction of damaged liver and kidneys. Therefore, all investigated signs of diabetes were improved by oral administration of aqueous leaf extract of *Medicago sativa*.

**Keywords:** *Medicago sativa*. diabetes, blood glucose, liver enzymes, medicinal plants

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# Evaluation of the effects of *Treculia africana* leaves on lipid profile, antioxidant activity and some biochemical parameters in Wastar Rats

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This study evaluated the potential effects of aqueous leaf extract of *Treculia africana* on cardiac function, lipid profile, antioxidant status and heart histology in male Wistar rats. Eighteen rats were divided into three groups and treated for 28 days with distilled water (control), 200 mg/kg and 400 mg/kg of the extract. Serum biochemical markers (Lactate dehydrogenase (LDH), creatine kinase (CK), cholesterol, triglycerides, HDL and LDL), cardiac antioxidant enzymes (SOD, CAT, GPx) and lipid peroxidation (MDA) were measured, while heart tissues were examined histologically. Results showed no significant changes ($p>0.05$) in lipid profile, cardiac enzymes and oxidative stress parameters between treated and control groups. Histological examination revealed normal cardiac structures across all groups. These findings suggest that *Treculia africana* leaf extract, at the tested doses, is safe for cardiac function and does not induce adverse biochemical or structural alterations in the heart.

**Keywords:** *Treculia africana*, cardiac function, antioxidant enzymes, lipid profile, medicinal plants

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# Biochemical Evaluation of *Andrographis paniculata* Leaf Extract on Liver Function Enzymes and Plasma Protein Parameters in Paracetamol –induced Hepatotoxic Wistar Rats

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*Andrographis paniculata* (AP), known as King of bitters is traditionally used in the treatment of Inflammation, gastrointestinal disorders, diabetes and liver diseases. The leaf extract was investigated on the levels of Plasma Proteins (Albumin, Globulin and Total proteins) and liver enzyme biomarkers (Alanine Amino Transferase, Aspartate Amino Transferase and Alkaline Phosphatase) of Wistar rats induced with overdose of paracetamol, N-acetyl-1,4-benzoquinoneimine (NAPQI) a paracetamol intermediate. The animals were divided into five groups of 10 rats administered different doses (*p.o)* of the aqueous leaf extract (ALE). Ctr 1: positive control group (n-saline), Ctr 2: negative control (2000mg/kg paracetamol), Group3: 250mg/kg bodyweight ALEAP, Group4: test group (500mg/kg ALEAP), Group5: test group (paracetamol + 250mg/kg ALEAP), Group 6: test group (paracetamol + 500mg/kg ALEAP). From the result, there was a slight reduction in the levels of Total Protein, Albumin and Globulin on the extract treated groups compared with the control but reduction was seen more when compared with the negative control though none was significant ($P>0.05$). This slight reduction in Total protein compared with the paracetamol group may signify amelioration of liver damage. Equally, the liver enzyme biomarkers showed ameliorative effect on the paracetamol induced rats when compared with the control though not statistically ($P>0.05$) significant. The GCMS result showed 60 bioactive components ranging from 3,6,9,12,15-Pentaoxanonadecan-1-ol with retention time of 1.319 to Hexasiloxane, 1,1,3,3,5,5,7,7,9,9,11,11-dodecamethyl with RT of 15.781 but has Phytol (RT 9.170) which is anticytotoxic and an antioxidant. Conclusively, this result suggests that *Andrographis paniculata* leaf extract may have hepatoprotective properties.

**Keywords**: *Andrographis paniculata,* Liver enzymes, Paracetamol, Wistar rats and Induced toxicity

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# S*yzygium aromaticum* Seed Extract Modulates Oxidative Stress and Glycaemic Indices in Alloxan-Induced Diabetic Rats

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The modulatory potentials of aqueous seed extract of *Syzygium aromaticum* on alloxan-induced diabetic Wistar rats were investigated. Eighty male rats weighing 100-130g were grouped into eight (n=10). Group 1 served as the normal experimental control. Groups 2-8 were fed a high-fat diet for 28 days and administered a single intraperitoneal injection of 150 mg/kg body weight of alloxan to induce diabetes. Diabetes was established after three consecutive days of Fasting Blood Sugar measurement between 11 and 13 mmol/L. Group 2 did not receive any treatment, and Group 3 received 500 mg/kg body weight of metformin. Groups 4, 5, 6, 7, and 8 were treated with 500, 1000, 1500, 2000, and 2500 mg/kg bodyweight of the extract, respectively, for 28 days. Biochemical indices and histology of the pancreas, liver and kidney were investigated. Results showed that treatment with 2500 mg/kg extract significantly ($p<0.05$) reduced fasting glucose from 10.47 ± 5.28 mmol/L to 4.81 ± 0.48mmol/L and amylase from 47.70 ± 33.05 to 28.72 ± 0.72. Also, there was a significant ($p<0.05$) decrease in nitric oxide and GSH from 9.71 ± 1.06 to 1.13 ± 0.28 µg/L and 62.74 ± 3.33 to 10.27 ± 1.22 nmol/L, respectively. There was a significant ($p<0.05$) increase in the activities of superoxide dismutase (from 1.38 ± 0.23 to 4.58 ± 0.06 U/ml), and catalase (39.67±10.43 to 53.64± 3.04 U/ml). The photomicrographs showed atrophic pancreatic islets in Group 2. However, the treatment groups were ameliorated by different concentrations of the extract and can therefore be explored in the management of diabetes.

**Keywords:** *Syzygium aromaticum*, High-fat-diet, diabetes, Pancreas, Histology

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# Bioanalytical Assessment of Lectin Content and Haemagglutination Potential in Selected Tropical Plants: Implications for Biomedical Use

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Lectins, carbohydrate-binding proteins prevalent in tropical plants, exhibit haemagglutination activity that influences their nutritional and therapeutic potential. The binding specificity of lectins to cell surfaces primarily relies on monosaccharides and simple or complex oligosaccharides, which can block lectin-mediated interactions when introduced. This study evaluated protein concentration, lectin-specific activity, haemagglutination potential, carbohydrate specificity, and antioxidant activity in ten selected tropical plants: *Gnetum africanum*, *Stachytarpheta cayennensis*, *Jatropha tanjorensis*, *Gongronema latifolium*, *Phyllanthus niruri*, *Ocimum gratissimum*, *Andrographis paniculata*, *Telfairia occidentalis*, *Talinum triangulare*, and *Hibiscus sabdariffa*. Lectins from the plants were extracted and partially purified, and their haemagglutination, carbohydrate-binding, and antioxidant activities were evaluated. Protein content was determined by the Bradford assay, and chemical constituents were characterized by LC-MS analysis. Protein concentration ranged from 0.01 mg/mL in *Telfairia occidentalis* to 0.53 mg/mL in *Hibiscus sabdariffa*. Lectin-specific activity was highest in *Gnetum africanum* (224.33 mg/protein) and *Phyllanthus niruri* (177.39 mg/protein). Haemagglutination titres were elevated in *Phyllanthus niruri* and *Gnetum africanum* against blood type A (177.39 and 224.33 LA, respectively). *Jatropha tanjorensis* and *Talinum triangulare* showed broad carbohydrate specificity (100% reactivity with A, B, and O types). Antioxidant activity via DPPH scavenging was highest in *Gnetum africanum* (24.14%). LC-MS analysis revealed a diverse array of bioactive compounds. Compounds like hexadecanoic acid and 9,12-Octadecadienoic acid were identified in multiple plants, corroborating their traditional medicinal uses. These findings highlight biochemical diversity, suggesting potential applications in food processing to mitigate antinutritional effects and in developing glycan-targeted therapeutics.

**Keywords:** Lectins, Haemagglutination, Tropical plants, Bioanalytical methods, LC-MS

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# Protective Effects of Cinnamic Acid Against Manganese Chloride-Induced Hematological and Reproductive Alterations in Female Wistar Rats

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Manganese chloride ($MnCl_2$) is an environmental toxicant that disrupts reproductive hormones and hematological parameters in female Wistar rats via oxidative stress and dysregulation of the hypothalamic-pituitary-gonadal axis. This study investigated the protective efficacy of cinnamic acid (CA), a phenolic antioxidant with metal-chelating properties, against $MnCl_2$-induced toxicity. Thirty female Wistar rats were randomly allocated to six groups (n=5): Group A (control), Group B ($MnCl_2$ 10 mg/kg), Group C (CA 50 mg/kg), Group D (CA 100 mg/kg), Group E ($MnCl_2$ + CA 50 mg/kg), and Group F ($MnCl_2$ + CA 100 mg/kg). Treatments were administered orally for 90 days; a sub-chronic duration selected to mimic occupational/environmental exposure patterns. $MnCl_2$ exposure significantly reduced serum progesterone (2.45 ± 0.71 ng/mL), estradiol (0.70 ± 0.22 pg/mL; measured by ELISA), red blood cell count (RBC, 6.35 ± 0.43 $\times 10^{12}$/L), hemoglobin (HGB, 11.70 ± 0.77 g/dL), and hematocrit (HCT, 34.03 ± 3.68%), while elevating granulocyte count (GRAN#, 0.60 ± 0.32 $\times 10^9$/L) ($p < 0.05$ vs control). Co-administration of CA, particularly at 100 mg/kg (Group F), dose-dependently ameliorated these alterations, restoring progesterone to 17.66 ± 0.46 ng/mL, estradiol to 2.19 ± 0.13 pg/mL, RBC to 7.59 ± 0.46 $\times 10^{12}$/L, HGB to 13.50 ± 0.74 g/dL, and HCT to 43.93 ± 8.24%, with GRAN# reduced to 0.20 ± 0.10 $\times 10^9$/L ($p < 0.05$ vs MnCl group). Data were analyzed by one-way ANOVA followed by Tukey's post-hoc test. These findings demonstrate that cinnamic acid exerts significant protective effects against $MnCl_2$-induced hematological and reproductive toxicity in a dose-dependent manner, supporting its potential as a natural therapeutic agent.

**Keywords**: Manganese chloride, cinnamic acid, reproductive hormones, hematological parameters, oxidative stress, female Wistar rats, ELISA, sub-chronic toxicity.

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# Evaluation of Nutritional Composition and Anticancer Potential of *Chenopodium album*

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This study evaluated the nutritional composition, phytochemical constituents, antioxidant, and anticancer activities of *Chenopodium album* leaves, a plant known for its nutritional and therapeutic properties. Dried leaves sequentially extracted with *n*-hexane, ethyl acetate, and methanol were analysed for proximate, phytochemical, mineral, vitamin, and antinutrient contents. Antioxidant (DPPH, TAC, FRAP) and cytotoxic (MTT) assays were also determined. The leaves contained 6.25 ± 0.29% moisture, 32.10 ± 0.71% ash, 2.58 ± 0.34% fat, 6.22 ± 0.75% protein, 8.34 ± 0.51% fiber, and 44.51 ± 0.94% carbohydrates, indicating a high mineral and carbohydrate composition. Antinutrient assessment showed moderate levels of oxalate (0.94 ± 0.16%), phytate (2.22 ± 0.17%), tannins (1.85 ± 0.24%), and saponins (3.01 ± 0.21%), while mineral analysis demonstrated substantial concentrations of potassium (6,932 ± 87.51 mg/kg), calcium (3,832 ± 79.10 mg/kg), magnesium (2,588 ± 56.19 mg/kg), and iron (1,920 ± 150 mg/kg). The methanol fraction showed the highest vitamin C (18.04 ± 4.62 mg/dL), vitamin E (48.85 ± 4.57 mg/dL), total phenolic (182.51 ± 3.82 mg GAE/g) and flavonoid (43.57 ± 0.30 mg QE/g) concentrations, along with the strongest antioxidant activity (DPPH $IC_{50}$ = 21.10 ± 0.36 µg/mL; TAC = 568.50 ± 39.74 µg AAE/mL and ferric FRAP = 210.25 ± 8.12 µmol $FeSO_4$/g). *In vitro*, the fraction moderately inhibited HeLa cancer cell viability (80.53% at 200 µg/mL) compared to doxorubicin (23.76%). These findings suggest that *C. album* leaves are nutritionally rich, contain potent antioxidants and moderate anticancer potential, supporting their potential use in functional food and therapeutic applications.

**Keywords:** Chenopodium album, antioxidant activity, antinutrients, proximate composition, cytotoxicity

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# Effect of Cinnamic Acid on Lipid Profile and Kidney Function of Female Rats exposed to Manganese Chloride

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Manganese is a trace element and an environmental pollutant widely used in industries, but excessive exposure is associated with multi-organ toxicity. While its neurotoxic effects are well documented, its impact on metabolic and renal functions is less explored. Manganese toxicity is known to promote oxidative stress, which can disrupt lipid metabolism and damage renal tissues. Cinnamic acid (CA) is a natural phenolic compound that has potent antioxidant and anti-inflammatory properties, which may offer a promising therapeutic benefit in ameliorating manganese chloride toxicity. This study evaluated the effect of cinnamic acid (CA) on the lipid profile and kidney function of female rats exposed to Manganese Chloride. Thirty (30) adult female rats were randomly divided into six (6) groups (n=5); group 1 (normal control), group 2 (10mg/kg MnCl2), group 3 (CA low dose, 50 mg/kg), group 4 (CA high dose, 100mg/kg), group 5 (MnCl2 + 50mg/kg CA) and group 6 (MnCl2 + 100mg/kg CA). Treatment was orally administered daily for 90 days. Thereafter, the rats were sacrificed under anesthesia and blood samples were collected for lipid profile and kidney function analysis. The results revealed that the group exposed to MnCl2 without treatment had significantly ($p<0.05$) impaired renal function, indicated by elevated serum urea and creatinine levels, electrolyte imbalance when compared to the normal control group. It also induced a dyslipidemic state with increased total cholesterol, triglycerides, low density lipoprotein (LDL) and decreased high density lipoprotein (HDL) levels. Co-treatment with CA demonstrated a dose-dependent ameliorative effect, as it was observed that group 6 (MnCl2 + CA high dose) showed better protection nearly normalizing the kidney function and lipid profile markers. No significant alterations were observed in groups 3 and 4 compared to the normal control. Findings from this study suggest that CA possesses renal protective and hypolipidemic potential against MnCl2-induced toxicity in a dose dependent manner. The mechanism is likely attributed to the antioxidant activity of CA which counteracts MnCl2 induced oxidative damage.

