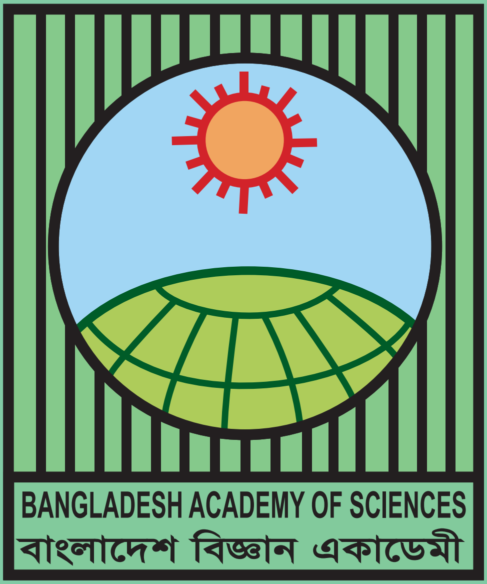
6th YOUNG SCIENTIST CONGRESS
04-05 April 2026
Dhaka, Bangladesh

ISSN
2224-7270 (Online)
0378-8121 (Print)

JOURNAL OF
BANGLADESH ACADEMY OF SCIENCES

Volume 50 Supplement 1 April 2026



A Publication of Bangladesh Academy of Sciences
http://www.bas.org.bd

COUNCIL OF
THE BANGLADESH ACADEMY OF SCIENCES
(July 2025 - June 2028)

JOURNAL OF
BANGLADESH ACADEMY OF SCIENCES

EDITORIAL BOARD

J. Bangladesh Acad. Sci. Volume 50, Supplement 1, April 2026

ISSN 2224-7270 (Online), 0378-8121 (Print)

Journal of Bangladesh Academy of Sciences is published four times a year (March, June, September and December comprising one volume) in English. Original research articles, review articles, and short communications of all branches of Science and Technology are considered for publication in this journal. Review articles are generally by invitation.

Disclaimer

Submission

All correspondence regarding contributions for publication in the journal should be addressed to the Editor, Journal of Bangladesh Academy of Sciences <jbas.editor@yahoo.com>. Authors should consult the contributor's guideline at the back of the journal before submitting their manuscripts.

Published by

Bangladesh Academy of Sciences, National Science and Technology Complex, Agargaon, Dhaka-1207.

Design and Printed by

Sucharu Desktop Publishing, 1/E/1, Paribagh, Dhaka-1000, Bangladesh

Annual Subscription: Tk. 500.00 (Bangladesh); US $ 60.00; £ 21.50 plus postage.
Single Copy: Tk. 250.00 (Bangladesh); US $ 30.00; £ 11.25 plus postage.

JOURNAL OF BANGLADESH ACADEMY OF SCIENCES

BANGLADESH ACADEMY OF SCIENCES
বাংলাদেশ বিজ্ঞান একাডেমী

Volume 50, Supplement 1, April 2026
ISSN 0378-8121 eISSN 2224-7270
Available at: http://www.bas.org.bd/publications/jbas.html

Journal of Bangladesh Academy of Sciences is currently indexed in the following online scholarly journal database:

ISSN INTERNATIONAL STANDARD SERIAL NUMBER INTERNATIONAL CENTRE
R^G
OJS Open Journal Systems
Crossref
doi DIGITAL OBJECT IDENTIFIER
Google Analytics
CiteFactor Academic Scientific Journals
ROAD DIRECTORY OF OPEN ACCESS SCHOLARLY RESOURCES
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ABSTRACTS

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BANGLADESH IN THE AGE OF AI: A NATION THAT CHOOSES TO SHOW UP

Dr Ehsan Hoque

Professor of Computer Science, University of Rochester, New York, USA

What would it take for Bangladesh to become an AI-powered nation within this decade, not by competing with global giants on compute, but by building systems that work for its people?

I grew up in Dhaka. I attended Udayan School and Dhaka College, where I founded the Science Club - which recently celebrated its 30th anniversary. I left for Penn State, then Memphis, then MIT. But I never stopped thinking about what the tools we were building could mean for the country I came from. During my graduate years, an IEEE Gold Humanitarian Fellowship brought me back to deploy some of the first AI-based tools in Bangladeshi autism centers. In 2016, I helped found Kolpokoushol, a mentorship initiative for underserved students in Dhaka. Several of those students went on to become PhD researchers in my lab. I write regularly for Prothom Alo and Biggan Chinta. I collaborate closely with faculty at BUET and the National Institute of Neurosciences (NINS). Bangladesh is not a talking point in this work; it is the motivation for it.

Bangladesh already possesses what many countries underestimate: scale, urgency, and a digitally active population. With 170 million people and over 300 million Bengali speakers, the country generates rich, real-world data across health, education, and daily life. These are not constraints. They are strategic assets if Bangladesh chooses to treat them that way.

Over the past several years, I have helped design and deploy AI systems across one of the largest healthcare ecosystems in the Kingdom of Saudi Arabia, reaching hundreds of thousands of users. These systems operate in local language, run on everyday devices, and are embedded into clinical workflows - not prototypes. My lab has built AI that detects Parkinson's disease from a 30-second video, monitors health passively through a smart speaker in the home, trains clinicians in empathy and listening, and coaches children through speech therapy in their own language. This experience offers a concrete blueprint for how a nation moves from research to real-world impact.

The key insight is this: the future of AI will not be defined solely by those who build the largest models, but by those who build systems that work in the most constrained, real-world settings.

No one is better placed to build that AI for Bangladesh than Bangladesh itself.

The bottleneck is not talent, not data, and not even compute. It is coordination.

Bangladesh has a narrow window to align its institutions, infrastructure, and incentives. This talk will be direct about what Bangladesh is getting wrong, and specific about what it could get very right. The opportunity is immediate. The cost of waiting is high.

PL0I

HUMAN INTELLIGENCE VS ARTIFICIAL INTELLIGENC

Prof Hasan Sarwar

School of Science and Engineering, United International University, Dhaka, Bangladesh

Is Artificial Intelligence replacing Humans?

Will civilization be at stake?

Will people lose jobs?

Do Humans have to compete with the Robots?

How is AI going to be beneficial for us?

This lecture discusses the applicability of Artificial Intelligence (AI) in human life with the perspective of the above questions. The relationship between human intelligence and artificial intelligence (AI) has been explored with a focus on their implications on society. Human intelligence is characterized by emotion, awareness, consciousness, while AI operates through data-driven pattern recognition, optimization, and computational efficiency without true understanding or subjective experience. The discussion highlights how humans learn through limited examples, intuition, and contextual reasoning, whereas AI requires vast datasets and lacks self-awareness.

The role of emotion in learning in human cognition has been translated to machine equivalents such as reward and loss functions, emphasizing that AI can simulate decision-making but cannot experience feelings. AI is capable to scale while human effort is inherently sequential. Machines enable parallel processing, AI systems achieve massive distributed scaling, fundamentally transforming productivity and problem-solving capacity.

The lecture also examines physical intelligence through robotics, noting that while robot movements can be precisely defined using kinematics and control theory, they lack the adaptability and fluidity of human motion. Despite advances, no universal robot or artificial general intelligence (AGI) currently exists, and significant challenges remain in achieving general-purpose intelligence.

Finally, the lecture frames AI as a powerful dual-use technology, comparable in impact to nuclear energy, requiring careful governance and ethical oversight. Drawing on perspectives from leading technology figures, it concludes that the future lies not in competition but in collaboration-where humans leverage AI to augment, rather than replace, human capability.

PL02

TRANSLATIONAL ARTIFICIAL INTELLIGENCE: FROM RESEARCH TO SOCIETAL IMPACT

Prof Dr Tanzima Hashem

Department of Computer Science and Engineering, Bangladesh University of Engineering and Technology, Dhaka, Bangladesh

The true potential of Artificial Intelligence (AI) lies in its ability to address complex real-world challenges and create meaningful societal impact. This talk presents a broader perspective on Translational Artificial Intelligence as an interdisciplinary process that begins with real-world problems and brings together expertise from multiple domains to co-create impactful AI solutions.

The talk will then present a few of my research projects. First, I will discuss a smartphone-based dehydration detection system that leverages mobile image analysis and AI to provide accessible, non-invasive health assessment, particularly for underserved populations. Next, I will discuss our solution to address the challenge of detecting attentiveness levels of students with Autism Spectrum Disorder (ASD), who often struggle to adapt to online learning environments. Our model analyzes real-time video data to detect behavioral cues (e.g., unusual movements, gaze patterns, and activity levels) and uses these features to classify attentiveness into low, medium, and high levels. Following this, I will present our research on crime prediction and lightning prediction using AI models that incorporate environmental and sensor data to improve early warning systems. Together, these case studies demonstrate how AI can move beyond theoretical contributions to deliver societal impact.

The talk concludes by outlining future directions for Translational AI, emphasizing cross-disciplinary collaboration, stakeholder engagement, and a problem-first approach. It underscores the importance of aligning technological innovation with societal needs to achieve sustainable and scalable impact, particularly in the context of Bangladesh and other resource-constrained settings.

PL03

AI FOR ONE HEALTH: BUILDING A SMART AND SUSTAINABLE HEALTH ECOSYSTEM IN BANGLADESH

Prof Dr Mohammad Ali Moni

Centre for AI and Digital Health Technology, AI and Cyber Futures Institute, Charles Sturt University, Australia; School of Information Technology,Washington University of Science & Technology, USA

Bangladesh stands at the nexus of multiple, interrelated health challenges driven by rapid urbanisation, climate vulnerability, agricultural dependence, and high population density. These challenges cut across human, animal, plant, and environmental health, reflecting the principles of the One Health paradigm. Addressing such complexity requires integrated, data-driven approaches that transcend traditional sectoral boundaries. This plenary talk will present a unified AI framework that integrates heterogeneous and multimodal data sources, including clinical and public health records, veterinary surveillance data, agricultural and crop monitoring systems, environmental and climate datasets, satellite imagery, and socio-economic indicators. By leveraging advanced machine learning and deep learning techniques, along with federated learning for privacy-preserving data sharing, the framework supports real-time monitoring, predictive modelling, and cross-sectoral decision-making. This integrated approach enables a more holistic understanding of the dynamic interactions between human, animal, plant, and environmental systems.

In the field of human health, AI can significantly enhance disease surveillance, early diagnosis, and the efficiency of the health system. Predictive models can identify emerging trends in infectious and non-communicable diseases, enabling timely interventions and improved resource allocation. In animal health, AI-driven systems support early detection of livestock and poultry diseases, strengthening biosecurity and reducing the risk of zoonotic transmission. The integration of sensor-based monitoring and precision livestock technologies further enhances productivity and animal welfare.

Plant health and agriculture are critical pillars of Bangladesh’s economy and food security. The plenary will highlight how AI-based image analysis, remote sensing, and predictive modelling can detect crop diseases, optimise irrigation and fertilisation, and support climate-resilient farming practices. These innovations not only improve agricultural productivity but also reduce environmental impact by more efficiently utilising resources. Besides, environmental health underpins all other domains and is particularly relevant in Bangladesh, given its vulnerability to climate change, flooding, and pollution. AI techniques can analyse large-scale environmental data to monitor air and water quality, assess climate risks, and predict extreme events. By linking environmental indicators with human and animal health outcomes, AI enables a comprehensive risk assessment framework that informs policy and public health interventions.

The central focus of the talk is on developing scalable, inclusive solutions. The integration of Internet of Things (IoT) devices, mobile health platforms, and low-cost sensing technologies ensures data collection and service delivery in rural and resource-limited settings. By applying AI across human, animal, plant, and environmental health, Bangladesh can transition towards a proactive, resilient, and sustainable ecosystem that supports improved health outcomes, food security, and environmental stewardship.

IL01

AI-DRIVEN DECODING OF HOST-MICROBE INTERACTIONS FOR CRISPR-EDITED CLIMATE-SMART WHEAT

Prof Dr Md Tofazzal Islam

Professor and Founding Director of the Institute of Biotechnology and Genetic Engineering (IBGE), Gazipur Agricultural University, Gazipur, Bangladesh

The 2016 wheat blast outbreak, which devastated 15,000 hectares in eight districts of Bangladesh with up to 100% yield losses, necessitated a paradigm shift in agricultural biosecurity. Through an international open data sharing and open-science collaboration involving 31 researchers across four continents, we utilized AI-driven field pathogenomics and machine learning to rapidly identify the pathogen as a South American lineage of Magnaporthe oryzae. By leveraging Nobel-winning AlphaFold technology, we modeled the structural recognition of the fungal effector AVR-RMG8 by the wheat resistance gene Rmg8, elucidating the kinase fusion protein-triggered immunity pathway. Our integrated computational approach further identified three CRISPR-editable susceptibility genes, TaSULTR3-3B, TaSTP3-4D, and TaMLO1-5A from epidemic-derived genomic data. To bridge the gap between discovery and field application, we employed computational biology to identify natural fungicides like 3-methyl pentanoic acid and their targets, such as UGE, while developing genome-specific primers for a point-of-care diagnostic tool. Furthermore, we utilized AI-optimized guide RNA design to navigate the complex 17-GB hexaploid wheat genome, enabling precise CRISPR editing for durable resistance. Our transcriptomics experiments have since yielded a library of new candidate genes involved in wheat-blast interactions. Collectively, these discoveries demonstrate that the synergy of AI, ML, and genome editing provides an accelerated, high-precision framework for tackling emerging fungal threats and engineering climate-smart wheat varieties to ensure global food security.

IL02

EMERGING SMART NANOBIOTECHNOLOGY PLATFORMS FOR NEXT-GENERATION-DRUGDELIVERY

Prof Dr Md Zaved Hossain Khan

Professor and Chairman, Dept of Chemical Engineering, Jessore University of Science and Technology, Jessore, Bangladesh

Recent advances in nanotechnology and biotechnology are transforming the field of drug delivery by enabling the development of smart, targeted, and highly efficient therapeutic systems. Conventional drug delivery methods often suffer from limitations such as poor bioavailability, nonspecific distribution, rapid degradation, and unwanted side effects. Smart nanobiotechnology platforms provide innovative solutions to these challenges by integrating nanoscale materials with biological functionalities to create responsive and controlled drug delivery systems. Nanocarriers such as nanoparticles, liposomes, polymeric nanocapsules, dendrimers, and nanoemulsions have demonstrated significant potential in imoving the pharmacokinetics and therapeutic efficacy of drugs. These nanosystems can protect sensitive drug molecules from degradation, enhance solubility of poorly water-soluble drugs, and facilitate targeted delivery to specific tissues or cells. By engineering particle size, surface charge, and surface functionalization, nanocarriers can be designed to interact selectively with biological targets, thereby minimizing systemic toxicity and improving treatment outcomes. Smart nanobiotechnology further introduces stimuli-responsive drug delivery systems, which can release therapeutic agents in response to specific biological or environmental triggers such as pH, temperature, enzymes, light, or magnetic fields. Such controlled release mechanisms allow precise dosing at the disease site, making them particularly valuable for the treatment of cancer, infectious diseases, and chronic disorders. Additionally, biofunctionalization with ligands, antibodies, peptides, or nucleic acids enables active targeting to diseased cells, significantly enhancing therapeutic precision. Despite these promising developments, several challenges remain, including large-scale manufacturing, long-term safety evaluation, regulatory approval, and cost-effective commercialization. Continued interdisciplinary research involving nanotechnology, materials science, molecular biology, and biomedical engineering will be essential to translate these technologies from laboratory research to clinical applications. This talk will highlight recent advances in smart nanobiotechnology platforms for drug delivery, discuss key design strategies for functional nanocarriers, and explore future opportunities for developing next-generation therapeutic systems that enable precise, safe, and efficient treatment of complex diseases.

IL 03

BREATHING A MIXED PARTICLE SOUP: COMPUTATIONAL AND AI MODELS OF MICROPLASTIC–POLLUTANT DEPOSITION IN HUMAN AIRWAYS

Dr Suvash C Saha

School of Mechanical and Mechatronic Engineering, University of Technology Sydney (UTS), Ultimo, NSW 2007, Australia

Microplastics are no longer just an environmental contaminant, they are an inhalation exposure. Airborne fibres and fragments can originate from resuspended indoor and outdoor dust, and important “hotspots” include cigarette smoke from conventional cigarettes and particles released from cigarette butts, as well as aerosols generated by e-cigarettes. Yet real-world exposure rarely involves a single particle type: the lung receives a mixed “particle soup” in which microplastics co-inhale with pollutant particulates (e.g., soot-like carbonaceous particles and PM), potentially altering where particles deposit, how long they persist, and what biological interfaces they encounter. In this talk, I will present a multi-scale modelling framework that links (i) CT-resolved computational fluid–particle dynamics in anatomically realistic conducting airways to predict regional deposition and dose, (ii) molecular dynamics simulations that resolve nano-plastic interactions with lung surfactant components to probe interface-level mechanisms that may influence agglomeration, wetting, and clearance, and (iii) in vivo mouse inhalation experiments that provide biological evidence for pulmonary exposure, retention, and early response markers under controlled conditions. To extend predictions into the deep lung where direct imaging and meshing are challenging, I will also describe a machine-learning approach for rapid, structure-aware modelling of acinar transport and deposition, enabling scalable sensitivity studies across ventilation patterns and particle property distributions. Together, these computational, AI, and experimental components provide a pathway from exposure sources to mechanistic understanding and risk-relevant dosimetry. The outcomes support more realistic assessment of mixed-particle inhalation, inform inhaled exposure mitigation strategies, and establish validation anchors for next-generation digital-twin models of respiratory particle transport.

IL04

AL-POWERED BY HEALTHCARE SERVICES: TRANSFORMING PATIENT CARE

Prof M Shamim Kaiser

Institute of Information Technology, Jahangirnagar University, Savar, Dhaka, Bangladesh

Artificial Intelligence (AI) and Machine Learning (ML) are rapidly transforming healthcare systems by enabling intelligent, data-driven, and efficient patient care. In Bangladesh, where healthcare systems face challenges such as limited resources, unequal access, and growing patient demands, AI offers significant opportunities to enhance diagnostic accuracy, optimize clinical decision-making, and expand access through digital and remote healthcare services. A key paradigm shift in modern healthcare is the move toward patient-centric care, which emphasizes personalized treatment, continuous monitoring, and active patient engagement. AI technologies play a critical role in this transformation by enabling predictive analytics, personalized medicine, and real-time health monitoring, ultimately improving patient outcomes and satisfaction. However, the adoption of AI in healthcare is not without challenges. In Bangladesh, barriers include limited digital infrastructure, lack of standardized and high-quality healthcare data, concerns over data privacy and security, and a shortage of skilled professionals. Institutional resistance and policy limitations further hinder large-scale implementation. Looking forward, the future of AI-enabled healthcare in Bangladesh depends on developing scalable, ethical, and interoperable systems. Strengthening digital infrastructure, fostering collaboration among academia, industry, and government, and investing in capacity building are essential. Emerging technologies such as explainable AI and smart health systems will further drive innovation, ensuring more accessible, inclusive, and sustainable healthcare services.

IL05

COMPUTATIONAL MODELING AND DEVELOPMENT OF TESEPTIMAVIRUS-BASED PHAGO-BIOSENSOR FOR SENSITIVE DETECTION OF SALMONELLA SPP. FROM HUMANS TO AGRICULTURAL PRODUCTS: A ONE HEALTH APPROACH

Prof Dr Munawar Sultana

Dept of Microbiology, University of Dhaka, Bangladesh

.Tail fiber proteins are the primary determinant of bacteriophage host specificity, making them promising tools for phage therapy and biosensor development in clinical, food and agriculture settings. In order to elucidate the function of the tail fiber proteins in host interaction and the infection cycle, we carried out a thorough whole-genome investigation of the Salmonella phage Teseptimavirus Sal_R1S, which was previously identified against Salmonella Typhi strain DMS A1. Genomic analysis showed a high degree of sequence conservation among

Salmonella Typhi-specific phages while phylogenetic classification using VICTOR and genome-BLAST distance phylogeny (GBDP) confirmed the taxonomic placement of Sal_R1S . AlphaFold2 was used to predict the tail fiber protein's structure, and InterProScan was used for functional annotation, which revealed conserved motifs linked to bacterial surface contacts, enzymatic changes, and host interactions. Notably, the presence of a Phage T7-like tail fiber domain, along with carbohydrate esterase and serralysin-like metalloprotease motifs, suggests a complex mechanism involved in phage bacteria interaction and infection cycle. Tail fibers sequence of homologous phages of Teseptimavirus Sal_R1S were aligned using MEGA11 revealed conserved region N terminal domain (1-155AA) in Salmonella Typhi specific phages. Despite sequence divergence, the analysis showed that all phages have conserved SGNH-type acetyl esterase domains with the classic Ser-His-Asp catalytic triad. AlphaFold3 models placed this domain in the middle of long tail fibers. Using DiffDockL and Glide SP processes, the docking of the Vi capsule monomer (3-O-acetyl-N-acetyl-D-galactosaminuronic acid) revealed convergent orientations among phages, with acetyl groups oriented toward catalytic serine. Docking scores showed a poor association (r=0.25) with MM-GBSA calculations, highlighting energetic refinement. Remarkably, the binding energetics and catalytic geometry of crystalline acetyl esterase (PDB:5B5S) were mirrored in Sal_R1S phage (biosensor-validated). These results showed that Teseptimavirus tail fibers use conserved esterase structures to recognize Vi capsules. Teseptimavirus was used as biorecognition element of the biosensor. The electrochemical response of the biosensor was assessed using differential pulse voltammetry (DPV) following immobilization of the RBP. The reduction peak current showed significant increase when Salmonella Typhi (106 CFU/ml) was added, suggesting that the phage and the target bacterial antigen were strongly bound. This study provides novel directions into the molecular determinants of phage-host interactions, supporting the rational design of bacteriophage-based therapeutics and biosensors for targeted Salmonella detection and control.

IL 06

TOWARD NET-ZERO RICE CULTIVATION: MITIGATION STRATEGIES FOR GREENHOUSE GAS EMISSIONS

SM Mofijul Islam

Bangladesh Rice Research Institute (BRRI), Soil Science Division, Gazipur, Bangladesh

Efficient fertilizer and water management, and the adoption of climate-smart rice cultivars, have the potential to reduce greenhouse gas (GHG) emissions from rice fields. However, studies on the impacts of urea deep placement (UDP), alternate wetting and drying (AWD) irrigation, and climate-smart rice cultivars on GHG emissions and rice yield are limited. Therefore, this study aimed to examine the impacts of UDP, AWD irrigation and climate-smart rice cultivars on GHG emissions, global warming potential (GWP) and rice productivity. We conducted field experiments during the dry seasons to compare the effects of alternate wetting and drying (AWD) and continuous flooding (CF) irrigation, as well as urea deep placement (UDP) and broadcast prilled urea (PU). Four rice cultivars, including BRRI dhan50, BRRI dhan67, BRRI dhan92, and BRRI hybrid dhan3 were evaluated under two N rates. Methane (CH4) and nitrous oxide (N2O) emissions were measured using the closed gas chamber technique, and their concentrations were determined using a gas chromatograph. Methane and N2O emissions varied across fertilizer and water regimes, as well as among rice cultivars. UDP significantly

($p < 0.05$) reduced CH4 emissions and greenhouse gas intensity by 9-10% and by approximately 25%, respectively, compared to the broadcast application of PU. Similarly, AWD irrigation reduced CH4 emissions by about 35-40% compared to CF. Although AWD irrigation significantly ($p < 0.05$) increased cumulative N2O emissions, the contribution of N_2O to total GWP was minor, resulting in lower GWP and GHG intensity under AWD. Among the cultivars, BRRI dhan67 reduced CH4 emissions by 11-14% at 139 kg N ha−1 and by 9-12% at 174 kg N ha−1 compared to BRRI dhan50 and BRRI dhan92 in the Boro season. Similarly, BRRI hybrid dhan3 reduced emissions by 6-9% at 139 kg N ha−1 and by 11-14% at 174 kg N ha−1 relative to BRRI dhan50 and BRRI dhan92. Both BRRI dhan67 and BRRI hybrid dhan3 produced higher grain yields than BRRI dhan50 and BRRI dhan92. AWD maintained yields comparable to CF irrigation, while UDP increased rice yield by 15-20% compared to the broadcast application of PU. These findings suggest that the combined use of urea deep placement (UDP) and AWD, along with BRRI dhan67 and BRRI hybrid dhan3, can be considered low-carbon and environmentally friendly strategies for sustainable rice production.

IL08

VECTOR-BORNE DISEASES AND THEIR PREVENTION: EMERGING CHALLENGES AND THE ROLE OF AI

Maj Gen (Retd) Prof Dr ASM Matiur Rahman

Bangladesh Academy of Sciences, Dhaka, Bangladesh

This presentation provides a generalized overview of vector borne diseases, with particular focus on dengue as a growing public health challenge in Bangladesh. It outlines the epidemiology, transmission dynamics, clinical features, and prevention strategies of major mosquito-borne infections, highlighting why dengue has evolved into a persistent and nationwide problem.The discussion further examines the structural and systemic factors contributing to recurring outbreaks and emphasizes the limitations of current reactive control approaches. It introduces the potential role of artificial intelligence (AI) in strengthening surveillance, enabling early warning, and guiding targeted interventions. Thus , the presentation aims to connect foundational knowledge with emerging technological solutions, encouraging young scientists to explore innovative, data-driven approaches for dengue prevention in Bangladesh.

IL10

ENVIRONMENTAL PROVIDENCIA STUARTII BCSIR AS A HIDDEN RESERVOIR OF ANTIMICROBIAL RESISTANCE AND VIRULENCE FACTORS: A GENOMIC AND PAN-GENOMIC PERSPECTIVE

Nizam Uddin

Genomic Research Laboratory, Bangladesh Council of Scientific and Industrial Research, Dhaka

Providencia stuartii is a Gram-negative, rod-shaped, facultative anaerobic bacteria commonly found in soil, water, and sewage. It is acknowledged as an opportunistic nosocomial pathogen exhibiting escalating multidrug resistance. The ecological durability and genetic traits of environmental isolates are inadequately comprehend-ed. This work is intended to isolate P. stuartii from the Buriganga River and examine its genomic characteristics, encompassing antibiotic resistance genes, virulence factors, prophage areas, mobile genetic elements, CRISPR-Cas systems, and secondary metabolic gene clusters. A pan-genome analysis of 31 genomes was performed to ascertain if the species exhibits an open genomic architecture. Buriganga River water was collected, diluted and cultured on MacConkey and Cetrimide agar. After incubation, a single bacterial colony was targeted and identified through biochemical assays (catalase, oxidase, IMViC, carbohydrate fermentation, and hemolysis tests). Antimicrobial susceptibility testing and biofilm formation assays were also performed. Genomic DNA was extracted and sequenced using the Illumina MiniSeq platform at BCSIR. Sequence quality was assessed with FastQC, and genome annotation was conducted using Prokka and RAST Server. Antimicrobial resistance genes and virulence factors were identified using CARD and VFDB, respectively. Prophage regions, mobile genetic elements, and CRISPR-Cas systems were analyzed through Proksee, while biosynthetic gene clusters were predicted using antiSMASH. Pan-genome analysis of 31 strains was performed using Roary. The isolate was identified as P. stuartii via PubMLST analysis. Phenotypic and genomic investigations demonstrated significant biofilm formation capabilities and considerable drug resistance. The genome contains resistance determinants for aminoglycosides (AAC(2')-Ia), β-lactams (mutated PBP3), polymyxins (arnT), and fosfomycin (FosA2). It comprises 229 mobile genomic components and a Type I-F CRISPR-Cas system. Biosynthetic clusters, including azole-containing RiPP, betalactone, terpene precursor, and Ni-siderophore, were identified. Pan-genome investigation of 31 strains indicated an open genome characterized by accessory genes, implying significant genomic plasticity and adaptive capacity. This study emphasizes environmental P. stuartii as a possible reservoir of clinically significant antibiotic resistance. The results underscore the significance of environmental monitoring and the implementation of a One Health strategy to reduce the emergence and dissemination of highly resistant pathogens

IL12

AI FOR DEVELOPMENT: EMPOWERING YOUTH AND TRANSFORMING EQUITY

Prof Dr Khondaker Abdullah Al Mamun

IRII, United International University, Dhaka, Bangladesh

Artificial Intelligence (AI) refers to systems that learn from data to support prediction, decision-making, and automation. Globally, AI is applied across economies to improve productivity, manage complexity, and deliver services at scale. From education and healthcare to agriculture, finance, and climate management, AI is increasingly embedded into how modern systems operate. Its adoption reflects a shift from isolated digital tools to integrated, data-driven approaches that enable efficiency, informed decisions, and innovation. For Bangladesh, AI represents both an opportunity and a challenge. While digital connectivity and economic growth have increased, structural inequalities remain. Education faces uneven quality and limited access to digital resources, healthcare is constrained by workforce shortages and urban-rural disparities, and agriculture suffers from low productivity, climate risks, and limited advisory and market information. Rapid urbanization strains infrastructure and public services, while fragmented governance and data systems reduce efficiency and accountability. Without strong foundations, AI risks remaining limited to pilots or benefiting only a small segment of the population. Effective adoption depends on reliable data systems, interoperable platforms, skilled human resources, and clear governance frameworks. Youth are central to realizing AI’s transformative potential in Bangladesh. The country’s digitally native population has the capacity to create locally grounded AI technologies that address national development challenges while driving reverse innovation, shifting from a one-way flow of technology from high-income countries to a two-way, global exchange. By applying AI across education, healthcare, agriculture, and governance, youth can design solutions that improve system efficiency, expand access, and strengthen decision-making. They can develop tools for personalized learning, predictive diagnostics, crop monitoring, and data-driven public service management, all adapted to low-bandwidth, mobile-first, and community-oriented environments. In doing so, these innovations are cost-effective, equity-focused, and scalable, enabling Bangladesh to not only enhance national systems but also offer models for other developing and developed contexts. Through their engagement, youth become drivers of AI transformation, turning local challenges into opportunities for systemic improvement, inclusive growth, and global knowledge exchange. AI can strengthen education through personalized learning, healthcare through affordable, accessible, and quality service, agriculture through predictive advisory tools, and governance through data-driven decision support. Ultimately, AI for development in Bangladesh is about building inclusive, efficient, and resilient systems, empowering youth, fostering Global South–originated innovations, and creating equitable pathways for national growth and global knowledge exchange.

IL 14

TARGETED DISRUPTION OF FOODBORNE BIOFILMS AND INNOVATIVE ANTIMICROBIAL STRATEGIES FOR SEAFOOD SAFETY

Md Ashikur Rahman

Bangladesh Fisheries Research Institute, Mymensingh, Bangladesh

Aquatic foods are essential sources of protein and micronutrients; however, their safety is increasingly compromised by foodborne pathogens persisting in biofilm form across aquaculture, processing, storage, and retail environments. Biofilms, embedded within extracellular polymeric substances (EPS), exhibit enhanced tolerance to conventional sanitation, contributing to recurrent contamination, spoilage, and economic losses.This study focuses on the targeted disruption of foodborne biofilms and highlights innovative antimicrobial strategies for seafood safety. Advanced interventions, including antimicrobial peptides, phenolic compounds, quorum sensing inhibitors, postbiotic metabolites, and nano-enabled systems, are discussed for their ability to disrupt EPS structure, inhibit microbial adhesion, induce oxidative stress, and destabilize bacterial membranes. In addition, artificial intelligence-enabled approaches, including environmental sensing, imaging-based detection, and omics-driven analysis, are emerging as powerful tools for real-time monitoring and identification of biofilm-associated traits. The integration of these technologies within digital twin frameworks enables predictive modeling and optimization of targeted interventions. Collectively, the convergence of advanced antimicrobial strategies and intelligent monitoring systems supports a shift from reactive sanitation to predictive, precision-based biofilm control, improving safety, shelf life, and sustainability in aquatic food systems.

IL 15

WINNING THE BID: AI-POWERED COMMERCIAL INTELLIGENCE FOR BANGLADESH'S RMG SECTOR

Tanzeem Haque | Tahsin Tasnia Simi

ACI AI Business, Dhaka, Bangladesh

Bangladesh's garment sector earned $39.35 billion in FY2024-25 - over 80% of national exports. And yet, factories are quietly losing buyers. Not because of wages. Not because of quality. Because the gap is not on the factory floor. It is in the infrastructure for turning market intelligence into a competitive quote, fast. The problem is structural. When a buyer sends a tech pack, the clock starts. The CAD team calculates consumption, the merchant team builds multiple quotes, and everyone converges on a designated bidding day - a buyer portal where factories submit and find out if they've won. The process is time-pressured and high-stakes. But the inputs going into those quotes are still being assembled manually: commodity prices pulled from wherever, freight rates looked up individually, FX movements tracked by hand. Days of preparation for a few minutes of submission. We propose a platform built around two modules. The first is an Order Pattern Forecasting Engine - combining Prophet-based seasonal modeling with LSTM sequence modeling to read buyer demand one to two seasons ahead. The goal is simple: a tech pack shouldn't be a surprise. Factories that can anticipate order volume, category mix, and buyer-specific patterns can allocate capacity and brief their merchant teams before the formal process begins. The second is a Bid Intelligence Engine - built to support the merchant team's costing process, not replace it. It surfaces live commodity prices, freight differentials, FX movements, and factory-specific cost profiles automatically, benchmarked against OTEXA, Eurostat Comext, and UN Comtrade export price proxies. A quote matrix maps cost variations across fabric types, construction details, and order volumes in one view - so the merchant isn't rebuilding the same calculations from scratch for each variant. A bidding day countdown tracks the designated submission date and works backwards, flagging when inputs need to be locked to meet it. The merchant still owns the quotes. They just arrive at the bidding day with better numbers, built faster. We applied a Design Science Research methodology - meaning instead of studying the problem, we designed a solution for it. We reviewed existing literature on RMG competitiveness and digital transformation, consulted with industry practitioners to map how the merchant costing process actually works, and stress-tested the architecture against real operational constraints. The platform draws on publicly available trade datasets and is built to integrate with factory ERP systems already in use. No exotic infrastructure required. The ask is a structured pilot with BGMEA and willing factory partners to validate the framework against live tech packs and real bidding cycles. The design is ready. The data exists. What's needed now is the room to test it.