**Keywords**: Cinnamic acid, Manganese Chloride, Renoprotective, Dyslipidemic, Hypolipidemic

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# Effect of High-Dose Ethanol Leaf Extract of *Alchornea cordifolia* on Liver Enzymes in Ulcer-Induced Albino Rats

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*Alchornea cordifolia*, also known as Christmas bush tree or goat weed, is a medicinal plant widely recognized for its antioxidant and anti-inflammatory properties. Peptic ulcer disease (PUD) remains a global health concern, and conventional treatments often present adverse hepatic side effects. This study investigated the Effect of High-Dose Ethanol Leaf Extract of *Alchornea cordifolia* on Liver Enzymes in Ulcer-Induced Albino Rats. Ulcers were induced by a single dose of indomethacin (200 mg/kg), after which treatment groups received the *A. cordifolia* leaf extract at 200 mg/kg body weight for 21 days. The ulcer control group exhibited significantly elevated liver enzyme biomarkers, including Alanine Aminotransferase (ALT), Aspartate Aminotransferase (AST), and Alkaline Phosphatase (ALP), confirming hepatocellular stress due to indomethacin. The ulcer control group showed depleted antioxidant defense systems (GSH, GPx, SOD, CAT) and increased lipid peroxidation (MDA). Treatment with the high-dose *A. cordifolia* extract significantly attenuated these detrimental effects. Liver enzyme levels were restored closer to the normal control group, and antioxidant status (GSH: 11.97 \pm 0.21 mg/dl; MDA: 0.27 \pm 0.01 mmol/L) was maintained comparably to the standard drug group. The protective effect is likely mediated by the plant's abundant phytochemicals (alkaloids, tannins, saponins), which possess strong antioxidant and anti-inflammatory properties. These findings validate the traditional use of *A. cordifolia* and indicate that the high-dose ethanol leaf extract is both hepatoprotective and anti-ulcerogenic, suggesting its potential as a safe, natural alternative in PUD management.

**Keywords:** *Alchornea cordifolia*, Hepatoprotection, Peptic Ulcer Disease, Liver Enzymes (or ALT/AST/ALP), Antioxidant Activity

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# Liver and Haematological Responses to Varying Doses of *Andrographis paniculata* Leaf Extract in Indomethacin-Ulcerated Rats

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*Andrographis paniculata* (King of Bitters) is a medicinal plant widely recognized for its hepatoprotective, anti-inflammatory, and antioxidant properties. This study evaluated the Liver and Haematological Responses to Varying Doses of *Andrographis paniculata* Leaf Extract in Indomethacin-Ulcerated Rats. Thirty Wistar rats were divided into six groups: normal control, negative control, low dose (100 mg/kg), high dose (200 mg/kg), and positive control (omeprazole). Extracts were administered orally for 21 days, after which blood and organs were collected for biochemical and haematological analysis. Results revealed significant dose-dependent effects on liver biomarkers and haematological indices. The low-dose group showed elevated ALT and AST levels, suggesting possible hepatic stress, whereas the high-dose group exhibited improved liver profile parameters, closer to the standard control. Total protein and globulin were higher in the high-dose and standard drug groups compared to the negative control. Body and organ weight changes indicated that the extract influenced growth and metabolic responses. Haematological parameters revealed mild variations, with the high dose maintaining relatively stable values compared to controls. In conclusion, *A. paniculata* demonstrated both protective and dose-related effects on liver and haematological functions in ulcer-induced rats. While the high dose showed hepatoprotective tendencies, the low dose may induce mild hepatic stress. Further research is recommended to clarify its therapeutic margin and safety profile for clinical applications.

**Keywords:** *Andrographis paniculata*, hepatoprotective, haematology, indomethacin-induced ulcer, medicinal plant

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# *In-vitro* and *In-vivo* Antioxidant Potentials of Methanol Extract and Aqueous Fraction of *Ficus platyphylla* Stembark in Albino Rats

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Oxidative stress arises from an imbalance between free radicals and antioxidants in biological systems. This study aimed to evaluate the phytochemical profile as well as the *in-vitro* and *in-vivo* antioxidant potentials of methanol extract and aqueous fraction of *Ficus platyphylla* stem bark in albino rats. Phytochemical screening revealed the presence of alkaloids, saponins, glycosides, phenols, flavonoids, and tannins, with anthraquinones absent in both extracts. *In-vitro* assays demonstrated a dose-dependent increase in ferric reducing antioxidant power (FRAP) in vitamin E, while the aqueous fraction of *Ficus platyphylla* exhibited comparable reducing activity at concentrations of 5, 10, and 15 mg/mL. *In vivo,* a significant ($p<0.05$) reduction in biomarker enzymes and malondiadehyde (MDA) concentrations were observed in both extract-treated groups and the positive control compared to the negative control. Conversely, antioxidant enzymes—including catalase (CAT) and superoxide dismutase (SOD), were significantly ($p<0.05$) elevated in extract-treated groups and the positive control relative to the negative control. Similarly, concentrations of vitamins A, C, E and reduced glutathione (GSH) were markedly increased in extract-treated and positive control groups. The ability of *Ficus platyphylla* stem bark to restore antioxidant enzyme activity and reduce lipid peroxidation highlights its potential as a natural therapeutic agent against oxidative stress-related disorders. In conclusion, both the methanol extract and aqueous fraction of *Ficus platyphylla* stem bark contain diverse bioactive phytochemicals with strong pharmacological relevance and exhibit potent antioxidant activity in-vitro and *in-vivo*.

**Keywords:** Phytochemicals, antioxidant activity, *Ficus platyphylla*, stem bark, oxidative stress

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# Antimalarial Efficacy of *Enantia chlorantha* Aqueous Stem Bark Extract: Modulation of Redox Homeostasis and Biochemical Dysfunctions in *Plasmodium berghei*-Infected Mice

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Malaria remains a leading cause of death globally, with the rapid emergence of resistance to frontline therapies compounding control strategies. This necessitates the exploration of novel antimalarial agents with distinct mechanisms of action. *Enantia chlorantha* stem bark is traditionally used in the management of malaria, yet its pharmacological basis requires scientific validation. We investigate the antimalarial efficacy of *Enantia chlorantha* aqueous stem bark extract (*Ec*ASBE), elucidating its mechanistic role in restoring redox homeostasis and malaria-induced biochemical dysfunctions in *Plasmodium berghei*-infected mice. Using curative, prophylactic, and suppressive test models, we assessed the antimalarial activity of *Ec*ASBE against *P. berghei* infection *in vivo*. Antioxidant enzyme activities, lipid peroxidation markers, liver and kidney function indices, and pro-inflammatory mediators were also determined. *Ec*ASBE significantly ($p < 0.05$) reduced parasitaemia as concentration increased, with the curative model showing the highest suppression (80.4%) and prolonged survival (mean survival time, MST = 20 days). Extract treatment restored hepatic enzyme levels (ALT, AST, ALP, GGT) and renal biomarkers (creatinine, urea) to near-normal ranges. *Ec*ASBE enhanced antioxidant defence by elevating CAT, SOD, GPx, and GSH, while reducing NO and MDA. Additionally, TNF-α levels were significantly ($p < 0.05$) attenuated, indicating anti-inflammatory effects. *Ec*ASBE exerts potent antimalarial activity while simultaneously re-establishing redox balance and modulating inflammatory responses. These findings provide mechanistic support for its ethnopharmacological use and highlight *E. chlorantha* as a promising source of bioactive compounds for integrated antimalarial drug discovery. Further molecular characterisation of its active principles is warranted.

**Keywords:** Malaria, *Plasmodium berghei*, Natural product pharmacology, Oxidative stress, Drug discovery

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# Contragestive activity of *Citrullus colocynthis* (L.) Schrad (bitter apple) extract through oestrogen-progesterone suppression

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*Citrullus colocynthis* fruit is commonly used in traditional medicine as therapy for numerous diseases which entails antifertility, and uterus washing. This study investigated the contragestive activity of *Citrullus colocynthis* in pregnant Wistar rats. Pregnant rats were randomized into six (n=5 rats/group): Control (receives olive oil), Mifepristone (1.84 mg/kg mifepristone) while other groups were administered with 100, 200, 400, and 800 mg $kg^{-1}$ ethanol extract of *Citrullus colocynthis* (EECC) from day $6^{th}$ through $14^{th}$. Abortifacient parameters and the reproductive hormone levels were evaluated. The result obtained during the *in vitro* analysis of EECC revealed the presence of bioactive constituents like cucurbitacin B and gallic acid while the treatment with EECC, *p.o* for 9 days led to a dose-dependent decrease ($p < 0.05$) in foetus survival ratio at 81.48%, 66.66%, 18.75%, and 0% respectively. Likewise, the influence of the treatment resulted in a dose-dependent elevation in abortion, pre- and post-implantation losses, and resorptive index. In contrast, a decrease in implantation index and *Corpora lutea* were recorded. Mifepristone and 800 mg/kg EECC showed 100% post-implantation loss. Furthermore, a dose-dependent reduction in progesterone, oestrogen, follicle-stimulating hormone, luteinizing hormone, and prolactin in the serum was recorded in EECC-treated rats. The findings support the folkloric usage of *Citrullus colocynthis* as a contragestive. Moreover, the groups containing 800 mg/kg EECC have comparable abortifacient effects with the mifepristone-treated group. Hence, cucurbitacin B and gallic acid present in EECC extract could be responsible for contragestive potential.

**Keywords:** Contragestive, abortifacient, *Citrullus colocynthis,* mifepristone, progesterone

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# In-Silico Studies of GC-MS Identified Botanicals from *Azanza garckeana* Extracts Presents Promising Druggability Against Type 2 Diabetes

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Diabetes mellitus affects 589 million adults globally, projected to reach 853 million by 2050, causing 6.7 million deaths and USD 966 billion in costs. Current antidiabetic drugs have side effects, high cost, and limited efficacy, necessitating novel multitarget therapies such as *Azanza garckeana*, rich in antidiabetic phytochemicals. Two GC-MS identified compounds from *A. garckeana* TYR; 2-threonyltyrosylarginine and Carazolol were evaluated using in-silico molecular docking against five key diabetic enzymes (α-amylase, α-glucosidase, hexokinase, protein tyrosine phosphatase, and glucokinase), with acarbose as a reference inhibitor. Molecular mechanics generalized Born surface area (MM/GBSA) binding free energy calculations, pharmacokinetic profiling, and toxicity predictions were performed to assess drug likeness and safety. TYR; 2-threonyltyrosylarginine showed the strongest affinity for α-amylase (–10.165 kcal/mol), with additional inhibition of glucokinase (–7.051 kcal/mol) and α-glucosidase (–6.892 kcal/mol). Despite hydrophilicity (LogP –1.94) and a relatively safe $LD_{50}$ of 2400 mg/kg, it demonstrated poor gastrointestinal absorption, no BBB penetration, predicted nephrotoxicity, respiratory, and cardiotoxicity risks. Carazolol exhibited strong binding to hexokinase (–9.110 kcal/mol) and glucokinase (–7.995 kcal/mol), alongside moderate α-amylase inhibition (–8.454 kcal/mol). It satisfied Lipinski's rules, showed high gastrointestinal absorption, and crossed the BBB; however, toxicity profiling flagged carcinogenicity, CYP2D6 inhibition, immunotoxicity, and a lower $LD_{50}$ of 145 mg/kg. TYR; 2-threonyltyrosylarginine demonstrates promising α-amylase inhibition, suggesting potential to reduce postprandial hyperglycemia, but its poor pharmacokinetic profile limits direct therapeutic use. Carazolol displayed multitarget antidiabetic activity but presented notable toxicity concerns. Structural optimization and toxicological validation are essential for advancing these compounds as antidiabetic candidates.

**Keywords**: *Azanza garckeana*, diabetes, bioactive compounds, molecular docking, ADMET

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# Modulatory Effects of Ageratum conyzoides and Costus afer Extracts on Serum Lipid Profiles in Plasmodium berghei-Infected Mice

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Malaria, caused by *Plasmodium* species, it is associated not only with hematological disturbances but also with alterations in lipid metabolism. This study evaluated the effects of combined methanolic Stem bark extract of *Ageratum conyzoides and Costus afer* on lipid profile in Plasmodium berghei infected mice. Infection was established via intraperitoneal inoculation with *P. berghei*, and treatment was administered orally for five days. After treatment, mice were sacrificed and serum was analyzed for total cholesterol (TC), triacylglycerol (TG), high-density lipoprotein (HDL), and low-density lipoprotein (LDL). Sixty adult Swiss albino mice (25-35g) were randomly assigned into six groups of ten; normal control, infected control, infected + artesunate, and infected + combined extracts at 250, 500, and 1000 mg/kg body weight. Infection was established via intraperitoneal inoculation with *P. berghei* and treatment was administered orally for five days. After treatment, mice were sacrificed and serum samples were analysized for total cholesterol (TC), triacylglycerol (TG), high-density lipoprotein (HDL) and low-density lipoprotein (LDL). The infected untreated group showed elevated TC (4.53±0.06 mmol/L), TG (6.36±0.20 mmol/L), and LDL (5.87±0.06 mmol/L), levels with a reduction in HDL (0.83±0.35 mmol/L), indicating malaria-induced dyslipidemia. In contrast, extract-treated groups demonstrated significant ($p < 0.05$) dose-dependent decreases in TC (3.12±0.31, 2.50±0.22 and 2.19±0.72 mmol/L), TG (3.92±0.15, 2.14±0.22, 1.90±0.12 mmol/L) and LDL (2.83±0.18, 2.01±0.17 and 3.66±0.24 mmol/L), along with increased HDL (1.69±0.01, 2.70±0.61 and 4.03±0.08 mmol/L), for the 250, 500 and 1000 mg/kg body weight groups respectively. These effects were comparable to the artesunate-treated group (2.04±0.12, 2.18±0.16, 2.53±0.02 and 4.15±0.31 mmol/L). The combined extracts appeared to restore lipid balance disrupted by malaria infection. Overall, the coadministration of *A. conyzoides* and *C. afer* extracts shows potential in ameliorating malaria-associated lipid abnormalities, suggesting the presence of bioactive constituents with therapeutic relevance.

**Keywords:** *Ageratum conyzoides*, *Costusafer, Plasmodium berghei* and lipid profile

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# Synergistic Antihypertensive Effect of Camel Milk and Urine on L-NAME Treated Rats

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Milk and urine mixture reconstituted from some lactating Arabian camels (*Camelus dromedarius*) within Sokoto locality, Nigeria synergistically exhibited antihypertensive effect for some L-NAME-mediated hypertensive rats via non-invasive pressure measurements. Many unverified therapeutic claims were ascribed for them against varied diseases. This research aimed validation; verifying regimen's antihypertensive effect. Three used controls [normal, hypertensive negative (L-NAME only [50mg/kg body weight/day]) and hypertensive positive; amlodipine (10mg/kg body weight/day)]; with 3 treatment tests administered to all except normal control which is treatment-less were instituted. Para nitro-l-arginine methyl ester chemical; L-NAME ensured daily hypertension exposure. This followed OECD acute toxicity up-and-down procedures from 50 to 5000 mg/kg that was monitored through non-invasive regular measurements. Hypertension was checked with amlodipine or three CT regimens as 100, 300 and 500 mg/kg body weights of rats/day up to 28 days. Rats' blood pressure measured in mmHg was documented daily and weekly. All SBPs/DBPs and MABP were in mmHg. 4$^{th}$ week's significantly elevated ($p < 0.05$) hypertensive negative control's mean arterial blood pressure (146.7±1.8**), reduced to (111.8 ± 2.0) with CT3 [500mg/kg b.w], while PC's and normal control's MABP were (107.6 ± 2.6) and (95.4±1.4). NC's initial SBP (115.8± 2.1) compared to CT's SBP (138.6±2.3); increased by end of same 4$^{th}$ week to (119±1.3); all CT's SBPs however decreased to (129.6±2.6) for CT3, CT1 and 2 has (133.2±4.0) and (136.0±2.5) from their initials of (139.6±4.3) and (142.8±2.6) respectively. Findings suggest CT displaying significant synergistic antihypertensive impact, comparable to (amlodipine's) action, thus indicating promising natural alternative for hypertension management.

**Keywords**: Camel milk; combination treatment; systolic blood pressures and antihypertensive effect

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# Evaluation of Immunoglobulin G Response and Lipid Peroxidation in Mice Immunized with an *Azadirachta indica*–Silver Nanoparticle–Adjuvanted Inactivated Rabies Vaccine

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Rabies remains a major public health concern in low-resource regions, with high fatality and limited access to effective vaccines. Current inactivated rabies vaccines rely on aluminum-based adjuvants that can cause side effects and induce suboptimal immune responses. This study evaluated the efficacy and safety of silver nanoparticles (AgNPs) synthesized using the aqueous leaf extract of *Azadirachta indica* as an alternative adjuvant for inactivated rabies vaccine. The nanoparticles were characterized by UV–Vis spectrophotometry, dynamic light scattering, and thermogravimetric analysis, revealing a λmax of 460 nm, an average size of 33.72 nm, and thermal stability up to 400 °C. Mice (n = 8 per group) were divided into eight groups: negative and positive controls, AgNPs only (600 µg/mL), vaccine alone, or vaccine adjuvanted with 200, 400, or 600 µg/mL AgNPs or alum (600 µg/mL), administered intramuscularly. Serum IgG was quantified by ELISA, while brain malondialdehyde (MDA) levels were assessed using the method of Akanji et al. (2009). Vaccines adjuvanted with 400 µg/mL and 600 µg/mL AgNPs induced significantly higher IgG titres ($p < 0.05$) and lower MDA levels compared to controls and the alum group. These findings suggest that *A. indica*–derived AgNPs enhance humoral immunity and antioxidant capacity, supporting their potential as safe and effective adjuvants for inactivated rabies vaccines.

**Keywords:** *Azadirachta indica*, silver nanoparticles, rabies vaccine, IgG, antioxidant

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# Effect of *Azadirachta indica*–Silver Nanoparticle Adjuvant on Serum Immunoglobulin A Response and Toxicity in CVS-11 Inactivated Rabies Vaccine

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Rabies is a fatal zoonotic infection of the central nervous system, responsible for about 35% of global rabies deaths in Africa. Despite vaccination efforts, current inactivated rabies vaccines require multiple doses and elicit weak mucosal immune responses. This study evaluated the immunogenic and toxicological effects of *Azadirachta indica*–derived silver nanoparticles (AgNPs) as adjuvants in the CVS-11 inactivated rabies vaccine. AgNPs were synthesized using aqueous *A. indica* leaf extract and characterized by UV–Vis spectrophotometry, dynamic light scattering (DLS), and FTIR, showing λmax at 460 nm, mean particle size 21.21 nm, and phytochemical capping. Mice (n = 8 per group) were assigned to negative and positive controls, AgNPs only (600 µg/mL), vaccine alone, or vaccine adjuvanted with 200, 400, or 600 µg/mL AgNPs or alum (600 µg/mL), administered intramuscularly. Serum IgA was quantified using anti-rabies IgA ELISA, and renal and hepatic biomarkers (urea, creatinine, ALT, AST, ALP) were analyzed with standard biochemical kits. The 600 µg/mL AgNP-adjuvanted group showed a significant ($p < 0.01$) 23.09-fold increase in IgA titre compared to controls. Liver and kidney function indices remained within normal limits, indicating no detectable toxicity. These results demonstrate that *A. indica*–AgNPs enhance mucosal immune response without adverse effects, supporting their potential as safe adjuvants for inactivated rabies vaccines.

**Keywords:** *Azadirachta indica*, silver nanoparticles, rabies vaccine, IgA, toxicity

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# Enzymatic Production and Characterization of Antioxidant Hydrolysates from Pumpkin Seed Protein Concentrate

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Pumpkin seeds are recognized as nutrient-dense foods with therapeutic value across various traditional diets. Despite their high protein content, limited research has explored the bioactive hydrolysates derived from pumpkin seed proteins and their potential health-promoting effects. This study aimed to produce, characterize, and evaluate the antioxidant properties of pumpkin seed protein hydrolysates generated using three proteolytic enzymes including alcalase, bromelain, and papain. Protein concentrate obtained from defatted pumpkin seed flour was subjected to enzymatic hydrolysis under optimal pH, enzyme-to-substrate ratio, and temperature for 8 hours. Hydrolysates collected at hourly intervals were analyzed for antioxidant activity using DPPH radical scavenging, ferric reducing antioxidant power (FRAP), and metal ion chelating assays. Bromelain-derived hydrolysates exhibited the strongest antioxidant properties, showing the highest ferric reducing power, DPPH radical scavenging, and metal chelation activities after 7 hours of hydrolysis. The highest degree of hydrolysis was recorded for alcalase after 6 hours. SDS–PAGE and amino acid profiling revealed low-molecular-weight peptides rich in essential amino acids such as lysine, leucine, and isoleucine. These findings highlight the potential of bromelain-generated hydrolysates as natural functional ingredients for mitigating oxidative stress–related disorders. Future studies should focus on peptide isolation, sequence identification, and validation of bioactivity using cellular and clinical models to advance their application in functional food and nutraceutical development.

**Keywords:** Pumpkin seed protein, enzymatic hydrolysis, antioxidant activity, functional food, bioactive peptides

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# Evaluation of the Nutritional and Physiological Effects of Two Locally Formulated Aphrodisiacs, *Tsimi* and *Gumba*, in Adult Women

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Herbal aphrodisiacs are widely used for enhancing sexual health, yet their biochemical and physiological safety remains poorly defined. This study assessed the nutritional composition, antioxidant potential, and selected hematological and toxicological parameters of two locally formulated aphrodisiacs, *Tsimi* and *Gumba*, in 150 healthy adult female volunteers aged 25–50 years. Participants were randomized into three groups (n = 50 per group): *Tsimi*, *Gumba*, and placebo. Each received 10 mL of the respective formulation daily for eight weeks under controlled dietary conditions. Proximate and phytochemical analyses revealed appreciable carbohydrate (45–52%), protein (12–16%), and lipid (8–11%) contents, along with detectable levels of flavonoids, tannins, and alkaloids. Both formulations demonstrated moderate antioxidant activity, with mean vitamin C and E concentrations of 24.5 ± 2.3 mg/100 g and 3.2 ± 0.4 mg/100 g, respectively. Hematological profiles showed no significant changes ($p > 0.05$) in RBC, WBC, or platelet counts compared to baseline, though *Tsimi* slightly increased hemoglobin by 4.8%. Liver and renal function markers (AST, ALT, urea, creatinine) remained within reference ranges across all groups. No clinical or biochemical signs of toxicity were observed. These findings suggest that *Tsimi* and *Gumba* are nutritionally rich, exhibit antioxidant potential, and appear safe for short-term use under controlled conditions. However, broader toxicological and immunological evaluations are recommended to confirm long-term safety and efficacy.

**Keywords:** Phytochemical, Hematology, Proximate Analysis, *Tsimi*, *Gumba*

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# FTIR and GC-MS Analysis of *Anthonotha macrophylla* Leaf Extract

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Medicinal plants are important source of medicines and have been used to treat different ailments due to their ease of availability, and presence of bioactive compounds. *Anthonotha macrphylla* is a plant used in the treatment of skin infection, malaria, diarrhoea and headache in traditional medicine. However, there is a dearth of scientific report about its phytoconstiuents. This study aims to identify the bioactive constituents present in *Anthonotha macrophylla* leaves. Powdered *Anthonotha macrophylla* leaves were extracted in ethanol for 72 hours, filtered and concentrated using a rotary evaporator. The extract was characterized by Fourier transform infrared (FTIR) spectroscopy and gas chromatography-mass spectrometry (GC-MS) techniques. FTIR analysis showed significant peaks for C≡C,–OH, C=C, C-H, C=O functional groups. GC-MS profiling revealed the presence of various compounds 4-O-Methylmannose, n-Hexadecanoic acid, 2-Piperidinone, N-[4-bromo-n-butyl]-, 4-((1E)-3-Hydroxy-1-propenyl)-2-methoxyphenol, Methyl 18-methylnonadecanoate, squalene, and phytol. These compounds have been shown to have numerous functions such as antibacterial, antimicrobial, antioxidant, anti-inflammatory and hepatoprotective activity. The results of this study suggest that *Anthonotha macrophylla* leaves contain bioactive compounds that may have therapeutic potentials and thus are beneficial to human health.

**Keywords**: *Anthonotha macrophylla*, bioactive compounds, FTIR, GC-MS, Medicinal plants

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# Evaluation of Selected Neem Compounds as Potential Inhibitors of Trehalose-6-Phosphate Synthase (TPS) in *Anopheles gambiae*

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Trehalose metabolism plays a critical role in the growth, development, and survival of insects, particularly in the malaria vector, *Anopheles gambiae*. Trehalose-6-phosphate synthase (TPS) catalyses the first committed step in trehalose biosynthesis, hence, disrupting its activity offers a promising molecular strategy for the control of *A. gambiae*. The neem plant, *Azadirachta indica*, presents a source of insecticidal and bioactive phytochemicals. In this study, molecular docking analyses were used to evaluate the potential of some neem-derived phytochemicals as inhibitors of TPS in *A. gambiae*. A total of 310 neem compounds were retrieved from the IMPPAT and Dr Duke's phytochemical databases. Three-dimensional (3-D) structure of *A. gambiae* TPS was modelled and molecular docking simulations were performed using the iDock platform. Known TPS inhibitors such as camptothecin and rocaglaol as well as the natural substrates, UDP-glucose and glucose-6-phosphate, were used as reference ligands. Binding affinities and molecular interactions were analysed to identify high- affinity inhibitors. Higher binding affinities to TPS were demonstrated by neem limonoids, Deacetyl-7-benzoylepoxyazadiradione (−11.760 kcal/mol) and 7-Deacetyl-7-benzoylgedunin (−11.206 kcal/mol), and other neem compounds, Lupeol (−11.067 kcal/mol) and 7-deacetylgedunin (−11.013 kcal/mol), compared to camptothecin (−9.005 kcal/mol) and strobilurin (−8.261 kcal/mol). These neem metabolites also bound more strongly than the enzyme's natural substrates, UDP-glucose (−8.313 kcal/mol) and glucose-6-phosphate (−5.231 kcal/mol). The higher binding affinity of neem-derived phytochemicals, particularly limonoids, over the known inhibitors and natural substrates, highlight their promising inhibitory potential against the TPS of *A. gambiae*. This positions neem plant as a source of eco-friendly bioactive molecules for malaria vector control strategies that targets trehalose biosynthesis. There is need for further validation through *in vitro* and *in vivo* studies.

**Keywords:** *Anopheles gambiae*, Trehalose-6-phosphate synthase, Neem-derived phytochemicals, Molecular docking, Binding affinities, Potential inhibitors.