IL 16

AI-Driven Pharmaceutical Innovation: Integrating Drug Discovery, Process Analytical Technology (PAT) and Smart Manufacturing

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The global pharmaceutical industry is undergoing a profound transformation, driven by artificial intelligence (AI), advanced analytics, and digital manufacturing systems. From accelerating drug discovery timelines to enabling real-time quality assurance through Process Analytical Technology (PAT) and achieving operational excellence via smart manufacturing, AI is redefining how medicines are developed, produced, and delivered. In this evolving landscape, Bangladesh has emerged as a resilient and rapidly growing pharmaceutical hub. With a strong domestic market, regulatory maturity, and increasing footprint in export markets, the country is already recognized for its capability in generic drug manufacturing. However, to transition from a generics-driven industry to a globally competitive innovation-led ecosystem, Bangladesh must strategically embrace AI-driven tranformation across the pharmaceutical value chain. AI-powered drug discovery can significantly reduce time, cost, and failure rates by enabling predictive modeling, target identification, and in-silico trials. Integrating AI with PAT frameworks allows continuous monitoring and control of critical quality attributes, ensuring compliance with global regulatory expectations such as Quality by Design (QbD). Furthermore, smart manufacturing—leveraging IoT, digital twins, and machine learning-can enhance efficiency, reduce variability, and support agile production systems aligned with Industry 4.0. Despite these opportunities, several structural challenges remain. Limited collaboration between industry and academia, insufficient investment in advanced research infrastructure, and gaps in AI talent development are key barriers. Additionally, policy frameworks have yet to fully incentivize high-risk R&D, data sharing, and digital transformation. To unlock the full potential of AI-driven pharmaceutical innovation, a coordinated, multi-stakeholder approach is essential: Industry must invest in digital capabilities, adopt PAT and smart manufacturing systems, and move towards data-driven decision-making cultures. Strategic partnerships with global technology providers and research institutions will be critical; Academia should align curricula with emerging industry needs, emphasizing AI, bioinformatics, pharmaceutical engineering, and translational research. Establishing centers of excellence and fostering industry-linked research programs can bridge the innovation gap; Policy and Regulatory Bodies need to create enabling frameworks that support innovation, including incentives for R&D, fast-track approvals for AI-integrated processes, data governance policies, and public-private collaboration platforms. By integrating AI across drug discovery, quality assurance, and manufacturing, Bangladesh has the opportunity to reposition itself from a volume-driven generics manufacturer to a value-driven, innovation-centric pharmaceutical leader. The convergence of technology, talent, and policy will determine how effectively the country can compete in the global pharmaceutical arena and contribute to improving healthcare outcomes worldwide. This session will explore practical pathways, real-world use cases, and strategic priorities for embedding AI into pharmaceutical operations-highlighting how Bangladesh can leverage this transformation to achieve sustainable growth and global relevance.

OP-01

REGULATING HEPATITIS B VIRUS REPLICATION THROUGH ENDOPLASMIC RETICULUS-TRESS MODULATION

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Hepatitis B virus (HBV) resistant to several antiviral drugs due to viral genomic mutations, has been reported which aggravates chronic infection and leads to hepatocellular carcinoma. Therefore, host cellular factors/signaling modulation might be an alternative way of treatment for drug-resistant HBV. Here, we investigated the viral protein expression, replication, and virion production using endoplasmic reticulum (ER) stress-modulating chemicals; tunicamycin (an ER-stress inducer) and salubrinal (an ER-stress inhibitor). We found that ER stress could be induced by HBV replication in transfected HepG2 cells as well as by tunicamycin as demonstrated by dual luciferase assay. HBV intracellular core-associated DNA quantified by qPCR has been significantlincreasedby tunicamycin in transfected HepG2 cells. Inversely, intracellular core associated and extracellular particlDNA has been significantly decreased in a dose-dependent manner in salubrinal-treated HepG2 cells transfected with HBV replicating plasmid pHBI. Similar results were found in stably HBV-expressing hepatoblasma(HB611) cells treated with salubrinal. However, increased or decreased ER stress by tunicamycin or salubrinal treatment respectively has been confirmed by expression analysis of grp78 using Western blot. In addition, Western blot results demonstrated that expression of HBV core protein and large HBsAg is increased and decreased by tunicamycin and salubrinal respectively. In conclusion, the sal-mediated inhibition of the HBV replication and virion production might be due to the simultaneous reduction of core and large HBsAg expression and maintaining the ER homeostasis. These results of HBV replication regulation by modulation of ER stress dynamics would be useful for designing/identifying anti-HBV drugs targeting cellular signaling pathways.

OP-02

EFFECTS OF TEMPERATURE ON GROWTH PERFORMANCE AND PHYSIOLOGICAL RESPONSES IN ASIAN SEABASS, LATES CALCARIFER

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Rising water temperatures driven by climate change poses a significant threat to aquaculture sustainability in tropical regions. Identifying species capable of maintaining physiological stability under elevated temperatures is therefore essential for future aquaculture development. Asian seabass (Lates calcarifer), a euryhaline and temperature-tolerant species, has gained considerable attention as a potential candidate for climate-resilienmarculture. This study investigated the growth performance, physiological responses, and gene expression patterns of Asian seabass under different thermal regimes to evaluate its suitability for aquaculture under warming conditions. An eight-week experiment was conducted with 20 fingerlings per tank in triplicate at four temperatures (28°C, 30°C, 32°C, and 34°C) maintaining 10 ppt salinity to all treatments. Fish reared at 34°C exhibited significantly reduced growth performance, including lower weight gain (30.12 ± 1.89) and specific growth rate (1.69 ± 0.05), along with elevated blood glucose levels (81.83 ± 9.27 mg dL^{-1}) and noticeable cellular and nuclear abnormalities. In contrast, fish maintained at 32°C showed the highest growth performance (WG: 42.88 ± 2.46, SGR: 1.94 ± 0.04) and significant upregulation of growth-related genes, including growth hormone (gh) in the pituitary and insulin-like growth factors (igf-1 and igf-2) in the liver. Immune-related genes (IL-1β and lysozyme) were also strongly expressed at this temperature. Meanwhile, expression of HSP70 increased at 34°C, indicating intensified thermal stress at elevated temperatures. Collectively, these results demonstrate that Asian seabass can maintain optimal growth and physiological stability at temperatures up to 32°C, underscoring its strong potential as a climate-resilient species for sustainable mariculture in warming tropical ecosystems.

OP-03

COMPARATIVE BACTERIOME DIVERSITY AND COMPOSITION IN QUARTER AND BULK MILK IN WATER BUFFALO (BUBALUS BUBALIS) IN BANGLADESH

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Water buffalo is critically important to Bangladesh's dairy sector, yet subclinical mastitis (SCM) prevalent in up to 50% of local herds silently threatens milk yield, quality, and public health. No study has characterized the milk bacteriome across udder health states or compared quarter-level microbiota with bulk tank milk in Bangladeshi buffalo, limiting effective diagnostics and interventions. This study aimed to provide the first 16S rRNA-based characterization of bacteriome diversity, taxonomic composition, indicator microbial signatures, and zoonotic risk across healthy milk (HM), SCM, and bulk tank milk (BM). A cross-sectional study was conducted on 15 small-scale buffalo farms across three upazilas of Bangladesh (Noakhali, Mirsarai, Godagari). Forty-five milk samples (HM=15, SCM=15, BM=15) were aseptically collected; SCM was diagnosed using the California Mastitis Test. Genomic DNA was extracted and V3–V4 regions of the 16S rRNA gene were sequenced on the Illumina MiSeq platform. Bioinformatics analysis used QIIME2 with SILVA database (v132); diversity and indicator species analyses were performed in R. A total of 251 bacterial genera and 491 species were identified. SCM showed significantly

reduced microbial diversity versus HM ($p=0.005$), dominated by Staphylococcus aureus (55.43%) with enrichment of mastitis indicator S. schleiferi (r.g=0.35, $p<0.001$). HM harboured a stable commensal microbiota associated with Propionibacterium spp. (r.g=0.52) and Clostridium spp. (r.g=0.50). Most strikingly, bulk tank milk was dominated by zoonotic Streptococcus suis (20.9%) negligible in quarter milk alongside S. equinus and Salmonella enterica, implicating post-milking contamination as a major public health hazard. SCM drives pathogen-dominated dysbiosis in the buffalo udder, while bulk tank milk harbors a distinct zoonotic bacteriome shaped by poor hygiene practices. Identified indicator taxa offer promising targets for microbiome-based mastitis diagnostics. Urgent hygiene improvements are needed to mitigate zoonotic transmission risks, with direct implications for food safety and sustainable dairy management in Bangladesh.

OP 04

BIOSYNTHESIS AND DIVERSE BIOACTIVITY OF GLYCOSYLATED OXYGENATED POLYENE ANALOGUES DERIVED FROM BACILLUS SPECIES

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Natural microbial pigments are emerging as sustainable and bioactive alternatives to synthetic colorants. This study investigates the production of an orange pigment and a yellow pigment using Bacillus thuringiensis OKS FPP1 (S1) and Bacillus wiedmannii OKS FPP2 (S2), respectively. The pigment-producing strains were identified through 16S rRNA sequencing. Both strains were cultivated in modified Tryptone Soya Broth under standardized conditions (30°C, 140 rpm) to evaluate their biosynthetic efficiency, structural characteristics and bioactivity. The FTIR spectra revealed significant oxygenation, evidenced by broad hydroxyl (3200–3500 cm^{-1}) and C–O stretching (1000–1200 cm^{-1}) signals, along with conjugated C=C (1600 cm^{-1}) and aliphatic C–H (2850–2950 cm^{-1}) signals. The 1D ^1H NMR analysis confirmed the presence of a shared conjugated polyene backbone, exhibiting olefinic signals ranging from 5.16 to 5.36 ppm, along with a polyol/sugar head group observed between 3.53 and 4.25 ppm. S2 was differentiated from S1 by the presence of an oxygenated marker at 3.27 ppm and additional aromatic signals detected within 8.17 to 8.34 ppm. The aliphatic regions, from 0.87 to 1.33 ppm, revealed branched iso and anteiso methyl groups characteristic of Bacillus metabolites. S1 exhibited a higher antioxidant capacity in the ABTS (2.23±0.02 mmol TE/g) and FRAP (94.15±2.18 mmol TE/g) assays compared to S2, which showed values of 1.53±0.02 and 72.15±4.00 mmol TE/g, respectively. However, there was no significant difference in DPPH activities ($p > 0.05$). The brine shrimp (Artemia salina) lethality assay revealed low toxicity for both S1 and S2, with an LC_{50} of approximately 3000 ppm. Additionally, S1 produced 30% more pigment than S2, underscoring strain-dependent variability. This study showcases the potential of oxygenated polyenes derived from Bacillus as non-toxic, multifunctional natural compounds suitable for high-value applications in the food, pharmaceutical and biotechnological sectors.

OP-05

INTEGRATING UAV BASED MULTISPECTRAL IMAGING AND DSSAT CROP MODELING TO SUPPORT CLIMATE-SMART WHEAT PRODUCTION UNDER LATE SOWING CONDITIONS

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The production of wheat in South Asia faces two main challenges which include climate variability and increasing temperature stress. The limited land resources in Bangladesh during the optimal growing season led farmers to use late sowing methods which result in wheat crops experiencing heat and drought stress at the end of their growth cycle. The research investigates how selected wheat cultivars perform during late sowing conditions through UAV-based multispectral imaging and the DSSAT crop simulation model. We conducted a field experiment through a randomized complete block design (RCBD) which included four experimental replications and also conducted evaluations of four wheat cultivars BWMRI-1, BWMRI-2, BWMRI-3 and BARI-28 under two different stress conditions which included heat stress and combined heat-drought stress. By multispectral UAV imagery to track physiological parameters which included leaf area index (LAI) and crop vigor and also collected phenological and yield data to establish the calibration and validation standards for the CERES-Wheat module of the DSSAT model. By assessed model performance through two measurements which included normalized root mean square error (RMSE) and coefficient of determination (R^2). The calibrated model successfully predicted anthesis and maturity and LAI and biomass accumulation across treatments which demonstrated strong predictive accuracy through its results ($R^2 = 0.8737$; adjusted $R^2 = 0.855$). BWMRI-1 wheat cultivar showed the greatest tolerance to stress when it produced only 6% lower yield under heat stress compared to its total yield under combined heat-drought conditions which results in 58% yield loss. UAV-based monitoring combined with crop modeling creates a decision-support system that farmers can use to implement climate-smart agricultural practices. The research results enable policymakers and extension services to choose stress-tolerant cultivars while developing adaptive sowing strategies for agricultural planning which supports climate services and early warning systems and anticipatory agricultural planning

OP 06

SYNTHESIS AND CHARACTERIZATION OF SPINEL FETI2O4 CRYSTALS FOR DEVICE APPLICATIONS

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The transition metal oxides of the spinel structure has a wide range of excellent electrical, optical and magnetic properties. Among them FeTi2O4 is a multipurpose material with with a.

Wide range of applications because of its chemical stability, wide band gap and structural features. The FeTi2O4 might be used in spintronics and non-volatile memory devices. It bcan be used as UV photodetectors, thin film transistor and in photovoltaic applications. In this work solid state reaction techniques was successfully used to synthesize high quality FeTi2O4 crystals. The thermogravimetric and differential thermal analysis were used to examine thermal behavior and phase formation. The X-ray diffraction was used to confirm phases and determine

crystal structure. The crystal structure and phases were established by Fourier transform infrared spectroscopy (FTIR) analysis. The UV-Visible spectroscopic technique was used to characterize optical properties and the two probe method was employed to assess the electrical characteristics of the materials. The optical characteristics reveal that the materials can be used in optoelectronic devices and coating materials. The electrical properties characterization results reveal that the prepared crystalline materials were semiconductors and can de used in memory devices.

OP 07

ASSESSING THE CLIMATE CHANGE IMPACTS ON BORO RICE PRODUCTION IN THE BARIND REGION OF BANGLADESH USING THE DSSAT MODEL

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Climate change has been posing a serious threat to rice production in Bangladesh, especially in the semi-arid Barind tract encompassing the Rajshahi, Rangpur, and Bogura districts. This study evaluated the estimated effects of climate change on grain production, crop water requirement (CWR), and growth period of boro rice (BRRI dhan29) through the DSSAT-CERES Rice model driven by CMIP6 climate projections from the ACCESS-CM2 General Circulation Model (GCM). The simulation was done under two socioeconomic shared pathways (SSP2-4.5, SSP5-8.5) for two periods: baseline period (1995-2014), future period (2030-2060). Findings show that the response of the yield was different across locations and situations. At Rangpur, the grain yield is projected to decline by 0.72% and 14.11% under SSP2-4.5 and SSP5-8.5 respectively as compared to the baseline yield of 6352 kg/ha. Under SSP2-4.5, Rajshahi shows an increase of 15.78% in yield and a drastic decrease of 18.88% under SSP5-8.5. Bogura exhibited modest declines of 0.85% and 13.86% under SSP2-4.5 and SSP5-8.5, respectively. The crop water requirement in all three locations shows a uniform increment under the two scenarios, with the most pronounced rise observed in Rajshahi under SSP5-8.5 (+27.53%). The duration of growth is expected to be reduced at all sites, due to the effect of warmer future conditions, ranging from 5% to 9% for all three locations. These results raise concerns that the high-emission trajectories might significantly undermine the food security in the Barind region in terms of concomitant yield losses, high irrigation pressure, and loss in the crop cycles. Strategies of adaptation, such as the development of a heat-tolerant variety and better irrigation control, will be important to maintaining the productivity of boro rice under estimated climate change.

OP 08

COMPARATIVE STUDY OF DOUBLE-DIFFERENTIAL NUCLEON EMISSION IN PROTON-INDUCED REACTIONS USING TALYS

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Double-differential cross sections (DDX) of emitted nucleons provide important insight into nuclear reaction. Mechanisms by simultaneously describing the energy and angular distributions of emitted particles. In this work, the TALYS nuclear reaction code is used to investigate proton-induced reactions on medium and heavy nuclei. Proton emission from 58Ni(p,xp) at an incident energy of 100 MeV and neutron emission from 208Pb(p,xn) at 103 MeV and 209Bi(p,xn) reactions at 11.2 MeV and 98 MeV are studied. The calculated double-differential cross sections are compared with available experimental data measured at laboratory angles between 30° and 150°. The results show clear variations in emission mechanisms depending on incident energy and target mass. The 209Bi(p,xn) reaction at 11.2 MeV is dominated by compound nucleus evaporation, while reactions at higher energies exhibit significant pre-equilibrium contributions, particularly at forward emission angles. Overall, the TALYS calculations reproduce the main features of the experimental spectra and provide insight into nucleon emission mechanisms in proton-induced reactions.

OP 09

MOUSE SERUM ALBUMIN-COATED PACLITAXEL-LOADED GELATIN NANOPARTICLES FOR STEALTH TARGETED CANCER THERAPY

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Following parenteral administration, drug-loaded nanoparticles (NPs) are rapidly coated by serum proteins, forming a ‘protein corona’ that promotes opsonization and recognition by phagocytic cells. This immune recognition often leads to premature clearance, reducing therapeutic efficacy. Surface functionalization with blood-derived proteins is hypothesized to minimize protein adsorption, providing a stealth effect and enhancing circulation time. This study aimed to develop stealth-bioinert nanoparticles by coating paclitaxel (PTX)-loaded gelatin NPs with mouse serum albumin (MSA) to reduce protein adsorption and unwanted clearance. The structural and compositional characteristics of the MSA-coated NPs were analyzed using FT-IR, FE-SEM/EDX, and TGA. Particle size (~200 nm), size distribution, and zeta potential were evaluated via dynamic light scattering (DLS) and zeta analysis. In vitro drug release studies assessed the pH-sensitivity and time-dependence of PTX release from the coated NPs. MSA-coated PTX-loaded gelatin NPs demonstrated significantly reduced non-specific protein adsorption when exposed to mouse blood, suggesting successful stealth behavior. The coating minimized immune activation, potentially enhancing nanoparticle retention

in circulation. In vivo studies in tumor-bearing mice confirmed reduced immune rejection and improved cytotoxic efficacy of PTX. These findings provide valuable insights into (1) achieving stealth properties in NPs for chemotherapeutics drug delivery, and (2) utilizing degradable, protein-based materials for biocompatible nanocarrier design.

OP 10

INVESTIGATION OF THE AGGREGATION BEHAVIOR OF TETRADECYLTRIMETHYLAMMONIUM BROMIDE WITH LEVOFLOXACIN HEMIHYDRATE: EFFECTS OF HYDROTROPES ON THE PHYSICO-CHEMICAL PARAMETERS

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Surfactant aggregation is a fundamental physico-chemical phenomenon that governs key processes such as detergency, solubilization, and surface tension reduction, which play crucial roles in cleaning systems, advanced drug delivery process, and various innovative industrial applications. Levofloxacin hemihydrate (LFH) drug is a fluroquinolone antibiotic, is widely used for the treatment of bacterial infections. This study aims to investigate the aggregation behavior of tetradecyltrimethylammonium bromide (TTAB) with LFH in the presence of hydrotropes at variable temperatures. In this exploration, conductivity method has been used to explore the aggregation behavior of TTAB + LFH system under the influence of hydrotropes (sodium salicylate (NaSal), sodium benzoate (NaBenz), para-aminobenzoic acid (PABA), and caffeine) within the temperature ranges of 288.15 to 323.15 K with 5 K differences. Critical micelle concentration (CMC) and relevant thermodynamic parameters were determined. A single CMC value was observed for the TTAB + LFH mixture in each solvent system. The CMC increased in the presence of NaSal and caffeine, whereas it decreased with NaBenz and PABA. At 5 mmol kg-1 concentration of HDTs, the CMC values followed the sequences as: CMC (aq. NaSal) > CMC (aq. Caffeine) > CMC (aq. PABA) > CMC (aq. NaBenz). Increasing temperature hindered the micellization process. The analysis of the thermodynamic parameters revealed that the Gibbs free energy change (Δ) values were found negative, suggesting the spontaneous process of aggregation. Enthalpy changes (ΔHmo) were positive at lower temperatures (endothermic) and negative at higher temperatures (exothermic), while entropy changes (ΔSmo) were attained positive at all thorough selected temperature ranges. The process is governed by hydrophobic, electrostatic, H-bonding, and ion-induced dipole interaction forces. The plot of ΔHmo vs. ΔSmo of the mixture was linear in fashion, confirming that the enthalpy and entropy compensate each other. The current research findings might be highly suitable in drug delivery and drug carrier system, new drug design, development of excipient formulations in the pharmaceutical industry.

OP 11

NEURAL SIGNATURES OF AUDITORY AND VISUAL PROCESSING: AN EEG ANALYSIS USING THE MNE SAMPLE DATASET

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Understanding how the brain processes sensory information is fundamental to cognitive neuroscience. Auditory and visual perception rely on partially distinct neural pathways that can be examined with high temporal precision using electroencephalography (EEG). Establishing transparent and reproducible EEG analysis pipelines using well-characterized benchmark datasets is an essential step before extending these methods to clinical and mental health research. This study aimed to demonstrate a reproducible EEG preprocessing and analysis pipeline for auditory and visual evoked responses and to illustrate modality-specific temporal and spatial neural activation patterns at the sensor level. EEG data were obtained from the publicly available MNE-Python sample dataset involving an auditory–visual stimulation paradigm recorded from a healthy adult participant. Data preprocessing was conducted using MNE-Python following standard best practices, including band-pass filtering, event extraction, epoching (−200 to 500 ms), baseline correction, artifact handling, and averaging to compute evoked responses. Event-related potentials (ERPs) were calculated separately for auditory and visual stimuli. Sensor-level waveform comparisons and scalp topographies were examined at key post-stimulus latencies associated with early sensory processing. Auditory and visual stimuli produced clearly differentiated evoked response profiles. Auditory stimulation elicited earlier peak activity compared with visual stimulation, indicating modality-specific temporal dynamics. At approximately 100 ms post-stimulus, auditory-evoked responses demonstrated a spatially organized scalp distribution consistent with early auditory sensory processing. In contrast, visual-evoked responses exhibited a distinct topographic pattern reflecting modality-specific cortical engagement. Difference topographies further highlighted spatial contrasts between auditory and visual neural responses. The study demonstrates a transparent and reproducible EEG analysis pipeline capable of identifying modality-specific neural signatures of sensory processing. This methodological framework provides a foundation for future multi-subject EEG research integrating behavioral and mental health measures.

OP 12

MOLECULAR-LEVEL INVESTIGATION OF ANTIOXIDANT ACTIVITY OF THYMOL IN DIVERSE SOLVENT ENVIRONMENTS: A DENSITY FUNCTIONAL THEORY STUDY

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Oxidative stress caused by excessive generation of reactive oxygen species (ROS) plays a critical role in cellular damage and various chronic diseases. Natural phenolic compounds have attracted considerable attention as effective antioxidants due to their ability to neutralize free radicals. In this study, the antioxidant potential of thymol (5-methyl-2-isopropylphenol), a naturally occurring phenolic monoterpenoid present in thyme and oregano essential oils, was systematically investigated using density functional theory (DFT) computations.

All geometrical optimizations and thermochemical calculations were performed at the B3LYP/6-311++G(d,p) level of theory in the gas phase and several solvent environments including water, dimethyl sulfoxide, methanol, ethanol, dichloromethane, chloroform, benzene, and cyclohexane using the IEFPCM solvation model. The antioxidant activity was evaluated through three principal mechanisms: hydrogen atom transfer (HAT), sequential proton loss electron transfer (SPLET), and single electron transfer–proton transfer (SETPT). Key thermochemical parameters such as bond dissociation enthalpy (BDE), proton affinity (PA), ionization potential (IP), electron transfer enthalpy (ETE), and proton dissociation enthalpy (PDE) were calculated to determine the most favorable radical scavenging pathway. The results reveal that the phenolic OH group of thymol exhibits the lowest BDE values across all environments, indicating that HAT is the most favorable mechanism for free radical scavenging. Electronic descriptors including HOMO–LUMO energies, chemical hardness, electrophilicity, Fukui functions, and molecular electrostatic potential further support the strong antioxidant capability of thymol. Spin density analysis confirms significant delocalization of the radical formed after hydrogen abstraction, which enhances radical stability. Overall, this study provides molecular-level insight into the antioxidant behavior of thymol and highlights its potential as an efficient natural antioxidant for pharmaceutical, nutraceutical, and food preservation applications.

OP 13

NON-INVASIVE ABDOMINAL FAT ESTIMATION FROM SKIN SURFACE TEMPERATURE: A FINITE ELEMENT APPROACH

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Accurate quantification of abdominal fat distribution is essential for understanding metabolic and thermoregulatory processes in the human body. Simpler indices like BMI cannot distinguish between visceral and subcutaneous fat, while traditional imaging techniques like CT and MRI, though accurate, are costly and involve radiation exposure or complex procedures i.e., invasive. This study aims to develop and validate a physics-informed computational framework to investigate the relationship between abdominal fat distribution and skin surface temperature, enabling the possibility of non-invasive fat estimation. A two-dimensional finite element model (FEM) of the human abdomen was developed using COMSOL Multiphysics, which incorporated anatomically representative tissue-layers including skin, subcutaneous fat, visceral fat, muscle, and internal organs. Each layer was assigned experimentally validated thermophysical properties. Thermal conduction and perfusion-driven heat-transfer in tissues were simulated using the steady-state Pennes' bioheat equation, with convective and radiative heat loss at the skin surface as boundary conditions representing interaction with the ambient environment. Two different abdominal profiles representing slim and obese conditions were modeled to analyze the influence of fat thickness on skin surface temperature distribution. Simulation results indicated that increased fat thickness lowers skin surface temperatures due to adipose tissue insulation and reduced heat conduction from internal organs. The slim model predicted 32.0–33.8 °C (experimental 32.7–35.0 °C), and the obese model predicted 32.5–33.6 °C (experimental 31.4–33.2 °C). The FEM predictions closely matched with experimental thermographic data in previous studies, including by Shimano et al., validating the developed model accuracy. The validated FEM framework demonstrates that variations in abdominal fat thickness can be reflected in measurable changes in skin surface temperature. This study provides a computational basis for developing computational approaches for non-invasive abdominal fat estimation using thermal data, potentially offering a safer, non-invasive and more accessible alternative to conventional imaging techniques.

OP 14

ADVANCING LARGE-SCALE SCREENING OF Β-THALASSEMIA TRAIT WITH NOVEL COMBINATIONS OF DISCRIMINANT FORMULAS AND MACHINE LEARNING ALGORITHMS

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β-thalassemia poses a considerable public health burden in Bangladesh, where a high carrier frequency underlies widespread disease risk. Hence, diagnosis of β-thalassemia trait (βTT) is indispensable to ensure genetic counseling and enable effective prevention strategies. Despite the availability of multiple discriminant formulas and machine learning algorithms (MLAs), their comparative diagnostic performance within the Bangladeshi population has not been comprehensively investigated. This study aimed to assess different discriminant formulas and MLAs as well as to propose novel combinations of formulas for population-specific screening of βTT. The study screened 2,514 individuals and categorized them as normal, βTT, and anemia cases, as well as other hemoglobin variants. 47 discriminant formulas and 12 MLAs were applied to identify the most effective predictors of βTT. DF-6 and DF-27 were two new formulas constructed by integrating high-performing formulas. Multi-criteria decision-making (MCDM) techniques, TOPSIS (Technique for Order Preference by Similarity to Ideal Solution) and SECA (Simultaneous Evaluation of Criteria and Alternatives), provided the final ranking for performance. Cluster analysis was performed to identify groups with similar diagnostic performance. Population-specific optimal cut-off values were determined for the discriminant formulas. The newly proposed formulas, DF-6 and DF-27, ranked among the top ten performers. DF-6 achieved the best overall performance (AUC: 0.9707). Assessment of MLAs revealed that XGBoost (XGB) (AUC: 0.9823) and Support Vector Machine (SVM) (AUC: 0.9743) provided the highest diagnostic accuracy. The reliability of ensemble MLAs was confirmed by MCDM and cluster analyses. The combination of novel discriminant formulas and integration of MLAs can substantially strengthen nationwide screening programs to reduce the burden of thalassemia in Bangladesh.

OP 15

A BI-OBJECTIVE LINEAR PROGRAMMING MODEL FOR COST-MINIMIZED AND NUTRITIONALLY ADEQUATE DIET PLANNING FOR UNIVERSITY HALL STUDENTS IN BANGLADESH: A SEASONAL SCENARIO ANALYSIS

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Dietary inadequacy among university residential hall students in Bangladesh represents a critical but underexplored dimension of food insecurity. Students operating under constrained daily food budgets of 60-200 BDT frequently achieve caloric sufficiency while remaining deficient in protein, calcium, and iron, underscoring a hidden burden of micronutrient shortfalls. This study aims to quantify the minimum daily budget required for full nutritional adequacy and to characterize cost-nutrition trade-offs across seasonal price environments. A bi-objective linear programming model was developed to simultaneously minimize daily food cost and maximize a composite Nutritional Adequacy Score (NAS) across six essential nutrients, evaluated under three seasonal price scenarios: Winter Baseline (S1), Monsoon Disruption (S2), and Ramadan/Festive (S3). The model was solved using two complementary approaches: the Gurobi epsilon-constraint method to generate exact Pareto-optimal solutions and the Non-dominated Sorting Genetic Algorithm II (NSGA-II), implemented via the pymoo framework, to obtain a dense approximation of the Pareto frontier and verify cross-solver consistency. Results indicate that full nutritional adequacy is estimated to be achievable at approximately 100 BDT/day in winter, rising to 110 BDT in monsoon and 120 BDT during Ramadan, a 20% seasonal budget premium. Knee-point optimal diets recommend culturally appropriate food combinations, including rice, rui fish, red lentils, spinach, banana, and milk. Budget sensitivity analysis reveals a steep NAS cost trade-off below 90 BDT, identifying a critical indicative threshold for hall dining subsidy policy design. NAS weight sensitivity analysis confirms that policy thresholds are robust to moderate variation in nutrient importance weights.

OP 16

CUO-GO NANOSTRUCTURE EMBEDDED ELECTROSPUN NANOFIBROUS SCAFFOLDS: A POROUS, AND CYTOCOMPATIBLE PLATFORM FOR ACCELERATED WOUND HEALING AND SKIN REGENERATION

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Electrospun nanofibrous scaffolds are artificial structures that mimic the natural extracellular matrix (ECM) using a fabrication process called electrospinning. Electrospun nanofibers derived from polymer–inorganic nanocomposites (NCs) have emerged as next-generation candidates in wound healing, largely owing to their inherent biocompatibility, biodegradability, tunable porosity, and the remarkable synergy achieved by coupling the flexibility of polymers with the unique functionalities of inorganic nanoparticles (NPs). In this study, we report, for the very first time, the design and fabrication of a nanofibrous scaffold engineered from copper oxide–graphene oxide (CuO-GO) NCs incorporated polyvinyl alcohol–chitosan (PVA/CS) polymeric solution. The resulting scaffolds displayed a highly porous architecture (>70%) and mechanical properties (σ =2.5–7 MPa, ε =9–18%, and E =12–120 MPa) strikingly reminiscent of the physiological microenvironment of skin, suggesting a structural compatibility ideal for tissue integration. The CuO–GO NCs were incorporated at finely tuned concentrations (0.75–2 wt%), ensuring a delicate balance between functionality and cytocompatibility, as confirmed by cell viability values exceeding 95%. Equally compelling were the scaffold's hydrophilic features, imparted by the PVA and CS matrix, which resulted in water contact angles ranging from 38° to 64.4° and an exceptional swelling capacity (>350%). Such characteristics are vital for absorbing wound exudates and maintaining a moist healing environment. Interestingly, the scaffold degraded by more than 70% within 14 days, a rate that harmonized with the natural timeline of wound closure. In vivo investigations using Swiss albino mice revealed a striking outcome: the nanofiber mats not only promoted re-epithelialization and granulation tissue formation but also facilitated complete wound closure within just 14 days. The CuO–GO/PVA/CS nanofibers stand at the intersection of biomaterials engineering and therapeutic innovation, holding immense promise for accelerating full-thickness wound repair and potentially redefining clinical strategies in tissue regeneration.

OP 17

COMPUTATIONAL INTELLIGENCE IN DRUG DISCOVERY: IDENTIFYING NOVEL DFRA1 INHIBITORS TO COMBAT TRIMETHOPRIM-RESISTANT KLEBSIELLA PNEUMONIAE AND ESCHERICHIA COLI

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Trimethoprim resistance in Klebsiella pneumoniae and Escherichia coli is largely driven by the DfrA1 protein, which reduces antibiotic binding efficacy. Addressing this global health threat requires accelerating traditional drug discovery. This study leverages advanced computational modeling and predictive artificial screening to rapidly discover novel drug candidates targeting DfrA1 in these resistant pathogens.We employed high-throughput computational screening a data-driven predictive approach to evaluate and optimize 3,601 synthesized chemical compounds from the ChemDiv database against the DfrA1 protein. Promising candidates were assessed for thermodynamic properties and binding interactions. Furthermore, advanced predictive molecular dynamics simulations were conducted to evaluate structural stability and inhibition dynamics over time. Finally, in vitro plate assays were utilized to validate the antibacterial efficacy of our top computationally predicted candidates against superbugs.Our computational models identified six promising drug candidates (DC1–DC6) with strong binding affinities comparable to the control antibiotic, Iclaprim. Molecular dynamics simulations confirmed their robust structural inhibition capabilities. Notably, the in silico profiling of DC4 (an organofluorinated compound) and DC6 (a benzimidazole compound) showed superior predicted efficacy, enhanced stability, and optimal binding site interactions. Crucially, our computational predictions were successfully validated by in vitro studies, where DC4 actively inhibited the growth of superbugs in plate assays.DC4 and DC6 emerge as potent DfrA1 inhibitors, showcasing the power of computational intelligence and predictive modeling in accelerating antimicrobial drug discovery. While these computer-aided predictions and in vitro validations are highly encouraging, further in vivo and clinical studies are necessary to validate these compounds as therapeutics.

OP 18

NETWORK PHARMACOLOGY AND MOLECULAR DYNAMICS-GUIDED MECHANISTIC ELUCIDATION OF NIFEDIPINE AND LERCANIDIPINE IN ISOPROTERENOL-INDUCED CARDIAC DYSFUNCTION

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Calcium channel blockers show cardioprotective potential in myocardial injury. To map their underlying molec-

ular mechanisms, we integrated computational approaches - network pharmacology, molecular docking, and molecular dynamics to compare nifedipine and lercanidipine, alongside in vivo echocardiographic, biochemical, and histological validations. In silico evaluations utilized network pharmacology to map intersecting therapeutic targets between the drugs and cardiac hypertrophy pathways. Molecular docking and 100 ns molecular dynamics (MD) simulations evaluated target-ligand binding affinities. For in vivo validation, Long-Evans rats were divided into six groups, including control, isoproterenol alone (ISO, 50 mg/kg), ISO with nifedipine (20 mg/kg), and ISO with lercanidipine (5 mg/kg). Echocardiography was performed on day 14. Following imaging, animals were sacrificed for histopathological profiling and evaluation of key oxidative stress, antioxidant, and cardiac toxicity markers. Principal Component Analysis (PCA) was applied to map complex redox and functional data distributions. Computational analyses identified core hub genes linked to cardiac inflammation and remodeling, with molecular docking revealing high binding affinities for both nifedipine and lercanidipine. Validating these in silico predictions, in vivo ISO administration reduced ejection fraction, induced severe cardiomyocyte disarray, and disrupted redox homeostasis. Treatment with nifedipine and lercanidipine substantially attenuated these changes. The interventions preserved myocardial architecture, mitigated fibrosis, and restored the antioxidant balance alongside circulating markers of cardiac injury. Furthermore, PCA revealed distinct restorative clustering patterns for both drugs across echocardiographic and biochemical profiles, moving treated groups away from the disease model. Computational modeling provided deep mechanistic insights into the comparable cardioprotective pathways of nifedipine and lercanidipine. These in silico network predictions strongly correlate with our in vivo physiological and multivariate biochemical findings, confirming that pathological remodeling is halted and myocardial function is substantially preserved.

OP 19

DEVELOPMENT AND EVALUATION OF A LOW-COST, MACHINE LEARNING ASSISTED BIOASSAY FOR RAPID IDENTIFICATION AND ANTIBIOTIC RESISTANCE ASSESSMENT OF UROPATHOGENIC KLEBSIELLA SPP.

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Urinary tract infections (UTIs) are among the most common bacterial infections worldwide, posing a significant healthcare burden due to high morbidity, recurrence, and rising antimicrobial resistance. Timely diagnosis and appropriate therapy are critical to prevent complications and limit resistant pathogen spread. Conventional culture-based identification and antibiotic susceptibility testing (AST) are time-consuming, while automated platforms like VITEK are costly and may not reflect recent breakpoint updates. Klebsiella spp. have emerged as clinically important uropathogens in both hospital and community-acquired UTIs, highlighting the need for rapid, low-cost diagnostic platforms capable of simultaneous detection, identification, and resistance profiling in resource-limited settings. The system uses an optimized broth medium with pH-sensitive indicators to reflect Klebsiella spp. metabolic behaviour. A novel biochemical panel allows genus-level identification, standardized with reference strains, and evaluated on clinical isolates. Gram profiling was also performed. Organism-induced colour changes are monitored via an RGB sensor-integrated microplate, and resulting colorimetric patterns are

analysed through a machine learning framework for identification and AST. Susceptibility testing is compared with standard reference methods following established guidelines. AI-assisted analysis is planned to track metabolic responses, aiming to reduce diagnostic turnaround time. The modified broth system successfully detected and identified Klebsiella spp. among UTI-associated pathogens using the novel biochemical panel. Evaluation with 21 clinical isolates demonstrated good antimicrobial susceptibility testing (AST) performance. Identification showed 100% sensitivity and specificity, with results interpreted via the machine learning–assisted device. Notably, interpretable results were obtained within 4 hours, highlighting the platform's potential as a rapid diagnostic approach. The MBS provides rapid, low-cost detection, identification, and AST of uropathogenic Klebsiella spp., achieving 100% sensitivity for detection. Future work will enhance AST accuracy, automate interpretation, and streamline the platform for broader clinical deployment.

OP 20

BIOPROSPECTING MARINE ENDOPHYTIC FUNGI ALTERNARIA PRUNICOLA AND FUSARIUM PERNAMBUCANUM ISOLATED FROM ULVA LACTUCA COLLECTED FROM THE BAY OF BENGAL

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Endophytic fungi isolated from marine macroalgae are recognised as abundant sources of many bioactive secondary metabolites. The objective of this study was to isolate and identify endophytic fungi from the green seaweed U. lactuca sourced from the Bay of Bengal, assess their antibacterial and cytotoxic properties, and then isolate bioactive chemical compounds. Endophytic fungi were isolated from surface-sterilised U. lactuca and characterised by molecular and morphological methods. Potato dextrose agar was used for large-scale culturing, and then ethyl acetate was used to extract the fungal metabolites. Disc diffusion method was used to test the crude extracts for antimicrobial activity and the brine shrimp lethality bioassay (BSLB) to test them for cytotoxicity. Bioactivity-guided fractionation with different chromatographic methods, such as column chromatography, size exclusion chromatography, thin layer chromatography, etc., were used for compound isolation. The isolated compounds were identified by utilizing nuclear magnetic resonance and mass spectroscopy. Alternaria prunicola and Fusarium pernambucanum were isolated and identified from U. lactuca. Both ethyl acetate extracts displayed substantial antibacterial efficacy and notable cytotoxicity in the BSLB. Mycochemical study of F. pernambucanum and A. prunicola results in three compounds from each. From F. pernambucanum ergosterol, ergosterol peroxide, and p-hydroxybenzaldehyde were isolated and from A. prunicola ergosterol peroxide, alternariol, and altenuene were isolated. These chemicals, especially the ergosterol peroxide and alternariol, are known for having a wide range of biological activities, including antifungal, antioxidant and anticancer properties. This study successfully identified U. lactuca from the Bay of Bengal as a host for bioactive endophytic fungi. The extraction of specific sterols and polyketides suggests that marine-derived fungi from the Bangladesh coast could be a valuable source of therapeutic lead compounds.

OP 21

PATTERNS, PREDICTORS AND DYNAMICS OF ANTIBIOTIC USE AND FARM-LEVEL RISK FACTORS IN BANGLADESHI POULTRY PRODUCTION SYSTEMS

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Antimicrobial resistance (AMR) in livestock is a major public health concern, driven by high animal density, poor sanitation, and irrational use of antibiotics, especially in resource-limited areas such as Bangladesh. The study aimed to identify antimicrobial usage patterns and risk factors for AMR, and to examine their associations with poultry mortality. We conducted a cross-sectional study in 204 commercial poultry farms across 42 sub-districts of Bangladesh (April–August 2025). Data was collected through face-to-face interviews using a semi-structured questionnaire. Statistical analyses included descriptive statistics, Chi-square, multivariable regression models, machine-learning–based AMR risk prediction (random forests, XGBoost), structural equation modeling (SEM), hierarchical clustering of antibiotic-use behaviors, and geospatial mapping of antimicrobial use patterns. The findings indicated that Antibiotics were the most prevalent drug (18.5%), with Quinolones being the most frequently used class (12.4%). Notably, 57% of antibiotics were administered prophylactically outside illness periods, and 54.6% of treatment recommendations were made by non-veterinarians. Multivariate analysis identified that poor sanitation was a critical driver of both increased antibiotic use and higher mortality rates. SEM identified prophylactic antibiotic use as the primary causal pathway driving AMR risk. Machine learning identified high-risk antibiotic use and advice from unqualified practitioners as the most influential predictors of AMR risk. Geospatial analysis revealed dynamic intensity shifts, with Rajshahi emerging as the region with the highest exposure over 14 days. These findings highlight the need to strengthen regulatory controls on critical antibiotic sales, enhance biosecurity, and establish effective surveillance systems. Comprehensive farmer training and targeted stewardship programs are also essential to shift the industry from routine drug-based prevention to evidence-based management.

OP 22

FIELD-LEVEL CONSTRAINTS AND FARMER-PRIORITIZED SOLUTIONS FOR ADOPTION OF BRRI-RELEASED BORO RICE VARIETIES IN BANGLADESH

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This study examined the socio-demographic characteristics of Boro rice farmers and identified field-level constraints and farmer-prioritized solutions influencing adoption of BRRI-released Boro rice varieties in Bangladesh. A total of 371 farmers were selected proportionately and randomly from 12 blocks across Cumilla, Mymensingh, Tangail, and Bogura districts. Data

were collected between 3 September and 31 December 2021through structured interviews. Descriptive statistics were applied, and constraints and recommendations were quantified using the Problem Faced Index (PFI) and Standardized Suggestion Index (SSI). Most respondents were middle-aged (41.78%), formally educated, and experienced in rice cultivation, though training exposure was limited. Farmers reported medium (38.55%) to high (37.20%) levels of adoption problems. Major constraints included unavailability of high-yielding variety Boro seed (PFI 89.67%), limited access to credit (PFI 88.95%), and high fertilizer costs (PFI 86.07%). Additional barriers involved inadequate technical knowledge, weak extension services, and poor market information. Farmers prioritized seed and input support (SSI 22.46%), improved credit facilities (SSI 18.56%), and irrigation incentives (SSI 18.21%). Addressing input supply, financial access, and institutional support is essential to accelerate adoption of BRRI-released Boro rice varieties and strengthen varietal dissemination at the farm level.

OP 23

ARTIFICIAL INTELLIGENCE (AI) AND MACHINE LEARNING (ML) FOR SUSTAINABLE MANAGEMENT OF MASTITIS IN DAIRY ANIMALS

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Bovine subclinical mastitis (SCM) costs the global dairy industry more than US$53 billion annually. SCM reduces milk yield and increases antibiotic use, thereby accelerating antimicrobial resistance. This study combined AI and ML with shotgun metagenomics, whole-genome sequencing (WGS), and computational analyses to characterize the milk bacteriome and resistome in SCM, and to identify genomically validated probiotics as antibiotic alternatives. Whole-metagenome shotgun sequencing was performed 30 milk samples from 20 crossbred cows grouped as SCM (n=10), antibiotic-treated SCM (ANT; n=10), and healthy (HM; n=10) to assess microbiome dysbiosis and resistome profiles. Three lactic acid bacterial strains Pediococcus pentosaceus MBBL4 and MBBL6, and Enterococcus faecium MBBL3 were characterized by WGS for probiotic attributes. Molecular docking and dynamics simulations assessed bacteriocin-virulence protein interactions, with results validated in a murine mastitis model. Microbial diversity was significantly higher in HM than SCM and ANT ($p<0.05$). SCM milk was dominated by Acinetobacter johnsonii (39.7%) and Escherichia coli (15.0%), whereas ANT milk showed increased Pseudomonas monteilii (4.03%), P. putida (2.91%), and Raoultella ornithinolytica (2.0%). HM milk harboured beneficial taxa including Pseudomonas lundensis (34.7%), Actinoalloteichus spp. (4.4%), and Lactococcus lactis (1.15%). Resistome profiling identified 194 ARGs, with SCM harbouring the largest repertoire (n=161). However, macrolide, aminoglycoside, and β-lactam resistance genes were significantly ($p<0.01$) enriched in ANT samples. Molecular docking showed high-affinity binding of bovicin (Pediococcus) to the Rho prptein, and enterolysin_A (Enterococcus) to usher protein of S. aureus, E. coli, and K. pneumoniae. In in-vivo, probiotic-treated mice showed complete resolution of mammary inflammation by day 14, with histopathological evidence of tissue recovery. This study highlights AI and ML as powerful tools for precision mastitis surveillance. Integrating metagenomics, resistome mapping, and AI-driven drug target prediction offers a strong One Health approach to combat AMR and advance sustainable, evidence-based probiotic therapies for the dairy industry.

OP 24

FARMERS ATTITUDE MEDIATES PREVENTIVE PRACTICES AGAINST INCLUSION BODY HEPATITIS AND FOWL ADENOVIRUS (FADV) CIRCULATION IN POULTRY IN BANGLADESH

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Inclusion Body Hepatitis (IBH), caused by Fowl Adenoviruses (FAdVs), is an emerging threat to the poultry industry in Bangladesh, leading to economic losses and increased mortality. Integrating farmer awareness, biosecurity practices and molecular approaches is essential for comprehensive disease management. This study aimed to (i) assess knowledge, attitudes, and practices (KAP) regarding IBH among poultry stakeholders, (ii) identify behavioral determinants influencing preventive practices, and (iii) detect and genetically characterize circulating FAdV strains. A cross-sectional KAP survey was conducted among 389 poultry stakeholders. Logistic regression and structural equation modelling (SEM) were used to assess associations and pathways among KAP variables. Concurrently, tissue samples (liver, spleen, kidney) from suspected IBH cases in selected districts were analyzed using conventional PCR targeting the hexon gene, followed by sequencing and phylogenetic analysis to determine genetic relationships. Knowledge showed no significant correlation with attitude ($r=0.09$, $p>0.05$) and a weak association with practice ($r=0.11$, $p<0.05$), whereas attitude was strongly correlated with practice ($r=0.47$, $p<0.001$). SEM demonstrated that knowledge significantly influenced attitude ($\beta=0.207$, $p=0.001$), and attitude strongly predicted biosecurity practices ($\beta=0.499$, $p<0.001$). The direct effect of knowledge on practice was non-significant ($\beta=0.117$, $p=0.079$), while the indirect effect via attitude was significant ($\beta=0.103$, $p=0.004$), indicating full mediation. PCR confirmed FAdV infection with a 590 bp amplicon, and sequencing identified serotype 8b. Phylogenetic analysis showed clustering with Bangladesh and neighboring countries, indicating regional persistence. The study establishes a direct link between farmer awareness, and confirmed viral circulation, demonstrating that attitude is the key mediator translating knowledge into preventive practices. Effective IBH control requires integrating attitude-focused training, strengthened biosecurity, and continuous molecular surveillance.

OP 25

DETERMINANTS OF FOOD SECURITY IN BANGLADESH: A TIME-SERIES ANALYSIS USING THE GLOBAL FOOD SECURITY INDEX (2012-2022)

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As Bangladesh navigates its demographic dividend, identifying the key factors associated with food security is important for long-term stability. While much of the literature focuses on broader regional patterns, this study examines the Bangladeshi context specifically. The objective was to assess how selected macroeconomic, agricultural, nutritional, and environmental variables relate to the four pillars of food security: Affordability, Availability, Quality & Safety, and Sustainability & Adaptation. A quantitative time-series analysis was conducted using Bangladesh data from 2012 to 2022 within the Global Food Security Index (GFSI) framework. The explanatory variables were GDP per capita (GDPpc), rice production (million tonnes), animal protein supply, inflation, and annual rainfall. Statistical analysis was performed in R using descriptive statistics, Pearson correlation, and pillar-wise linear regression to examine associations between the selected variables and food security outcomes. GDP per capita showed a very strong positive association with Affordability ($r=0.993$, $p<0.001$), while rice production was very strongly positively associated with Availability ($r=0.964$, $p<0.001$). Quality & Safety was also strongly positively associated with animal protein supply ($r=0.881$, $p<0.001$). Inflation showed a weak negative correlation with Affordability ($r=-0.242$), and rainfall showed a weak positive correlation with Availability ($r=0.229$); however, neither variable was statistically significant in the supporting regression models ($p>0.05$). The overall regression model further showed that GDP per capita and rice production were significant positive predictors of GFSI. The findings indicate that improvements in food security in Bangladesh during 2012–2022 were most closely associated with economic growth and staple crop production, while animal protein supply was linked to Quality & Safety. In contrast, inflation and rainfall showed weak and non-significant relationships in the tested models.

OP 26

DECODING INSECT COMMUNICATION SIGNALS USING ARTIFICIAL INTELLIGENCE FOR THE DEVELOPMENT OF SMART PEST SURVEILLANCE SYSTEMS IN AGROECOSYSTEMS

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Insects rely on a diverse repertoire of chemical, acoustic, and vibrational communication signals to coordinate mating, foraging, and aggregation behaviours. Exploiting these signals offers a biologically targeted, non-toxic avenue for pest surveillance. However, the complexity and variability of insect signal datasets have historically limited their application in real-time monitoring systems. Artificial intelligence (AI), particularly machine learning and deep learning, provides the analytical capacity to decode these multimodal communication channels and translate them into actionable pest surveillance intelligence. This study aimed to design and evaluate an AI-powered smart surveillance system capable of identifying and classifying insect pest species from acoustic and chemical signal data in agroecosystems. Acoustic and pheromone-associated volatile organic compound (VOC) datasets were collected from controlled laboratory colonies and field populations of six economically important pest species, including Helicoverpa armigera, Spodoptera frugiperda, Bemisia tabaci, and Bactrocera dorsalis. Acoustic signals were recorded using directional microphones; VOC profiles were captured via proton-transfer-reaction mass spectrometry (PTR-MS). Signal datasets were processed using short-time Fourier transform (STFT) for acoustic spectrogram generation and principal component analysis (PCA) for VOC feature reduction. A hybrid AI model combining a long short-term memory (LSTM) network for temporal signal patterns and a random forest classifier for chemical fingerprint matching was developed and tested. The hybrid LSTM–random forest model achieved a species-level classification accuracy of 93.7% across all six pest species. Acoustic signal decoding yielded an F1-score of 91.2%, while VOC-based classification attained 94.5%. Real-time field deployment of the prototype smart trap, integrating onboard signal processing and IoT-based data transmission, successfully detected pest presence with a 15-minute alert latency and a 96.1%

true-positive rate across 45 monitored field plots. AI-driven decoding of insect communication signals enables unprecedented specificity in pest surveillance without reliance on broad-spectrum chemical applications. The smart surveillance prototype demonstrated high accuracy, low detection latency, and practical deploy ability in open agroecosystems. Scaling this technology offers transformative potential for early warning systems, reducing economic losses and supporting environmentally responsible integrated pest management.

OP 27

SOIL SALINITY INDUCED MICROBIAL SHIFTS IN COASTAL REGIONS OF BANGLADESH

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Coastal agriculture in Bangladesh increasingly faces salinity stress, which can restructure soilmicrobial communities and impair nutrient cycling. This study showed comparison between the diversity, composition and predicted functional traits of microbiomes in saline versus non-salinecropland soils from the coastal region of Bangladesh. 10 saline and 8 non-saline soil samples were collected from 6 locations around the coastal region of Kuakata. The saline soils are taken from 10 to 15 cm depth in proximity of agricultural land in the coastal zone where the entire crop yield was lost due to salinity. Soils with EC greater than 4 dSm-1 were selected as saline soil samples and soils with EC less than 1.5 dSm-1 were selected as non-saline soil samples. Soil physiochemical parameters and metagenomics were carried out using standard protocol. Saline soils showed significantly different physicochemical profiles, including higher EC (median 4.82 vs 0.50 dS/m) and elevated SAR, ESP, sulfur, pH and CEC. Microbial evenness was reduced in saline soils (significant differences in Simpson and Inverse-Simpson), whereas richness-focused indices (Observed, Chao1, Shannon) were not significantly different. Community structure separated clearly by salinity (PERMANOVA ≤ 0.01 for Bray– Curtis and Jaccard). At the phylum level, both groups were dominated by Proteobacteria and Chloroflexi, with saline soils enriched for Desulfobacterota and Deferrisomatota, and non-saline soils enriched for Myxococcota, Methylomirabilota, Gemmatimonadota, Verrucomicrobiota, Spirochaetota and Planctomycetota. At the genus level, saline soils were characterized by higher relative abundances of taxa associated with sulfur cycling and facultative anaerobes (e.g., Desulfobacca, Pseudomonas, Thioalkalispira-Sulfurivermis), whereas non-saline soils were enriched in taxa linked to iron oxidation, nitrification and organic-matter turnover (e.g., Sideroxydans, Candidatus Nitrotoga, Candidatus Solibacter). Phenotype interpretation indicated a higher proportion of predicted anaerobes in saline soils (36.4%) then non-saline (29.3%). Salinity in coastal croplands is associated with lower microbial evenness, distinct community structure, and enrichment of anaerobic and sulfur-cycling taxa, conditions that can favor denitrification and sulfate reduction. These shifts highlight microbial indicators relevant to managing soil health and crop productivity in salt-affected agroecosystems.

OP 28

MICROPLASTIC POLLUTION IN THE TURAG RIVER, BANGLADESH: IMPLICATIONS FOR ENVIRONMENTAL MONITORING AND CLIMATE-RESILIENT WATER MANAGEMENT

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Microplastic pollution has become a major environmental threat because it endangers aquatic ecosystems and degrades water quality and poses risks to human health. Developing countries such as Bangladesh experience increased microplastic pollution in their rivers because of growing urban areas and industrial waste disposal and ineffective plastic waste management practices. This study investigates the presence and distribution and polymer makeup of microplastics found in the waters of the Turag River which serves both ecological and economic functions for the area around Dhaka city. By executed a field study that collected data from eleven sampling sites which were spaced 1.5 kilometers apart along the Turag River water that passed through regions affected by industrial activity. And we collected water samples which processed to extract microplastic particles from the samples and used macro- and microscopic analysis to examine the morphological characteristics of the samples which included color shape and size distribution while they determined particle size through ImageJ software. Fourier Transform Infrared Spectroscopy (FTIR) useed to identify polymers and compared the acquired spectra with reference specta from SpectraBase™ to achieve precise polymer identification. The research showed that microplastics contaminated all areas of the Turag River shoreline water because researchers discovered six different types of microplastics: fibers and fragments and films and granules and pellets and foam particles. The testing process showed that polyethylene became the main type of plastic material because its presence was strongest at sites which lay close to the Dhour Bridge because industrial companies dumped their plastic waste and people disposed of their garbage inappropriately. The level of microplastic contamination in different locations around the riverbanks depended directly on human activities which occurred at those sites. The study gives foundational information which environmental organizations need to monitor environmental changes and manage climate-resilient water resources and establish pollution detection systems. The findings provide useful information for policymakers and environmental managers because they want to develop better river pollution monitoring systems and effective plastic waste management techniques and they aim to add microplastic studies into climate services and upcoming environmental conservation programs.

OP 29

SENSITIVITY ANALYSIS OF MICROPHYSICS, PBL AND CUMULUS SCHEMES IN WRF: ACCURATE TROPICAL CYCLONE SIMULATION AND LANDFALL PREDICTION OVER THE BAY OF BENGAL USING IN- SITU OBSERVATIONS

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With respect to the coastal regions of Bangladesh, tropical cyclones (TCs) over the Bay of Bengal (BoB) are considered to be one of the most destructive natural calamities, which cause considerable loss of life and property due to strong winds, storm surges, and rainfall. In order to enhance the accuracy of cyclone trajectory, intensity, and landfall predictions by incorporating local in-situ data, this study aims to identify the optimal combination of Planetary Boundary Layer (PBL), Cumulus Convection, and Microphysics schemes of the Weather Research and Forecasting (WRF) Model. In this study, the WRF Model has been employed to simulate two pre-monsoon cyclones over the BoB, namely Mocha (9-15 May 2023) and Remal (24-28 May 2024). In-situ data have been employed to drive different combinations of PBL schemes (MYJ, YSU), Cumulus Convection schemes (BMJ, KF), and Microphysics schemes (Thompson, WSM6). MYJ-BMJ-Thompson has been found to be the optimal combination in terms of minimum central pressure (946 hPa, 982 hPa), closest maximum wind speed (40 ms^{-1}, 24 ms^{-1}), and minimum cyclone track errors (234.8 km, 68.8 km). Peak rainfall, however, was consistently underestimated in both situations. For the BoB, the study offers a locally customized, well verified WRF configuration that greatly enhances landfall prediction and cyclone simulation. In Bangladesh, this ready-to-use structure can improve community resilience and fortify early warning systems.

OP 30

INTEGRATING VEGETATION, CLIMATE, SOIL MOISTURE DATA AND CROP MODELING FOR DISTRICT-LEVEL DROUGHT ASSESSMENT IN THE BARIND TRACT

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Drought is a common weather risk that poses threats to the agriculture, water supply, and rural livelihoods in northwestern Bangladesh. Frequent rainfall deficits and prolonged dry seasons in the Barind region highlight the need for effective drought monitoring systems to strengthen climate services and enable proactive response. In this study, appropriateness of various satellite-based drought indices to monitor the conditions in the districts is assessed. With multi-source remote sensing data, a number of indicators are created, such as the Vegetation Condition Index (VCI) and Temperature Condition Index (TCI) based on the NDVI and land surface temperature of the MODIS, the Precipitation Condition Index (PCI) based on satellite precipitation products and the Soil Moisture Condition Index (SMCI) based on the SMAP soil moisture. Also, the Scaled Drought Condition Index (SDCI) is formulated as a composite indicator which combines the variables of vegetation, temperature, precipitation and soil moisture to

form a composite measure of the combined impacts of meteorological and agricultural drought. These are indices that are being measured against the Standardized Precipitation Index (SPI) that is determined using the rainfall measurements received at the Bangladesh Meteorological Department. To assess agricultural impacts, the DSSAT crop simulation model was applied for rice cultivation, using drought indices as inputs to evaluate yield sensitivity under varying rainfall and soil moisture conditions. Results reveal significant spatial variability in drought signals, with severe impacts in Naogaon and Chapainawabganj where vegetation and soil moisture indices were most sensitive. DSSAT simulations confirmed yield reductions in these hotspots, demonstrating the agricultural relevance of the composite index. This research contributes to SDG 13 (Climate Action) and SDG 2 (Zero Hunger) by advancing drought preparedness and food security strategies in high-risk regions of Bangladesh.

OP 31

SPATIO-TEMPORAL DYNAMICS OF LAND SURFACE TEMPERATURE AND ITS RELATIONSHIP WITH BIOPHYSICAL INDICATORS IN A RAPIDLY DEVELOPING REGION: A CASE STUDY OF RAJSHAHI DISTRICT, BANGLADESH

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Rajshahi district, located in the northwestern part of Bangladesh, has experienced intensified urbanization, agricultural shifts, and climatic stress over the last thirty years due to the region's unplanned development. Examining the relationship between Land Surface Temperature (LST) and biophysical indicators is essential for understanding the thermal and ecological changes. This study aims to investigate the temporal relationship between LST and multiple biophysical indicators over the period from 1995 to 2025 to highlight the areas experiencing climatic and ecological stress. Normalized Difference Vegetation Index (NDVI), Normalized Difference Water Index (NDWI), Normalized Difference Built-up Index (NDBI), and Normalized Difference Bare Soil Index (NDBSI) were considered in this study to derive biophysical information from satellite images. Satellite imagery from Landsat was utilized to derive LST and biophysical information using established remote sensing algorithms. Correlation between LST and the selected indices was evaluated through scatter plot-based analysis. Results indicate that from 1995 to 2025, LST increased significantly, with maximum temperature rising from 36.43°C to 46.87°C and minimum going from 21.94°C to 26.39°C. At the same time, NDVI indicated a tendencytowards an increase (minimums: –0.400 to –0.132), suggesting recovery of vegetation. It also shows significant improvement in vegetation health, as unhealthy vegetation cover reduced (~80% to lower levels) and moderate vegetation increased (12.15% to 27.90%), highlighting successful land restoration efforts. Result also indicates that NDBI values were increased (minimum value ranges from -0.38 to -0.54 and maximum value ranges from 0.22 to 0.54) during the study period. On the contrary, NDBSI was reduced, representing less bare soil exposure (maximum NDBSI: 0.490 to 0.142) and more dispersed urban expansion, respectively. NDWI declined considerably (0.611 to 0.307), indicating a decrease in water extent. Results obtained from the correlation analysis revealed that lower vegetation cover, bare soil area, less water availability and increased built-up areas are associated with higher surface temperatures. This study effectively provides essential insights into the climatic and ecological transformations occurring in Rajshahi District over the past three decades, which can help relevant stakeholders to formulate sustainable land use planning, vegetation restoration, and water resource management strategies that address the region's development needs while preserving ecological balance.

OP-33

A COMPREHENSIVE MACHINE LEARNING FRAMEWORK FOR HIGH-THROUGHPUT DENGUE TRANSCRIPTOME ANALYSIS, BIOMARKER DISCOVERY, FUNCTIONAL ANNOTATION AND VISUALIZATION OF THERAPEUTIC TARGETS

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Dengue is a viral disease transmitted by the mosquito and is a significant epidemic issue of global health concern. Host transcriptomic responses are crucial to understanding the mechanisms of disease progression and predicting possible disease diagnostic or treatment targets. Nevertheless, the growing amount and the complexity of transcriptomic data demand sophisticated methods of computation. This paper creates a machine learning model that can be used to perform high-throughput analysis of dengue transcriptome data to establish the most significant gene expression patterns related to infection. Publicly available transcriptomic data GSE140809 (136 samples) RNA-seq data was analyzed with differential gene expression analysis with DESeq2. Classification and feature prioritization were performed by machine learning models such as Random Forest, LASSO-regularized logistic regression, and XGBoost. The consensus feature selection was the method used to identify candidate genes that were related to dengue infection. STRING and Cytoscap were used to build protein-protein interaction networks to identify hub genes. Functional enrichment analyses were performed using Gene Ontology (GO), KEGG, Reactome, and WikiPathways. The analysis of the differential expression was made to identify 504 dysregulated genes (366 upregulated and 138 downregulated). Prioritization on the basis of machine learning narrowed those 36 candidate genes that could separate acute dengue infection and convalescent dengue infection. The important hub genes were CXCL11, IFI27, USP18, GBP1, MX1 and TNFAIP6 that are linked with interferon signaling and immune regulation. Pathway analysis revealed interferon-mediated antiviral response, cytokine signaling, and the innate immune pathways. The analysis of protein-drug interaction revealed that ADAMTS5 is a possible therapeutic target. The article is a computationally integrative system that show the host-virus interactions, as well as important genes that are being used in antiviral immune responses and can serve as a scalable platform to discover biomarkers and therapeutics.

OP 34

AI-ASSISTED COMPUTER VISION FOR NON-DESTRUCTIVE FRESHNESS PREDICTION OF NILE TILAPIA USING RGB EYE IMAGE FEATURES

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Accurate and rapid assessment of fish freshness is critical for ensuring food quality, safety, and market value. This study proposes a non-destructive, image-based analytical framework to evaluate Nile tilapia freshness using quantitative eye-color features and multivariate modeling. Temporal image data were acquired at 3-hour intervals over a 24-hour period at 22˚C, and key optical parameters, including mean red (R), green (G), and blue (B) intensities, and

overall brightness, were extracted. Concurrently, mechanical hardness measurements were recorded as a reference indicator of textural degradation. Results revealed a progressive increase in RGB and brightness values with storage time, reflecting biochemical and structural changes during spoilage. Correlation analysis revealed a consistent inverse relationship between optical features and hardness, indicating that higher reflectance corresponds to lower tissue firmness. Principal Component Analysis (PCA) confirmed clear temporal separation of freshness stages, highlighting the discriminative capability of the proposed features. A multivariate regression model was developed to predict fish hardness from extracted image features, achieving strong predictive performance ($R^2 = 0.835$; RMSEP = 0.276). The findings underscore the potential of RGB-based imaging as a cost-effective, rapid, and non-invasive alternative to conventional freshness assessment methods. This approach is particularly suitable for real-time quality monitoring in supply chains and retail environments.

OP 35

DECIPHERING ANTIMICROBIAL RESISTANCE FROM BACTERIAL GENOMES THROUGH EXPLAINABLE ENSEMBLE MACHINE LEARNING FRAMEWORK

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The rapid rise of antimicrobial resistance (AMR) requires strong predictive models that can connect genomic factors with phenotypic resistance. This study developed a comprehensive machine learning-based approach to forecast antimicrobial resistance (AMR) among clinically relevant bacterial pathogens utilizing extensive genomic datasets. Data on whole-genome resistomes and antimicrobial susceptibility testing (AST) were obtained from the NCBI Pathogen Detection Isolate Browser. Resistance genes were encoded into binary matrices, and AST results were converted to binary labels. Stratified five-fold cross-validation addressed class imbalances. Five machine learning methods were evaluated: Logistic Regression, Random Forest, Gradient Boosting, Support Vector Classifier, and XGBoost. A stacking ensemble model combined Random Forest, Gradient Boosting, and Support Vector Classifier, with Logistic Regression as the meta-learner. Performance was measured using accuracy, precision, recall, and F1-score, while interpretability was assessed through LIME. The maximum classification accuracy was 79.5%-99.5% in 14 antibiotic datasets, with a high F1-score, precision, and recall, which does not show poor predictive outcomes. The stacking ensemble model recorded the best accuracy (99.55%) on Escherichia coli using imipenem, and a number of E. coli datasets recorded accuracy of more than 98%. XGBoost also works with Campylobacter jejuni with clindamycin (98.96%) and Salmonella enterica with kanamycin (98.68%) using XGBoost. In contrast, comparatively lower accuracy was noted for Pseudomonas aeruginosa–meropenem (79.54%) with Gradient Boosting and E. coli-doripenem (84.66%) with the stacking ensemble model. LIME analysis identified key resistance determinants, including blaCTX-M, blaNDM, blaKPC, blaOXA variants, mecA, and the 23S rRNA A2075G mutation as determinants of AMR because of certain genomic peculiarities. The integration of multiple machine learning models with ensemble learning and interpretable AI enables accurate and scalable AMR prediction. The stacking ensemble consistently delivered top performance, although no single model universally outperformed others. This framework supports genomic surveillance and informed antimicrobial decision-making.