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# Phytochemical Screening and Chemical Composition of Aqueous Extract of Mesocarp of Doum Palm (*Hyphaene thebaica*) Fruit

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Doum Palm (*Hyphaene thebaica*) is an edible fruit commonly grown and also consumed as traditional beverages in the northern axis of Nigeria due to its acclaimed source of essential nutritional and medicinal substances. The study was conducted to evaluate both qualitative and quantitative phytochemical screening, proximate analysis, mineral and vitamin compositions of aqueous extract of air-dried powdered sample of the mesocarp of Doum palm (DP) fruits. The analyses of the aforementioned parameters were analyzed according to the official methods of analysis described by Association of official analytical chemists (AOAC, 2005). The results obtained revealed the presence of phytochemicals of 34.31%, 36.06%, 27.60%, 0.55%, 0.23%, 0.42% and 0.82% for saponin, alkaloid, total phenol, flavonoid, terpenoid, tannin and steroid respectively; the percentage proximate composition with moisture content (11.63%), crude protein (15.17%), crude fiber (22.17%), nitrogen free extract (55.23%), ash (3.10%), and crude fat (4.32%). The percentage minerals revealed sodium (0.18%), magnesium (0.20%), calcium (0.19%), potassium (0.57%), and iron (98.84%) while vitamins A, C and E were present at 50.61%, 43.62% and 5.76% respectively. Therefore, aqueous extract of mesocarp of DP fruit could be employed as a good source of nutrients, dietary antioxidant and some essential secondary plant metabolites. The high content of elemental iron may also help in combating anemia.

**Keywords:** Doum palm, mesocarp, phytochemicals, minerals, vitamins

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# Comparative Studies and Bioactive Compounds Analysis on Tea Leaves Sample (*Camellia sinensis*) and Jackfruit (*Artocarpus heterophyllus*)

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*Camellia Sinensis* generally known as green tea leaves found majorly in Taraba, Northeast, Nigeria is the second most consumed drink after water worldwide due to its promising benefit and *Artocarpus heteropyllus* known as Jackfruit leaves found mostly in Southeast Nigerian believed to have similar good bioactive compounds and benefit as tea was proven by this research work. As per Antioxidant, two antioxidants (DPPH and HRSA) were considered and had significant value of 10mg/ml, 20mg/ml and 100mg/ml for Jackfruit, Camellias and Ascorbic Acid respectively in terms of percentage which show a mere significant value for the observed leaves in focus for DPPH, while for the HRSA there is a slight decline having camellia and jackfruit close with 20mg/ml and Ascorbic acid as the standard having 97mg/ml, which show a significant value. The result suggested that jackfruit is a good source of antioxidant.

**Keywords:** Jackfruit, Phytochemicals, Antioxidant, DPPH, *C. sinensis*

FASBMB2025/MB-042

# Anti-Diabetic, Antioxidant and Hypolipidemic Activities of *Bridelia ferruginea* Stem Bark Methanol Extract on Alloxan-Induced Diabetic Rats

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*Bridelia ferruginea*, is widely consumed medicinal plant that grows in the Savannah or rain forests of Africa to treat diabetes with reported antioxidant properties. This work investigates the anti-diabetic, antioxidant and hypolipidemic activities of methanol stem bark extract of *Bridelia ferruginea* in Alloxan induced diabetic rats. The rats were randomly divided into 6 groups: positive and negative control, diabetic untreated, and three treatment groups receiving 100, 200, and 300 mg/kg body weight of extract respectively for 24 days. Blood glucose level, oxidative stress markers and lipid profile were determine using standard biochemical techniques. Results showed significant ($P$<0.05) reduction in blood glucose and MDA levels in extract treated groups compared to diabetic controls. While SOD and catalase activities were significantly increased, suggesting a dose -dependant antioxidant effect. Serum total cholesterol, TG, and HDL showed significant difference ($P$<0.05) between treated groups when compared to untreated control. However, serum low density lipoprotein revealed a non-significant difference in all the treatment groups when compared to normal, and untreated groups. The present study revealed that *B. ferruginea* stem bark methanol extract showed strong antioxidant potentials, average hypolipidemic effect and revealed strong glucose lowering potentials.

**Keyword**: *Bridelia ferruginea*, Glucose, Lipid profile, Antioxidant and oxidative stress marker (MDA)

FASBMB2025/MB-043

# Neurochemical and Behavioral Antidepressant-Like Effects of *Portulaca oleracea* Extract in Sleep-Deprived Rats

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Depression is a debilitating mental disorder associated with increased risk of criminal behaviour, substance abuse, and suicide. This study evaluated the antidepressant potential of hydro-ethanolic extract of *Portulaca oleracea* in Wistar rat model. Thirty male Wistar rats weighing 180±20 grams were divided into five groups. The animals were subjected to stress by preventing them from sleeping for 24 hours after which they were treated. Group 1 (control) received no treatment, group 2 was treated with fluoxetin (5mg/kg b.w.) while groups 3, 4 and 5 were treated with *Portulaca oleracea* (200, 400 and 600 mg/kg b.w. respectively) for 14 days. The forced swim test (FST) and tail suspension test (TST) were used to investigate the antidepressive effect of *Portulaca oleracea* in the rat model. Cerebral cortex, cerebellum, medulla oblongata, midbrain and basal ganglia were isolated to elucidate the extract's impact on monoaminergic neurotransmission, acetylcholinesterase activity, and calcium homeostasis across the brain region. There were significant reductions of the immobility times in the FST and TST following oral administration of extract 2 hours prior to testing when compared to the control group and no significant difference in dose variation when compared to FXT group. After treatment with *Portulaca oleracea*, dopamine, norepinephrine and serotonin were significantly increased in the studied brain region, acetylcholinesterase was increased in all brain regions except in the cerebellum while there was a decrease in calcium concentration of the brain cortex. The results suggest that *Portulaca oleracea* exhibit antidepressant-like effect and the ability to modulate key neurochemical pathways implicated in depression.

**Keywords:** Antidepressant, *Portulaca oleracea,* neurochemical pathways, brain, mental disorder.

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# Protective Role of Virgin Coconut Oil against Kidney Dysfunction Induced by Spent Vegetable Oils from Different Sources in Rats

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The repeated use of vegetable oils for frying leads to the formation of thermal oxidation products, which pose significant health risks, including renal damage. Virgin coconut oil (VCO), rich in medium-chain fatty acids and antioxidants, has been reported to possess protective properties against oxidative stress. This study aimed to evaluate the protective effect of VCO against kidney dysfunction induced by spent vegetable oils from different dietary sources in Wistar rats. Forty-five adult Wistar rats were divided into nine groups and exposed to either spent vegetable oils (from fish and bean cake vendors) at single and double doses for 14 days, followed by treatment with 1 mL of VCO for another 14 days. Serum levels of urea, creatinine, uric acid, and electrolytes were measured. Kidney tissues were also examined histopathologically. Spent vegetable oils significantly increased serum urea, creatinine, and uric acid levels, an indication of renal impairment. Histopathological examination revealed tubular necrosis, glomerular damage, and inflammatory changes. Administration of VCO significantly ameliorated these biochemical alterations and improved kidney function markers, although it had limited effect on reversing structural damage. Virgin coconut oil demonstrates a protective role against kidney dysfunction induced by spent vegetable oils by mitigating biochemical disturbances and oxidative stress such as malondialdehyde (MDA). These findings suggest that VCO may serve as a potential therapeutic agent in reducing renal toxicity associated with the consumption of repeatedly heated oils.

**Keywords:** virgin coconut oil, spent vegetable oil, kidney dysfunction, oxidative stress, Wistar rats, nephroprotection.

FASBMB2025/MB-045

# Ethanolic Leaf Extract of *Abrus precatorius A*meliorates Arsenic-Induced Ionoregulatory Disruptions in Rats

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Arsenic is a naturally occurring and pervasive metalloid found in soil, water, food, and the environment. Chelation therapy has a number of adverse effects that restrict its clinical utility when used to treat arsenic poisoning, thus this study investigated the protective effects of ethanol leaf extract of *Abrus precatorius* against arsenic-induced ionoregulatory disruptions in male Wistar rats. Forty-nine (49) rats were divided into seven groups: control, *A. precatorius* low dose (300 mg/kg bw), *A. precatorius* high dose (600 mg/kg bw), arsenic (100 ppm) plus *A. precatorius* low dose, arsenic (100 ppm) plus *A. precatorius* high dose, arsenic (100 ppm) plus vitamin C (50 mg/kg bw) and arsenic (100 ppm),. Treatments were given orally for 6 weeks. Arsenic exposure reduced body weight gain, altered liver and brain weight coefficients, disrupted electrolyte balance, and inhibited total-, $Na^+/K^+$-, $Ca^{2+}$-, and $Mg^{2+}$- adenosine triphosphatases (ATPases) in liver and brain. Co-administration of *A. precatorius* dose-dependently restored these parameters. Findings suggest that *A. precatorius* at the doses administered ameliorated arsenic-induced ionoregulatory disruptions, and there may be some scope in the use of *A. precatorius* in the management of arsenic intoxication especially in cases where the subjects cannot be removed from the source of arsenic exposure, such as in occupational and environmental exposure.

**Keywords**: Arsenic, Ethanolic leaf extract, *Abrus precatorius*, ATPases, ionoregulatory disruptions

FASBMB2025/MB-046

# Green-Synthesized *Detarium microcarpum* Silver Nanoparticles Induce Cell-Cycle Arrest and Modulate BAX, BCL-2, and p53 to Promote Apoptosis in Oral Cancer Cells

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Green synthesized nanoparticles offer a promising alternative for cancer therapy due to their biocompatibility and potent bioactivity. This study investigated the antiproliferative and pro-apoptotic effects of *Detarium microcarpum*–mediated silver nanoparticles (DM-AgNPs) on OECM oral squamous carcinoma cells. DM-AgNPs were synthesized using aqueous plant extract and characterized using UV–Vis spectroscopy, FTIR, XRD, and scanning electron microscopy. Cytotoxicity was assessed through dose response analysis using CellTiter-Glo, while glutathione depletion was evaluated using the GSH/GSSG assay. Apoptosis and cell-cycle arrest were assessed by measuring intracellular ROS levels, and the gene expression of BAX, BCL-2, and p53 was quantified using qPCR. DM-AgNPs significantly ($P < 0.05$) reduced cell viability in a dose-dependent manner (12.5–200 µg/mL), yielding an $IC_{50}$ of 16.52 µg/mL, identified as the optimal concentration for treatment. Treated OECM cells showed increased ROS generation and glutathione depletion, serving as prognostic biomarkers. Gene expression analysis revealed upregulation of BAX and p53, along with downregulation of BCL-2, resulting in a markedly elevated BAX/BCL-2 ratio (15.98), confirming activation of the inherent apoptotic pathway. *Detarium microcarpum*–derived AgNPs exhibit strong antiproliferative, apoptosis-inducing, and cell-cycle arrest effects in oral cancer cells. These findings support their potential as a natural, nanotechnology-based therapeutic candidate for oral cancer management.

**Keywords:** *Detarium microcarpum*, Biogenic-silver nanoparticles, OECM oral cancer cells, Apoptosis, Cell cycle arrest, BAX/BCL-2 ratio, p53 gene expression

FASBMB2025/MB-047

# Bioactivity-Guided Fractionation, Gastroprotective Evaluation and *In Silico* Characterization of Antiulcer Phytochemicals from *Brassica Oleracea* in Ethanol-Induced Ulcer in Male Wistar Rats

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Gastric Ulcer Disease (GUD) remains prevalent due to drug side effects, comorbidities, and recurrence, highlighting the need for new management strategies. Cabbage (*Brassica oleracea*), rich in bioactive phytochemicals, is traditionally valued for gastroprotective effects, though the specific compounds remain underexplored. This study investigated bioactivity-guided fractionation, gastroprotective evaluation, and *in silico* characterization of *B. oleracea* extracts in ethanol-induced ulcer in rats. Cabbage extracts (n-hexane, ethyl acetate, methanol) were screened, with n-hexane (HEBO) and ethyl acetate (EtBO) showing higher activity. Their fractions (HEBOF, EtBOF) were evaluated in 40 rats, randomized into eight groups (n=5): control, negative control, cimetidine (50 mg/kg), rabeprazole (20 mg/kg), HEBOF (250/500 mg/kg), and EtBOF (250/500 mg/kg). Treatments lasted seven days. Biochemical assays measured GSH, MDA, IL-6, TNF-α, catalase, SOD, and $H^+/K^+$-ATPase. EtBOF demonstrated superior gastroprotective effects, with 500 mg/kg significantly lowering ulcer index, increasing catalase, SOD (7.33 ± 0.31; 9.02 ± 0.17 U/mg protein), and GSH (59.67 ± 0.22 µmol/g), while reducing MDA (4.02 ± 0.20 µmol/g). Elevated IL-6, TNF-α (2.63 ± 0.06; 2.64 ± 0.06 ng/mL), and $H^+/K^+$-ATPase (9.21 ± 0.29 µmolPi/mg/hr) in negative control were decreased in EtBOF 500 mg/kg (0.51 ± 0.02; 0.57 ± 0.02 ng/mL; 1.10 ± 0.05 µmolPi/mg/hr). GC-MS identified 20 compounds and HPLC revealed 12 polyphenolics. *In silico* analysis highlighted CPT, APA, naringenin, and quercetin as lead candidates with strong binding to $H^+/K^+$-ATPase, urease, muscarinic, and histamine receptors. CPT complied with Lipinski's, Veber's, and lead-likeness rules. EtBOF significantly protected against ethanol-induced ulcers, suggesting CPT and APA as promising antiulcer drug candidates.