OP 36

DECODING IMMUNE SIGNALING IN SEVERE COVID-19: SINGLE-CELL TRANSCRIPTOMICS AND MACHINE LEARNING INSIGHTS

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Severe COVID-19 is characterized by extensive transcriptional reprogramming, yet the signaling logic that bridges innate and adaptive immune responses remains poorly understood. This study elucidates the crosstalk between Neutrophils and Plasma Cells by integrating single-cell transcriptomics with an interaction-driven machine-learning framework. We reanalyzed scRNA-seq data from 136,236 PBMCs (7 COVID-19 patients and 6 controls). After batch correction, we mapped intercellular communication using LIANA and identified the S100A8/S100A9/ITGB2 "Signaling Trio" as a key regulatory axis. We developed a Stacking Ensemble Model (Random Forest and XGBoost) with SMOTE-Tomek resampling to predict disease severity. To ensure robustness, we performed external validation on 318,894 independent cells from the CellXGene Census. Finally, we utilized Local Interpretable Model-agnostic Explanations (LIME) to ensure model transparency. Our analysis reveals that Plasma Cells serve as a central signaling hub that drives inflammatory responses in Neutrophils through the S100A8/S100A9/ITGB2 axis. Our bias-corrected model demonstrated consistent performance, achieving an ROC-AUC of 0.66 in the internal cohort and 0.65 in the independent external validation cohort ($P < 0.001$). LIME analysis further confirms that this signaling trio is a more powerful predictor of cell fate than traditional lineage markers, indicating that a cell's "signaling state" is more crucial than its static identity during systemic inflammation. We establish the S100A8/S100A9/ITGB2 axis as a universal molecular signature for severe COVID-19. By combining explainable AI with large-scale validation, we show that maturing Plasma Cells functionally reprogram into pro-inflammatory hubs. This research offers a scalable, interpretable template for discovering signaling-based biomarkers in complex immune diseases.

OP 37

COMPUTATIONAL INVESTIGATION OF ANODIC CHLORINE EVOLUTION REACTION ON PLATINUM-TETRAPHENYL PORPHYRIN ELECTROCATALYST

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Chlorine, a vital industrial chemical, is predominantly produced via the chlor-alkali process, where dimensionally stable anodes (DSAs; RuO_2, IrO_2, TiO_2) are commonly employed. However, their reliance on scarce metals, limited selectivity, and environmental concerns necessitate alternative catalysts for the chlorine evolution reaction (CER). Carbon nanomaterials (CNMs) have recently emerged as promising supports owing to their high conductivity, tunable surfaces, and stability. In this work, we theoretically explored the CER activity of platinum-tetraphenyl porphyrin

(PTPP), as a Pt-doped graphene analogue, using density functional theory (DFT) along with B3LYP functional and Stuttgart/Dresden triple-ζ basis set with effective core potentials for Pt and the 6-311++G(d,p) for others in Gaussian 16. The calculated adsorption energy (ΔE) of Cl onto PTPP substrate was –0.073 eV, indicating spontaneous yet weak adsorption, enabling facile desorption of chlorine in the next step according to the Volmer–Heyrovsky pathway. The Gibbs free energy (ΔG) of adsorbed chlorine (Cl*) was 0.128 eV at 1.36 V, corresponding to a thermodynamic overpotential (η_CER) of 128 mV, consistent with literature benchmarks. Electronic structures analyses (FMO, NBO, MEP, spin density) confirmed favorable electronic features for CER. Importantly, PTPP also displayed strong selectivity toward CER over the competing oxygen evolution reaction (OER). The ΔE/ΔG of OER intermediates (HO*, O*, and HOO*) were calculated as 2.33/2.28 eV, 4.94/4.58 eV, and 4.82/4.37 eV, respectively, all significantly higher than those of Cl*. Moreover, CER proceeds via the Cl* intermediate (ΔG: 0.128 eV) rather than the ClO* pathway (ΔG: 3.150 eV), further ensuring selective chlorine production. These results establish PTPP as a selective, efficient, and cost-effective CNM mimic for chlorine generation.

OP 38

DEVELOPMENT OF CHROMACS: AN AUTOMATED AND FLEXIBLE GUI FOR END-TO-END REPRODUCIBLE ATAC-SEQ ANALYSIS ACROSS MULTIPLE SPECIES

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ATAC-seq is a powerful method for profiling chromatin accessibility, a key aspect in understanding gene regulation. Yet, ATAC-seq analysis remains technically demanding due to its multi-step workflows and diverse tool requirements. We aimed to develop a reproducible, user-friendly pipeline that enables both computational and experimental biologists to derive biological insights from ATAC-seq data. We introduce ChromAcS (Chromatin Accessibility Analysis Suite), a GUI-based, end-to-end pipeline integrating quality control, adapter trimming, alignment, coverage track generation, peak calling, annotation, differential accessibility analysis, motif enrichment, transcription factor footprinting, and multi-omics integration. The pipeline supports replicate-aware and replicate-free designs, flexible algorithm choices, parameter selection, multi-species genome support, and modular re-execution. Benchmarking was performed using publicly available datasets, including a case study of drug-tolerant persister (DTP) cells in EGFR-mutant PC9 lung cancer. ChromAcS analysis of drug-tolerant persister (DTP) cells in EGFR-mutant PC9 lung cancer reproduced published chromatin accessibility dynamics and revealed coordinated pathway-level chromatin remodeling. Peaks with increased accessibility were enriched in extracellular matrix organization, integrin signaling, focal adhesion, TGF-β, and MET pathways, consistent with adhesion-mediated drug resistance and bypass signaling. Conversely, decreased accessibility was observed in MAPK signaling and cytoskeletal regulation, reflecting attenuation of proliferative programs. ChromAcS automated ATAC-seq analysis with minimal setup friction, while retaining analytical depth. Benchmarking demonstrated reproducible outputs across datasets and highlighted how user-defined thresholds influence biological interpretation. ChromAcS provides a robust, open source solution for ATAC seq analysis, lowering barriers for non computational biologists while supporting advanced epigenomic studies. By combining analytical rigor with usability, ChromAcS enables reproducible discovery of regulatory mechanisms and accelerates chromatin biology research across diverse contexts.

OP 39

ANALYZING HEMATOLOGICAL PARAMETERS IN DIABETES: TOWARD A BETTER UNDERSTANDING OF PATHOPHYSIOLOGY

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Diabetes is an intricate public health burden. In Bangladesh, the cases of diabetes are rising drastically, and the scenario will be worrying if public awareness is not raised. Diabetic patients often have to handle significant systemic complications of comorbidities like hypertension, chronic kidney disease, coronary artery disease, etc all of which can be linked to altered levels of hematological markers. This study explores the interplay between hematological parameters and comorbidity variables of diabetic patients from Bangladesh. This study was an institutional cross-sectional comparison between 62 diabetic and 72 non-diabetic patients. SPSS and graph pad prism were used in the statistical analysis. Utilizing machine learning, we created a correlation matrix between different parameters. P-value of ($p<0.05$) was deemed statistically significant. The observation of our study is that the mean and standard deviation of RBS, FBS, SBP, WBC, ESR, Hb, MPV, PDW, PCT, and P-LCR were statistically significant. Contrarily, other parameters like RBC, neutrophil, platelet, RDW-CV, etc showed no statistical significance in comparison of diabetic patients and control non-diabetic group. In the correlation matrix between all the possible pairs of correlation coefficients, we observed very high positive and negative associations. Among diabetic patients, hypertension was highest in the case of comorbidity. Anemia (9.67%), ischemic heart disease (4.83%), coronary kidney diseases, and hyperglycemic patients (6.45%) were also found among the common co-morbidity factors. This study shows diabetic patients may undergo significant alterations in various parameters, which can be an indicator of diseases like anemia, hypertension, asymptomatic infection, etc. This undiagnosed stage can be an alliance for injurious comorbidity factors.

OP 40

RSENIC EXPOSURE–INDUCED HYPERTENSION: MECHANISTIC ASSOCIATION WITH ANGIOTENSIN-CONVERTING ENZYMES

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Arsenic toxicity is a major public health concern, including in Bangladesh, and is linked to increase the risk of cardiovascular disease (CVD) mortality. Hypertension, the most common risk factor of CVD causing millions of deaths worldwide. Angiotensin-converting enzyme (ACE), the main components of the renin-angiotensin system (RAS) convert angiotensin I to angiotensin II. Increased angiotensin II levels lead to the elevation of blood pressure because of its strong vasoconstrictive activity while ACE2 counteracts these effects by producing vasodilator, angiotensin (1-7) from angiotensin II. Although arsenic exposure is associated with hypertension, the underlying mechanism, particularly the effects of arsenic exposure on RAS components remains unclear. Therefore, this study aimed to explore the

association between arsenic exposure and serum ACEs levels with regard to hypertension. The study participants (n=200) were recruited from low-and high-arsenic exposure rural areas of Bangladesh. Participants' arsenic exposure levels (drinking water, hair and nail arsenic) were determined by ICP-MS. Commercially available immunoassay kits were used to measure the levels of ACEs. Participants from high-arsenic exposure areas showed significantly higher ACE and lower ACE2 levels ($p<0.001$) compared to those from low-exposure areas. After adjusting for age, sex, BMI, and smoking habit, each log unit increase in arsenic (water, hair, and nail) were significantly associated with increased ACE (0.09, 0.16, 0.21) and decreased ACE2 (−0.07, −0.17, −0.20) levels ($p<0.001$). Dose-dependent relationships between arsenic exposure and ACEs levels were also observed. Arsenic exposure and ACE levels were positively associated with systolic blood pressure and diastolic blood pressure, while ACE2 showed negative associations ($p<0.01$). Hypertensive individuals had higher ACE and lower ACE2 levels than normotensive participants ($p<0.01$).The results of this study suggest that arsenic exposure increases ACE levels and decreases ACE2 levels which may be implicated in arsenic-induced hypertension as well as CVD.

OP 41

BRIDGING THE DIAGNOSTIC GAPS FOR HEPATITIS E VIRUS (HEV) INFECTION IN RESOURCE-LIMITED SETTINGS

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Hepatitis E virus (HEV), a major form of enterically transmitted acute viral hepatitis, is endemic in many developing countries but still an underestimated emerging threat in the developed world. Although HEV infection is self-limiting; it can have a fulminant progression, especially among pregnant women, with case fatality risks up to 30%. However, scarce incidence data and lack of a gold standard in HEV diagnosis have been contributing factors to the assessment of morbidity and mortality [4,5]. Therefore, this study aims to fill the gaps by evaluating the performance of HEV rapid diagnostic tests (RDTs), including urine as a non-invasive specimen. We are conducting an ongoing evaluation of HEV diagnosis with a target sample size of 1,552 in Bangladesh. Suspected acute jaundice patients are tested with four RDTs, including three IgM RDTs using plasma (Assure, CTK, Wantai) and one Wantai urine antigen RDT. In parallel, we are performing serum IgM ELISA, and HEV RNA detection in plasma and urine by RT-qPCR. Diagnostic performance is being evaluated by sensitivity and specificity. To address the absence of a gold standard, we will use latent class modeling to estimate test performance. To date, we have tested 962 cases. Using ELISA and RT-qPCR (blood) as reference standards, Assure exhibited

the highest sensitivity (100.0% and 86.9%, respectively), whereas CTK showed the highest specificity (99.5% and 96.0%, respectively) among the IgM RDTs. In contrast, Wantai urine antigen RDT demonstrated relatively lower sensitivity (53.7%) despite high specificity (100%) compared to composite standard (either ELISA or RT-qPCR). After analysis of the complete study cohort, our findings will provide definitive estimates of diagnostic accuracy and reliability for each assay to offer a roadmap for scalable HEV screening strategies in high-burden, resource-limited settings as well as spatio-temporal dynamics of HEV outbreaks in Bangladesh.

OP 42

A POLYHERBAL FORMULATION ENHANCES GLUCOSE UTILIZATION AND ATTENUATES INSULIN RESISTANCE VIA UPREGULATION OF GLUT4 MRNA IN TYPE 2 DIABETIC RATS

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The rationale, role, and mechanism of action of the individual components in polyherbal formulations are not well investigated. To address this issue, a polyherbal formulation containing Gymnema sylvestre, Trigonella foenum-graceum, Momordica charantia, Swertia chirata, Cinnamomum cassia, and Camellia sinensis was developed based on the contributions of individual components, and their underlying cellular and molecular mechanisms were evaluated. Wistar rats were fed a high-fat diet for 6 months, followed by a low-dose streptozotocin injection (30 mg/kg) to establish a diabetic model. The diabetic rats were treated with the formulated polyherbal (1 g/kg) orally, once daily for 30 days. After this treatment period, fasting and postprandial blood glucose, insulin tolerance, serum insulin (ELISA), adiponectin (ELISA), β-cell function, and oxidative stress were measured. Glucose utilization was measured by [14C]2-deoxy D-glucose uptake assay, and Glut4 mRNA was monitored by RT-PCR. The polyherbal ameliorated fasting and postprandial hyperglycemia observed in model rats. Reduction in insulin resistance and improvement in insulin tolerance were also observed, along with elevated insulin and adiponectin levels, in polyherbal-treated rats. The insulin-stimulated and basal [14C] 2-deoxy D-glucose transport in adipocytes was increased significantly in the polyherbal-treated rats. The substantially decreased Glut4 mRNA expression observed in diabetic states was up-regulated substantially after 30 days of polyherbal treatments. Moreover, thiobarbituric acid-reactive substances and reduced glutathione were significantly modulated in the treatment group. The β-cell modulatory activity of cinnamaldehyde and cinnamic acid, 2 compounds derived from Cinnamomum cassia revealed that the number of β-cells was increased by the action of cinnamaldehyde but not by cinnamic acid. The cumulative effect of individual components in the polyherbal formulation optimally reduces hyperglycemia and insulin resistance by improving glucose utilization and up-regulating Glut4 mRNA expression in this type 2 diabetic rat.

OP43

DETERMINANTS OF METABOLIC SYNDROME CONTROL AMONG ADULTS PEOPLE WITH NON-COMMUNICABLE DISEASES RECEIVING SERVICES AT NCD CORNER IN BANGLADESHI HOSPITALS: MULTILEVEL ANALYSIS

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Metabolic syndrome (MetS) is a cluster of risk factors, including low HDL cholesterol,high blood pressure, elevated blood sugar, high triglycerides, and abdominal obesity.Uncontrolled MetS significantly raises the risk of ischemic heart disease, heart failure and stroke, leading to increased hospital admissions and higher healthcare costs. This study aimed to investigate the multilevel relationship between health service system factors and individual level factors influencing the control of MetS among adults with NCDs receiving healthcare services at NCD corner in hospitals across Bangladesh over 1-year period. The study was conducted in a cross-sectional manner with a descriptive and analytical approach from February to March 2025. Data were collected from primary, secondary and tertiary government hospitals in Bangladesh using a multistage stratified random sampling technique. A total of 14 hospitals (6 primary, 4 secondary, and 4 tertiary) were selected. 472 valid patients questionnaires and 14 doctor/nurses questionnaire were used. Data were analyzed using multilevel logistic regression analysis. In this study, 51% participants successfully controlled MetS within 1 year. In secondary hospitals are the most effective in controlling MetS with 62.3% of patients having controlled MetS compared to 37.7% with uncontrolled MetS. This contrasts with primary hospitals, where 59.9% of participants had uncontrolled MetS and only 40.1% had controlled MetS. Tertiary hospitals showed a nearly equal distribution with 50.3% of patients having uncontrolled MetS and 49.7% controlling their condition. Individual-level factors significantly influenced MetS control. Adults with a BMI >30 had an 83% lower chance of controlling MetS compared to those with BMI <18 (OR = 0.17, 95% CI: 0.05-0.53, p = 0.001). Regular physical exercise increased the odds of control by 2.83 times (OR = 2.83, 95% CI: 1.73–4.62, $p < 0.001$). Participants using ≥5 medications had a 70% lower chance of controlling MetS (OR = 0.30, 95% CI: 0.18–0.52, $p < 0.001$). High medication adherence increased the odds of control by 3.78 times (OR = 3.78, 95% CI: 1.93–7.36, $p < 0.001$). At the hospital level, comprehensive health behavior monitoring was associated with a 3.42 fold increase in MetS control compared to partial monitoring (OR = 3.42, 95% CI: 1.47–7.96, $p < 0.05$). This study highlights the critical role of individual factors such as BMI, physical activity, polypharmacy and medication adherence in controlling MetS. It also underscores the importance of comprehensive health behavior monitoring at the hospital level. These findings provide valuable insights for healthcare providers and policymakers to improve MetS management strategies in Bangladesh.

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OP 44

AI-DRIVEN GENOMIC INSIGHTS INTO HOST ADAPTATION AND VIRULENCE OF FISHPAOGENIC STREPTOCOCCUS AGALACTIAE IN AQUACULTURE IN BANGLADESH

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Streptococcus agalactiae (Group B Streptococcus) causes severe streptococcosis in tilapia, resulting in substantial economic losses to Bangladesh's aquaculture sector. As the nation leverages its demographic dividend to modernize agriculture, the application of artificial intelligence (AI) and frontier science, technology, and innovation (STI) tools is essential for food security. This study integrated AI-driven genomic analytics to investigate the evolutionary dynamics, virulence landscape, and host adaptation of three fish-pathogenic isolates. Bacterial isolates from infected tilapia underwent antimicrobial susceptibility testing, challenge test and whole-genome sequencing. High-throughput genomics included de novo assembly and functional annotation of isolates GIFTS6, GIFTS10, and GIFTS31. AI-enabled bioinformatics platforms including machine learning-based resistance gene predictors (CARD, ResFinder) and virulence factor databases (VFDB) were employed for annotation. Comparative phylogenetics, average nucleotide identity (ANI) clustering, and genome plasticity assessment were performed using computational workflows that leverage algorithmic pattern recognition for evolutionary inference. AI-assisted phylogenetic analysis positioned the GIFTS isolates within a distinct monophyletic "fish-origin" clade, suggesting host-specific adaptation. ANI-based heatmap analysis, facilitated by clustering algorithms, confirmed near-identity (>99.99%) among the three strains. Machine learning-augmented virulence profiling revealed a conserved repertoire, including adherence factors (fbsA, bibA, lmb, hylB), the complete cyl operon, and the cps cluster. Four antibiotic resistance genes (vanT, vanY, mprF, mreA/mreAS) were identified across all strains using AI-driven resistance databases. Multiple genomic islands indicated significant genome plasticity, underscoring the organism's adaptive capacity. Integrating AI-powered genomic tools provides transformative insights into S. agalactiae pathogenicity within Bangladeshi aquaculture. The conserved virulence profile among fish-pathogenic lineages points to a dominant clonal lineage, with AI-enabled surveillance offering a scalable framework for molecular diagnostics and sustainable disease management. This study exemplifies the role of young scientists in harnessing artificial intelligence to address critical challenges in food security and One Health.

OP45

ESTIMATION OF NUTRIENT FLOWS AND BALANCE IN AGRICULTURE FOR BETTER FERTILIZER MANAGEMENT USING MACHINE LEARNING ALGORITHM

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Background and objectives: Lack of a holistic understanding of the nutrient flows and GHG emissions in agroecosystems is a constraint to sustainable agriculture and food security. Nitrogen (N), phosphorus (P), potassium (K) and sulfur (S) input and output pathways for an annual maize-rice, rice-rice-rice, potato-rice-rice-rice were measured after two consecutive years of cropping in Floodplain soils. The experiment consisted of: (i) two levels of residue (NR, no residue vs. CR, 30 cm residue amounting for 2 t ha-1) as main plots and (ii) four levels of fertilizer (control [CL]; farmers' practice [FP]; recommended dose [RD]; and 125 % of RD [125RD]) as subplots. CR application together with fertilizer significantly improved the soil nutrient balance. Nutrient balances exhibited significant positive relationships with the total nutrient contents in soils suggesting that positive nutrient balance enhanced nutrient buildup in soils. Leaching was a significant pathway for nutrient loss from the soil (ca. 3–4, 6–8, 7–8 and 1.5–2 % of total N, P, K and S fertilizer). Volatilization, denitrification and leaching caused 27–37, 5–7 and 4–5 % loss of the applied N. Volatilization was 7.5 % higher in the RD with CR than in the RD without CR. The N, P, K and S addition via irrigation and rainfall ranged between 2.9 and 5.1, 2.4 to 4.2, 3.2 to 5.7 and 2.6–5.1 kg ha-1, respectively. Addition of CR with RD resulted in a positive balance for P and S while decreasing the negative balances for N and K. A 25 % increase in N and K and 25 % reduction in P and S coupled with 30 cm CR addition reduced excessive P and S fertilization while reducing the negative N and K balances. N2O emissions ranged from 0.5 to 1.3% of the applied N fertilizer, irrespective of crops while CH4 emissions ranged from 200-300 kg CH4 ha-1, irrespective of seasons. Our results suggest that balancing nutrient input-output in crop field helps avoid inadequate or excessive fertilization for sustainable crop production but also decreaes negative environmental impacts.

OP 46

SYSTEMATIC PROCESS DEVELOPMENT FOR THE HETEROLOGOUS EXPRESSION OF THE NOVEL LANTIBIOTIC, 'HOMICORCIN'

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Lantibiotics are peptide antibiotics that serve powerful tools against antibiotic-resistant bacteria. Homicorcin, a class-I lantibiotic, is naturally produced by the jute endophyte Staphylococcus hominis MBL_AB631. Native production of homicorcin is hindered by the host's pathogenic nature. This study aims to transfer the homicorcin

biosynthetic pathway into Lactococcus lactis NZ9000-a "Generally Recognized as Safe" (GRAS) organism-to facilitate safer and more efficient large-scale production. In silico modeling and protein-protein docking were performed to map the biosynthetic machinery of homicorcin. Following computational analysis, the immunity gene (homI) was cloned into the L. lactis expression vector-pMG36c. The expression of the homI was cross-checked by qPCR. To establish the full production pathway, the six-gene biosynthetic cluster and transporter genes were ligated into the same vector (pMGWT). Gene orientation and successful integration were verified via sequencing. Computational models demonstrated a coordinated assembly of homicorcin gene cluster: HomC functions as a cyclase, connecting the dehydratase HomB to the transporter. The suggested method entails HomB-facilitated dehydration and HomC-mediated cyclization, succeeded by HomT secretion and subsequent maturation by the protease HomP. Predictions of subcellular localization corroborated these functional roles2. For heterologous expression, the immunity gene was cloned into pMG36c vector. The transformed strain demonstrated lantibiotic resistance relative to the wild type. Subsequently, the six-gene cluster and Protein interaction network for homicorcin maturatiom transporter genes were ligated in tandem into the vector (pMGWT), and the gene arrangement was verified using DNA sequencing. The Lactis-specific promoter of pMGWT demonstrated more expression in L. lactis pMGWT than in E. coli pMGWT, as determined by qPCR. The subsequent stage is the transformation of the construct into L. lactis and the assessment of expression efficiency. Heterologous expression of homicorcin in L. lactis, a food-grade GRAS organism, will provide cost-effective, large-scale fermentation, making it a promising platform for scalable homicorcin production.

OP 47

ANTIMICROBIAL RESISTANCE PROFILE, PHYLOGENY AND WHOLE GENOME ANALYSIS OF BIOFILM FORMING ACINETOBACTER BAUMANNII ISOLATED FROM DAIRY CATTLE FARM ENVIRONMENTS FROM MYMENSINGH IN BANGLADESH

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Multidrug resistant Acinetobacter baumannii have emerged as global public health threat. This study was conducted to isolate and identify A. baumannii from dairy cattle and farm environment along with determination of their abtibiogram phenotype and genotype, biofilm formation, and whole genome analysis. A total of 134 samples, including feed (15), manure (15), drinking water (15), drainage water (15), air (15), feed trap (15), rectal swab (14), nasal swab (8), and hand swab (7) were collected and analyzed using. Among these 74 (55.2%) were culture-positive and 53 (39.6%) PCR-positive for A. baumannii. Prevalence was highest in manure (86.7%), followed by drainage water (80%), air (73.3%), drinking water and feed trap (60%), rectal swabs (57.1%), and hand swabs (28.6%). blaOXA51 gene from three isolates were sequenced (PX662091, PX662092, PX662093), and phylogenetic analysis showing high similarity to CP169866, a human respiratory isolate from the USA. In disk diffusion antibiogram study high resistance was observed against ceftazidime (81%), trimethoprim–sulfamethoxazole (91%), piperacillin (96%), ceftriaxone (85%), and tetracycline (89%), while susceptibility to

meropenem (87%), imipenem (85%), doripenem (91%), and amikacin (92%).24 isolates were identified as MDR. In Congo red biofilm assay 40% isolate identified as strong, 26.7% intermediate, and 26.7% weak biofilm producers. Genotypically, blaTEM was detected in 30.2%, kpc in 3.8%, and tetA in 49.1%; int 50% (22 among 11) showed intermediate carbapenem resistance. Whole genome sequencing (WGS) of a manure isolate strain ABMTRAAP01M (BioProject ID: PRJNA1437284) was performed having a genome size of 3,431,271 bp in length with 136 contigs, and GC content of 39.05%. ResFinder identified two resistance genes, blaADC-25 and blaOXA-64 involved in carbapenem resistance. To the best of our knowledge this is the first study in Bangladesh describing detection and characterization of A. baumannii from in dairy cattle and farm environments that needs further investigation to evaluate their public health significance.

OP 48

GENOMIC CHARACTERIZATION OF WHEAT SEED ENDOPHYTIC BACILLUS USING AI APPROACHES FOR WHEAT BLAST MANAGEMENT

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Endophytic bacteria associated with wheat (Triticum aestivum) seeds represent a valuable resource for sustainable agriculture. Among these, Bacillus species are well known for their multifunctional plant growth-promoting traits (PGPTs), including biocontrol activity, phytohormone production, and nutrient acquisition. However, the genomic and functional basis of these traits in seed-associated endophytes remains insufficiently explored. Therefore, this study aimed to elucidate the genomic and post-genomic determinants of plant-beneficial traits in two wheat seed-endophytic Bacillus subtilis strains Ta5A1 and Ta4A2, isolated from the F6 (S-615 × BG33) wheat line. Whole-genome sequencing followed by functional annotation and genome mining was employed to identify PGPT-associated genes and biosynthetic gene clusters (BGCs). Post-genomic analyses, including functional pathway normalization, were conducted to assess trait enrichment across the isolates. In addition, in vitro dual culture assays and seedling bioassays were performed to evaluate antifungal activity and plant growth-promoting potential. A substantial repertoire of PGPT-associated genes was identified, with 4,418 genes in Ta5A1 and 4,419 in Ta4A2. Both strains exhibited strong inhibitory activity against Magnaporthe oryzae pathotype Triticum (MoT) in in vitro dual culture assays. Whole-genome analysis further revealed diverse biosynthetic gene clusters associated with antifungal metabolites and plant growth-promoting compounds. In wheat seedling bioassays, both strains significantly enhanced plant growth and markedly reduced the incidence and severity of wheat blast disease compared to untreated controls. Collectively, these findings highlight the biotechnological potential of Bacillus subtilis strains Ta5A1 and Ta4A2 as effective plant growth promoters and sustainable biocontrol agents, providing a foundation for eco-friendly management of wheat blast. These findings highlight the strong biotechnological potential of wheat seed-endophytic Bacillus subtilis strains as plant growth enhancers and sustainable biocontrol agents. Their diverse genomic architecture and functional capabilities support their application as next-generation bioinoculants for eco-friendly management of wheat blast and improved crop productivity.

OP 49

IDENTIFICATION OF NOVEL NRAS AND RB1 SOMATIC VARIANTS IN PAPILLARY THYROID CARCINOMA FROM A BANGLADESHI COHORT

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Papillary thyroid carcinoma (PTC) is the most prevalent thyroid malignancy, characterized by diverse genetic alterations. However, data on novel somatic variants in underrepresented populations remain limited. This study aimed to identify and characterize novel mutations in key oncogenes and tumor suppressor genes in a Bangladeshi PTC cohort to expand the current understanding of its molecular landscape. A cross-sectional study was conducted, including 110 PTC patients, individuals with benign thyroid conditions. Targeted next-generation sequencing (NGS) was performed to screen for mutations in NRAS, RB1, HRAS, and RET genes. Identified variants were validated by Sanger sequencing and analyzed in relation to clinicopathological features. Three novel variants—NRAS g.7775T>A, NRAS g.7797G>A, and RB1 c.2039T>A (p.Ile680Asn)—were identified and showed significant enrichment in PTC patients ($p < 0.0001$). Those variants were predominantly detected in non-smoking and non-familial cases, suggesting a sporadic mutational origin. The NRAS g.7797G>A variant was primarily associated with early-stage tumors (T1), indicating a potential role in tumor initiation. In contrast, the RB1 c.2039T>A variant was observed across both early and advanced tumor stages, suggesting involvement in both tumor development and progression. This study reports novel somatic variants in NRAS and RB1 genes in Bangladeshi PTC patients, expanding the mutational spectrum of thyroid cancer in an underrepresented population. These findings highlight the potential of these variants as early molecular markers and provide a foundation for future functional validation and precision oncology applications.

OP 50

DEVELOPMENT OF A FERMENTED NON-ALCOHOLIC BACK-SLOPED GINGER BEVERAGE: IMPACT OF DEALCOHOLIZATION ON PHYSICO-CHEMICAL PROPERTIES, ANTIOXIDANT ACTIVITY, SENSORY CHARACTERISTICS AND FLAVOUR PROFILE

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This study involved the preparation of back-sloped ginger beverage (GB) and observing the effects of dealcoholization on the physico-chemical characteristics, bioactive properties, sensory attributes and the flavour profile of fermented ginger beverage during storage at 4-6°C for a period of 30 days. GB was prepared by adding shredded ginger in water (1:25) and boiling it for 10 minutes. After cooling (30°C), the mixture was transferred to a borosilicate vessel, incorporated with 1% ginger bug and incubated at 30±1°C until the pH reached 4.0. Four samples were prepared: GB1 served as the control ginger beverage, while GB2 was prepared by sonicating the beverage at 40kHz for 30 minutes. GB3 was prepared by pasteurizing the beverage at 80±2°C for 5 minutes, and GB4 was

pasteurized for 10 minutes. Total soluble solids content remained constant, while the pH significantly decreased and acidity increased throughout the storage period for all samples. The lowest alcohol content (0.13±0.02 ABV) was observed in GB4 and the highest in GB1 (2.95±0.01 ABV). During storage, the alcohol content of GB1, GB2, and GB3 decreased significantly, whereas for GB4, the change was not significant. Initially, there was no significant difference in the total phenolic content and DPPH• scavenging activity among the samples; however, both parameters decreased during storage for all samples. GC-MS-based flavour analysis identified several volatile compounds, including 6-gingerol, 2(5H)-furanone, 2-ethyl-5-propylcyclopentanone, and 5-acetoxymethyl-2-furaldehyde. However, compounds with higher retention times were found in lower concentrations in GB3 and GB4 compared to GB1 and GB2. In terms of sensory evaluation, GB1 received the highest flavour score (7.5±1.05), whereas GB2 had the lowest score (6.33±0.52). GB3 achieved the highest score for taste (7±0.89) and the highest overall acceptability score (7.5±0.55). In contrast, GB4 recorded the lowest overall acceptability (6.83±0.41). These results suggest that GB3 is the optimal sample for producing ginger beverages.

OP 51

SUSTAINABLE STARCH-BASED BIODEGRADABLE FOOD PACKAGING FILMS REINFORCED WITH BIO-DERIVED OXIDE FILLERS FOR FOOD SECURITY ENHANCEMENT

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The increasing environmental burden associated with conventional petroleum-based food packaging materials has intensified the search for sustainable and biodegradable alternatives. In this context, the present study aims to develop and optimize maize starch (MS)-based biodegradable films with enhanced physicochemical and functional properties through the incorporation of plasticizers and green-synthesized bio-oxide fillers. Starch-based films were prepared via a solution casting method using different plasticizers, namely citric acid, glycerol, polyethylene glycol (PEG), sorbitol, and acetic acid, in the presence of Al_2O_3 and SiO_2 synthesized from neem and bamboo leaves, respectively. Key processing parameters, including time, temperature, concentration, and pH, were systematically varied to evaluate their effects on film properties. The fabricated films were characterized in terms of thickness, moisture content (MC), water absorption (WA), water solubility, and biodegradation behavior. The results demonstrated that PEG-plasticized films incorporated with Al_2O_3 exhibited the highest thickness (2.088 mm) and lowest water absorption (16.91%). Water absorption decreased with increasing temperature and concentration, reaching a minimum of 30.50% at 25 min, but increased to 44.43% at prolonged immersion (45 min), while a maximum value of 55.54% was observed at 30°C. Moisture content decreased to a minimum of 1.92% at 35°C but increased under alkaline conditions (5.54% at pH 13). The incorporation of bio-oxide fillers improved water resistance and reduced moisture sensitivity, with SiO_2-based films showing comparatively lower MC. Water solubility varied between 47.41% and 72.06%, with PEG–Al_2O_3 films exhibiting the highest solubility. Biodegradation studies revealed significant weight loss up to 32.34% within 10 days, confirming the environmentally friendly nature of the developed films.

OP 52

FACILE SYNTHESIS OF 2D MO2TIC2@PDA/MNO2 COMPOSITE-BASED ELECTRODE MATERIAL FOR CLEAN AND EFFICIENT ENERGY STORAGE

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Owing to their distinctive stacked layered structure, exceptional conductivity, large specific surface area, and abundance of redox active sites, two-dimensional transition carbon nitride, and metal carbides and nitrides efficiently store and transfer charges, thus becoming attractive electrode materials for supercapacitors. MXene-based supercapacitors are, however, seriously hindered by the low specific capacitance driven by severe self-discharge behavior and poor ambient stability due to oxidation. To overcome these limitations, herein, a Mo2TiC2@PDA/MnO2 composite was synthesized to functionalize a glassy carbon electrode (GCE) surface via a two-layer modification strategy, which enabled faster charge transfer and ion diffusion within the electrode material, thus boosting the capacitive performance of Mo2TiC2 MXene. The composite's structure and morphology were confirmed by X-ray diffraction, transmission electron microscopy, and scanning electron microscopy. Furthermore, the electrochemical behavior of the functionalized-electrodes was assessed by galvanostatic charge-discharge (GCD), cyclic voltammetry (CV), and electrochemical impedance spectroscopy (EIS), which all revealed that Mo2TiC2@PDA/MnO2 can be a promising electrode material for supercapacitor. The Mo2TiC2@PDA/MnO2 modified electrode delivered a high specific capacitance of 573 Fg-1 at a current density of 1 Ag-1 and demonstrated superior cycling stability with 87.43% capacitance retention over 5000 cycles. This study shows that integrating Mo2TiC2, PDA, and MnO2 can significantly improve the capacitance, stability, and eco-friendly operation in supercapacitors. However, the current work does not evaluate the performance in portable or flexible devices, and future studies may address this limitation through full-cell assembly and real-world testing. Overall, the composite provides a strong foundation for next-generation energy storage applications.

OP 53

ENVIRONMENTAL TOXICITY OF ETHYL PARABEN AND ITS IMPLICATIONS FOR RISK ASSESSMENT AND URGENT MONITORING

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Ethyl Paraben, a well-known toxicant present in cosmetics and pesticides causes severe toxicity in living organisms. Due to its widespread usage, Ethyl Paraben has been a contributor to environmental toxicity and associated genotoxicity. Onion roots were exposed to Ethyl Paraben concentrations (0.25, 0.5, 0.75, 1, 1.25 mg/mL) for 48 and 72 hours. After assessing LC50, DNA damage was identified by the exposure of Ethyl Paraben concentrations 0.25 mg/mL (1/2xLC50), 0.5 mg/mL (LC50) and 1 mg/mL (2xLC50) at 48 and 72-hr. LC_{50} was observed as 0.5 mg/mL, with statistically significant concentration-dependent inhibition of root growth ($p< 0.05$). Time and concentration-dependent increase in DNA damage ($p < 0.05$) was observed at 48 and 72-hr. Ethyl Paraben-induced

DNA damage in meristematic cells of onion root tips using comet assays highlighted the relevance for biomonitoring, toxicological and environmental risk evaluation. The significant time and concentration-dependent genotoxicity marked by reduced root length and increased DNA damage highlighted possible risks to the environment and health strengthening the United Nations Sustainable Development Goals (UN SDGs), emphasizing the need for improved monitoring and further regulation of Ethyl Paraben exposure in future.

OP 55

COMPARATIVE ANALYSIS OF AI MODELS FOR ALZHEIMER'S DISEASE: PERFORMANCE, INTERPRETABILITY AND CLINICAL READINESS

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Alzheimer's disease (AD) is a progressive neurodegenerative disorder and one of the leading causes of dementia worldwide. Early and accurate diagnosis remains challenging due to the complex nature of the disease and limitations of conventional diagnostic approaches. In recent years, artificial intelligence (AI) techniques have demonstrated significant potential in improving the detection, classification, and prediction of Alzheimer's disease using large-scale biomedical data. The objective of this study is to conduct a comparative analysis of different AI models used in Alzheimer's disease research, focusing on their diagnostic performance, interpretability, and readiness for clinical application. This study reviews and compares major categories of AI models applied to Alzheimer's disease diagnosis, including traditional machine learning methods, deep learning architectures, generative AI models, and hybrid multimodal systems. The analysis considers models such as support vector machines, random forests, convolutional neural networks (CNNs), recurrent neural networks (RNNs), graph neural networks (GNNs), and generative adversarial networks (GANs). These models are evaluated across multiple data modalities commonly used in AD research, including structural MRI, PET imaging, cognitive assessment scores, genomic biomarkers, and longitudinal electronic health records. Key evaluation metrics such as classification accuracy, robustness, interpretability, and potential clinical integration are considered.

The comparative analysis indicates that deep learning models, particularly 3D convolutional neural networks and transformer-based architectures, achieve higher diagnostic accuracy in identifying Alzheimer's disease andearly-stage mild cognitive impairment compared with traditional machine learning approaches. Multimodal models that integrate neuroimaging, cognitive, and biomarker data demonstrate improved predictive performance and more comprehensive disease representation. However, challenges remain regarding model interpretability, data availability, computational complexity, and clinical validation.AI-based models show considerable promise for improving Alzheimer's disease diagnosis and prognosis. While deep learning and multimodal frameworks provide superior performance, further research is required to enhance model transparency, generalizability, and clinical reliability before widespread adoption in healthcare systems.

OP 56

PADDY LEAVES SPAD VALUE PREDICTION FROM RGB CONTACT IMAGING USING ENSEMBLE DEEP LEARNI

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Assessment of chlorophyll content is important to understand plant nitrogen status in precision agriculture. Traditional destructive methods for chlorophyll quantification are time-consuming, labor-intensive, and unsuitable for high-throughput phenotyping applications. The SPAD meter provides a rapid, non-destructive alternative by measuring leaf greenness as a proxy for chlorophyll content. Recent technological advances in imaging sensors and computational methods have enabled the development of low-cost approaches for predicting SPAD values. In this study, we proposed an Ensemble Deep Learning model to predict SPAD values of paddy leaf. The proposed method leverages the usefulness of contact imaging to capture images through a smartphone camera. A total of 34 features, including color space features, textural features, and vegetation indices, were used to develop the ANN model without any preprocessing. The proposed ensemble model yielded *R2training*=0.9283 and *R2training*=0.7692, RMSE=2.24, RPD=2.038. Feature importance analysis revealed that the CIVE index, green channel intensity, Excess Green (ExG), and Brightness were the most influential predictors of chlorophyllcontent. Furthermore, an Android-based mobile application was developed to deploy the trained modforeal-time SPAD estimation. Field validation of the application yielded of 2 =0.7285 with an RMSE of 3.47,demonstrating that the proposed system maintained reliable predictive performance under real-worlconditions despite environmental variations such as illumination differences and leaf positioning. Overall, theresultsdemonstrate that smartphone-based RGB contact imaging combined with ensemble deep learninprovides promising non-destructive solution for rapid chlorophyll estimation, with potential applications in precision cromotoring.

OP 57

STUDY ON 3D VISION-BASED WEED DETECTION AND LOCALIZATION AND SITE-SPECIFIC SPRAYING WITH DEEP LEARNING

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Bangladesh, an agriculture-dependent nation, grapples with balancing crop yield and safe herbicide use. Farmers use herbicides to protect vegetables from weed infestation, but the use of fertilizers for this purpose is criticized for its potential environmental harm. Due to a lack of knowledge about safe herbicide use among many Bangladeshi farmers, traditional practices are prone to the overuse of the chemical. To minimize the need for herbicide, the suggested system used deep learning and 3D depth vision to identify, locate, and spray the correct weeds. The system is incorporated into a reliable and autonomous car. An Intel D435 depth camera is installed at the bottom of the autonomous vehicle. First, YOLOv12 is used to detect weeds using the RGB channel. For localization, the detected locations were then projected into depth data. The angle of the nozzle is then computed using linear transformation. A microcontroller controls nozzle actuation. The model's performance was evaluated under laboratory conditions at night, achieving a precision rate of 93.6%. Additionally, F1 scores of 0.805 under nighttime conditions demonstrate the model's effectiveness in nightlight conditions. This system offers several potential benefits, such as reduced herbicide use, improved crop yields, and sustainable weed control. This system paves the way for a more sustainable and efficient approach to weed control in Bangladesh's vegetable fields.

OP 60

INVESTIGATION OF CLINICALLY ACTIONABLE CYP2C19 ALLELES AND ASSOCIATED RISK-PHENOTYPES IN THE BANGLADESHI POPULATION FOR ADVANCING PRECISION MEDICINE

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The Clinical Pharmacogenetics Implementation Consortium (CPIC) guidelines recognized CYP2C19*2, *3, *9 and *17 as clinically actionable alleles. The frequency analysis of these alleles in the Bangladeshi population remains unexplored. This study, therefore aimed to undertake a frequency analysis to identify the risk-phenotypes among Bangladeshis and compare them with other Asian populations.Complying with the Fort Lauderdale principles, allele frequencies of CYP2C19*2, *3, *9 and *17 alleles were extracted from 1000 Genomes Project Phase III for Bangladeshi and other Asian populations, followed by the predictive phenotype assignment according to the CPIC guideline. Descriptive statistical analyses were utilized for estimating the frequency and 95% confidence interval (95% CI) of the alleles, and the risk-phenotypes. For comparing the prevalence among different population groups, the chi-square test was employed where $p<0.05$ was considered statistically significant.Among 86 Bangladeshis included, the frequencies of CYP2C19*2, *3, *9, *17were 32.6% (25.6%-39.3%), 2.3% (0.1-4.6%), 0%, 11% (6.4%-15.7%), respectively. The predictive prevalence of NMs, UMs, RMs, LIMs, IMs, LPMs, and PMs was 30.2% (20.5%-39.9%), 0%, 14% (6.6%-21.3%), 0%, 41.9% (31.4%-52.3%), 0%, and 14% (6.6%-21.3%), correspondingly. The predictive prevalence of high-risk (UM, RM, PM) and medium-risk (IM, LIM) phenotypes among Bangladeshis was 27.9% (18.4%-37.4%), and 41.9% (31.4%-52.3%) and this prevalence significantly differed from East-Asian ($p=0.00196$), Chinese ($p=0.00206$) and Vietnamese populations ($p=0.0212$). Identified risk-phenotypes may affect safety or effectiveness of at least 15 clinically important drugs. More than two-thirds of Bangladeshis are found to be predicted risk-phenotypes for several clinically important drug therapies due to the inheritance of clinically actionable CYP2C19 alleles. This strongly reinforces the need for clinical study and adoption of CYP2C19-guided therapy in Bangladesh for advancing precision medicine.

OP 61

PREVALENCE OF CLASS 1, 2, AND 3 INTEGRONS IN MULTIDRUG-RESISTANT ACINETOBACTER BAUMANNII ISOLATED FROM BURN WOUND INFECTIONS

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Acinetobacter baumannii is a significant antibiotic-resistant pathogen associated with high morbidity and mortality among hospitalized patients, particularly in burn units. The acquisition of mobile genetic elements such as integrons plays an important role in the development of multidrug-resistant (MDR) hospital isolates. Therefore, this study aimed to determine the prevalence of class 1, 2, and 3 integrons in A. baumannii isolates.Clinical isolates were collected from burn patients with wound infections admitted to theNational Institute of Burn & Plastic Surgery, Bangladesh. The isolates were identified usingstandard microbiological and biochemical tests and were further confirmed by 16S rDNAsequencing. The antibiotic resistance patterns of the isolates were evaluated using the diskdiffusion method. Genomic DNA was extracted using the boiling method. Finally, the presenceof integrons and antimicrobial resistance genes was assessed using PCR.A total of 17 Acinetobacter baumannii isolates were identified from 146 burn wound samples.The patients were 68% male and 32% female, with ages ranging from 1 to 80 years. The majorcauses of burn injuries were fire (52%) and electrical incidents (29%). The highest antibioticresistance (100%) was observed against aztreonam, cefuroxime, ceftazidime, and cefixime.Colistin was the most effective antibiotic, although 41% of isolates were resistant. All A.baumannii isolates were multidrug-resistant (MDR). The intI1 gene was detected in 47% of theisolates and intI2 in 12%, while intI3 was not detected. Among the 17 isolates, 18% wereblaTEM positive, 24% were blaSHV positive, 18% were blaCTX-M-15 positive, and 18% wereblaOXA positive.The high level of antibiotic resistance and MDR in Acinetobacter baumannii isolates from burnpatients suggests the inappropriate use of broad-spectrum antibiotics. This may facilitate thespread of integrons, particularly class 1 integrons. Therefore, further investigation and revisionof antibiotic prescription policies are necessary.

OP 62

RAPID IDENTIFICATION AND ANTIBIOTIC SUSCEPTIBILITY TESTING OF UROPATHOGEN PSEUDOMONAS AERUGINOSA USING AN AI-INTEGRATED NOVEL MULTIPLEX BIOASSAY

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Urinary Tract Infections (UTIs) rank among the most prevalent bacterial infections globally. Conventional diagnostics, though reliable, demand up to 72 hours for pathogen identification and antimicrobial susceptibility testing (AST), delays that worsen patient outcomes and accelerate antimicrobial resistance (AMR). Molecular techniques offer speed but remain cost-prohibitive and personnel-dependent, limiting their feasibility in resource-constrained settings. This study aimed to design and validate an AI-integrated multiplex novel bioassay capable of simultaneous identification of the uropathogen Pseudomonas aeruginosa along with AST within 6 hours, operable by non-specialized personnel. The system employs a novel modified broth medium incorporating pH indicators tailored to the metabolic profiles of Pseudomonas aeruginosa. Tested against both ATCC reference strains and 17 clinical isolates, the system captures pathogen-driven colorimetric shifts via an RGB sensor-based microplate reader. These colorimetric data points are processed through a machine learning (ML) framework to identify the species and determine resistance patterns. Integration with AI will enable high-speed observation of metabolic kinetics, with the potential to reduce time-to-result to under 2 hours. The modified broth successfully detected, identified, and performed AST across all 17 clinical isolates of Pseudomonas aeruginosa tested. Pathogen identification achieved 100% sensitivity and specificity. For AST, the system reached 88% sensitivity, reliably detecting resistant organisms; however, further standardization of the AST protocol is required, and validation with a larger cohort of clinical samples is necessary. This AI-integrated multiplex bioassay represents a rapid, cost-effective, and accessible alternative to conventional culture methods, compressing the diagnostic window from days to hours. While identification performance was absolute, the AST component warrants further refinement. Subsequent actions will incorporate validation with a larger number of clinical samples. Once optimized, this platform holds meaningful.

OP 63

CHARACTERIZATION OF MULTIDRUG RESISTANCE AND BIOFILM FORMATION IN CLINICALSTAPHYLOCOCCUS SPP. ISOLATES

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Staphylococcus spp. are among the most significant opportunistic pathogens associated with surgical site infections, bloodstream infections, and device-associated infections. Their remarkable biofilm forming ability and adaptability enables them to survive under harsh environmental conditions and develop resistance to multiple antimicrobial agents. However, such studies remain limited in Bangladesh. Therefore, this study aims to evaluate antibiotic and disinfectant resistance patterns, efflux pump activity, and biofilm-forming capacity among clinical Staphylococcus spp. isolates in Bangladesh. Clinical isolates were collected and reconfirmed using phenotypic and biochemical assays. Antibiotic susceptibility testing was performed using Kirby–Bauer disc diffusion method. Disinfectant susceptibility was assessed using disc and well diffusion methods. Efflux pump activity was determined by EtBr-agar Cartwheel method. PCR was performed to detect antibiotic and disinfectant resistant genes. Biofilm formation was evaluated using Congo red agar and microtiter plate assay. A total of 45 Staphylococcus spp. were collected, of which 57.78% (26/45) were methicillinresistant. The highest resistance was observed against ciprofloxacin (62.22%), while resistance to clindamycin (41%) and vancomycin (17.78%) was also detected. Notable resistance to disinfectants, including Savlon (57.78%) and hydrogen peroxide (44.44%), was observed. Efflux pump activity was observed in 37.5% of the isolates. The antibiotic

resistant mecA gene (57.78%), vanB (4.44%) and disinfectant resistance genes qacC (48.89%) qacA/B (38%) were detected. Additionally, 31.11% (14/45) of isolates produced strong slime on Congo red agar, while 22.22% (10/45) formed strong biofilms in microtiter plate assay. This study reveals a high prevalence of antibiotic and disinfectant resistance, along with biofilm formation among clinical Staphylococcus spp. in Bangladesh. Continuous surveillance, rational antibiotic use, and effective infection prevention strategies are essential to limit the spread of multidrug-resistant strains.

OP 64

BACTERIOPHAGE-BASED INTERVENTION TO REDUCE ANTIMICROBIAL RESISTANT BACTERIA ON SHARED MOTORCYCLE HELMETS

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The routine exchanges of bike helmets between the drivers and passengersof the rideshare business in the highly-dense urban areas present a potential public health risk due tomicrobial accumulation, biofilm formation, and transmission of antimicrobial-resistant (AMR) bacteria.The aim of this study was to determine the microbial contamination and resistance level on shared helmetsin Dhaka and to come up with a bacteriophage-based biocontrol strategy as a sustainable alternative to thetraditional disinfectants.A total of 157 drivers aged 18–35 years across four locations in Dhaka (Mirpur, Banani, Gulshan,and Merul Badda) completed a standardized survey assessing helmet-usage factors. Corresponding swabsamples were cultured, and the recovered isolates were characterized using Gram staining, morphological,and biochemical analyses. Antibiotic sensitivity was established by Kirby–Bauer disk diffusion and MARindexes computed. Phages were recovered from environmental sources and screened for strict lytic activity,breadth of host range, one-step growth parameters and genome security. A prototype spray preparation(aim 10^8–10^9 PFU/mL) incorporating PBS with trehalose and glycerol was prepared and tested in vitro forreduction of planktonic and biofilm on helmet-associated substrates.Helmet microbiomes were predominantly composed of Firmicutes and Proteobacteria, including-Staphylococcus, Corynebacterium, Pseudomonas, and Enterobacteriaceae.Some isolates exhibitingelevated MAR indexes and plasmid-mediated resistance. A panel of lytic phages demonstrated broadspectrum coverage of dominant resistant strains. The prototype cocktail achieved substantial planktonic reduction (≥3-log CFU) and significant biofilm biomass removal in bench testing, though compatibilitywith standard helmet construction materials requires further refinement.Bike helmets that are shared can serve as sources of AMR bacteria that is an underacknowledgedpublic health issue. Bacteriophage cocktail is a promising, focused environmentally friendlymethod of reducing bacterial contamination. It requires further optimization and validation in the field inorder to facilitate its practical use in metropolitan transport systems

OP 65

PROBIOTICS AND SPIRULINA IMPROVE GROWTH PERFORMANCE, HEMATOLOGY, GUT HISTOLOGY, AND FLESH COMPOSITION OF HEAT-STRESSED STRIPED CATFISH (PANGASIANODON HYPOPHTHALMUS)

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Global climate change-induced thermal stress is increasingly and profoundly threatening fishes, resulting in an uncertain future across worldwide aquaculture production. Probiotics and spirulina are promising nutritional interventions to mitigate such stress. The present study investigated the capability of probiotics and spirulina in restoring the thermal stress, ameliorating growth impairment, blood biochemical alterations, gut histopathomorphology and deterioration of proximate composition in a commonly cultured striped catfish, P. hypophthalmus. Fish with an average body weight of 13.54 g were distributed into four treatment groups: 30°C (ambient), 36°C (elevated), 36°C + Probiotics (1 ml/L), and 36°C + Spirulina platensis (50 g/kg in feed), each with three replicates over a 60-day period. The results found that elevated temperature (36°C) significantly ($p < 0.05$) reduced growth performance (final body weight, weight gain, specific growth rate) and feed utilization efficiency. In contrast, both 36°C + Pro. and 36°C + Spir. groups exhibited a marked improvement over 36°C, with growth parameters closely approaching those observed in 30°C, while 36°C + Pro. showing a greater effect than 36°C + Spir. The elevated temperature significantly altered various biomarker responses, such as lower hemoglobin level (g/dL) and higher glucose level (mg/dL), increased erythrocytic cellular (twin, fusion, teardrop, spindle) and nuclear anomalies (binucleated, nuclear bud, notched nuclei), in the fish. Intestinal histology revealed pronounced deformities in 36°C, which were substantially alleviated in probiotics supplemented group compared to spirulina. Additionally, Probiotics and spirulina supplementation substantially enhanced crude protein and lipid contents while regulating moisture and carbohydrate levels compared to the 36°C group, with probiotics showing more improvement in protein accumulation. The findings indicate that the overall improvements were more pronounced in the probiotic-supplemented group compared to spirulina, confirming that probiotics may provide a more effective strategy for mitigating thermal stress and enhancing fish health in sustainable aquaculture systems.

OP 66

NANOPORE SEQUENCING OF HBB GENE IMPROVED GENOTYPE–PHENOTYPE CORRELATIONS IN B-THALASSEMIA AND HBE/B-THALASSEMIA IN BANGLADESH

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β-thalassemia is a widespread inherited blood disorder caused by mutations in the HBB gene, which leads to chronic anemia. Oxford Nanopore sequencing, as a long-read sequencing platform, enables comprehensive detection of point mutations, insertions and deletions, splice site variants, rare mutations, and haplotype structures across the entire HBB gene. The study objective was to improve understanding of genotype–phenotype correlations in β-thalassemia and HbE/β-thalassemia in Bangladesh using Oxford Nanopore sequencing. The study enrolled 402 participants, including 225 healthy controls and 177 β-thalassemia patients. Hematological parameters were evaluated using complete blood count analysis and serum ferritin assays to understand the clinical context. The entire HBB gene was sequenced on the Oxford Nanopore MinION platform. Pathogenic variants were categorized into different genotypic groups to assess their genotypic and phenotypic correlations and disease severity in thalassemia. Nanopore sequencing identified 18 HBB gene variants, including 8 pathogenic mutations. The most frequent pathogenic variants were c.79G>A (HbE) and c.92+5G>C among double heterozygous cases. Haplotype phasing confirmed that these two variants came from both paternal and maternal chromosomes. Linkage disequilibrium analysis revealed overall weak LD across the HBB gene, indicating multiple independent mutation origins within this population. Significant changes in hematological parameters were observed in pathogenic variant groups compared with healthy controls. Conversely, transfusion interval and serum ferritin levels did not differ significantly across genotype groups. This indicates the burden of iron overload and transfusion dependence is consistently high across thalassemia patients, regardless of the specific HBB genotype subgroup. This study demonstrates substantial mutational diversity within the HBB gene. Oxford Nanopore sequencing facilitated reliable and comprehensive mutation detection, haplotype phasing, and detailed genotype-phenotype analysis of pathogenic variants. These findings provide valuable insights that may facilitate the management of effective treatment strategies.

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A PRODUCTION-READY MFS FRAUD DETECTION SYSTEM: FLUTTER-BASED MOBILE ARCHITECTURE WITH EMBEDDED ML INFERENCE AND FEDERATED FINE-TUNING

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Bangladesh's mobile financial services sector faces a 9.3% fraud victimisation rate across 110 million accounts, with attack patterns including SIM-swap chains, OTP-interception malware, and sequential investment scams that are absent from existing public fraud detection benchmarks. No labelled Bangladesh MFS transaction dataset is publicly available, and current fraud detection architectures cannot be directly deployed due to infrastructure constraints including 43% 3G connectivity, USSD-dependent user bases, and 80,000 agent-mediated transaction points. This study extends a validated two-stage anomaly detection framework (autoencoder on Kaggle + LSTM on PaySim, MMD=0.61 domain shift quantified) into a production-ready mobile architecture

that preserves detection fidelity while operating under Bangladesh's connectivity and device limitations. We implement the trained models as TensorFlow Lite quantised executables embedded within a Flutter application, achieving sub-50ms inference on sub-$200 Android devices. An adaptive threshold engine implements the tiered alert framework derived from Monte Carlo simulations, applying differential sensitivity thresholds (rural low-income: 0.62, urban mid-income: 0.78) to deliver the mathematically projected 31% false-positive reduction for low-income rural users. A federated learning pipeline enables privacy-preserving fine-tuning across distributed devices, targeting the 400,000 labelled transaction requirement identified by domain shift quantification. USSD fallback mechanisms maintain fraud protection when smartphone connectivity is unavailable, while offline SQLite buffering ensures operation during network interruptions. TFLite quantisation preserves model fidelity with AU-ROC degradation <0.8% relative to full-precision versions. The adaptive threshold engine formally operationalises the MMD-quantified domain gap, converting a 0.61 distributional shift into device-specific sensitivity calibrations. Federated architecture enables progressive fine-tuning without centralised raw data collection, addressing the 400,000-transaction target identified as necessary to close the domain gap to estimated AU-ROC above 0.94. Offline capabilities maintain fraud detection coverage across the 43% of connections operating on 3G or slower networks. This Flutter-based implementation transforms a formally characterised anomaly detection baseline into a deployable system that respects Bangladesh's infrastructure realities while preserving the mathematical rigor of the underlying detection architecture. The framework converts the open data-access problem into a federated learning protocol, establishing the first production pathway for USSD-based, agent-mediated MFS fraud detection in a high-growth inclusion-critical economy. The 31% false-positive reduction target becomes a measurable operational metric tied directly to MMD-monitored domain adaptation

OP 80

GIS-BASED ASSESSMENT OF SOCIO-ECONOMIC AND ENVIRONMENTAL IMPACTS OF COASTAL TOURISM IN MAHESHKHALI AND TEKNAF, BANGLADESH

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Coastal tourism is rapidly transforming the socio-economic and environmental landscape of Bangladesh, particularly in ecologically sensitive regions such as Maheshkhali and Teknaf in Cox's Bazar. While tourism contributes to economic growth, it also poses risks to environmental sustainability and cultural integrity. This study aims to assess the socio-economic benefits and environmental impacts of coastal tourism using geospatial and field-based approaches. The study employed a mixed-method approach combining primary data collection through household surveys, direct observations, and key informant interviews. Spatial analysis was conducted using Geographic Information Systems (GIS) tools, including ArcGIS and ENVI. Statistical analyses were performed using SPSS and KoboToolbox to evaluate patterns of tourism development and its impacts. The findings indicate that over 90% of respondents perceive tourism as a driver of economic growth, improving infrastructure and income opportunities. However, significant environmental concerns were reported, with more than 75% of respondents in Maheshkhali and 60% in Teknaf identifying increased pollution, including air, water, and noise pollution. Cultural degradation is also evident, as over half of the respondents believe tourism has negatively affected local traditions. Despite economic benefits such as employment generation and market expansion, these gains are unevenly distributed and often

dogs in the present study. Study of oxidant-antioxidant status of demodicosis, revealed a significant ($p<0.01$) reduction in the mean values TA (0.76±0.04 mM), GSH (0.33±0.03µM), SOD (3.41±0.20µ/ml), LPO (0.06±0.00nmol) in Demodex infected dogs. The therapeutic evaluation of herbal formulation against demodicosis revealed all the parameters viz, haemato-biochemical changes and oxidant-antioxidant status was improved on day 21 post therapy onwards which was similar with standard therapy i.e. Amitraz. From the present study it seems that Herbo-Nano medicine can be an effective alternative of Amitraz in case of demodicosis

OP 71

OPTOELECTRONIC PROPERTIES OF BORON-NITROGEN CO-DOPED BENZODITHIOPHENE AND BENZODISELENOPHENE: A DENSITY FUNCTIONAL THEORY STUDY

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The optoelectronic features of newly designed boron–nitrogen (BN) co-doped benzodithiophene (BDT) and benzodiselenophene (BDSe) were investigated, along with a comprehensive analysis of the comparative charge transport and optoelectronic properties of all possible BN co-doped and undoped isomers of BDT and BDSe using density functional theory (DFT). To accurately examine the optoelectronic properties, different DFT methods (B3LYP, CAM-B3LYP, WB97XD, MPW1PW91, M06, and BHandHLYP) were employed for both BN co-doped and undoped isomers to ensure reliable comparison. The ionization potentials (IP), electron affinities (EA), hole extraction potentials (HEP), and electron extraction potentials (EEP), as well as the frontier molecular orbital (FMO) distributions, were analyzed for both doped and undoped systems. Furthermore, the linear and nonlinear optical (NLO) properties were investigated in detail. To identify efficient charge-transport materials, hole and electron reorganization energies were calculated. Among the different methods, the MPW1PW91 functional provided the best agreement with the experimental band gap of undoped BDT, demonstrating its suitability for further analysis. The results indicate that, among the eleven isomers, three exhibit the most promisingoptoelectronic performance, characterized by the lowest hole and electron reorganization energies across all DFT methods. These findings are further supported by UV-vis spectral analysis.

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NOVEL ZINC DIARYL-DITHIOCARBAMATE COMPLEXES AS SINGLE SOURCE PRECURSORS(SSPS) FOR NANOSCALE ZINC SULFIDE(ZNS)

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Dithiocarbamates (DTCs) are monoanionic ligands that are widely used in agriculture, medicine, imaging and material science. Dialkyl dithiocarbamate zinc complexes [Zn(S2CNR2)] have been well studied but their diaryl counterparts are virtually ignored. Thus, we have investOigated them with a view to compare their structures,

reactivity and thermally-promoted degradation with respect to dialkyl derivatives. There are various ways for the synthesis of nanoscale ZnS, but the single source precursor (SSP) approach is especially intriguing since it provides control nanoparticulate shape-size structure without the requirement for sophisticated experimental equipment.Deprotonation of diarylamines by nBuLi results in Ar2NLi and further slowly dropwise addition of CS2 produces air and moisture stable diaryl dithiocarbamate salts Ar2NCS2Li. Li was replaced by Zn2+ salt through a room temperature reaction in water to produce [Zn{S2CN(p-tol)2}2] which was thermally decomposed in oleylamine solution by both heat-up and hot-injection methods. A series of diaryl ZnDTCs have been prepared and heat-up and hot-injection decomposition of [Zn{S2CN(p-tol)2}2] in OLA at 230 ◦C and produced nanorods of ZnS while irregular and large (10-300μm) sheet-like particles of wurtzite have also been found from the solid-state decomposition of [Zn{S2CN(p-tol)2}2] at 450 oC. ZnS nanorods were produced in both cases with average dimensions of 17×2.1 nm and 11×3.5 nm respectively that were shorter than those produced from [Zn(S2CNiBu2)2] under similar conditions. This is tentatively attributed to differing rates of amine-exchange between diaryl and dialkyl dithiocarbamate (DTC) complexes and their differing rates of DTC loss following amine-exchange. Probably both amine-exchange and DTC loss are faster for diaryl vs dialkyl DTC complexes. Thus, the electron-withdrawing nature of the aryl ligands should increase the electrophilicity of the backbone carbon, thus facilitating nucleophilic attack by the primary amine. Whatever the exact reason, our preliminary results suggests that diaryl-DTC complexes [Zn(S2CNAr2)2] are a significant addition to the arsenal of SSPs available to prepare ZnS nanomaterials.

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PEDOT: PSS-COATED NICOFE-LDH/NICKEL FOAM ELECTROCATALYST FOR HIGH-PERFORMANCE OXYGEN EVOLUTION REACTION

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The development of efficient catalysts to accelerate the sluggish oxygen evolution reaction (OER) is essential for achieving hydrogen production through water splitting. Herein, a novel PEDOT:PSS-coated NiCoFe-Layered Double Hydroxide (LDH) on nickel foam (denoted as PPS@0.2NCF-LDH/NF) is fabricated using a simple hydrothermal and electrodeposition method. The Ni:Co:Fe molar ratio was fixed at 3:2:1, and the total metal cation content was systematically optimized, with 0.2 mmol yielding the best electrocatalytic performance. The obtained PPS@0.2NCF-LDH/NF exhibits excellent OER activity, requiring an overpotential of 123 mV at 10 mA•cm-2 and a Tafel slope of 49.18 mV•dec-1 in 1 M KOH. The catalyst also exhibits remarkable long-term stability over 130 h, with the overpotential increasing by only about 5%. The enhanced performance may be attributed to the abundant active sites of NiCoFe-LDH, while the PEDOT:PSS layer improves electron transfer, increases surface conductivity, and stabilizes the LDH structure during OER. This work demonstrates that the synergistic design of multi-metal LDHs with conductive polymer coatings provides a powerful strategy for developing efficient, non-precious-metal OER electrocatalysts.

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ELECTROCHEMICAL DETECTION OF L-HISTIDINE USING ZNO NANOFLOWER-BASED SENSOR IN COPPER COMPLEX MEDIA

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L-histidine is an essential amino acid that plays a vital role in various physiological processes, including enzyme activity, metal ion coordination, and metabolic regulation. Abnormal levels of L-histidine in biological fluids are associated with several metabolic and neurological disorders, highlighting the need for sensitive and reliable detection methods. However, conventional analytical techniques often require complex instrumentation, time-consuming procedures, and high operational costs, limiting their practical applicability. In this study, we report a novel electrochemical sensing platform for the detection of L-histidine based on zinc oxide (ZnO) nanoflower structures in a copper-complex-mediated environment. The synthesized ZnO nanoflowers were comprehensively characterized using scanning electron microscopy (SEM), energy-dispersive X-ray spectroscopy (EDS), X-ray diffraction (XRD), and Fourier-transform infrared spectroscopy (FTIR), confirming their morphology, elemental composition, and crystalline structure. The electrochemical performance of the sensor was evaluated using cyclic voltammetry (CV), electrochemical impedance spectroscopy (EIS), and pH optimization studies. The developed sensor demonstrated a low detection limit of 0.01 µM and a wide linear range from 0.1 to 100 µM. The enhanced sensitivity is attributed to the high surface area of ZnO nanoflowers and the synergistic interaction with the copper complex, promoting efficient electron transfer. Moreover, the sensor was successfully applied for the detection of L-histidine in human blood serum, exhibiting good stability, reproducibility, and satisfactory recovery. This study presents a promising, cost-effective approach for amino acid detection in clinical diagnostics.