**Keywords:** Antiulcer phytochemicals, Bioactivity-guided fractionation, *Brassica oleracea*, Gastroprotection, $H^+/K^+$-ATPase

## SUB-THEME 5

## SINGLE CELL GENOMICS AND PRECISION MEDICINE (SPM)

FASBMB2025/SPM-001

# Probing the Lineage Path of Induced Pluripotent Stem Cells (iPSCs) to Pancreatic Beta Cells *In Vitro*

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Type 2 Diabetes (T2D) is a major cause of morbidity and mortality, affecting more than 30 million people in the US. T2D is a complex polygenic and multifactorial disorder, caused by both defective insulin secretion and insulin resistance in peripheral tissues. To date, more than 200 well-validated genetic variants have been identified as risk factors for T2D, but for most of those, the impact on Beta cell development and/or function is poorly understood. To facilitate the understanding of T2D pathophysiology, we have generated iPSC cell lines from the skin cells of 52 Finnish diabetic or nondiabetic individuals and are pursuing *in vitro* differentiation of these iPSCs to mature insulin secreting Beta cells. We are monitoring single-cell gene expression by scRNA-seq at multiple stages during differentiation. A major challenge of this project is to identify the lineage relationships of cell types over the month-long differentiation process, and to assess the effect of genotype. Several computational methods have been developed and employed by the single-cell research community to reconstruct developmental trajectories, and these methods have provided valuable insights for other systems into developmental lineages of multiple cell types. After considering several options, our preliminary approach is to utilize pseudotime and realtime analysis programs including CellRouter and Waddington Optimal Transport (WOT) to identify gene expression changes that occur during the seven stages of differentiation. Unsupervised CellRouter analysis of over 20,000 cells across iPSC to Beta cell developmental stages revealed that the cells in stages 0, 1, 4, 6, and 7 are readily distinguished by their patterns of gene expression. We observed expression of developmentally regulated Beta cell progenitor genes such as NANOG, PDX1, and NKX6-1, and subsequently the transcription of mature beta cell genes such as INS and ABCC8. We also observed bihormonal cells expressing both GCG and INS in stage 4, but monohormonal INS-producing cells characteristic of mature beta cells were observed by stage 6. We anticipate this type of analysis will shed light on the complexities of beta cell differentiation and provide opportunities to define the consequences of T2D risk variants on the development and function of human pancreatic beta cells.

**Keywords**: Type II Diabetes, pancreatic beta cells, iPSCs

FASBMB2025/SPM-002

# Non-Invasive Profiling of Maternal Blood Reveals Candidate Placental Cell Regulatory Signatures in Healthy Pregnancies Including CGB3, PGF, ERVFRD-1, GCM1, SNAI1, and EPAS1

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Placental dysfunction is a major cause of pregnancy complications like preeclampsia and fetal growth restriction, threatening maternal and fetal outcomes. Many of these disorders arise from epigenetic changes that disrupt gene regulation in the placenta. Monitoring placental health is critical, yet direct tissue sampling is invasive and impractical. Emerging evidence suggests that placental cells circulate in maternal blood, offering a non-invasive window into placental health. This study aimed to determine whether regulatory signatures of placental marker genes are detected in maternal PBMCs by profiling chromatin accessibility. Blood samples were collected from four healthy second-trimester pregnant women at Yusuf Dantsoho Memorial Hospital, Kaduna, Nigeria. PBMCs were isolated using Ficoll-Paque density centrifugation, libraries prepared with the OMNI-ATAC-seq protocol, and sequencing performed. Thousands of accessible chromatin regions were identified, many annotated to promoters and enhancers of well-validated placental regulatory genes. Significant promoter accessibility was observed at multiple placenta-associated regulatory genes (MACS2 peaks at q < 1e-4; gene-level FDR < 0.05).These included CGB3 ($p = 2.34 \times 10^{-28}$), central to chorionic gonadotropin production; ERVFRD-1 ($p = 1.60 \times 10^{-19}$), and GCM1($p = 1.19 \times 10^{-21}$), key regulators of syncytiotrophoblast fusion; SNAI1($p = 4.74 \times 10^{-27}$), an epithelial–mesenchymal transition driver of trophoblasst invasion; EPAS1($p = 8.50 \times 10^{-22}$) and PGF ($p = 2.22 \times 10^{-45}$), hypoxia and angiogenesis mediators linked to preeclampsia. The detection of these canonical regulators demonstrates that placental cell regulatory signatures are reproducibly detectable in maternal PBMC chromatin accessibility profiles. These findings provide proof-of-principle that PBMC-based ATAC-seq can non-invasively capture placental regulatory programs in healthy pregnancy, supporting their potential as early biomarkers of placental dysfunction.

**Keywords:** Chromatin Accessibility, Non-Invasive Prenatal Testing, Placental Cells Marker Genes, Peripheral Blood Mononuclear Cells (PBMC), Materna-Fetal Health.

FASBMB2025/SPM-003

# Single-Cell Transcriptomic Profiling of Reticulocytes Reveals Heterogeneity and Distinct Subpopulations within Stress Erythroid Progenitors with Increased Fetal Hemoglobin Expression

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Stress erythroid progenitors (SEPs) are specialized cells derived from short-term hematopoietic stem cells that proliferate mainly in extramedullary sites like the spleen in response to hypoxia, inflammation, and anaemia, producing erythrocytes with high fetal haemoglobin (HbF) expression. Understanding the cellular diversity and developmental trajectory of SEPs is therefore crucial. In this study, we performed comprehensive single-cell transcriptomic profiling and annotation of different cell types from reticulocytes enriched from whole blood of sickle cell anaemia patients and apparently healthy controls. Libraries were prepared using the 10X Genomics pipeline, demultiplexed with CellRanger, and analysed with Seurat. Stringent QC metrics were performed to filter out low quality cells. The filtered data were integrated, normalized and scaled. Principal components that capture the variation within the data were determined. Cells were clustered using a KNN graph, and the Louvain algorithm optimized modularity. Clusters were defined using standard globin canonical gene markers. Focusing on the stress erythroid progenitors (SEPs) and F-cells, we applied high-resolution sub-clustering analysis to uncover previously un-reported heterogeneity within these populations. The SEP population revealed five cell states while the F-cell population showed six cell states, characterized by unique marker genes, suggesting functional diversity within these cell populations. These cell states are evidence of developmental changes during stress erythropoiesis. Pseudotime trajectory analysis further revealed the developmental paths of the cell states within SEPs, providing insight into their temporal gene expression dynamics during stress erythropoiesis. These findings provide a refined cellular diversity of SEPs and F-cells, laying the foundation for understanding how SEPs activation increase HbF expression, thus increasing production of F-cells. Further studies on the functional and developmental state transitions within SEPs could improve our understanding of stress erythropoiesis and production of F-cells.

**Keywords:** Stress erythropoiesis, Single-cell transcriptomics, Fetal hemoglobin (HbF), Reticulocyte heterogeneity, Stress erythroid progenitors.

FASBMB2025/SPM-004

# Single- nuclei RNA Sequencing Reveals Cellular Heterogeneity and Specific Gene Ontology Profiles (DUSP9, XAGE3, PEG10 and LGALS2) in Third Trimester Human Placenta of Nigerian Origin

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The human placenta is a vital organ that performs the functions analogue to those of the lungs, liver, kidney for the growing foetus during pregnancy. It achieves these through the coordinated activity of different cell types and any malfunctioning of these cell types can lead to adverse pregnancy outcome. Single-nuclei RNA sequencing provides a powerful approach to understanding of the placenta cell types. However, there is a limited knowledge of the placental cell type composition and transcriptional activities during physiological condition also, individuals of African origin have been underrepresented in genomic research, to fill in these gaps, biopsies were collected from the four regions of third trimester human placenta from two women with term labor who were of Nigerian origin. Single nuclei were isolated from the four regions, single nuclei were barcoded using the 10X genomic pipelines, cDNA libraries were constructed. Quality checks of the libraries were done using tape station and the qubit fluorometer. Sequencing of the libraries were done using the Illumina sequencing platform. Raw sequencing data was processed using cell ranger version 8. A total of 2,761 cells were obtained, with 100% mapping to the human reference genome (GRCh38). A count matrix was generated and analyzed using Seurat, resulting in the identification of 13 distinct clusters corresponding to 9 different cell types. Canonical markers were used to assign marker genes (P value < 0.01 and log2foldchange > 0.05 were set as the threshold for significantly differential expression of the marker genes). Our analysis reveals a set of functionality significant genes including PEG10, DUSP9, LTF and XAGE3 marker genes, each playing critical roles in cellular signaling, immune regulation and trophoblast biology. This research findings provides novel insight into the transcriptomic profile of Nigerian third trimester placenta and identifies top markers genes for further investigation in the maternal- fetal health research.

**Keywords**: Single nuclei RNA sequencing, Third Trimester Human Placenta, Cell Types, Gene Ontology, Transcriptomic

## SUB-THEME 6

## MATERNAL, INFANT AND YOUNG CHILD HEALTH (MIY)

FASBMB2025/MIY-001

# Assessment of Infant and Young Child Feeding Practices by Mothers Attending Post-Natal Clinic at Abuja Municipal Area Council

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Feeding during the first two years of life are important for growth and mental development of a child and the prevention of malnutrition and child mortality. This study aimed at assessing the Infant and Young Child Feeding (IYCF) Practice by mothers attending postnatal care at Family Health Clinic, Area 2 Garki, Abuja Municipal Area Council**.** A descriptive cross-sectional study design technique was utilized using semi structured interviewer-administered questionnaire to collect data from randomly selected 100 mothers. Data on sociodemographic and economic characteristics, hygienic practices, breastfeeding and complementary feeding practice were collected. Among respondents, 74.4% were married women, mostly aged 26–30 (45.2%), and 57.3% had senior secondary education. Nearly half (46.3%) were traders or businesswomen. Children studied were mostly under 6 months (46.3%), followed by 7–12 months (32.9%) and 13–23 months (20.7%). Most (81.7%) had normal weight-for-height. Breastfeeding was prevalent (87.7%), with 58.3% feeding on demand and 58.0% breastfeeding over 8 times daily. Weaning occurred mainly at 12–23 months, with 80% weaned by mothers and 30% self-weaned. Complementary feeding was initiated by 79.0%, mostly at 6 months (52.5%) due to perceived readiness. Pap was the sole complementary food for 69.5%. Breastfeeding and complementary feeding practices were generally appropriate. Educational efforts are crucial to ensure the WHO guidelines and underscore the significance of the first 1,000 days in child development.

**Keywords**: Feeding practices, breast feeding, complementary feeding, caregivers, malnutrition.

FASBMB2025/MIY-002

# Investigating *Pentadiplandra brazzeana* Root-Supplemented Diet Intervention on Selected Biomarkers in a Postpartum Uterine-cleansing and Involution Rat Model

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Poor uterine cleansing and involution contributes to poor postpartum recovery, causing undesirable complications and death. *Pentadiplandra brazzeana* Baill root has been traditionally used for enhancing uterine cleansing and involution during early postpartum, but without scientific validation. This research investigated the effect of *P. brazzeana* Root-Supplemented Diet (PBRSD) intervention on selected biomarkers in a postpartum uterine-cleansing and involution rat model. Thirty female Wistar rats were randomly distributed into six groups (n = 5): non-pregnant rats fed with basal diet; lactating rats fed with basal diet (Control Group (CG)), positive control diet (100 g/kg *Zingerber officinale*), test diet (TD) I (50 g/kg PBRSD), TD II (100 g/kg PBRSD) and TD III (200 g/kg PBRSD). The effects of PBRSD on weight, uterine indices and morphology were measured. Furthermore, serum oestrogen, Matrix Metalloproteinase 9 (MMP9), Tumor Necrosis Factor α (TNF-α) and Nuclear Factor Kappa B (NF-κB) were measured in the postpartum lactating rats (dams), using commercial enzyme-linked immunosorbent assay kits. Expression of Phospholipase $A_2G_3$ (*Pla2g3*) gene was investigated using real-time quantitative polymerase chain reaction. Investigations showed, PBRSD at 50, 100, and 200 g/kg concentrations, significantly decreased ($p < 0.05$) weight, uterine indices, MMP9 activity, TNF-α and NF-κB levels. Additionally, PBRSD significantly downregulated ($p < 0.05$) *Pla2g3* ($1.70 \pm 0.07$ in CG to $0.03 \pm 0.02$ treated group) gene expression in dams compared to the CG. The PBRSD exhibited uterine cleansing and involution effect in Wistar rats, corroborating the ethnobotanical use of *P. brazzeana* root, for improving postpartum uterine cleansing and involution.

**Keywords**: Gene expression, *Pentadiplandra* brazzeana, *Pla2g3,* Postpartum, Uterine cleansing model.

FASBMB2025/MIY-003

# Infant and Young-Child Feeding Practices for Under-two Children Involved in Community Infant and Young Child Feeding Programme in Zaria, Nigeria

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Infant and young child feeding practices have substantial consequences for the growth, development, and survival of infants and children during the first two years of life and throughout life. The study aimed to assess the infant and young child feeding practices among the caregiver of children (0 -23 months) enrolled in a community infant and young child feeding programme. A validated semi-structured questionnaire was used to collect information's. The major food consumed was legumes (62.7%) and cereals (60.8%). Over (74.8%) of the caregivers were still breastfeeding during the period of the study, (22%) of caregivers-initiated breastfeeding within one hour of birth and 8.2% exclusively breastfed their children; the majority (91.7%) of the caregivers breastfed on demand. Only (24.5%) of the caregiver met minimum meal frequencies, (10.1%) diversified their diet, while (47.5%) met the minimum acceptable diet. Almost two third of the indices measured for the quality of Community Infant and Young Child Feeding programme was rated very good in Wucicciri, rated poor in Rafin Magaji and also poor in Babban Dodo primary health care. This study revealed inappropriate infant and young child feeding practices in study area, despite being enrolled in the Community Infant and Young Child Feeding programme. Therefore, these poor practices needed urgent action and aggressive sustained intervention.