OP 77

DFT AND TD-DFT STUDY OF NATURAL CAROTENOID-BASED PHOTOSENSITIZERS FOR DYE-SENSITIZED SOLAR CELL

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The development of environmentally benign and efficient sensitizers remains a key challenge for improving the performance of dye-sensitized solar cells (DSSCs). Natural carotenoid pigments, characterized by extended π-conjugated frameworks and strong visible-light absorption, offer promising potential as sustainable alternatives to conventional metal-based dyes. In this study, a comprehensive theoretical investigation was conducted on four carotenoid dyes namely, bixin, norbixin, lutein, and zeaxanthin, to evaluate their suitability as DSSC sensitizers. Structural geometry, Electronic structures (frontier molecular orbitals, electrostatic potential surface), optical absorption properties, and the key photovoltaic parameters were calculated using density functional theory (DFT) and time-dependent density functional theory (TD-DFT) methods implemented in Gaussian. Frontier molecular orbital analysis revealed HOMO energies ranging from -6.192 to -4.411 eV and

LUMO energies from −2.792 to −1.622 eV, demonstrating appropriate energy alignment for efficient electron injection into semiconductor electrodes. The calculated excitation energies (2.177–2.834 eV) and simulated UV–visible spectra indicate strong absorption in the visible region, with maximum absorption wavelengths at 569.4 nm (bixin), 437.6 nm (norbixin), 474.5 nm (lutein), and 470.5 nm (zeaxanthin), primarily originating from HOMO→LUMO transitions. Photovoltaic performance indicators further highlight their potential. The calculated light-harvesting efficiencies are remarkably high (LHE = 0.996–1.000), indicating excellent photon-capture capability. Favorable electron-injection driving forces (−0.642 to −2.224 eV) and significant open-circuit voltage values (1.208–2.378 V) suggest efficient charge transfer and minimized recombination losses. Additionally, the predicted excited-state lifetimes (0.055–0.132 ns) support rapid electron injection processes. In summary, the results demonstrate that carotenoid-based dyes possess desirable electronic and optical characteristics for DSSC applications. Among the investigated candidates, bixin exhibits the most balanced photovoltaic properties, including a narrow band gap, red-shifted absorption, and longer excited-state lifetime, highlighting its strong potential as a sustainable sensitizer for next-generation DSSC technologies.

OP 78

INTEGRATING HYBRID DEEP LEARNING FOR REAL-TIME MONITORING OF PROHIBITED FISHING GEAR AND JUVENILE (JATKA) HILSA PROTECTION

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In Bangladesh, one of the national economic resources is the Hilsa fish. Additionally, it is a source of protein, also. Preservation of juvenile Hilsa (Jatka) is crucial for economic growth and for supporting the health of the Bangladeshi people. It is strictly prohibited in our country to fish Jatka. However, our administrative and related authorities are having great difficulty minimizing or maintaining this. In this study, the deep learning architectures YOLO, Faster R-CNN, and Mask R-CNN are employed to address illegal Jatka catching. The objective of this work is to give a technology-based solution for illegal jatka catching as well as mitigating the use of invalid gears or elements during fishing in coastal areas in our country. The proposed architecture combines YOLO, Faster R-CNN, and Mask R-CNN to detect illegal activities in river and coastal areas. This combined structure is connected to a drone (UAV) to perform its function. The YOLO V8 is utilized for live streaming from the drone. Its functionality is the detection of boats or trollers when they are in high speeds for illegal activity. As the YOLO architecture is highly speedy and applicable in real-time data extraction, so suspicious boats can be identified through this. When the drone is closer to a suspicious boat, the Faster R-CNN is activated, and using its region proposal network, it identifies the current jal as well as a collection of jatka in the boat. If the sky or environmental scenario is not clear, then there may arise difficulty in identifying or obtaining clarity of tiny ingredients. In the last phase, the mask R-CNN employs its pixel-level segmentation not only to measure the mesh size of the net but also to detect whether the mesh size is more or less than the government-approved mesh size of the net. Additionally, it measures the fish size, whether it is standard length or smaller than the authority-given reference value. This study idea has been implemented using Python programming in a simulated environment. The YOLO, Faster R-CNN, and Mask R-CNN have shown accuracy such 94%, 92% and 90% respectfully. In conclusion, this work proposes a solution utilising the advanced computer vision structure regarding the illegal catching of jatka fish as well as paves the way to take crucial measures for protecting the invalid absorption of fish.

OP 79

A PRODUCTION-READY MFS FRAUD DETECTION SYSTEM: FLUTTER-BASED MOBILE ARCHITECTURE WITH EMBEDDED ML INFERENCE AND FEDERATED FINE-TUNING

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Bangladesh's mobile financial services sector faces a 9.3% fraud victimisation rate across 110 million accounts, with attack patterns including SIM-swap chains, OTP-interception malware, and sequential investment scams that are absent from existing public fraud detection benchmarks. No labelled Bangladesh MFS transaction dataset is publicly available, and current fraud detection architectures cannot be directly deployed due to infrastructure constraints including 43% 3G connectivity, USSD-dependent user bases, and 80,000 agent-mediated transaction points. This study extends a validated two-stage anomaly detection framework (autoencoder on Kaggle + LSTM on PaySim, MMD=0.61 domain shift quantified) into a production-ready mobile architecture that preserves detection fidelity while operating under Bangladesh's connectivity and device limitations. We implement the trained models as TensorFlow Lite quantised executables embedded within a Flutter application, achieving sub-50ms inference on sub-$200 Android devices. An adaptive threshold engine implements the tiered alert framework derived from Monte Carlo simulations, applying differential sensitivity thresholds (rural low-income: 0.62, urban mid-income: 0.78) to deliver the mathematically projected 31% false-positive reduction for low-income rural users. A federated learning pipeline enables privacy-preserving fine-tuning across distributed devices, targeting the 400,000 labelled transaction requirement identified by domain shift quantification. USSD fallback mechanisms maintain fraud protection when smartphone connectivity is unavailable, while offline SQLite buffering ensures operation during network interruptions. TFLite quantisation preserves model fidelity with AU-ROC degradation <0.8% relative to full-precision versions. The adaptive threshold engine formally operationalises the MMD-quantified domain gap, converting a 0.61 distributional shift into device-specific sensitivity calibrations. Federated architecture enables progressive fine-tuning without centralised raw data collection, addressing the 400,000-transaction target identified as necessary to close the domain gap to estimated AU-ROC above 0.94. Offline capabilities maintain fraud detection coverage across the 43% of connections operating on 3G or slower networks. This Flutter-based implementation transforms a formally characterised anomaly detection baseline into a deployable system that respects Bangladesh's infrastructure realities while preserving the mathematical rigor of the underlying detection architecture. The framework converts the open data-access problem into a federated learning protocol, establishing the first production pathway for USSD-based, agent-mediated MFS fraud detection in a high-growth inclusion-critical economy. The 31% false-positive reduction target becomes a measurable operational metric tied directly to MMD-monitored domain adaptation.

OP 80

GIS-BASED ASSESSMENT OF SOCIO-ECONOMIC AND ENVIRONMENTAL IMPACTS OF COASTAL TOURISM IN MAHESHKHALI AND TEKNAF, BANGLADESH

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Coastal tourism is rapidly transforming the socio-economic and environmental landscape of Bangladesh, particularly in ecologically sensitive regions such as Maheshkhali and Teknaf in Cox's Bazar. While tourism contributes to economic growth, it also poses risks to environmental sustainability and cultural integrity. This study aims to assess the socio-economic benefits and environmental impacts of coastal tourism using geospatial and field-based approaches. The study employed a mixed-method approach combining primary data collection through household surveys, direct observations, and key informant interviews. Spatial analysis was conducted using Geographic Information Systems (GIS) tools, including ArcGIS and ENVI. Statistical analyses were performed using SPSS and KoboToolbox to evaluate patterns of tourism development and its impacts. The findings indicate that over 90% of respondents perceive tourism as a driver of economic growth, improving infrastructure and income opportunities. However, significant environmental concerns were reported, with more than 75% of respondents in Maheshkhali and 60% in Teknaf identifying increased pollution, including air, water, and noise pollution. Cultural degradation is also evident, as over half of the respondents believe tourism has negatively affected local traditions. Despite economic benefits such as employment generation and market expansion, these gains are unevenly distributed and often compromise long-term environmental sustainability. The study highlights the need for sustainable tourism management strategies that balance economic development with environmental conservation and cultural preservation. Effective policy interventions, community participation, and eco-friendly practices are essential to ensure sustainable coastal tourism in Bangladesh.

OP 83

IN SILICO PREDICTION OF A CONSERVED MULTI-EPITOPE VACCINE FOR HUMAN METAPNEUMOVIRUS USING PAN-GENOMIC REVERSE VACCINOLOGY

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Human metapneumovirus (HMPV) causes significant respiratory infections globally, particularly in vulnerable populations, yet lacks an approved vaccine. This study computationally designed and evaluated a multi-epitope

HMPV vaccine candidate using integrated immunoinformatics, reverse vaccinology, and pan-genomic approaches.Sixty-five HMPV genomes were analyzed for virulence, antigenicity, toxicity, and solubility, leading to three promising vaccine constructs (HMPV_V1, HMPV_V2, HMPV_V3). Fifteen conserved B-cell, MHC-I, and MHC-II T-cell epitopes were identified and linked with AAY, GPGPG, and KK linkers, plus a 50S ribosomal protein L7/L12 adjuvant. Physicochemical and immunological profiling confirmed antigenicity, non-allergenicity, and non-toxicity. High-quality 3D models were generated and validated. Molecular docking to the TLR4 immune receptor and molecular dynamics (MD) simulations assessed binding and structural stability. In silico immune simulations predicted adaptive responses, and codon optimization for HMPV_V2 was performed.Molecular docking showed strong TLR4 binding, with HMPV_V1 exhibiting the lowest binding energy (-1141.9). MD simulations revealed HMPV_V2's superior structural stability, with minimal RMSD and RMSF fluctuations over 100 ns, supporting its selection as the optimal candidate. Immune simulations predicted a robust adaptive response, including early antigen clearance, antibody class switching (IgM, IgG), memory B-cell formation, T-helper and cytotoxic T-cell activation, and IFN-γ and IL-2 production. Codon optimization indicated high expression feasibility for HMPV_V2 in E. coli K-12.These computational findings strongly support HMPV_V2 as a safe and effective preventative vaccine candidate against HMPV. However, Experimental validation through in vitro and in vivo studies is essential to confirm its immunogenicity and protective efficacy in clinical settings.

OP 84

ASSOCIATION OF DIETARY OIL WITH BODY MASS INDEX, WAIST-HIP RATIO AND BLOOD PRESSURE AMONG RURAL BANGALEE REPRODUCTIVE AGED WOMEN

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Dietary oil constitutes a major source of visible fat in Bangladeshi diets and plays an important role in energy intake. Excessive consumption of dietary oil may contribute to overweight, central obesity, and hypertension, particularly among women of reproductive age who are undergoing rapid nutrition transition in semiurban settings. This study aimed to evaluate the association of dietary oil intake with body mass index (BMI), waist–hip ratio (WHR), and blood pressure among rural Bangalee women of reproductive age, and to assess the independent associations after adjusting for sociodemographic, dietary, clinical, and anthropometric factors. A community-based cross-sectional study was conducted among 200 rural Bangali women aged 15–55 years. Data was collected from the rural area of Munshiganj district following convenient sampling technique. Sociodemographic and dietary information, including daily per-capita oil consumption, were collected using a structured questionnaire. Data were analyzed following standard procedures using IBM-SPSS V-26. $p \leq 0.05$ was considered as the level of significance. Among the study subjects, more than 60% were overweight or obese, 90% had a high-risk WHR and 13% of women were hypertensive. Daily oil consumption showed a significant positive association with BMI in unadjusted analyses and correlation analysis ($r = 0.204$, $p = 0.004$), with obese women consuming higher amounts of oil than underweight and

normal-weight women. However, oil consumption was not significantly associated with WHR or blood pressure. Age was positively associated with BMI (p=0.001), WHR (p=0.002) and blood pressure (SBP, p=0.001& DBP, p=0.002). In multivariable analyses, BMI emerged as an independent predictor of hypertension, while oil consumption did not remain independently associated with BMI, WHR, or hypertension after adjustment. Excess body weight and central obesity are highly prevalent among urban Bangali women of reproductive age. While higher dietary oil intake is associated with increased BMI, its independent effect is weakened after adjustment for confounders.

OP 85

AVAILABILITY AND ACCESSIBILITY OF PRIMARY HEALTH CARE SERVICES IN A DISTRICT OF BANGLADESH WITH BETTER HEALTH OUTCOMES: A STUDY BASED ON CONSUMER PERCEPTIONS

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Consumer perspectives in Primary Health Care (PHC) need further exploration in Bangladesh. The present study aimed to explore consumer-perception-based availability and accessibility of PHC services, along with their equity aspects, in a district with higher health outcomes. A cross-sectional observational study was conducted in Naogaon district, which is high-performing district (HPD) from the viewpoints of Human Development Index and and, Self-Reported Availability Score (SRAvS) and Self-Reported Accessibility Score (SRAcS) were derived official mortality data. Adult (n=421) Health Care Consumers (HCCs), attending PHC facilities (PHCFs), were purposively selected and data were collected through face-to-face interviews. Individual questions were weighed selected and data were collected through face-to-face interviews. Individual questions were weighed (0%-100% scale). Equities in availability and accessibility were explored by analyzing gender (male-female), location (rural-urban), and Income-Quintile (InQ)-based subgroups, using appropriate bivariate and multivariate statistics. The perceived availability of PHC services in HPD was average, with gaps in diagnoses (49%), emergency-related services (74%), health and nutrition education (64%), and regular access to drugs (40% most of the time). 54% respondents visited alternative facilities for diagnostics, though referrals (43%) were mainly to the public sector (86% of the total). Access was favourable: 86% arrived within 30 minutes at facilities, 86% travelled without interruption, 30% could travel on foot, and 94% spent ≤BDT 100. Median SRAvS was moderate (53-59) and showed no significant difference in gender, location, and income (p>0.05). There was strong median SRAcS (80-88) and even across groups (p>0.05). Gender (p=0.003) and occupation (p=0.035) influenced availability by regression analysis and accessibility was primarily determined by the type of facility. PHC services are moderate in this HPD of Bangladesh, and there is a significant gap in diagnostics and referral services. The accessibility generally is good and equal among groups. Socioeconomic status is not as important as facility type, gender, and occupation in determining remaining disparities.

OP88

PROPORTION OF DEMENTIA AND ITS ASSOCIATION WITH DIETARY VITAMIN B6 INTAKE AMONG ELDERLY TYPE 2 DIABETIC SUBJECTS IN A DHAKA-BASED COMMUNITY

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Diabetes raises the risk of dementia by 1.5 times for Alzheimer's and 2.5 times for vascular dementia. It has been reported that 1 in every 12 Bangladeshi individuals aged 60 years or above has dementia. Vitamin B6 deficits in older people may cause dementia. However, the extent of the association has not yet been studied among Type 2 diabetic (T2DM) subjects. The objectives of the study were to explore the proportion of dementia and its association with vitamin B6 among T2DM subjects in a Bangladeshi urban community. A Cross-sectional study with 145 elderly T2DM participants (age ≥60 years) was conducted in Dhaka city. Dementia was screened and categorized by ACE-III scores derived from Addenbrooke's Cognitive Examination. A pre-designed 24-hour recall method was used to measure dietary consumption of vitamin B6. Among the study participants, 69% had dementia, of which 30.3% had Alzheimer's disease (AD) and 38.6% had vascular dementia (VAD). Of all T2DM subjects, 84.14% had Vitamin B6 deficiency. The proportion of inadequate vitamin B6 intake was significantly higher (p= 0.016) in VAD (34.43%) as compared to AD (33.61%) subjects. Dietary total vitamin B6 intake was significantly lower in VAD as compared to Nondementia or ND (p=0.001) and AD (p=0.002). Total dietary vitamin B6 intake was significantly lower in AD as compared to ND (p= 0.001). Total vitamin B6 (r/p= 0.541/0.001) intake from diet was positively correlated with ACEIII score. The proportion of dementia is very high among elderly T2DM subjects in Dhaka City, with 7 out of 10 persons suffering from the cognitive dysfunction. VD is about 9% more prevalent among these persons as compared to AD, and deterioration of the cognitive function marker (ACEIII score) has an association with dietary deficiency of vitamin B6.

PP001

ECONOMIC LOSSES OF MARGINAL FARMERS DUE TO LUMPY SKIN DISEASE (LSD) IN SYLHET DISTRICT, BANGLADESH

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Lumpy Skin Disease (LSD), a devastating cow virus, affects the global industry and economy, particularly in Bangladesh. LSD's financial impact on Sylhet's smallholdings was underreported. To fill this knowledge gap, LSD prevalence among bovine exposure risk factors in Sylhet District, Bangladesh, and demographic and managerial factors impacting dissemination were examined. Kobo Toolbox was used to collect data from May 2024 to March 2025 in a longitudinal survey. We chose cattle-owning smallholder farmers over 18 years old. Seven Sylhet District subdistricts were randomly selected from all subdistricts using basic random selection. We developed a roster of smallholder households in each subdistrict with local livestock officials and randomly chose them for participation. From these families, 388 LSD-positive cattle were included. Face-to-face interviews were conducted to collect data on cattle demographics, risk factors, management practices, and economic effects using structured questionnaires. Direct observation and herd record verification were also part of the survey. Ten residents from Sylhet Sadar were randomly selected to pre-test and refine the questionnaire in a pilot study between April 2 and 6, 2024. Losses for LSD-affected cattle rose to 130 USD. More prevalence occurred in calves with 298 cases (≤12 months) than in 59(12-24 months), statistically significant ($p<0.001$). Bulls (236) suffered more than females (152). Crossbred animals outnumbered indigenous breeds, 325(71%) against 63 (69%). The most genotype-positive animals were discovered in Indigenous × Sahiwal (185), followed by Indigenous × HF (147). Vaccination is crucial to preventing LSD spread, as unvaccinated people had 360 infections compared to 25 for vaccinated people. This is the first micro-level economic burden evaluation of LSD among Sylhet smallholders. Integrated epidemiological and economic evidence linked a significant regional gap and advanced a livelihood-centered disease resilience concept in resource-constrained cattle syste

PP0002

PREVALENCE AND RISK FACTORS ANALYSIS OF FELINE PANLEUKOPENIA (FPV) VIRAL INFECTION IN CATS AT CENTRAL VETERINARY HOSPITAL (CVH), DHAKA

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Feline panleukopenia is a highly contagious, often fatal viral disease of cats, particularly kittens, yet robust epidemiological data from Dhaka are lacking, potentially delaying outbreak recognition and vaccination planning. This study therefore aimed to estimate FPV prevalence and identify key demographic and seasonal risk factors in hospital-presented cats. A hospital-based cross-sectional study was conducted using records of 2,678 infectious and non-infectious cats presented to the CVH in Dhaka from January to December 2024. Eligible cats were companion animals aged ≥8 weeks, including emergency, stray, and owned cats; those with inadequate records, recent FPV diagnosis or treatment, or unrelated fatal conditions were excluded. FPV infection was diagnosed using rapid antigen testing confirmed by RT PCR, supported by clinical signs, post mortem findings, and hematobiochemical profiles. Associations with age, sex, and season were assessed using chi-square tests at $p<0.05$. The overall prevalence of FPV infection was 19.7% ($p<0.001$). Kittens aged 0–6 months showed the highest infection rate (10.8%). Male and female cats were similarly affected, with prevalences of 9.9% and 9.8%, respectively. FPV was most frequent in winter (13.4%), followed by the rainy season (5.2%) and summer (1.1%), with significant associations between age, season, and infection ($p<0.01$). This first hospital-based epidemiological assessment of FPV in Dhaka demonstrates a substantial disease burden during winter months and underscores the need for targeted, seasonally responsive FPV vaccination, strengthened clinical surveillance, and enhanced biosecurity measures to inform evidence-based feline health policy in urban Bangladesh.

PP0003

COMPANION CAT OWNERSHIP AND HUSBANDRY PRACTICES IN SYLHET SADAR, BANGLADESH: EMERGING GAPS AND OPPORTUNITIES

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Cat ownership is increasing in Sylhet Sadar, yet limited owner knowledge of vaccination, nutrition, hygiene, and disease prevention may compromise feline health and welfare. This study aimed to describe companion cat husbandry, including breed and sex preferences, feeding and hygiene practices, common health problems, and vaccination uptake, to identify priority areas for veterinary outreach and owner education interventions. A descriptive cross-sectional study was conducted between October 2024 and February 2025. A simple random selection of 250 pet cats was obtained through structured interviews with cat owners in Sylhet Sadar. The questionnaire captured cat demographics, breed and sex preferences, feeding patterns, housing and hygiene, history of illness, accidental injuries, and preventive health practices, including vaccination. Descriptive statistics (frequencies and percentages) were used to summarize responses. Local breeds were most common (56%), followed by Persian (24%) and hybrid cats (20%). Male cats (56%) were preferred over females (44%) to avoid unwanted offspring, as kitten rearing was perceived as difficult. Feeding patterns showed that 32% of cats were mainly given specially prepared boiled fish and 24% received boiled chicken meat, while 16% were fed regular human food (rice, vegetables, and fish from curry) and 12% consumed kitchen scraps. Frequently reported health problems included accidental injuries (24%), respiratory tract infections (16%), and urinary tract infections (8%). Despite growing awareness, only 20% of owners reported vaccinating their cats. This first owner-based assessment of companion cat husbandry in Sylhet Sadar reveals notable gaps in nutrition, preventive care, and injury prevention and underscores the need for targeted veterinary outreach, systematic owner education, and strengthened vaccination promotion to support evidence-based feline health and welfare strategies in urban Bangladesh.

PP0004

A NONFERMENTABLE HERBAL FORMULATION RELIEVES DYSMENORRHEA (DM), INHIBITS YEAST GROWTH BUT NOT PROBIOTIC BACTERIA: A NATURAL MICROBIOME FRIENDLY HOME REMEDY FOR DM WITH NO DETECTABLE SIDE EFFECTS

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Dysmenorrhea (DM), commonly known as menstrual cramps, affects nearly half of women worldwide and is primarily caused by uncontrolled contractions of uterine muscles during menstruation. While some women experience severe symptoms, many suffer from mild to moderate pain that can disrupt daily activities. Conventional treatments such as non-steroidal anti-inflammatory drugs (e.g., ibuprofen), hormonal contraceptives, and lifestyle modifications may provide relief but can also lead to side effects or hormonal disturbances. The objective of this study was to develop a natural herbal formulation that may help alleviate menstrual cramps safely and conveniently. An herbal formulation named HER-Flex was developed using a combination of chamomile, ginger, mint leaves, turmeric, fennel seeds, and cinnamon. The ingredients were processed into a powdered formulation that can be dissolved in boiling water and consumed as a soup two to three times daily. In vitro experiments were conducted to evaluate antifungal activity and compatibility with probiotic bacterial growth. The formulation inhibited yeast growth in vitro, indicating antifungal potential and suggesting that the product is non-fermentable. At the same time, the formulation did not inhibit probiotic bacterial growth, indicating microbiome-friendly characteristics. The selected herbal ingredients are traditionally associated with anti-inflammatory, antispasmodic, and digestive benefits, which contribute to relieving menstrual discomfort & assured by the 122 volunteers who consumed the formulation during their menstrual cycle. HER-Flex represents a promising herbal formulation designed to help relieve menstrual cramps while maintaining microbiome compatibility. The product provides a convenient and potentially safe dietary option for managing dysmenorrhea.

PP0005

EMERGING THREATS TO BOTTLE GOURD PRODUCTION IN THE NORTHEASTERN BANGLADESH: A FARMERS' PERSPECTIVE

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Bottle gourd (Lagenaria siceraria) is a popular year-round vegetable crop in Bangladesh, contributing significantly to farmers' income and national nutritional security. Recently, bottle gourd production in the northeastern part of Bangladesh is facing new threats. To enlist the problems from the farmers' point of view, a cross-sectional survey was conducted among randomly selected 200 farmers through face-to-face interview from four districts of the Sylhet division of Bangladesh, along with laboratory analyses. Results revealed that about 80.5% farmers reported sudden wilting of bottle gourd plants at either vegetative or reproductive stage as the most severe threat. Laboratory analysis of the bottle gourd infected plant samples collected from the farmer's field confirmed the causal agent for the sudden wilting was nematodes. About 65.5% of the farmers noticed that a lepidopteran larva caused a scarring injury on the fruit surface of bottle gourd. Further life cycle study of the larvae in the laboratory confirmed the species as cucumber moth (Diaphania indica). Moreover, 54.5% farmers of this region also found sap beetle (Epuraea sp.) as major threat of bottle gourd in the reproductive stage. It consumed the pollen of bottle gourd male flower voraciously which increased the number of unset fruits. Bottle gourd fruit with whitish pale green rough surface was also mentioned by 18% of the farmers. The etiology of this symptom is unclear and need further research. These findings suggest that nematodes, cucumber moths, sap beetles, and fruit malformation by irregular surface are emerging as significant constraints to bottle gourd production in the northeastern Bangladesh. Further diagnostic research, strengthening integrated pest management (IPM) strategies, and farmer training is essential to mitigate these emerging challenges and ensure sustainable bottle gourd production in Bangladesh.

PP0006

EFFECTS OF WATER MANAGEMENT AND CLIMATE-SMART RICE CULTIVARS ON GREENHOUSE GAS EMISSIONS AND RICE YIELD

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Efficient water management and adoption of climate-smart rice cultivars have the potential to reduce greenhouse gas (GHG) emissions from rice fields. However, studies on the impacts of alternate wetting and drying (AWD) irrigation and climate-smart rice cultivars on GHG emissions and rice yield are limited. Therefore, this study aimed to examine the impacts of AWD irrigation and climate-smart rice cultivars on GHG emissions, global warming potential (GWP) and rice productivity. We conducted field experiments during the dry seasons to compare the effects of AWD versus continuous flooding (CF) irrigation. Four rice cultivars including BRRI dhan50, BRRI dhan67, BRRI dhan92, and BRRI hybrid dhan3 were evaluated under two N rates. CH4 and N2O emissions were measured using the closed gas chamber technique and their concentrations were determined using a gas chromatograph. CH4 and N2O emissions varied across water regimes and rice cultivars. AWD irrigation reduced CH4 emissions by about 35-40% compared to CF. Although AWD irrigation significantly increased cumulative N2O emissions, the contribution of N_2O to total GWP was minor, resulting in lower GWP and GHG intensity under AWD. Among the cultivars, BRRI dhan67 reduced CH4 emissions by 11-14% at 139 kg N ha−1 and by 9-12% at 174 kg N ha−1 compared to BRRI dhan50 and BRRI dhan92 in the Boro season. Similarly, BRRI hybrid dhan3 reduced emissions by 6-9% at 139 kg N ha−1 and by 11-14% at 174 kg N ha−1 relative to BRRI dhan50 and BRRI dhan92. Both BRRI dhan67 and BRRI hybrid dhan3 produced higher grain yields than BRRI dhan50 and BRRI dhan92, while AWD maintained yields comparable to CF irrigation. These findings imply that AWD combined with BRRI dhan67 and BRRI hybrid dhan3 may be considered environmentally favorable technologies for sustainable rice production

PP0007

DEEP LEARNING–DRIVEN EARLY DETECTION OF CROP INSECT PESTS USING UAV IMAGERY FOR PRECISION AGRICULTURE

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Timely detection of insect pest infestations is a fundamental prerequisite for effective crop protection. Conventional scouting methods are labor-intensive, spatially limited, and often fail to capture early-stage infestations before economic thresholds are breached. Unmanned aerial vehicles (UAVs) equipped with high-resolution cameras offer unprecedented spatial coverage and revisit frequency, yet their full potential can only be realized when combined with robust automated image analysis. This study aimed to develop and validate a deep learning framework for early-stage identification and spatial mapping of economically important crop insect pests using UAV-acquired multispectral imagery. UAV surveys were conducted across wheat, cotton, and maize fields in Punjab, Pakistan, during the 2023 growing season. RGB and multispectral imagery were captured at 20 m altitude using a DJI Matrice 300 RTK platform. A labelled dataset of 12,450 annotated image patches representing six target pest species including aphids, thrips, whitefly, armyworm, stem borer, and leaf hopper was constructed. Three convolutional neural network (CNN) architectures YOLOv8, EfficientDet-D4, and ResNet-50 were trained, validated, and compared using five-fold cross-validation. Precision, recall, F1-score, and mean average precision (mAP) were used as performance metrics. YOLOv8 achieved the highest overall mAP of 91.4%, with species-level F1-scores ranging from 87.3% (thrips) to 94.6% (armyworm). EfficientDet-D4 and ResNet-50 returned mAP values of 88.1% and 84.7%, respectively. Early infestation foci were detected with a spatial accuracy of ±1.2 m. The framework reduced false-positive rates by 34% compared to conventional threshold-based image segmentation. Geo-referenced pest density maps generated from UAV outputs demonstrated strong agreement ($r = 0.91$) with ground-truth field counts. The integration of deep learning with UAV remote sensing constitutes a practical, scalable solution for real-time, early-stage pest detection in precision agriculture. YOLOv8-based models demonstrated superior detection performance across multiple pest categories, and the geo-referenced output maps provide actionable spatial data for site-specific pesticide application, thereby reducing chemical inputs and improving crop protection efficiency.

PP0008

MACHINE LEARNING PREDICTION OF WHITEFLY (BEMISIA TABACI) POPULATION DYNAMICS AND BEGOMOVIRUS TRANSMISSION RISK IN AGROECOSYSTEMS

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Bemisia tabaci (Gennadius) is among the most destructive agricultural pests globally, causing direct feeding damage and serving as the exclusive vector of over 200 Begomovirus species, including tomato yellow leaf curl virus (TYLCV) and cotton leaf curl virus (CLCuV). Population outbreaks are driven by complex interactions among temperature, humidity, host plant phenology, and natural enemy activity, making accurate population forecasting a persistent challenge for crop protection practitioners. Machine learning (ML) offers a data-driven pathway to model these non-linear interactions and generate predictive risk assessments. This study developed and validated ML models to forecast B. tabaci population dynamics and associated Begomovirus transmission risk

under field conditions in Pakistan. Weekly B. tabaci population counts and Begomovirus incidence data were collected from tomato and cotton fields across five districts of Punjab over three consecutive growing seasons (2021–2023). Concurrently, meteorological variables (temperature, relative humidity, rainfall, wind speed), host plant growth stage, and natural enemy abundance were recorded. Five ML algorithms random forest (RF), gradient boosting machine (GBM), support vector regression (SVR), artificial neural network (ANN), and XGBoost, were trained and evaluated. Model performance was assessed using root mean square error (RMSE), mean absolute error (MAE), and coefficient of determination (R^2). XGBoost outperformed all competing models, achieving an R^2 of 0.94, RMSE of 3.2 adults/leaf, and MAE of 2.1 for population density prediction. Temperature and relative humidity were identified as the most influential predictors via SHAP (SHapley Additive exPlanations) analysis. Begomovirus transmission risk classification attained an area under the ROC curve (AUC) of 0.96. The model accurately predicted epidemic-threshold exceedance events 14 days in advance with 88.6% sensitivity and 91.3% specificity. Machine learning-based predictive models provide a robust and interpretable tool for forecasting B. tabaci population outbreaks and Begomovirus epidemic risk. XGBoost demonstrated the strongest predictive performance, and SHAP-based feature importance analysis identified actionable environmental drivers for proactive intervention. Integrating these models into digital decision-support platforms can substantially improve the timing and precision of whitefly management, reducing virus disease losses in vulnerable agroecosystems.

PP0009

EVALUATING THE PHYSIOLOGICAL AND MOLECULAR RESPONSES OF ASIAN SEABASS IN DIFFERENT SALINITY GRADIENTS

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Salinity plays major role in controlling physiological function and growth performances in fish. This study determined the impact of variable salinity levels on growth, survivability, hematology, histopathology, proximate composition, and gene expression of Asian seabass fry (Lates calcarifer). For a period of 45 days, seabass fry (10.13 ± 0.56 g) were exposed in varying salinity levels of 0, 5, 10, and 15 ppt. Highest growth (~57–58 g) and specific growth rate(1.85 %/day) were observed at 10 ppt, followed by 15, 0, and 5 ppt. However, the highest survivability was observed at 0 ppt (100%) followed by 5, 10, and 15 ppt. The highest blood glucose levels was observed at 0 ppt followed by 5, 10, and 15 ppt, while hemoglobin levels remained unchanged across the treatments ($p = 0.676$). As salinity increased from 0 to 15 ppt, chloride cells in the gills gradually increased. Proximate analyses indicated that increasing salinity from 0 to 15 ppt led to a general decline in crude lipid and carbohydrates, but notable rise in crude protein and ash content. The molecular result of growth (GH, IGF1 & IGF2) and immune (IL-1β & Lysozyme) related genes suggest that exposure to moderate salinity (5–10 ppt) increases the activity of growth and immune genes in seabass, with 10 ppt being the best level, Higher salinity (15 ppt) slightly reduces this activity. However, all the parameters in the fish reared at o ppt were not so affected. So, overall, it can be said that farming the seabass in freshwater will not cause any negative effects. This study will help the researchers, policymakers, entrepreneurs, and aquaculturists to introduce seabass for freshwater culture in our all regions.

PP010

PROBIOTICS AND SPIRULINA RELIEVE SALINITY-INDUCED GROWTH OBSTRUCTION IN ROHU (LABEO ROHITA) BY UPGRADING INTESTINAL MORPHOLOGY AND GROWTH-RELATED GENES EXPRESSION

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Salinity intrusion in coastal regions poses a significant challenge to the cultivation of freshwater fish species. This study aimed to evaluate the potential of multispecies probiotics (1 ml/L in water) and Spirulina platensis (50 gm/Kg in feed) to mitigate the negative effects of elevated salinity on the growth of rohu, Labeo rohita. Fingerlings were reared for 60 days under four experimental conditions: 0 ppt (freshwater, positive control), 8 ppt (elevated salinity, negative control), 8 ppt with probiotics, and 8 ppt with Spirulina platensis supplementation. At the end of experiment, growth parameters such as weight gain (WG), specific growth rate (SGR) was significantly lower in 8 ppt saline water condition with higher feed conversion ratio (FCR). Incorporation of either probiotics or Spirulina platensis significantly improved growth and FCR. Protein and lipid content in the fish were reduced under elevated saline conditions but were restored and enhanced in both treatment groups. Elevated salinity also abruptly affected the morphology of intestine and reduce the abundance of goblet cells (GC) and enterocyte cells (EC). Both probiotic and S. platensis supplementation markedly improved intestinal morphology, including villus dimensions, wall thickness, muscular layer integrity, and epithelial cell abundance. The relative mRNA level of three growth-relevant genes (growth hormone, gh, in the pituitary; insulin-like growth factor 1 and 2, igf-1 and igf-2, in the liver) decreased in elevated saline condition. Whereas notable upregulation regarding the expression of these genes were found in case of both treatments. These findings suggest that probiotics and Spirulina platensis effectively alleviate salinity-induced growth suppression in Labeo rohita, likely through the improvement of intestinal morphology and modulation of the GH–IGF growth axis.

PP011

HARNESSING PROBIOTICS AND SPIRULINA TO COUNTERACT SALINITY INDUCED STRESS IN LABEO ROHITA

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Salinity is widely recognized as a critical environmental parameter, and salinity-induced stress can significantly reduce aquaculture productivity. The use of probiotics and the dietary microalga Spirulina platensis in aquaculture has been increasing because of their consistently positive effects as environmentally sustainable agents. Rohu (Labeo rohita) fingerlings were reared for 60 days under four experimental treatments: a control group maintained at 0‰ salinity, a negative control at 8‰ salinity, and two additional groups at 8‰ salinity supplemented with probiotics (1 mL/L) and S. platensis (50 g/kg of feed), respectively. Growth performance metrics, such as weight gain (WG) and specific growth rate (SGR) markedly declined, whereas feed conversion ratio (FCR) and condition factor (CF) exhibited a notable increase at the elevated salinity (8‰). Notably, the probiotic and spirulina groups

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maintained at 8‰ significantly mitigated the WG, SGR, FCR and CF. Under elevated salinity condition (8‰), blood analyses revealed a significant decrease in glucose level and increase in hemoglobin concentration, accompanied by a significant increase of erythrocyte cellular (twin, fusion and tear dropped) and nuclear (nuclear bridge, notched nuclei and nuclear bud) abnormalities. Conversely, probiotics and spirulina groups significantly ameliorated these changes. Gill structures exhibited pronounced structural damage under elevated salinity conditions (8‰), while using of probiotics and spirulina offered complete recovery. At 8‰ salinity, gene expression of Na^+ K^+ ATPase, MAPK, and Aquaporin were significantly upregulated, while hepcidin was downregulated, reflecting differential gene regulation under osmotic stress. Antioxidant genes, GPx and SOD were upregulated at 8‰ salinity. Exposure to 8‰ salinity elicited pronounced upregulation of IL 1β, TNFα, LyZ C, and IgM genes, while probiotics and spirulina supplementation downregulated their expressions. Therefore, the findings of study advocate for the inclusion of probiotics or spirulina as effective bio-amelioration against high salinity-induced stress and physiological wellbeing, thereby enhancing aquaculture productivity.

PP012

THE EVOLUTIONARY LANDSCAPE OF DIVERSITY-GENERATING RETROELEMENTS (DGR) IN SOUTH ASIAN GUT COMMENSALS

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Diversity-generating retroelements (DGRs) act as molecular regulators, enabling microbes to quickly diversify particular proteins to adapt to changing environmental conditions. In the South Asian gut, which has distinctive dietary and microbial characteristics, these systems are likely key to the coevolution of hosts and their symbionts. This research examines the prevalence of common DGRs and their functional roles in promoting hypervariation among South Asian gut commensals. Metagenomes and Metagenome-assembled genomes (MAGs) sequences from South Asian gut cohorts, mainly from Bangladesh and India, were retrieved from NCBI and analyzed

Potential DGR loci were identified by screening predicted proteomes for homology to reverse transcriptase (RT) using curated reference databases. Candidate systems were further validated by searching for hallmark 10 kb genomic windows containing template repeat (TR) and variable repeat (VR) pairs. To identify hypervariable regions, adenine-specific mismatches were detected via iterative sequence alignments, and the functional domains of target gene-encoded proteins were annotated to predict their ecological functions. We identified four high-confidence DGR systems within key South Asian gut bacteria, including Prevotella stercorea, Bacteroides fragilis, and Lactococcus garvieae. Two of these systems are located in prophage neighborhoods, indicating that bacteriophages are likely the main vectors for spreading hypervariation mechanisms. In B. fragilis and P. stercorea, we observed complex copy-paste behavior in which a single template repeat diversifies multiple distant target genes simultaneously. These target genes encode surface-adhesion domains (Glyco_hydro_59_C and DUF6273), indicating that DGRs actively modify the microbial interactome to enhance gut colonization and evade host immune responses. Our findings show that DGR-driven hypervariation actively influences evolution in South Asian gut microbial communities. The identification of multi-target diversification in important commensals indicates a specialized system for environmental detection and competitive advantage. This research offers a biological basis for understanding how targeted mutations impact the stability and functionality of the human mucosal ecosystem.

PP013

COMPUTER VISION-BASED DETECTION OF TOMATO LEAF DISEASES FOR FARMERS AND AGRICULTURE

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Tomato is one of the most widely cultivated vegetable crops, but its leaves are affected by various leaf diseases. Early detection of these diseases is very important for reducing crop loss and increasing agricultural productivity. In recent years, deep learning techniques have been widely used for plant disease detection using image data. The main aim of this study is to detect various types of tomato leaf diseases, like Early Blight, Late Blight, and identify healthy leaves. In this study, YOLO, ResNet, and MobileNet deep learning models are used. The tomato leaf image dataset utilizes for training and testing these models. These models were trained using the images to learn the patterns of different tomato leaf diseases and evaluate their performance. All experiments were done by using Python in Google Colab with GPU support. Using these models, we achieved reliable results in detecting tomato leaf diseases. The YOLO model achieved an accuracy of 97.7%, the Resnet model had given 95.5% accuracy, and most importantly, the Mobilenet model had achieved 100% accuracy on the dataset. This result indicates that deep learning models can highly identify leaf diseases using image data. This system will help farmers to detect leaf diseases at early stages, and they can take necessary steps to prevent these leaf diseases. In the future, this idea can be developed into a monitoring system in the agricultural sectors and improve our agricultural productivity.

PP014

CORRELATION OF THE TESTICULAR SONOGRAPHIC BIOMETRIC FEATURES AND SEMEN QUALITY AS TOOLS IN BREEDING SOUNDNESS EXAMINATION OF RED SOKOTO BUCKS

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Breeding soundness evaluation (BSE) is a vital component in the selection of fertile sires for livestock production, particularly among indigenous breeds such as the Red Sokoto goat (RSG) buck. This study aimed to investigate the correlation between testicular sonographic biometric features and semen quality as tools for evaluating breeding soundness in Red Sokoto bucks. Sixty mature Red Sokoto bucks in Sokoto, Nigeria, were subjected to detailed semen analysis and ultrasonographic evaluation of testicular dimensions. Semen parameters assessed included volume, progressive motility, live ratio, morphology, pH, and sperm concentration. Sonographic measurements included testicular length, height, width, and volume, with echotexture also examined. Mean semen volume was 0.85±0.299 ml, progressive motility 77.33±14.305%, live spermatozoa 89.18±9.118%, and sperm morphology 80.07±7.481%. Sperm concentration was 374 ± 138.923 × 10^9/ml. Testicular volumes were larger on the right side (115.23±5.264 cm^3) than the left (89.95±18.280 cm^3), with uniform hypoechoic echotexture and scattered hyperechoic spots. A positive correlation was observed between testicular volume and sperm concentration. The combination of ultrasonographic testicular measurements and semen quality parameters provides a reliable approach to breeding soundness examination in Red Sokoto bucks. Testicular volume and echotexture are valuable predictors of semen quality, and their evaluation should be considered a standard tool in reproductive soundness assessment for breeding selection in small ruminants.

PP015

THERMAL STRESS MITIGATION IN NILE TILAPIA (OREOCHROMIS NILOTICUS) THROUGH SUPPLEMENTATION WITH PROBIOTICS AND DIETARY SPIRULINA

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Extreme warming poses a serious threat to aquaculture throughout the world by lessening fish growth, physiology, and immune function. Fishes are more susceptible to this climate induced thermal fluctuation even if it is a little. This study was conducted to evaluate the mitigating effects of multispecies probiotics and dietary Spirulina platensis on thermal stress in juvenile Nile tilapia (Oreochromis niloticus). A total of 240 fish were assigned to four treatments with triplicates for 60 days rearing period: control (31°C), negative control (37°C), probiotics group (37°C + probiotics, 1 mL L^{-1}), and dietary Spirulina group (37°C + 10% S. platensis diet). Growth performance, hemato-biochemical parameters, erythrocytic abnormalities, intestinal histomorphology, and expression of growth, stress, antioxidant, and immune-related genes were analyzed. Exposure to 37°C (negative control) well markedly or significantly reduced growth performance, survival, hemoglobin levels, and the expression of GH, IGF-1, IGF-2, SOD, CAT, TNF-α, IFN-γ, and IL-1β while increasing feed conversion ratio, erythrocytic abnormalities, intestinal damage, and HSP-70 expression. However, supplementation with probiotics or dietary Spirulina markedly alleviated these adverse effects by improving growth and survival, restoring hemato-biochemical indices, reducing erythrocytes abnormalities, enhancing intestinal structure, suppressing HSP-70, and promoting antioxidant and immune gene expression. These findings demonstrate that multispecies probiotics and dietary Spirulina can effectively mitigate extreme warm temperature-induced stress in Nile tilapia, offering promising nutritional strategies for improving fish resilience under climate-driven warming conditions in aquaculture.

PP016

ENZYMATIC CONVERSION OF INSOLUBLE DIETARY FIBER FROM POST-EXTRACTION SWEET POTATO LEAF PROTEIN FRACTION: PHYSICOCHEMICAL, STRUCTURAL, IN VITRO BIOACTIVITY AND EFFECTS ON ANTI-OBESITY, SERUM LIPID PROFILE AND GLYCEMIC LEVELS IN SWISS ALBINO MICE

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The by-product obtained from protein extraction of sweet potato leaves is an underutilized agro-industrial waste that is still rich in insoluble dietary fiber (IDF). In this study, IDF was converted to modified insoluble dietary fiber (MIDF) using α-amylase, xylanase, and cellulase enzymes. The structural, physicochemical, and functional properties as well as its in vitro glucose and cholesterol binding capabilities were evaluated for both IDF and MIDF. Furthermore, MIDF was also utilized to prevent metabolic disorders in Swiss albino mice specifically by assessing its effects on blood glucose levels and cholesterol profiles in comparison to the high-fat diet group. MIDF showed substantial enhancement in water-holding capacity, increasing from 5.98 to 7.11 g/g; swelling capacity, from 6.81 to 10.05 g/g; oil-holding capacity, from 1.86 to 1.89 g/g; and solubility, from 12.77% to 19.38% as compared to IDF. MIDF exhibited pronounced surface and structural changes under SEM (500–20 μm), with enhanced porosity, and ATR-FTIR (4000–400 cm^{-1}) revealed corresponding functional group modifications. The

glucose adsorption capacity of MIDF increased by 46% and was 231% higher than that of IDF at 2 hours and 6 hours, respectively. Furthermore, the cholesterol-binding capacity of MIDF improved by 67% under gastric conditions (pH 2) and by 8% under intestinal conditions (pH 7) compared to IDF. Supplementation with MIDF (3 g/kg BW/d) in mice on a high-fat diet led to a reduction in body weight gain, decreasing from 2.95 g to 1.62 g, which represents a 45.1% reduction. Additionally, total cholesterol levels decreased from 186.6 mg/dL to 156.6 mg/dL, and blood glucose concentration fell from 4.48 mmol/L to 3.89 mmol/L, compared with mice fed the high-fat diet alone. Results suggest that MIDF may serve as a supplementary diet, potentially leading to significant metabolic improvements and offering a protective effect against obesity, serum lipid profile and glucose concentration.

PP017

CONSTRUCTION OF HOMICORCIN VARIANTS WITH ENHANCED PRODUCTIVITY AND ACTIVITY THROUGH IN SILICO AND IN VIVO TECHNIQUES

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Homicorcin, novel class I lantibiotic from Staphylococcus hominis MBL_AB63 exhibiting potent antimicrobial activity against Gram-positive pathogens including MRSA. This study aimed to enhance the biosynthesis rate and antimicrobial potency of homicorcin through in-silico NNK mutagenesis. Molecular Operating Environment (MOE) tool was used to dock wild-type Homicorcin to its cognate biosynthetic enzymes (HomB, HomC, HomP and HomT) to establish baseline interaction profiles. In-silico site saturation mutagenesis generated a comprehensive mutant library, identifying three superior variants: K52R, K52W, and D54W. Interaction with HomB increased by 2.7, 9.1, and 3.2 kcal/mol and with HomC by 1.12, 5.64, and 7.02 kcal/mol for K52R, K52W, and D54W mutant variants respectively. The binding affinity of K52R and D54W increased with HomP by 0.1658 and 0.1310 kcal/mol respectively. Notably, D54W exhibited maximum interaction with Lipid II by an increament of 0.0381 kcal/mol). The structural stability and interaction dynamics were validated by performing molecular dynamics simulation of the complexes using GROMACS. The simulation results revealed that, the mutants demonstrated enhanced enzyme recognition and processing efficiency while maintaining stable conformations. These carefully crafted mutants serve as attractive candidates for experimental validation and establish a framework for building lantibiotics with improved biosynthesis rates and therapeutic efficacy against a broad spectrum of antibiotic-resistant bacteria.

PP018

COMBINED EFFECTS OF SUMITHION AND MERCURY ON HEMATOLOGY, HISTOPATHOLOGY AND ANTIOXIDANT-IMMUNE RESPONSE OF NILE TILAPIA WITH IMPLICATION FOR FISH HEALTH AND SUSTAINABLE AQUACULTURE

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Aquatic ecosystems have been greatly threatened by the widespread use of pesticides and industrial pollutants. Notably, Sumithion (Su), an organophosphate insecticide which is used to remove hazardous insects. However, excessive Su use can harm the ecosystem. Mercury (Hg), a heavy metal, has detrimental effects on fish physiology and overall health. The present study aims to investigate the combined effects of Hg and Su on hemato-

logical and assess the histomorphological alterations after exposure to Su, Hg and their combination. A total of 240 fingerlings of Nile tilapia (Oreochromis niloticus) were randomly distributed in four experimental tanks, including T1 (Control), T2 (Hg: 0.03 mg/L), T3 (Su: 0.6 µg/L), T4 (Su + Hg), with three replicates each. The result showed that single exposure to Su and Hg increases both hemoglobin (Hb) and blood glucose levels but in combined exposure of Su and Hg, the increase is significantly higher compared to the control group (Hb: 12.58 g/dL, glucose: 85.33 mg/dL). Moreover, combined exposure of Su + Hg alters physiological parameters of gill, liver and kidney. The number of cellular (twin, fusion, echinocyte, spindle, teardrop, and elongated shaped) and nuclear (bi-nuclei, nuclear buds, karyopyknosis, and notched nuclei) abnormalities in erythrocytes was higher in the Su and Hg-exposed group. In addition, the combined exposure significantly upregulated antioxidant genes, with a noticeable increase in SOD and CAT activities, suggesting elevated oxidative stress in fish. These findings indicate that such contamination threatens aquatic biodiversity and negatively affects food safety, nutritional value and aquaculture production. The observed alterations suggest that combined exposure to Su and Hg resulted in more severe adverse effects on Nile tilapia compared to individual treatments, highlighting the need for effective monitoring and management strategies to ensure healthy fish populations and safe aquatic food resources

PP019

PROBIOTICS AND SPIRULINA EFFECTIVELY COUNTERACT MERCURY-INDUCED GROWTH SUPPRESSION, HEMATOBIOCHEMICAL DISTURBANCES, INTESTINAL HISTOPATHOLOGY AND GH/IGF AXIS DYSREGULATION IN NILE TILAPIA (OREOCHROMIS NILOTICUS)

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Mercury (Hg) is a highly toxic, non-essential element that readily accumulates in fish via respiratory, dietary and integumentary pathways, causing severe physiological impairments. In Nile tilapia (Oreochromis niloticus), Hg exposure disrupts growth performance, intestinal architecture, hematobiochemical indices, and endocrine regulation through the GH/IGF axis. This study evaluated the protective efficacy of probiotics and dietary Spirulina against Hg-induced toxicity. A 42-day trial was conducted with 240 fingerlings randomly distributed into four triplicated treatments: control (no Hg, probiotics, or Spirulina), Hg (0.03 mg/L), Hg + probiotics (0.03 mg/L + 1 mL/L), and Hg + Spirulina (0.03 mg/L + 50 g/kg feed). Fish exposed to Hg exhibited reduced weight gain, specific growth rate, and survival rate, alongside elevated feed conversion ratio and impaired intestinal histology. Moreover, Hg toxicity altered hematobiochemical parameters, including glucose and hemoglobin levels, and suppressed GH/IGF axis markers of gh, igf-1, igf-2. In contrast, supplementation with probiotics and Spirulina significantly alleviated these adverse effects, improving growth performance, restoring intestinal functions, correcting hematobiochemical alterations and stabilizing GH/IGF axis regulation. Collectively, these findings highlight the eco-friendly potential of probiotics and Spirulina as effective bioremediation strategies to mitigate Hg-induced growth retardation and physiological dysfunctions in Nile tilapia

PP020

AI-DRIVEN SYNTHETIC LOGIC CIRCUITS: ENGINEERING MULTI-FLOOD RESILIENT "SMART RICE" FOR BANGLADESH'S CLIMATE FUTURE

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Bangladesh's agricultural landscape is increasingly threatened by two distinct, unpredictable flooding patterns: sudden flash floods and prolonged deep-water submersion. Current rice varieties typically carry either the Sub1A gene (quiescence strategy) or SNORKEL genes (escape strategy), but none can dynamically switch between both. The objective of this research is to use Generative AI to design a synthetic genetic "Smart Switch"- a biological logic circuit, that enables a single rice variety to sense flood depth in real-time and activate the appropriate survival mechanism. We employed Generative Adversarial Networks (GANs) and Deep Learning to engineer synthetic promoter sequences that function as a multi-input biological "AND-gate." The circuit is designed to integrate three environmental inputs: Ethylene accumulation, Hypoxia (low oxygen), and the Red:-Far-Red (R:FR) light ratio, which serves as a biological depth gauge. The circuit's performance was validated through "Digital Twin" kinetic modeling to simulate gene expression under varying flood durations. The proposed lab workflow involves CRISPR-Cas9 mediated insertion of this optimized circuit into high-yielding Bangladeshi varieties like BRRI dhan29. In silico simulations predict that the AI-designed circuit maintains 100% specificity, triggering the Sub1A pathway during shallow flash floods while suppressing elongation. Conversely, it switches to the SNORKEL pathway only when the R:FR ratio drops below a specific level, indicating deep water. This dual-response capability is predicted to increase crop survival rates by 40% in hydro-topographically diverse regions of Bangladesh compared to traditional mono-strategy varieties. This study demonstrates that coupling Artificial Intelligence with synthetic biology can transcend the limitations of conventional breeding. By creating "climate-intelligent" crops with built-in decision-making logic, this approach offers a robust, scalable solution for ensuring food security in the face of climate instability in the Bengal Delta.

PP021

IMPACTS OF SALINITY ON GROWTH, PHYSIOLOGY AND TISSUE INTEGRITY OF NILE TILAPIA: IMPLICATIONS FOR COASTAL AQUACULTURE UNDER CLIMATE CHANGE

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Climate change is responsible for salinity intrusion in coastal areas, which is significantly threatening the sustainability of aquaculture. This investigation focused on evaluating growth performance, proximate composition, blood morphology, and histopathological modifications in Nile tilapia (Oreochromis niloticus) exposed to varying salinity levels. Therefore, this trial was performed with a total of 300 fingerlings exposed to five different triplicated setups (0, 3, 6, 9, and 12 ppt), over 42 days. Salinity concentrations ranging from freshwater to 9 ppt provided favorable conditions, with notable improvements in growth metrics, weight gain (WG), specific growth rate (SGR), and feed conversion ratio (FCR) for fish. In terms of nutritional profile, Nile tilapia reared at intermediate salinities (3, 6, and 9 ppt) showed elevated protein contents. Furthermore, the glucose level was found to have declined significantly by 12 ppt in comparison with other treatments, while the hemoglobin levels showed an opposite trend, and the prevalence of erythrocytic anomalies (cellular and nuclear) was markedly elevated with increasing salinities. Mild histopathological anomalies in gills (hypertrophy of chloride cells, epithelial lifting, telangiectasia, and hyperplasia pillar system distortion), liver (hemorrhage, blood congestion, hypertrophy, the presence of melano-macrophage centers, and hemochromatosis), kidney (hemorrhage, renal shrinkage corpuscles, necrosis, glomerular damage, and occurrence of melano-macrophage centers) and intestine (beheading villi, shifting lamina propria, fusion of brush border, degeneration of columnar epithelium and vacuolization of submucosa) were diagnosed in 9 ppt but pronounced anomalies were found at higher salinity (12 ppt). In summary, the findings of the current investigation suggest that Nile tilapia is a viable candidate for farming in low-salinity environments, with salinity levels up to 10 ppt.

PP022

PROTECTIVE ROLES OF PROBIOTICS AND SPIRULINA IN ALLEVIATE MERCURY-INDUCED HEMATOLOGICAL, OXIDATIVE STRESS AND IMMUNE RESPONSES IN NILE TILAPIA (OREOCHROMIS NILOTICUS)

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Mercury (Hg) is one of the most hazardous heavy metals that poses serious threats to aquatic ecosystems and impairs fish health over the long term. An experiment was conducted to observe the role of probiotics and Spirulina in mitigating the adverse effects and damage in Nile tilapia (Oreochromis niloticus) due to mercury toxicity. The experiment was carried out with a total of 240 fingerlings (10.74 ± 1.23 g; 8.93 ± 0.43 cm) assigned in four treatments with three replicates for each, including T1 (control), T2 (Hg: 0.03 mg/L), T3 (Hg: 0.03 mg/L + probiotics: 1 ml/L), and T4 (Hg: 0.03 mg/L + Spirulina: 50g/kg feed) for 42 days. The results exhibited that exposure to Hg (T2) caused elevated hemoglobin (g/dL) and glucose levels (mg/dL); however, the use of probiotics and Spirulina reversed these effects in T3 (Hg + probiotics) and T4 (Hg + Spirulina).The frequencies of nuclear (notched nuclei, nuclear bud, and nuclear bridge) and cellular (spindle, elongated, and twin) abnormalities of erythrocytes increased in the Hg-exposed group (T2); however, these were significantly recovered after probiotic and Spirulina administration (T3 and T4). Mercury (Hg) exposure upregulated antioxidant genes (SOD and CAT) ($p < 0.05$), and downregulated immune (IL-1β, TNF-α, and IFN-γ) mRNA expressions compared with the control. Moreover, higher deformities (degeneration, hypertrophy, and hyperplasia) were observed in the gills of fish exposed to Hg, while water additives probiotics and dietary Spirulina effectively reduced these alterations. The findings of the present study suggest that water additives probiotics and dietary spirulina contribute significantly to the mitigate the negative physiological effects.

PP023

FUNCTIONAL RESTRUCTURING OF THE RICE RHIZOSPHERE MICROBIOME INDUCED BY BURKHOLDERIA CONTAMINANS NZ

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Burkholderia contaminans NZ bacterium, isolated from jute seed, has significant plant growth-promoting potentials including nitrogen fixation, siderophore production, Indole Acetic Acid (IAA) production with ACC deaminase activity. This study is to evaluate the efficiency of this bacterium at the field level through understanding the mechanisms by which it modulates the soil microbiome and support plant growth. For field application, a Polyvinylpyrrolidone (PVP) based liquid formulation was prepared. To compare the rice rhizosphere microbiome, the field was divided into three different plots: first one was untreated control, second plot treated with NZ biofertilizer and the third one was a combined chemical (50%)-microbial (50%) (CheNZ) treatment plot. The morphological parameters of rice, soil physicochemical parameters and the rhizosphere microbiome was analyzed via high depth shotgun metagenomics. CheNZ treated plants showed significantly improved tiller and panicle number, final yield as well as soil organic matter compared to other treatment plots. Metagenomic analysis exhibit stable taxonomic diversity with increased microbial functions related to nutrient recycling, signaling, glycan metabolism and plant-microbe interactions in CheNZ treatment. Metagenome assembled genome (MAG) reconstruction revealed abundant plant growth promoting traits including nitrogen and phosphorus metabolism, phytohormone biosynthesis, stress mitigation particularly in CheNZ treatment. These findings revealed that NZ effectively boosts crop growth synergistically with chemical fertilizer by maintaining regular microbial abundance while enhancing functionally critical microbial genomes. These provide insights into microbe mediated crop enrichment and validate B. contaminans NZ as an efficient bioinoculant capable of performing as a biofertilizer under field condition.

PP024

PROTECTIVE ROLE OF VITAMIN E AND SELENIUM AGAINST MERCURY-INDUCED TOXICITY IN NILE TILAPIA (ORECHROMIS NILOTOCUS)

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Globally, aquatic pollution is acknowledged as a major threat to environmental integrity, agricultural sustainability, and rural livelihood development. Heavy metals are one of the major contributors to aquatic pollution. Among these, mercury (Hg) is particularly toxic to fish, even at low concentrations. In addition to disrupting aquatic ecosystems, this kind of contamination poses serious hazards to animal production systems that depend on aquaculture resources. Vitamin E and selenium (Se) supplementation with diet may mitigate the toxic effects of mercury; hence, this study was implemented to evaluate the role of dietary Vitamin-E and Selenium (Se) nano particles in mitigating the adverse effects of Hg on Nile tilapia (Oreochromis niloticus) a species

with significant economic value in animal and agricultural production. This experiment was carried out with a total of 240 fingerlings of Nile tilapia (10.82 ± 1.05 g) with 3 replicates that were distributed in four treatments including control, Hg (0.03 mg/L), Hg + Vit-E (0.03 mg/L + 100 mg/kg feed), and Hg + Selenium (0.03 mg/L + 3 mg/kg) for six weeks. The results showed that growth performance of fish such as weight gain (WG), and specific growth rate (SGR) were enhanced and feed conversion ratio (FCR) was declined in dietary exposure with Hg, but the opposite results were recorded in Hg treated fish. However, histological examination of the intestinal parameters exhibited significant negative alterations and decrease immune related gene (IFN-α, IGF-I, IGF-II, GH, TNF-α) in the Hg-treated group. Whereas Vit-E and selenium-supplemented diet played a fundamental role in counteracting the changes caused by mercury toxicity. Overall, Vit-E and Selenium.

PP-025

AI-ENABLED EARLY WARNING OF ANTHRAX USING FLY-DERIVED DNA IN A ONE HEALTH APPROACH IN BANGLADESH

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Zoonotic diseases are a major concern within the One Health framework, particularly in endemic regions. Anthrax, caused by Bacillus anthracis, continues to threaten humans and livestock in Bangladesh, with recurrent outbreaks since 2010 in districts such as Meherpur, Sirajganj and Rangpur. Conventional diagnostics rely on invasive sampling and strict biosafety protocols, limiting rapid, large scale surveillance. Non-invasive environmental sampling offers a safer, scalable alternative, as flies frequently interact with contaminated environments and can carry pathogen DNA. This study combines fly derived invertebrate DNA (iDNA) with AI based predictive modeling to create a practical early warning system for anthrax, aiming to streamline surveillance by identifying high risk areas before outbreaks and enabling proactive One Health monitoring. A total of 150 flies were collected from 10 sites in Rangpur, including outbreak farms, a wet market and a control site, under strict biosecurity protocols. DNA was extracted and analyzed by qPCR targeting protective antigen (PA) and capsule (CapC) genes of B. anthracis. Historical outbreak data were compiled from national surveillance reports (2012–present). A conceptual AI framework integrated iDNA results (presence/absence and Ct values) with spatial and temporal patterns. Supervised machine learning models were used to analyze fly derived DNA with historical outbreak data, detect predictive patterns and generate high risk area maps. Preliminary analysis of 50 samples showed 23% tested positive for anthrax specific DNA, while control sites had no detection. Positive samples occurred across outbreak prone farms and the wet market, suggesting environmental persistence of B. anthracis. The data pipeline demonstrated feasibility of combining iDNA with historical outbreaks for predictive modeling. Fly derived iDNA, combined with AI based predictive models, provides a safe, non-invasive, scalable approach for zoonotic surveillance, enabling early warning by identifying high risk areas before outbreaks and supporting proactive, data driven One Health monitoring in Bangladesh.

PP0265

DEVELOPMENT AND VALIDATION OF A CLIMATE DEVICE FOR REAL-TIME DAIRY SHED MONITORING

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Heat stress is a global challenge in dairy production. In Bangladesh, this problem is especially important because hot-humid conditions can compromise cow comfort, alter physiological responses, and increase the need for timely shed management. Climate devices can support heat-stress surveillance, but imported systems may be expensive, difficult to service locally, and not always independently verified under Bangladesh conditions; English-only outputs may also reduce farmer usability. This study developed and validated three cloud-connected climate devices for monitoring dairy shed temperature, relative humidity (RH), temperature-humidity index (THI), and carbon dioxide (CO2). Each device used an integrated temperature-RH-CO2 sensor module marketed by the manufacturer as using NDIR-based CO2 sensing. Two devices used sensors purchased from Bangladeshi vendors at about USD 20 each, whereas one device used a directly imported higher-priced sensor costing about USD 70. Validation was conducted in a psychrometric chamber using six mid-lactation HF crossbred cows tested in two batches of three at THI 72, 77, and 82 for 3 days each, with 3-day acclimation before each chamber round and 7-day washout between rounds. The higher-priced device showed the best agreement with chamber-controller reference values, with mean absolute errors of 0.077 C for temperature, 0.765% for RH, 0.174 THI units for THI, and 18.2 ppm for CO2. Concordance correlation coefficients were 0.999, 0.864, 0.998, and 0.958, respectively. In contrast, the lower-priced devices showed larger errors, especially for RH and CO2. Physiological responses increased with heat load. Mean rectal temperature rose from 38.75 to 39.41 C, respiration rate from 49.70 to 78.89 breaths/min, and heart rate from 72.51 to 86.62 beats/min as THI increased from 72 to 82. These findings indicate that sensor grade and module quality substantially affect monitoring reliability and that the better-performing device offers stronger evidence for accurate, farmer-oriented dairy shed heat-stress surveillance under Bangladesh conditions.

PP027

DEVELOPMENT AND VALIDATION OF AN INTELLIGENT FEEDER FOR MONITORING FEEDING BEHAVIOR IN CROSSBRED DAIRY COWS UNDER DIFFERENT THI CONDITIONS

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Heat stress adversely affects feed intake and feeding behavior in dairy cattle, yet practical feeder-based systems for continuous behavioral monitoring are limited in Bangladesh. This study developed a cloud-connected intelligent feeder for real-time remote monitoring of feeding behavior and evaluated its performance in Holstein Friesian (HF) crossbred dairy cows exposed to different temperature-humidity index (THI) conditions

under controlled chamber settings. Three mid-lactation HF crossbred cows (average milk yield >12 L/day) were exposed to three Temperature-Humidity Index (THI) levels (72, 77, and 82) for 3 days each in a psychrometric chamber. Before each measurement phase, cows were acclimated to the chamber for 3 days under thermo-neutral conditions, and each experimental round was separated by a 7-day recovery period in a normal shed. Based on the results, mean dry matter intake declined from 10.96 ± 0.53 kg/day at THI 72 to 9.97 ± 0.44 kg/day at THI 77 and 9.03 ± 0.46 kg/day at THI 82. Mean feeding duration decreased from 194.1 to 145.5 min/day, feeder visits declined from 16.0 to 10.7 visits/day, and milk yield decreased from 13.26 to 12.43 L/day as THI increased from 72 to 82. Validation against manual dry matter intake showed excellent agreement. Feeder-recorded intake had a Pearson correlation of 0.995 and Lin's concordance correlation coefficient of 0.994. Mean bias was 0.014 kg DM/day, with 95% limits of agreement from −0.123 to 0.151 kg DM/day, mean absolute error of 0.055 kg DM/day, root mean square error of 0.067 kg DM/day, and mean absolute percentage error of 0.56%. These findings indicate that the intelligent feeder can accurately quantify intake and detect THI-associated changes in feeding behavior, supporting its potential as a precision-livestock tool for dairy management in Bangladesh.