**Keywords**: Under-two Children, Dietary Intake, caregivers, Infant and Young child feeding practice, (C-IYCF) programme

FASBMB2025/MIY-004

# Ribramo: Potential Remedy for the Reversal of Oxidative Stress in Children with Severe Acute Malnutrition

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Severe Acute Malnutrition (SAM) is a global health crisis, responsible for over 50% of child deaths in vulnerable regions. Mortality and morbidity in SAM are critically compounded by Oxidative Stress (OS), a metabolic imbalance that drives cellular damage, growth faltering, and long-term non-communicable disease risk. Standard Ready-to-Use Therapeutic Foods (RUTF) though effective, are limited by sustainability and coverage. RIBRAMO (*Moringa oleifera* fortified rice bran RUTF), a novel, locally produced alternative RUTF designed to provide essential nutrition while delivering high phyto-components. In this study, acceptability, safety and shelf-life quality of this product were evaluated. Results showed high overall sensory acceptability mean score (8.8) and excellent antioxidant properties, high in vitro protein digestibility (76.55%) and solubility (89.78%). Safety analysis confirmed low levels of total aflatoxin (3.305µg/kg), antinutrients that ranged from 0.007± 0.0038 to 104.32mg/100g, and heavy metals (Chromium, 6.743; Mercury,0.674; Arsenic, 0.514; Cadmium, 0.011and Lead 0.063mg/Kg). Shelf life of the product as indicated by water activity (0.34) microbial counts, in addition to peroxide and acid value of 2.82±0.104 to 3.88±0.13mEqO/Kg and 0.132±0.014g/kg respectively, were below standard limits thereby confirming the product's stability over a period of 12-weeks.Thus RIBRAMO could provide a sustainable, acceptable, and promising dual-action intervention that can combat SAM and reverse the detrimental effects of oxidative stress in affected children.

**Keywords**: Severe Acute Malnutrition, Heavy Metals, Aflatoxin, Shelf Life.

FASBMB2025/MIY-005

# Impact of Optimized Complementary Foods on Anthropometric and Biochemical Parameters in Children Under Five in Takalau, Kebbi State

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In Nigeria, inadequate complementary feeding practices contribute significantly to childhood malnutrition. This randomized controlled trial evaluated the impact of optimized complementary foods (OCF) on anthropometric and biochemical parameters in children aged 6-59 months in Takalau, Kebbi State, Nigeria, over an eight-week period. 140 children aged 6-59 months attending the Out-patient Therapeutic Centre in Takalau were randomly assigned to receive either OCF or standard commercial complementary food. The intervention group received optimized complementary foods, while the control group received standard care. Anthropometric measurements (weight, height, MUAC) and biochemical measurements were taken at baseline and after eight weeks. Data obtained were subjected to one way ANOVA and the results revealed significant improvements in weight, mid upper arm circumference, skin fold thickness and selected biochemical parameters in the OCF group compared to the control group ($p<0.05$). The findings suggest that eight weeks of feeding trial resulted in improved anthropometric and biochemical parameters of children aged 6-59 months in Takalau, Kebbi State, Nigeria.

**Keywords**: Complementary feeding, malnutrition, anthropometry, biochemical parameters, child nutrition.

FASBMB2025/MIY-006

# Dietary Patterns and Nutritional Status of Vesico Fistula Patients: A Study from Birnin Kebbi, Nigeria

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Vesicovaginal fistula (VVF) is a serious health issue affecting women's quality of life, particularly in low-resource settings. Nutritional status is a crucial indicator of overall wellbeing and a predictor of future health outcomes. Assessing nutritional status is vital for individuals with health conditions like Vesicovaginal Fistula (VVF). This study evaluated the nutritional status and dietary patterns of 41 women with VVF at the VVF Centre in Birnin Kebbi, Nigeria. Data on socio-demographics, dietary habits, anthropometry and biochemical parameters were collected using questionnaires, 3-day food recall, blood samples and standard tools. Results of socio-demographics revealed that 95% of participants were Muslim, married, and engaged in some form of work. Additionally, majority of participants (83.3%) had poor dietary diversity, with low consumption of fruits, vegetables, protein-rich foods and high reliance on carbohydrate-based foods. Biochemical analysis revealed 52% had low albumin levels, 71% and 76% of participants had low PCV and hemoglobin levels, respectively, suggesting high prevalence of anemia. Significant associations were found between nutritional status and factors like age, education, and duration of illness. The study highlights the need for targeted nutrition interventions to improve dietary patterns and nutritional outcomes among VVF patients.

**Keywords:** Vesicovaginal fistula, nutritional status, dietary patterns, anemia, VVF patients

FASBMB/MIY-007

# Effects of Poor Community Infant and Young Child Feeding Practices on the Nutritional Status and Micronutrients of 0-23 months Children in Kubau LGA, Kaduna, Nigeria

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Infant and young child feeding practices have substantial consequences on the growth, development, and survival of infants and children during the first two years of life and throughout life. This study assessed the nutritional status and feeding practices of under-two children involved in Community Infant and Young Child Feeding (C-IYCF) programme in Kubau LGA. This cross-sectional study was conducted among 159 randomly selected mother-child pair attending the C-IYCF programme in three primary health centres in Kubau LGA, Kaduna. Validated semi-structured questionnaire was used to harness data on socio-demographic variables and feeding practices. Weight, length and mid upper arm circumference (MUAC) measurements were assessed to determine the anthropometric indices of the children. Vitamin A, zinc and iron were measured using standard instruments. Results showed that 11.9% of the children were severely wasted, 5.0% severely underweight and 23.3% were severely stunted. Majority of the mothers (76.1%) practiced exclusive breastfeeding, though 22.0% initiated breastfeeding within the first one hour after birth, however, 54.7% of the children met the minimum dietary diversity (MDD). There was high zinc (97.4%) deficiency among the children. Significant association was observed between C-IYCF practices and nutritional status (Weight-for-Age Z-score $p=0.024$; Weight-for-Height Z-score $p=0.046$). Education and social status showed significant association with MDD at $p=0.006$ and $p=0.001$ respectively. Education status ($p=0.041$) and occupation ($p=0.013$) showed significant association with zinc level. Significant relationships ($p<0.05$) were observed between MUAC and zinc level and between vitamin A and iron level. This study revealed inappropriate infant and young child feeding practices in the LGA.

**Keywords**: Anthropometry, Food consumption pattern, Micronutrient, Feeding practices, Kubau LGA

FASBMB2025/MIY-008

# Bridging Gaps in Maternal Health Services through Community Education and Health Systems Strengthening: Evidence from Sabo Gari, Kaduna State, Nigeria

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Maternal health remains a key indicator of national development, yet Nigeria continues to record one of the highest maternal mortality ratios globally. Despite several policy interventions, disparities in access, affordability, and quality of maternal health services persist, especially in semi-urban areas such as Sabo Gari LGA, Kaduna State. To assess the availability, affordability, accessibility, quality, and utilization of maternal health services among women of reproductive age in Sabo Gari LGA and identify barriers to effective service delivery. A descriptive cross-sectional design was adopted, involving 385 women aged 15–49 years selected through stratified random sampling. Data were collected using structured questionnaires and analysed with SPSS version 23 using descriptive statistics and chi-square tests. The Andersen Healthcare Utilization Model provided the theoretical framework for evaluating determinants of service use. Findings revealed that while 92.7% of respondents accessed antenatal care, only 59.5% received postnatal services. Cost of care and distance to health facilities were major barriers; 24.2% of respondents paid over ₦2000 for delivery, leading some to opt for traditional birth attendants. Availability and quality of care were constrained by inadequate infrastructure and personnel. Education and occupation were significant predictors of service utilization ($p < 0.05$). Maternal health services in Sabo Gari LGA remain suboptimal despite availability. Financial barriers, cultural practices, and inadequate service quality impede full utilization. Strengthening healthcare infrastructure, subsidizing maternal services, and enhancing community health education are crucial for improving maternal and child outcomes.

**Keywords:** Maternal health, accessibility, utilization, affordability, women of childbearing age

FASBMB2025/MIY-009

# Consumption Pattern of Selected Spices and Serum Malonaldehyde Among Pregnant Women in Samaru Primary Healthcare Center

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Pregnancy is a critical physiological period characterized by increased nutritional and metabolic demands, which heighten oxidative stress and the need for adequate antioxidant intake. Spices, rich in bioactive compounds with antioxidant properties, may play an important role in mitigating oxidative stress and promoting maternal well-being. This study assessed the consumption pattern of selected spices and serum malonaldehyde (MDA) levels among pregnant women attending antenatal care at Samaru Primary HealthCare Center, Zaria. A descriptive cross-sectional study was carried out using a semi-structured interviewer-administered questionnaire to collect information on socio-demographic characteristics, obstetric history, and spice consumption pattern. A convenient sampling technique was used to select 50 apparently healthy pregnant women aged 15–49 years. Blood samples were collected, and serum MDA concentration was determined using the Thiobarbituric Acid Reactive Substances (TBARS) method. Data were analyzed using SPSS version 23, and results were presented as means ± standard deviation. Statistical significance was set at $p \leq 0.05$ The study revealed that majority (54%) of the respondents are in the active reproductive age group, 48% had a secondary level of education. Many (57.1%) of the women are in their third trimester, and the majority of respondents (89.8%) did not experience any complications during pregnancy. The majority (92%) of respondents regularly consumed spices, with clove, garlic, ginger, and turmeric being the most frequently used. Most pregnant women (59.2%) have good knowledge of spices but lack knowledge of nutrient-dense spices (55.1%). The majority also agrees that spices improve the baby's health (30%) among other benefits. Almost half of the women (47.6%) stated that taste influences their spice choice, and health benefits (45.6%) is a factor that influences more spice consumption. The mean serum MDA level was 2.41 ± 0.95 nmol/ml, lower than the reference value of 3.71 ± 1.24 nmol/ml, suggesting reduced oxidative stress among the respondents. Although no significant associations were observed between socio-demographic variables and MDA levels ($p \leq 0.05$), clove consumption showed a significant positive correlation ($p = 0.05$) with serum MDA. The study concludes that frequent consumption of antioxidant-rich spices may enhance oxidative balance, and nutrition education should be strengthened during antenatal care.

**Keywords:** Pregnancy, Spices, Consumption pattern and malonaldehyde

FASBMB2025/MIY-010

# Fluorescence-Based Characterization of the Tumor Microenvironment in Cervical Cancer: Integrating Spatial Imaging and Molecular Profiling to Advance Therapeutic Strategies

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Cervical cancer progression is driven by a highly dynamic tumor microenvironment (TME), where immune suppression, extracellular matrix (ECM) remodeling, hypoxia-driven angiogenesis, and metabolic adaptations collectively contribute to tumor heterogeneity and therapy resistance. Cervical cancer tissues were analyzed using multispectral fluorescence imaging to segment tumor cores, stromal regions, and immune infiltration zones. Quantification of DAPI, Alexa Fluor 488, and Alexa Fluor 594 intensities enabled evaluation of nuclear organization, cytoskeletal remodeling, immune marker expression, and angiogenic activity. Fluorescence profiles were correlated with molecular findings related to CD151-mediated immune suppression, hypoxia-driven metabolic shifts, and TIE2+ macrophage–associated angiogenesis. Inter-patient variability in immune infiltration, ECM structure, and vascular remodeling was assessed. Three immune zones were identified: high-immune (mean intensity: 194.26), moderate-immune (154.61), and immune-excluded regions (79.49). Hypoxic tumor cores showed markedly reduced intensities (60–120), corresponding to elevated HIF-1α/VEGF expression and fibrotic expansion. Tumors overexpressing CD151 demonstrated increased ECM rigidity and immune exclusion (mean intensity: 110.34). Vascular-rich regions contained clusters of TIE2+ macrophages (180–240 intensity), consistent with angiogenic activation. Substantial inter-patient heterogeneity was observed in vascularity, fibrosis, and immune distribution. Findings reveal a coordinated interplay between hypoxia, immune suppression, and ECM remodeling in promoting cervical cancer progression and therapy resistance. Fluorescence-based spatial profiling effectively captures this heterogeneity and links biomarker distribution with microenvironmental states. Fluorescence-guided histopathological profiling enables precise characterization of TME subtypes in cervical cancer. This work underscores the importance of precision oncology approaches tailored to microenvironmental complexity in HPV-driven cervical cancer.

**Keywords:** Tumor Microenvironment, Fluorescence Imaging, Immune Suppression, ECM Remodeling, Hypoxia and Angiogenesis

## SUB-THEME 7

## NUTRITIONAL AND FOOD BIOCHEMISTRY (NFB)

FASBMB2025/NFB-001

# Nutritional Characterization, Antioxidant Activity and Effects of *Duranta Repens* (Yellow Bush) Extracts on Biochemical Parameters in Rats

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Nutritional characterization, antioxidant activity, and effects of *Duranta repens* aqueous extracts on biochemical parameters in rats were investigated using the seed and leaf samples of the plant with standard methods. Vitamins observed for the seed were A (6.82±0.50 mg/kg), B1 (0.02±0.01 mg/kg), and C (69.47± 1.07 mg/kg); while the vitamins observed for the leaf were A (5.07±0.31 mg/kg), B2 0.018±0.01 mg/kg), D (3.15±0.44 mg/kg), and E (15.46±0.90 mg/kg). The proximate composition values for the leaf were moisture (4.45±0.70g/100g), fiber (9.11±1.04 g/100g), and protein (7.70±0.63 g/100g), while observed proximate composition for the seed were fiber (11.98±1.90 g/100g), fats (1.53±0.42 g/100g), and carbohydrates (54.50±2.17 g/100g). Palmitic acid, oleic acids, myristic acids, lauric acid, and linoleic acids were among the important fatty acids observed in both the leaf and seed samples of *D. repens*. All the essential amino acids and minerals such as iron, magnesium, calcium, phosphorus, and sodium were appreciably observed in the samples studied. The Hb, PCV, and the associate indices of Hb such as MCH, MCV, and MCHC as well as liver and kidney indices of rats placed on the extracts from the leaf and seed samples were significantly ($p<0.05$) decreased against their control. The liver and kidney tissues of rats placed on the extracts had massive deterioration against their control. The samples had nutritional constituents of biological importance but are basically not meant for consumption, due to their toxic biochemical effects observed in this study. This study has revealed the nutritional characterization, antioxidant activity and effects of *D. repens* extracts on biochemical parameters in rats.

**Keywords**: Antioxidant activity, biochemical studies, fatty acids, nutritional characterization, aqueous extracts.

FASBMB2025/NFB-002

# Quantitative Evaluation of the Nutritional and Antinutritional Factors in Dried *Solanum lycopersicum* (tomato) Sold in Gboko Market, Benue State

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*Solanum lycopersicum* (tomato) is an admired and widely consumed fruit that has the challenge of being seasonal due to its short shelf life and limited processing facilities. The drying of tomato has gradually been embraced as a traditional way to bridge the gap created by its availability during the wet and dry seasons. This study was carried out to determine the quality of dried *Solanum lycopersicum* through proximate analysis and the measure of the antinutritional factors in the fruit since the value of food is determined by the presence of the nourishing compounds or the measure of the deleterious antinutrients. The result of the proximate analysis revealed 63% of carbohydrates, 24% moisture, 7% protein, 4% ash content, 1% crude fat and 1% crude fibre. The amount of antinutrients in phytic acid (0.64285%), saponin (0.63935%), oxalate (0.2747%), HCN (0.19135%), trypsin inhibitor (0.1246%) and tannins (0.064715%) were also determined. The result shows that the dried tomato obtained from the area has good energy content, an appreciable amount of protein and an ash content that is indicative of its vitamins. The low antinutrients found in most of the factors analyzed attract their potential health importance. The drying of tomato could also be embraced and used as a local method of preservation owing to its good nutritional content, low antinutrients and cost friendliness.

**Keywords**: Dried tomato, *Solanum lycopersicum*, Antinutrients, Proximate analysis, Preservation

FASBMB2025/NFB-003

# Evaluation of *Adenium obesum (forssk.)* Roem. & schult. Stem Bark Extract as a Potential Diet Supplement for Vincristine-induced Peripheral Neuropathy in Albino Rats

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Nutrient deficiency leads to reduced level of one or more nutrient affecting the body's normal function leading to diseases like Peripheral Neuropathy. The study was designed to evaluate the effect of *A. obesum* stem bark as a dietary supplement for vincristine induced peripheral neuropathy in albino rats model. The stem bark was shed dried then turned into powder. The powder was extracted with ethanol and fractionated with hexane, ethyl acetate, butanol and water. Safety of the plant was ascertained using $LD_{50}$. Twenty-eight rats weighing 200-250gram were used. Vincristine sulphate (0.1mg/kg *i.p*) was used to induce peripheral neuropathy. The rats were grouped into seven: normal control, vincristine control, pregabalin, *A. obesum* ethanol extract (300mg/kg) and *A. obesum* ethylacetate fractions (100, 200 and 300mg/kg) treated groups. Vincristine group were not treated. Ethylacetate fractions were administered orally. Behavioral test was done on day 0, 1, 5 and 10 vincristine induction. Rats were sacrificed on day 31, the blood was collected for nutritional assessment. Behavioral changes were observed on day 10 after vincristine induction. Ethylacetate (300mg/kg) fraction showed significant ($p<0.05$) increase in the serum level of vitamin E, Cu, Mg and Zn. Based on this research, it will be concluded that *A. obesum* ethylacetate (300mg/kg) fraction can be used as a potential diet supplement for the management of diseases that are caused as a result of nutrient deficiency such as peripheral neuropathy. Further studies are recommended to analyse the metal chelating activity of the *A. obesum* stem bark.

**Keywords:** *A. obesum* stem bark, medicinal plant, peripheral neuropathy, dietary supplement

FASBMB2025/NFB-004

# Physicochemical, Mineral Profiling and Fat-soluble Vitamins Evaluation of *Telfairia occidentalis* (Fluted Pumpkin) Seed Oil

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*Telfairia occidentalis* (Fluted pumpkin) seed oil is a high-quality vegetable oil reported for its numerous nutritional and medicinal benefits. This study investigated the physicochemical parameters, mineral profile (mineral composition, mineral ratios and mineral safety index), and fat-soluble vitamins composition of the seed oil. Fluted pumpkin seed oil was extracted with petroleum ether using soxhlet extraction method. Physicochemical parameters were determined according to standard AOAC procedures. Heavy metals were analyzed using Agilent FS240AAS and PG990, mineral ratios and mineral safety index (MSI) were calculated based on tabulated standards. Fat-soluble vitamins were evaluated using Agilent 1100 series HPLC system and GC-MS. Physicochemical parameters of the seed oil were found to be acid value (1.84±1.26 mg KOH/g oil), free fatty acid (0.92±0.63 %), peroxide value (8.60±0.35 mleq/kg), saponification value (115.01±7.01 mg KOH/g), thiobarbituric acid number (0.95±0.02 mg/kg), iodine value (71.90±0.01 g $I_2$/100 g), specific gravity (0.91±0.00 g/mL), viscosity (123.33±1.15 Mpa.s), smoke point (138.67±0.58 ºC), flash point (203.33±1.15 ºC), melting point (35.33±0.58 ºC), freezing point (2.37±0.06 ºC), refractive index (1.57±0.12 ºC), and moisture content (0.84±0.00 %). The mineral profile showed K (57.41±0.14 mg/l), Na (25.32±0.20), Ca (9.47±0.14), P (9.07±0.10), Mg (1.81±0.03), Mn (0.64±0.02), Fe (0.62±0.09), Se (0.43±0.04), Zn (0.40±0.01). The mineral ratios had Na/K (0.4), Ca/K, (0.2) Zn/Cu (2.2), Ca/Mg (5.2), Na/Mg (14.0), Fe/Cu (3.4), Ca/P (1.0), Fe/Co (8.9), Zn/Cd (4.4), [K/(Ca+Mg)] (5.1). The calculated MSI values for Na, Fe, Zn, Na, Ca, and P were within the standard MSI values, which may not pose health risk for consumers. The result of fat-soluble vitamins showed ergocalciferol (Vitamin $D_2$) (15.691 mg/L), cholecalciferol (Vitamin $D_3$) (13.054 mg/L), γ-tocopherol (5.806 mg/L), α-tocopherol (3.733 mg/L), β-tocopherol (0.004 mg/L), retinol (2.764 mg/L), Phylloquinone ($K_1$) (2.561 mg/L), and menaquinone ($K_2$) (0.912 mg/L). The result of the mineral ratios showed that Ca/Mg fell within the ideal range (3-11), Na/Mg fell outside the acceptable range (2-6), Ca/P met the ideal ratio. Fluted pumpkin seed oil can be regarded as a nutritionally dense oil with a diverse profile of vitamins A, $D_3$, E, and $K_1$.

**Keywords:** *Telfairia occidentalis*, physicochemical, mineral ratios, mineral safety index, fat-soluble vitamins

## SUB-THEME 8

## INDUSTRIAL AND ENVIRONMENTAL BIOCHEMISTRY (IEB)

FASBMB2025/IEB-001

# Optimization of Bio-Ethanol Produced from Sweet Potato Peel via Separate Hydrolysis and Fermentation

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Sweet potato peel, is a biowaste that is abundantly available in Nigeria as Nigeria is the highest producer of sweet potato in Africa. This study was aimed at bioconversion of sweet potato peels to ethanol, a useful energy product and optimization of bioethanol produced via hydrolysis of sweet potato peels using cellulase enzyme. The effects of substrate concentration, enzyme concentration, temperature, and pH during hydrolysis were determined using One Factor at a Time (OFAT) method. Separate hydrolysis and fermentation (SHF) method was used to optimize the substrate and enzyme concentrations, temperature and pH using *Saccharomyces cerevisiae* to facilitate the fermentation. The results obtained showed the optimum temperature and pH to be 50ºC and 5.0 respectively, and 48.26mg/ml of reducing sugar were obtained at the earlier stated temperature and pH. The optimum temperature and pH at which the hydrolysis yielded a higher ethanol of 41.80mg/ml are 50ºC and 4.0 respectively. Consequently, cellulase enzyme hydrolysis can be used to enhance reducing sugar concentration to maximize higher yield of bioethanol for industrial scale production.

**Keywords**: reducing sugar, sweet potato peel, cellulase, bioethanol, separate hydrolysis and fermentation.

FASBMB2025/IEB-003

# Hepatorenal Toxicity and Dyslipidaemia Induced by Crude Oil Soot Inhalation in Wistar Rats: Protective Effect of *Curcuma longa* Rhizome Extract

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This study investigated the effect of *Curcuma longa* rhizome (CLR) extract against crude oil soot (COS)-induced hepatorenal toxicity and dyslipidemia in Wistar rats. Twenty-eight female rats (weighing 130–150 g) were divided into seven groups, comprising four rats each. Group 1 was the normal control, while Groups 2, 3, and 4 were exposed to crude oil soot for 7, 14, and 28 days, respectively. Groups 5, 6, and 7 were administered 500 mg/kg of *Curcuma longa* in addition to soot exposure for 7, 14, and 28 days, respectively. Soot was generated in a closed chamber through thermal combustion of crude oil, and the animals were exposed for 30 minutes each day. The results showed that soot exposure in Groups 2, 3, and 4 elicited a significant increase ($p < 0.05$) in serum liver enzymes (ALT, AST, and ALP) activities and concentrations of urea, creatinine, total and LDL cholesterol, along with a decrease in HDL cholesterol in comparison with control. Administration of CLR extract to Groups 5, 6, and 7 significantly decreased serum enzyme activities and concentrations of urea, creatinine, total and LDL-cholesterol, coupled with an increase in HDL-cholesterol compared to Groups 2, 3, and 4, respectively. The results show that inhalation of soot for 7, 14, and 28 days induced hepatorenal toxicity and dyslipidemia in Wistar rats. *Curcuma longa* rhizome extract mitigated the crude oil soot-induced adverse effects in the Wistar rats, possibly through its antioxidative potential.

**Keywords**: Crude oil, soot, Liver function, Kidney function, lipid profile

FASBMB2025/IEB-004

# Inflammatory and neurotoxic effects of methylmercury and monosodium glutamate co-exposure in the lobster cockroach (*Nauphoeta cinerea*) are regulated by JNK and Rel genes

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There is a need to prevent food-related contamination by establishing safety profile for foods. The relevance of *Nauphoeta cinerea* (Lobster cockroach) in elucidating the redox dysregulation associated with exposure to methylmercury (MeHg), which is occasionally contained in food seasonings like sodium chloride and monosodium glutamate (MSG), has been established. The present study sought to establish a relationship between inflammatory and redox pathways in the lobster cockroach exposed to MeHg, NaCl and MSG. The cockroaches were exposed to these compounds for 21 days through their diet. Thereafter, mRNA levels of reactive oxygen species-generating Nox/Doux NADPH oxidases, and target of the UPD3/JAK/STAT, TOLL and JNK pathways were determined in the head of the cockroaches. Results showed that exposure to MeHg disrupted expression of genes associated with redox and inflammation. Expression of DUOX was upregulated in roaches exposed to MeHg only, expression of Reaper, UPD3 and SOCS36E was elevated in roaches administered MeHg and NaCl, while expression of Reaper was lowered in roaches administered MeHg and MSG. Exposure to both MeHg + MSG and MeHg + NaCl increased mRNA levels of PVF, REL and EGR, with a concomitant decrease of FOXO mRNA levels. Our findings suggest that the pathways of Rel, Nox/Doux NADPH oxidases and JNK, were activated upon exposure of lobster cockroach to a combination of monosodium glutamate and methylmercury. These findings support the relevance of *Naphoeta cinerea* as a practicable model for elucidating inflammatory and redox responses arising from heavy metal toxicity.

**Keywords**: Methylmercury, lobster cockroach, inflammation, dysregulation, monosodium glutamate

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# Modeling and Prediction of Bioethanol Production from Walnut Pod Waste using Artificial Neural Network and Modified Gompertz Kinetics

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Bioethanol production from lignocellulosic waste has gained significant attention over time; however, optimization and kinetics studies of the fermentation process are crucial in understanding the dynamics of the bioprocess. Hence, this study aimed to model and predict bioethanol production from walnut pod waste using an Artificial Neural Network (ANN) and modified Gompertz kinetics. The central composite face-centred design (CCFCD) was used to generate 32 experimental runs, with substrate concentration, incubation time, pH, inoculum size, and iron nanoparticle concentration serving as input variables, while bioethanol was the output variable. From the results obtained, ANN demonstrated a strong predictive capability in evaluating bioethanol production with a coefficient of determination ($R^2$) of 0.8944 and root mean square error (RMSE) of 4.3678. The $R^2$ value obtained in this study explains how well the model's prediction aligns with the experimental results, with a value close to 1 indicating a strong fit. Also, substrate concentration, pH, and iron nanoparticle were the most significant factors that affected bioethanol production. Optimum conditions for fermentation based on the predicted ANN model were substrate concentration (20 %), pH (4.0), time (5 days), nanoparticles (0.08 mg/mL), and yeast (2 %) with a bioethanol concentration of 61.38 mg/mL. Kinetic parameter estimation using the modified Gompertz model of product formation predicted a maximum bioethanol production ($B_m$) of 56.48 mg/mL, maximum bioethanol production rate ($R_m$) of 8.2 mg/l/h, lag time of 2 hours, with an $R^2$ of 0.983. From our findings, ANN demonstrated good modeling and predictive capabilities, making it a suitable tool for modeling biotechnological processes.

**Keywords:** Bioethanol, Artificial Neural Network, Modified Gompertz Model, Lignocellulosic Waste, Central Composite Face-Centred Design

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# Chlorophyll as A Biomarker for Evaluating the Impact of Hydrocarbons on Soil Ecosystem and Hence Soil Productivity

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Soil degradation resulting from pollution compromises the earth's self-renewing capacity and agricultural productivity. One major contributor to this pollution is the indiscriminate discharge of spent engine oil (SEO), which alters soil properties and affects plant growth. This study evaluated the uptake and accumulation of hydrocarbons in cucumber (*Cucumis sativus*) plants cultivated in SEO-contaminated soil and assessed its effect on chlorophyll content. Uncontaminated soil samples (1 kg) were spiked with SEO at concentrations of 0, 1, 5, 10, 15, 20, 25, 30, and 50 g/kg and allowed to equilibrate for five days before transplanting cucumber seedlings. The plants were monitored for 28 days, and chlorophyll levels were determined spectrophotometrically. Results showed a significant ($p < 0.05$) reduction in total chlorophyll content with increasing SEO concentration. The highest chlorophyll content (2.321 mg/g) was recorded in the control soil, while the lowest (0.766 mg/g) occurred in the 50 g/kg treatment. The study also revealed a marked difference between *chlorophyll a* and *chlorophyll b* concentrations across treatments. These findings demonstrate that hydrocarbon contamination adversely affects chlorophyll synthesis and photosynthetic efficiency, leading to vegetation stress and reduced crop productivity. The study underscores the need for effective soil pollution control and remediation measures to sustain agricultural productivity.

**Keywords**: Spent engine oil, Hydrocarbon contamination, Chlorophyll content, Cucumber, Soil pollution

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# Adsorption of Pb (II) ions from Polluted Water using Agricultural Wastes as Biosorbents

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Increase Industrial development and volume of sludge produced in urban areas, excessive use of synthetic pesticides in agriculture and illegal mining had contributed largely to widespread of heavy metal pollution globally. This has become a serious global issue and threat to public health. Conventional methods used in removing these toxic metals from our environment are costly, ineffective and not eco-friendly. Therefore, the present study exploited the use of non-living biomass, costless and environmentally agricultural waste (orange and banana peels) for the removal of Pb ions from aqueous solution. Physical properties of the orange and banana peels powder were evaluated using standard procedure and Fourier transform infrared spectroscopy (FTIR). Experimental conditions like agitation time, initial metal concentration, adsorbent dosage, temperature, and solution pH were studied. Orange peel had low bulk density, moisture, and ash contents compared to banana peel. The maximum uptake of Pb ion was observed at 35 $^0$C and 30 $^0$C and decreased with increasing temperature for orange and banana peels respectively. Optimum adsorption was attained at 60 minutes, with initial metal concentration of 50 mg/L, and solution pH of 5.45, and 6.14 for orange and banana peels respectively. The presence of functional groups such as hydroxyl, carbonyl, alkyl, aldehyde and ether confirmed using FTIR analysis and high bulk density of the orange and banana peels have indicated that these biomasses could be used as potential biosorbents for Pb ion from aqueous solution.

**Keywords:** Lead, Adsorption, Orange peel, Banana peel, Pollution

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# Pathophysiological Biomarker Alterations in Women Exposed to Chronic Gas Flaring in the Niger Delta

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Gas flaring emits harmful hydrocarbons that may disrupt both endocrine activity and heart health. This study aimed to assess the impact of chronic gas flare exposure on selected cancer, cardiac, and thyroid biomarkers in women (pregnant and non-pregnant) residing in gas flare host communities. Bonny and Omoku in Rivers State, Nigeria were the test locations, and Idah in Kogi State was the control. Criteria Air Pollutants (CAP), Polycyclic Aromatic Hydrocarbons (PAHs), Benzene, Toluene o-xylene, m-xylene, p-xylene and Ethylbenzene (BTEX) and Total Hydrocarbon (TPH) content in air were determined. Thyroid Stimulating Hormone (TSH), Triiodothyronine ($T_3$), Thyroxine ($T_4$), D-dimer, Troponin, C-Reactive Protein (CRP), Carcinogenic Embryonic Antigen (CEA) and Alpha Fetoprotein (AFP) were analysed in blood samples. PAHs, BTEX, and TPH were quantified by single extraction GC-MS while AFP, CEA, CRP, troponin, D-dimer, TSH, $T_4$, and $T_3$ were concurrently analyzed with the Boditech iChroma multi-test fluorescence immunoassay. Total PAHs and BTEX (ppm) were significantly higher ($p \leq 0.05$) in Omoku (1608.18±82.03), (31.00±0.76), relative to Bonny (1360.28±159.10), (23.62±1.00), for PAHs and BTEX, respectively. D-dimer (ng/ml) levels among non-pregnant women of Omoku (224.45±24.62) and Bonny (295.66±29.37) were significantly higher ($p \leq 0.05$) than those in Idah (79.04±10.03). CRP (mg/l) for non-pregnant women increased significantly ($p \leq 0.05$) from Omoku (6.03±0.35) to Bonny (8.64±0.48). The study confirmed hydrocarbon pollution. Although the control site showed background hydrocarbon pollution, with some pollutants unexpectedly elevated, overall, contamination levels were higher in the exposed communities. Despite this, most pathophysiological biomarkers showed minimal alteration, suggesting latency in pollutant-related health effects or possible adaptive mechanisms among exposed groups.

**Keywords:** Gas Flare, Criteria Air Pollutants, Polycyclic Aromatic Hydrocarbons, C-Reactive Protein, D-dimer

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# Green Valorization of Methanolic Extract of Watermelon Rinds for Sustainable Bioremediation of Cr (VI) Tannery Contaminated Environments

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The conversion of agro-wastes into wealth is a sustainable practice employed in the bioremediation of heavy metals such as Cr (VI), from polluted environments. Tannery industries contribute largely to the production of toxic Cr (VI) in the environments. This study evaluated the potential of methanolic extract of watermelon rinds (agro-waste) in the bioremediation of Cr (VI) from tannery effluent and soil, with respect to effects of process parameters such as concentration of watermelon rinds, contact time, temperature, and pH, as well as the kinetics and thermodynamics processes. Watermelon rinds (WMR) were extracted using the maceration method (70% methanol), and batch process was used for the study. Results showed that process parameters were highly significant in the bioremediation of Cr (VI) as 98% reduction rate were achieved within 5min at a temperature of $25^0$C, with a concentration of 1.0mg/mL and at pH 7.0 for tannery effluent and pH 12.0 for soil, respectively. Pseudo-second order best described the kinetic model. Thermodynamically, the bioremediation process was exothermic, feasible and spontaneous, as the values $\Delta H^o$, $\Delta G^o$, $E_a$ and $\Delta S^o$ were -13430 (J/mol), -15123 (J/mol), 16.12 (J/mol), and 35.21 (J/k/mol). These findings show that agro wastes like watermelon rinds can successfully clean up heavy metals from polluted environments, thereby converting wastes into wealth for sustainable living. Upscaling the use of agro-wastes in a continuous process is highly recommended.

**Keywords:** Agro-waste, bioremediation, watermelon rind, tannery environment, Cr (VI).

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# Valorization of Neglected Plantain (*Musa Paradisiaca*) Peel and Stalk for Co-Production of Pullulanase and Mannanase by *Pseudomonas Sp.* PAA2 in Submerged Fermentation

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The demand for enzymes of biotechnological importance is on the high side, hence, the need for their production from cheap and alternative sources. The valorization of agricultural wastes as cost-effective substrates offers sustainable solution for both waste management and industrial biotechnology. This study explores the utilization of neglected agro-residue from plantain (peel and stalk) as lignocellulosic substrates for the production of pullulanase and mannanase enzymes in submerged fermentation. Bacterial isolates capable of producing pullulanase and mannanase were isolated and screened before optimizing the production media for the organism with the highest potential. The results obtained showed significant enzyme yields with maximum pullulanase activity within 18 h of incubation when stalk was used, but plantain peel gave a higher yield which continued till the 3rd day. Optimum production of mannanase was observed with 1% (w/v) stalk and 2.5% (w/v) peel, whereas, 2.5% (w/v) gave the highest production yield for pullulanase using the two carbon sources. The combination of yeast extract and peptone was best for mannanase while urea was best for pullulanase when plantain stalk was used as substrate. Peptone alone gave the best yield of both enzymes when peel was used. The optimum pH for production of both enzymes falls within the slightly acidic region (4.5 – 6.5). The study demonstrated that plantain peel and stalk can serve as viable, low-cost substrates for industrial enzyme production, contributing to sustainable bioprocessing and reduction of environmental pollution associated with agricultural waste disposal.

**Keywords:** Bioprocessing, Valorization, Biotechnology, Enzyme, Agricultural wastes

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# Rhizobacterial Inoculants from Semi-Arid and Arid Trees of North-East Nigeria: Isolation, Characterization and Experimental Trials

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The search for Plant Growth Promoting Rhizobacteria (PGPR) in biofertilizer development is driven by the urgent need to mitigate the environmental damage caused by chemical fertilizers. This paper reports the conventional and metagenomic approaches to characterize microbial diversity and soil properties in the rhizospheres of selected tree species across semi-arid and arid regions of north-eastern Nigeria. Distinct microbial taxa were identified, leading to the formulation of a biofertilizer cocktail, which was subsequently experimented to evaluate its effectiveness in promoting the growth of millet crops. The rhizosphere soils showed bulk density of 1.63–1.77 g/cm³, with neutral pH in Adamawa, Borno, and Gombe, while sandy, slightly acidic soils were seen in Bauchi and Yobe states. Conventional microbiology and molecular characterization lead to the isolation and selection of four (4*)* free-living nitrogen fixing bacteria. The selected isolates are, BOR/BLN/002, AD/BB/005, BB/TM/001 and BOR/TM/002 and were used for the experimental trial as biofertilizer candidates. Millet inoculated with biofertilizer strain 40 showed the greatest nutrient efficiency, boosting shoot N (114.86%), P (165%), and K (73.58%) concentrations and achieving the highest phosphorus uptake (0.025 g $pot^{-1}$), outperforming controls and rivalling chemical fertilizers. The results reveal beneficial microbial communities in the rhizospheres of the selected trees underscoring their potential in sustainable biofertilizer development.

**Keywords:** Biofertilizer, Millet, Nitrogen-fixing, Nutrient uptake, Rhizosphere, Tree Crops

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# Effect of Four Biowaste Substrates on Growth and Lead (Pb) Accumulation of *Hermetia illucens* Larvae

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This study assesses growth performance and lead (Pb) accumulation potential of *Hermetia illucens* larvae reared on four biowaste substrates: brewers' spent grain (BSG), chicken droppings (CND), fruit waste (FRW), and kitchen waste (KTW). Recently, *H. illucens* larvae has attracted interest as a sustainable protein source for animal feed. However, their capacity to absorb toxic heavy metals like Pb from contaminated substrates raises safety concerns. Larval neonates were fed Pb spiked substrates (0, 10, and 100mg/kg Pb) for 15 days, with growth metrics (survival rate, prepupae development) and proximate composition analysed alongside larval Pb concentrations using standard analytical methods. Results demonstrated significant negative, substrate-dependent effects ($p<0.05$) with increasing Pb spike concentrations. Survival rates declined sharply in FRW (93% to 57%) and CND (90% to 51%), while BSG and KTW larvae maintained >75% survival. Prepupae formation increased greatly for CND (47% to 93%), with more moderate increases for BSG (7% to 23%) and KTW (17% to 41%), while FRW had no prepupae. Proximate analysis revealed substrate-specific variations, with only CND larvae having lowered protein, while lipid values were generally reduced under Pb exposure. Larval Pb concentrations increased with substrate Pb concentrations, up to 34.9 ppm (CND) in 100 mg/kg treatments, exceeding EU safety thresholds. In summary, with increased Lead concentrations, larval development to prepupae and mortality was significantly accelerated in all but FRW, which is a negative outcome. These findings underscore the need for substrate specific safety assessments to ensure the sustainable use of *H. illucens* larvae in animal farming.

**Keywords**: *Hermetia illucens*, cultivation, lead accumulation, toxicity

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# Housing Conditions and Behavioural Predictors of Malaria Prevalence Among University Students in Zaria

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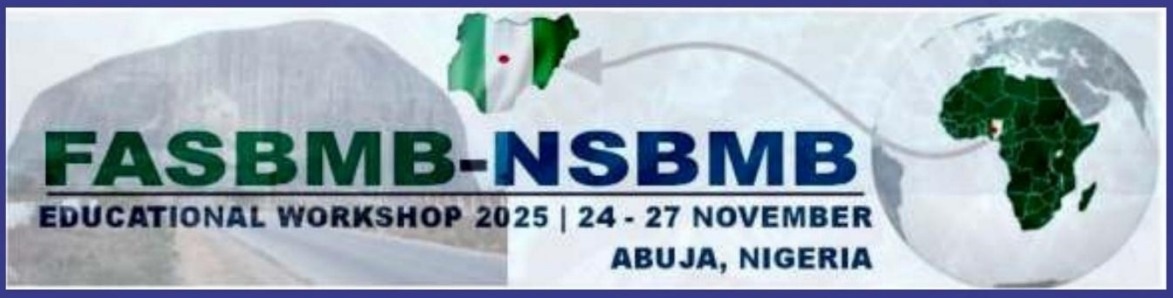
Malaria has remained a global health challenge, especially in the tropics despite the enormous effort expended towards its eradication largely through chemotherapeutic and behavioral practices. Vector control through housing conditions, especially among vulnerable student populations, has comparatively received limited attention. This study reports findings from a cohort of university students in Zaria, Northwest Nigeria. Malaria prevalence, measured by retrospective laboratory test results from 114 respondents was 25.4%. Not concurrently treating typhoid fever ($p=0.002$), age ($p=0.026$) and dirty surroundings ($p=0.033$) significantly predicted malaria in a binary logistic regression model that explained 35-51.2% of the variance. The odds ratio of reporting malaria was higher among females (OR=3.99), students treating cold and catarrh (OR=2.33), respondents who prevented malaria through closing doors and windows (OR=1.39) and occupants of rooms with gaps in walls, ceilings and openings (OR=1.34). We conclude that malaria is largely transmitted through gaps and openings within rooms and that commonly held preventive measures such as the use of ITNs, periodic spraying of insecticides and installing mosquito nets are ineffective in the study area. Improving housing and environmental conditions, reorientation and behavioral changes are key to malaria mitigation among university students.

**Keywords**: Malaria, Prevalence, Housing, Students, Behaviour

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