PP028

PERFORMANCE OF AN AUTOMATED THI-BASED ROOF-RAIN AND COW-SPRINKLER SYSTEM FOR CROSSBRED DAIRY COWS IN AN OPEN-SIDED SHED

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Heat stress is a major challenge for dairy cattle maintained in open housing under hot-humid conditions. This study evaluated an automated temperature-humidity index (THI)-based cooling system at the Climate Smart Dairy Research Station, Gazipur Agricultural University during June 2025. Crossbred dairy cows producing 14-15 L milk/cow/day were housed in an open-sided shed. A 12-day switchback design was used, consisting of 3 days control, 3 days treatment, 3 days control, and 3 days treatment. Hourly shed temperature and relative humidity were recorded using a climate-sensing device that automatically calculated THI and transmitted data to a controller. The controller generated ON/OFF commands for an automated roof-rain and cow-sprinkler system based on preset thresholds, activating at THI 80 and stopping at THI 75 according to sensor-recorded shed microclimate. Rectal temperature, respiration rate, milk yield, and water use were also assessed. Across all treatment hours, mean THI declined from 81.80 before cooling to 77.77 after cooling. During controller-triggered hours, THI decreased from 82.92 to 77.60. Equivalent valve-open time averaged 2.92 h/day, and mean water use during treatment was 1,750.9 L/day. Mean rectal temperature was lower during treatment than control (38.63 vs 38.77°C), respiration rate was reduced (50.7 vs 57.9 breaths/min), and daily milk yield was higher (14.66 vs 14.29 L/cow/day). The findings indicate that the automated cooling system reduced sensor-recorded heat load and was associated with favorable physiological and productive responses under summer field conditions. This approach may offer a practical heat-abatement option for crossbred cows in open housing. Further study is needed to validate these findings through longer-term field observations and independent measurement of airflow, controller performance, and animal responses.

PP029

RESISTOME MAPPING AND CHARACTERIZATION OF MICROORGANISMS FROM LOW-ANTHROPOGENIC-IMPACT HIGHLAND AQUATIC ENVIRONMENTS USING INTEGRATED CULTURE BASED AND MULTI-OMICS APPROACHES

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Antimicrobial resistance (AMR) is a major global health threat, exacerbated in Bangladesh by high population density and antibiotic misuse. While most studies focus on urban and industrial areas, limited research exists on low-impact regions like the Chittagong Hill Tracts (CHT). This study aimed to explore microbial diversity and AMR in these relatively pristine environments using culture-based and multi-omics approaches. Water samples from 10 sites in Khagrachari and Bandarban were collected. Shotgun metagenomic sequencing (Illumina MiSeq) was used for microbial profiling and AMR gene detection, alongside culture-based identification of Gram-negative bacteria. Antibiotic susceptibility was tested using the Kirby-Bauer method and VITEK 2. Selected strains underwent whole-genome sequencing (WGS) for detailed analysis. A multi-layered analysis revealed a complex antimicrobial landscape. Metagenomics showed dominance of Proteobacteria and Actinobacteria (~75%), with regional variation (Novosphingobium in Bandarban; Bradyrhizobium in Khagrachari) and a core microbiota including Pseudomonas, Caulobacter, and Mycobacterium. A total of 95 AMR genes were detected, mainly beta-lactam (20–25%) and trimethoprim (15–20%) resistance. Culture-based analysis identified 27 isolates, with Enterobacter cloacae dominating Bandarban, while Khagrachari showed greater diversity (e.g., Klebsiella, Serratia, Acinetobacter). High resistance to Ampicillin (91%) and Nitrofurantoin (83%) was observed, while Imipenem remained fully effective. WGS confirmed pathogenic strains (Klebsiella variicola ST347, Acinetobacter baumannii ST2887) harboring multiple resistance and virulence genes. Resistance genes were primarily chromosomal, associated with mobile genetic elements (IS, transposons), with no plasmids detected. This study demonstrates that even low-anthropogenic-impact highland aquatic environments harbor a substantial and diverse resistome. The integration of community-level metagenomics with isolate-level whole-genome sequencing reveals that while these environments appear pristine, they serve as natural reservoirs for clinically relevant resistance genes. These results establish a critical baseline for environmental AMR in the Chittagong Hill Tracts and emphasize the importance of monitoring remote ecosystems to understand the global evolution and dissemination of antimicrobial resistance.

PP030

CRISPR/CAS9 BASED KNOCKOUT OF HTA1 GENE TO IMPROVE HEAT TOLERANCE IN RICE (ORYZA SATIVA)

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Rice (Oryza sativa), a member of the Poaceae family, grows optimally at 25-30 °C and feeds more than half of the world’s population. However, rice is highly sensitive to heat stress, posing a serious threat to global food

security. GDSL lipases are enzymes characterized by a conserved N-terminal GDSL motif (GxSxxxxG), and the rice genome contains at least 113 GDSL lipase genes. HTA1, a rice GDSL lipase gene, negatively regulates abiotic stress responses; its suppression enhances heat tolerance by increasing survival, reducing reactive oxygen species (ROS), and boosting antioxidant enzyme activity under high temperatures. In this study, CRISPR/Cas9 technology was used to knock out the HTA1 gene to improve rice heat tolerance. To achieve this, sgRNA targeting HTA1 was designed using CRISPR-P 2.0, cloned into the pRGEB32 vector, and introduced into heat-sensitive rice varieties via Agrobacterium-mediated in planta transformation. Successful cloning was confirmed by colony and plasmid PCR. Currently, edited plants are under growth for phylogenetic and physiological screening. Phylogenetic analysis of the 115 members of GDSL lipase family was conducted to investigate their evolutionary relationships. This non-transgenic genome-editing approach may enhance rice thermo tolerance and support food security.

PP031

NATIVE PROBIOTICS AS BIO-ALTERNATIVES TO ANTIBIOTICS: ENHANCING PRODUCTIVITY IN FRESHWATER PRAWN (MACROBRACHIUM ROSENBERGII) AQUACULTURE

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The giant freshwater prawn (Macrobrachium rosenbergii) is an economically vital species, accounting for nearly 25% of Bangladesh's fisheries export earnings. Despite its importance, the industry in southwestern Bangladesh faces significant losses due to stunted growth and frequent viral and bacterial outbreaks. This study aimed to isolate and characterize native probiotic strains as sustainable, antibiotic-free alternatives to enhance growth, immunity, and disease resistance in M. rosenbergii. Five indigenous bacterial strains were isolated from shrimp "gher" soil and evaluated through comprehensive biochemical assays including enzymatic activity (protease, lipase, amylase) and bile salt tolerance alongside in vitro pathogen inhibition tests. All isolates exhibited robust enzymatic profiles and significant antagonistic activity against common pathogens, including Vibrio sp., Aeromonas veronii, and Aeromonas enteropelogenes. 16S rRNA gene sequencing identified the strains as Bacillus amyloliquefaciens GIFPSR-101, B. paramycoides GIFPSR-103, B. cereus GIFPSR-111, Priestia aryabhattai GIFPSR-118, and B. cereus GIFPSR-121. A 60-day feeding trial was conducted using prawn juveniles (initial weight ≈1.7 g) across six experimental groups. Probiotic supplementation significantly ($p < 0.05$) enhanced growth and survival compared to control. The highest weight gains were observed in groups treated with B. paramycoides (3.11 g) and B. cereus GIFPSR-111 (2.99 g), while the control group showed minimal gain (0.7 g). Immunological assays revealed significantly elevated phenoloxidase (PO) and prophenoloxidase (proPO) activity in probiotic-treated groups, alongside altered superoxide dismutase (SOD) levels, suggesting enhanced immune competency and reduced oxidative stress. These findings demonstrate that native probiotics, particularly B. cereus GIFPSR-111, are highly effective in boosting the productivity and health of M. rosenbergii, offering an eco-friendly strategy for sustainable aquaculture in Bangladesh.

PP032

EVALUATION OF SEED GERMINATION CAPACITY AND SEEDLING BEHAVIOUR IN DIVERSE CARROT (DAUCUS CAROTA L.) GERMPLASM

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An experiment was conducted to evaluate seed germination capacity and early seedling behaviour of 50 carrot germplasm at Postgraduate Laboratory, Department of Horticulture, Bangladesh Agricultural University, Mymensingh during August–September 2025. The single factor experiment was laid out in Completely Randomized Design with two replications. Among the 50 germplasm Jiyang, Acrya, Spring maki, PI 652143, Pusa Kesar, Koyogo Koyo No. 2 and Nantes Supreme demonstrate 100% germination while PI 226043, PI 249535, PI 261650, PI 279776, PI 294090, PI 289700, PI 232073, PI 341204, PI 419084 and PI 451759 unable to germinate. Among the germinated entries, R5 demonstrated superior performance regarding seedling radical length (5.63 cm), plumule length (4.11 cm), seedling height (9.74 cm) and leaves seedling–1 (4.0) at the final stage of data recording (19 days after seed placement in the petridish) followed by Autumn King and Honku (Red). Overall results indicated that the genotypes Jiyang, Acrya and Spring maki followed by Pusa Kesar, Koyogo Koyo No. 2 and Nantes Supreme are highly promising for rapid and uniform germination while R5, Autumn King 2 and Honku (Red) are particularly suitable for vigorous seedling growth which may be recommended for use in carrot improvement programs and quality seedling production.

PP033

GENOME MINING OF ENDOPHYTIC BACILLUS VELEZENSIS REVEALS ANTIFUNGAL ARSENALS AGAINST CORYNESPORA CASSIICOLA CAUSING TARGET LEAF SPOT OF CHIA

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Chia (Salvia hispanica L.) is an emerging high-value crop in Bangladesh. In March 2024, severe target leaf spot symptoms of chia were observed at Bangladesh Agricultural University, with field incidence of 23–47%. Morphological traits and ITS/TEF-1α sequence analyses identified the causal agent as Corynespora cassiicola, representing the first report of this disease on chia in Bangladesh. Employing antagonistic microorganisms represents an environmentally friendly and cost-effective approach to pathogen management. This study aimed to apply AI-oriented genome-guided analysis of endophytic B. velezensis to prioritize antimicrobial determinants supporting biocontrol. From 200 endophytic bacterial isolates, two antagonistic strains (BGERD-B1 and BGERD-B6) were selected and identified as Bacillus velezensis. Whole-genome sequencing of the selected strains was performed, followed by comprehensive computational analyses to identify biosynthetic gene

clusters, antimicrobial peptides, carbohydrate-active enzymes, and functional genes associated with antifungal activity, stress tolerance, and plant growth promotion. The selected B. velezensis strains significantly reduced disease severity by 80–90% under controlled conditions. Genomes encode multiple biosynthetic gene clusters, including those associated with known antifungal compounds such as lipopeptides and polyketides, alongside several putatively novel clusters. Additional features included bacteriocin-associated regions and enzymes involved in fungal cell wall degradation were identified. The genomes also harbored predicted functional genes associated with plant-beneficial traits, including chemotaxis, motility, biofilm formation, phytohormone production, nitrogen fixation, phosphate solubilization, and osmotic stress tolerance. Integrated genomic and predicted metabolomic insights demonstrate that B. velezensis possesses a diverse repertoire of bioactive compounds driving strong antifungal activity against C. cassiicola. Collectively, the findings support the development of these strains as promising biopesticide candidates for sustainable management of chia target leaf spot.

PP034

AI-DRIVEN GENOME MINING OF BACILLUS VELEZENSIS S-LA5 REVEALS BROAD-SPECTRUM ANTIFUNGAL AND PLANT GROWTH-PROMOTING LIPOPEPTIDES

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Biotechnology and sustainable strategies are increasingly recognized as essential pathways for ensuring global food security under rising demand and environmental challenges. Plant growth-promoting bacteria (PGPB) provide eco-friendly alternatives to chemical inputs, offering benefits such as enhanced crop productivity, improved soil fertility, and increased tolerance to biotic and abiotic stresses. In this study, Bacillus velezensis S-LA5, isolated from the anthosphere of the medicinal plant Leucas aspera, was evaluated for its antifungal potential against several economically important phytopathogens, including Magnaporthe oryzae triticum, M. oryzae oryzae, Bipolaris sorokiniana, Sclerotium rolfsii, Colletotrichum capsici, and Phytophthora infestans. In vitro dual plate assays revealed strong inhibitory activity against fungal growth and conidial germination demonstrating its capacity to suppress pathogen development. Whole-genome sequencing combined with AI-driven genomic insights uncovered diverse biosynthetic gene clusters responsible for antifungal metabolites and plant growth-promoting traits, with particular emphasis on unique lipopeptide pathways that may represent novel antifungal compounds. Seedling bioassays in wheat confirmed the ability of B. velezensis S-LA5 to stimulate plant growth while significantly reducing wheat blast disease severity and incidence compared to untreated controls. The integration of genomic insights with experimental validation highlights the dual role of this strain as both a growth promoter and biocontrol agent. These findings underscore its biotechnological promise for the development of eco-friendly strategies to manage wheat blast and other devastating crop diseases. By bridging genomic discovery with practical application, this study provides a foundation for future exploration of B. velezensis S-LA5 in commercial biocontrol formulations, contributing to sustainable crop protection and improved resource management within the broader framework of natural resource conservation and environmental sustainability

PP035

GENOTYPE-ENVIRONMENT INTERACTION STUDIES AND MOLECULAR CHARACTERIZATION TO IDENTIFY HIGH YIELDING AND UNIQUE STABLE BARLEY GENOTYPE

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Barley (Hordeum vulgaris L.) is a nutrient-rich grain, but an exotic item in Bangladesh. The major aim of the study was to analyze high yielding stable genotypes by genotypes-environment interactions (GEI) and to observe the unique genotype by employing molecular variations among them. The GEI was investigated using different methodologies viz. parametric and non-parametric stability statistics, MGIDI, AMMI, and GGE etc. using nine barley genotypes comprised of six exotic lines and three BARI released varieties. The study was conducted in a randomized complete block design across three locations (Dinajpur, Rangpur and Panchagarh) during the rabi season of 2022-2023. Various parametric and nonparametric stability statistics were calculated using a web-based STABILITYSOFT program. Based on the analysis, EEB_450, BARI Barley-7 and EEB_91 identified as superior and high yielding genotypes. The additive effects analysis of the additive main effects and multiplicative interaction (AMMI) model revealed significant effects of genotype, environment, and GEI on number of grains per spike (NGPS), yield per plant (YPP) and yield per plot (YPPLOT). EEB_450 and EEB_91 for NGPS, EEB_18 and EEB_152 for YPP, and EEB_450 and EEB_91 for YPPLOT emerged as stable genotypes with optimal performance according to the AMMI model. The likelihood ratio test indicated significant effects of genotype and GEI all studied traits. Regarding NGPS, YPP and YPPLOT, EEB_450, BARI Barley-7 and BARI Barley-9 had high best linear unbiased prediction (BLUP) value and were identified as suitable genotypes. The GGE biplot method proved useful in determining the most favorable location for specific genotypes. Among three experimental locations, Panchagarh was identified as the superior environment for barley cultivation with EEB_450 being the top performing genotype considering all traits. Using the multi-trait genotype ideotype distance index (MGIDI), EEB_450, BARI Barley-7 and BARI Barley-9 were deemed the most ideal genotypes. Analysis of genetic variation using SSR markers, the genotype EEB_450 revealed phenotypically stable and showed variations with the BARI released check varieties. Therefore, EEB_450 is recommended as a superior performing genotype in three locations and can be released as a variety in Bangladesh.

PP036

GENETIC VARIABILITY AND DIVERSITY OF PIGMENTED BORO RICE (ORYZA SATIVA L.) GENOTYPES THROUGH MORPHO-NUTRITIONAL AND MOLECULAR APPROACHES

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The prevalence of undernutrition is more common especially among children and women in Bangladesh. Considering this national issue, the major aim of the experiment was to observe the genetic variation and diversity using morpho-nutritional and molecular screening in boro rice (Oryza sativa L.). The experiment was conducted in a randomized complete block design (RCBD) with three replications at the research field and laboratory experiment was carried out in the molecular breeding laboratory of the Department of Genetics and Plant Breeding inHajee Mohammad Danesh Science and Technology University, Dinajpur. The thirty-six local landraces and three BRRI released varieties of rice were evaluated during the period from December 2021 to May 2022. Significant differences were found among the genotypes for all the traits under study. Several genotypes exhibited superior performance in both yield and nutritional characteristics, particularly concerning zinc, iron, phenolic, and flavonoid concentrations, as well as antioxidant activity. High heritability accompanied by high genetic advance were observed among the significant agronomic and nutritional traits, thereby suggesting strong genetic control. Correlation and regression analyses revealed that grain yield was positively associated with chlorophyll content, tiller number, grain weight, panicle traits, and zinc content. Cluster and principal component analyses demonstrated substantial genetic diversity, grouping genotypes into distinct clusters, with selected groups showing superior nutritional and agronomic performance. In molecular study, 63 highly polymorphic alleles were identified using 13 SSR markers and population structure analysis divided the genotypes into two primary groups. Considering overall morphological and molecular study, the genotypes Uliaboro, Aushaboro, Tepiboro2, Jamirboro, Purple1, Purple2, BRRI dhan28, BRRI dhan29 and BRRI dhan84 could be used as parents in hybridization program of high yielding and nutrient rich variety development in the country.

PP037

COMBINED EFFECTS OF MICROPLASTIC AND MERCURY ON GROWTH, HEMATOLOGY, TISSUE MORPHOLOGY, GH/IGF AXIS AND ANTIOXIDANT-IMMUNE RESPONSES IN NILE TILAPI

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Microplastics (MPs) and heavy metal mercury (Hg) have drawn global surveillance as major contaminants due to their toxic effects on aquatic organisms. The individual effects of both contaminants have been extensively characterized; however, their co exposure effects remain insufficiently explored. As aquatic o rganism s

areicreasingly exposed to multiple pollutants simultaneously in natural environments, this investigation explored the combined effects of polyamide microplastic (PA-MP) and mercury (Hg) on Nile tilapia (Oreochromis niloticus) fingerlings, focusing on survival, growth, hematological balance, tissue structure, GH/IGF axis regulation, and immune-antioxidant responses. Over a 42 day trial, 240 Nile tilapia fingerlings were allocated into four triplicated treatments: control (no PA MP or Hg), PA MP (10 mg/L), Hg (0.03 mg/L), and PA MP + Hg (10 mg/L + 0.03 mg/L), with 20 fingerlings per tank. The co-exposure group showed increased MP accumulation and mortality; suppressed growth indicators; substantial shifts in blood physiology, including elevated glucose (126.83 ± 2.40 mg/dL) and lowered hemoglobin (9.45 ± 0.85 g/dL), along with higher cellular and nuclear abnormalities. The histo-architectural assessment identified severe structural deformities in gills, intestine, and liver, of co-exposed fish compared to control and individual contaminants. At the transcriptional level, expression of growth hormone-secreting gene (gh) in the pituitary and insulin-like growth factors (igf-1 and igf-2) in the liver showed a significant downregulation under co-exposure treatment. Moreover, co-exposure to PA-MP and Hg induced hepatic oxidative damage by affecting antioxidant defense, as evidenced by altered activity of superoxide dismutase (sod) and catalase (cat), and simultaneously modulated immune responses by significantly upregulating interferon-γ (ifn-γ) and tumor necrosis factor-α (tnf-α) while downregulating interleukin-1β (il-1β), indicating an oxidative-inflammatory response. These outcomes collectively underscore that MP and Hg co-exposure aggravates both systemic and molecular impairments in Nile tilapia, resulting in weakened molecular responses, impaired physiological functions, and decreased survivability.

PP038

BIOCONTROL POTENTIAL OF PSEUDOMONAS AERUGINOSA PA_RV FROM WHEAT GENOTYPE S-615 CARRYING BLAST RESISTANCE GENE RMG8

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Fungal phytopathogens represent a major constraint to global crop production, with Magnaporthe oryzae Triticum (MoT), the causal agent of wheat blast, being particularly destructive. Conventional fungicide-based management is constrained by limited efficacy, environmental toxicity, and pathogen resistance. This study evaluated the biocontrol potential and plant growth-promoting properties of Pseudomonas aeruginosa strain PA_RV (GenBank accession JBTONL000000000), a seed endophyte of wheat genotype harboring the Rmg8 gene, against MoT, Bipolaris sorokiniana, Colletotrichum spp., Fusarium graminearum, and Corynespora cassiicola. Antifungal activity was assessed via dual culture, volatile organic compound (VOC), and seedling biocontrol assays. Phosphate solubilization and siderophore production were evaluated on Pikovskaya and chrome azurol S (CAS) agar, respectively. Growth promotion was quantified through hydroponic seedling assays. Whole-genome sequencing using Oxford Nanopore Technology (ONT) and coupled with GC–MS metabolomic profiling revealed strain PA_RV's genetic basis for antifungal activity, growth promotion, and metabolite production. PA_RV inhibited hyphal development by 46.3-79.8% in dual culture and by 58.6-82.5% through VOC-mediated antagonism, with MoT exhibiting the highest susceptibility. In seedling biocontrol assays, disease severity was reduced by 37.6-41.3%, with maximal suppression achieved via cell suspension

foliar spray. Bacterium-primed seedlings in hydroponic assays showed significantly enhanced germination rates and increased fresh and dry biomass. The strain demonstrated efficient phosphate solubilization and siderophore production. Genome mining identified BGCs encoding phenazines (pyocyanin, phenazine-1-carboxamide), siderophores (pyoverdine, pyochelin), hydrogen cyanide, nonribosomal peptide synthetase (NRPS)-derived metabolites. GC-MS analysis of PA_RV-MoT co-culture extracts confirmed the production of phenazine-1-carboxamide, 2,4-di-tert-butylphenol, diketopiperazines (cyclic dipeptides), and induced systemic resistance (ISR)-associated compounds including 2,3-butanediol. Notably, the genome lacked major virulence determinants, including exoS, exoU, toxA, and ExlA. Pseudomonas aeruginosa PA_RV exhibits broad-spectrum antifungal activity and multifunctional plant growth-promoting traits, supported by convergent genomic, metabolomic, and in vitro biocontrol assays. The absence of key virulence determinants supports its candidacy as a biocontrol agent, though field validation and biosafety evaluation remain essential.

PP039

AI-DRIVEN GENOMIC AND POST-GENOMIC INSIGHTS INTO WHEAT SEED-ENDOPHYTIC PROBIOTIC BACILLI WITH MULTIFUNCTIONAL PLANT-BENEFICIAL TRAITS

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Wheat (Triticum aestivum) seeds harbor endophytic bacteria with significant potential for sustainable agriculture. Among them, Bacillus spp. are known for multifunctional plant probiotic traits (PPTs), including nutrient acquisition, phytohormone production, and suppression of phytopathogens. This study aimed to discover new plant seed-endophytic probiotics bacilli and their functional bases using AI and machine-learning bases genomic and post-genomic analyses. Whole-genome-level sequencing, functional annotation and genome mining were performed using Oxford nanopore sequencer followed by advanced bioinformatic tools to identify PPT-associated genes and biosynthetic gene clusters (BGCs). Post-genomic analysis included functional pathway normalization to assess trait enrichment across isolates. A substantial repertoire of PPT-associated genes was identified, with total counts of 2294 (BaGV), 2489 (BsR6), 2485 (BsR7), and 2489 (BsR8). Indirect plant-beneficial mechanisms dominated, with 1538 genes in BaGV and ~1712–1716 genes in Bacillus subtiltis (Bs) strains. NRPS biosynthetic gene clusters (~12–15 per strain) containing key genes such as srfA (surfactin), ituD (iturin), and fenA (fengycin), along with siderophore genes (dhb) involved in bacillibactin production were consistently detected. IAA biosynthesis genes (~8–12 per strain), phosphate solubilization, and iron acquisition pathways were also identified. Functional enrichment analysis showed that osmotic stress neutralization was the most abundant trait (BaGV: ~2.38; Bs strains: ~2.75), followed by motility and chemotaxis (~1.10–1.12), surface attachment (~0.54–0.55), and secretion systems (~0.38), indicating strong colonization and adaptability. Siderophore (~0.56–0.66), phytohormone (IAA ~0.25; cytokinin ~0.34), vitamin (~1.35), and volatile compound (~0.56) pathways further support plant growth-promoting potential. Wheat seed-endophytic probiotic bacilli exhibit extensive genomic and functional potential for multifunctional plant-beneficial activities, highlighting their promise as next-generation bioinoculants for sustainable crop production.

PP040

AI-DRIVEN TRANSCRIPTOMIC ANALYSES REVEAL KEY GENES INVOLVED IN DROUGHT AND HEAT STRESS RESPONSES IN WHEAT

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Wheat is a major global cereal crop and the second most important staple in Bangladesh. However, its productivity is severely constrained by abiotic stresses, particularly drought and heat, which often co-occur and intensify yield loss. This study aimed to identify key genes involved in the molecular crosstalk between drought and heat stress and to elucidate the role of defense and priming-related genes in stress adaptation. Wheat RNA-seq reads from stress and control samples were quality-checked using FastQC, pseudo-aligned with Kallisto, analyzed in R for differential expression, and interpreted via heatmaps, GO enrichment, and crosstalk analysis. A total of 291 upregulated and 343 downregulated genes were identified, indicating extensive transcriptional reprogramming under stress conditions. Upregulated genes were primarily associated with antioxidant defense, protein folding, and cell wall modification, whereas downregulated genes were linked to photosynthesis and growth-related processes, suggesting a defense–growth trade-off. Enrichment analysis revealed significant involvement of stress signaling, plant–pathogen interaction, and hormonal pathways. Six key drought-responsive candidate genes were identified as potential targets for crop improvement. This study provides insights into the complex molecular mechanisms underlying combined drought and heat stress responses in wheat. The identified candidate genes offer promising avenues for developing climate-resilient wheat varieties through molecular breeding strategies

PP041

MOLECULAR DYNAMICS SIMULATION OF TYPE III METALLOTHIONEIN FROM HALOPHYTIC WILD RICE, O. COARCTATA AND SALT-SENSITIVE CULTIVATED RICE, O. SATIVA

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Salinity is a major abiotic stress limiting rice productivity. Metallothioneins (MTs), particularly Type III MTs (MT3), are cysteine-rich proteins that confer stress tolerance through Zn^{2+} chelation, metal homeostasis, and reactive oxygen species scavenging. While human MTs are structurally well characterized, plant MTs lack resolved apo- and holo-structures. The halophytic wild rice Oryza coarctata exhibits superior salt olerance compared to cultivated Oryza sativa. Previous molecular cloning studies have shown that O. coarctata MT (OcMT3) homologous to OsMT3a (Oryza sativa) confers enhanced salt tolerance relative to its cultivated counterpart, but the mechanistic basis remains unclear. A comprehensive in-silico analysis was performed integrating sequence, evolutionary, and structural approaches. Multiple sequence alignment and phylogenetic analysis were conducted to assess conservation and divergence between OcMT3 and OsMT3a and related plant MTs. Physicochemical properties and conserved cysteine motifs were examined. Three-dimensional models were generated and validated using Alphafold 3. Apo- and Zn^{2+}-bound (1–4 ions) forms were simulated to represent different metallation states. All-atom molecular dynamics simulations were performed using GROMACS under normal and 30 mM NaCl stress conditions. Structural stability and dynamics were evaluated using RMSD, RMSF, radius of gyration (Rg), and solvent-accessible surface area (SASA), along with hydrogen bonding, electrostatic surface potential, and Zn^{2+} coordination analysis. Sequence and phylogenetic analyses revealed conserved cysteine-rich motifs alongside key variations that may influence metal-binding behavior. OcMT3 displayed greater structural stability, reduced flexibility, and improved compactness compared to OsMT3a, particularly under salt stress and higher Zn^{2+} occupancy. Enhanced hydrogen bonding and favorable electrostatic environments supported stronger Zn^{2+} coordination in OcMT3. This integrative study links sequence divergence, evolutionary context, and structural dynamics to explain the superior performance of OcMT3. Its enhanced Zn^{2+}-chelating capacity and stability likely underlie improved salt tolerance, supporting its potential for engineering stress-resilient rice varieties and guiding future experimental validation.

PP042

HYDROBIOLOGICAL STUDY OF MANKHOLA HAOR AT KISHOREGANJ DISTRICT WITH SPECIAL EMPHASIS ON CLIMATE CHANGE AND PHYTOPLANKTON

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Mankhola Haor, a well-known wetland in Austagram Upazila, Kishoreganj, is the subject of the current study. The current study aims to investigate the relationship between the physico-chemical characteristics of the waterbody and the effects of climate change on phytoplankton communities. The present investigation was carried out from February 2024 to March 2025 on three selected sampling station on three different seasons. To assess the hydrobiology status of the water 33 physico-chemical and 3 biological parameters were measured. The following findings were made in order to examine the effects of climate change over the past 30 years: there has been a notable decrease in the area covered by bodies of water, which has eventually been replaced by various types of flora. Therefore, the growing vegetation may indicate a trend toward reforestation or natural regeneration in that area, which could have a variety of ecological and environmental ramifications.

PP043

ONE-STEP FABRICATION OF AUNP-ITO COMPOSITE AS A BIFUNCTIONAL ELECTROCATALYST FOR 4-NITROPHENOL DETECTION AND OXYGEN EVOLUTION REACTION: MECHANISTIC STUDY AND DFT INSIGHTS

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Considering the adverse effects of 4-nitrophenol and the global energy crisis, an effective electrocatalyst is necessary. To date, the existing catalyst has several drawbacks, including a high detection limit, a narrow dynamic range, and high overpotential. To overcome these challenges, our study aims to develop a new efficient electrocatalyst for the detection of 4-nitrophenol and for the oxygen evolution reaction (OER). To fulfill this demand, we synthesized a gold nanoparticle indium tin oxide composite (AuNP-ITO) for the detection of 4-nitrophenol and for OER. It is synthesized by a simple wet chemical method carried out at 70°C. The AuNP-ITO composite was characterized using FESEM, TEM, and the SAED technique. The AuNP-ITO was drop-cast onto a glassy carbon electrode (GCE) for 4-nitrophenol and nickel foam (NF) for OER. Electrochemical performance was evaluated for both 4-nitrophenol detection in 0.1 M PBS and for OER in 1 M KOH. The structure and composition of AuNP-ITO composite were characterized by the FESEM and TEM techniques. The electrocatalyst shows a very low detection limit of 50.45pM with a wide linear range of 1nM to 2000µM for 4-nitrophenol detection. The AuNPs-ITO on NF also shows a low overpotential of 329 mV at 20mA/cm2 at 1 M KOH for OER with high stability after 10h. DFT analysis reveals that the composite has a lower HOMO-LUMO gap than that of the single compound. Excellent recovery, high reproducibility, lower overpotential, and ultra-stability confirmed the reliability of these electrocatalysts in the practical assessment for 4-nitrophenol and for OER. The AuNPs-ITO/GCE sensor offers a cost-effective, simple, and stable platform for 4-nitrophenol detection with high sensitivity and selectivity. Similarly, low overpotential and high stability toward OER make it a promising bifunctional electrocatalyst for 4-nitrophenol and OER.

PP044

REMOVAL OF CIPROFLOXACIN FROM AQUEOUS SOLUTION USING GO/PVA /CALCIUM ALGINATE COMPOSITE BEADS AS AN ABSORBENT

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We prepared an eco-friendly graphene oxide (GO)- incorporated composite bead adsorbent, comprising sodium alginate (SA) and polyvinyl alcohol (PVA), via in situ cross-linking between GO and SA using calcium chloride as a cross-linking reagent, which is uniformly distributed within the PVA matrix. Fourier transform infrared (FTIR) spectroscopy analysis of the functional groups confirms the successful preparation of the composite. The batch

process is used to treat aqeous solution containing CPX. The composition adsorbent chrematistic is analyzed using moisture content, ash content, point zero charge (pHzpc), pore volume, ion exchange capacity, specific surface area, oxidative stability, thermogravimetric analysis (TGA), X-ray diffraction (XRD), scanning electron microscope (SEM), energy-dispersive spectroscopy (EDS), and X-ray spectroscopy analysis. Point zero charge, specific surface area, moisture content, ash content, pore volume, ion exchange capacity, and oxidative stability of the adsorbent were 7.07, 1991 mg/g, 11.72%, 78.92%, 1.7%, 0.7857%, and 96.45%, respectively. Adsorption experiments revealed that the beads achieved a maximum adsorption capacity under optimal conditions and that the highest removal efficiency is 89.82%. Among the four linear and non-linear isotherms, the Langmuir adsorption isotherm model indicates that the adsorption occurred by forming a monolayer. Thermodynamic studies of the adsorption indicate that the adsorption process is a spontaneous and exothermic process. The kinetics studied indicate that the adsorption process is pseudo-second-order. These findings highlight the GO/PVA/CA composite beads as promising, economical, and eco-friendly adsorbents for the removal of pharmaceutical contaminants (especially CPX) from wastewater.

PP045

SUSTAINABLE RGO–RICE HUSK ACTIVATED CARBON COMPOSITE MODIFIED GLASSY CARBON ELECTRODE FOR HIGHLY SENSITIVE ELECTROCHEMICAL DETECTION OF PARACETAMOL

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Paracetamol is a widely used analgesic and antipyretic drug, but excessive intake can cause serious liver damage. Therefore, sensitive detection of paracetamol is important. Conventional methods such as HPLC and UV–Vis spectroscopy are effective but require expensive instruments and lengthy sample preparation. To overcome these limitations, the development of sensitive and cost-effective electrochemical sensors has gained significant attention. In this work, an efficient electrocatalytic composite of reduced graphene oxide and rice husk activated carbon (rGO–RHAC) was synthesized and used to modify a glassy carbon electrode (GCE) for the electrochemical detection of paracetamol. In this study, reduce graphene oxide and rice husk activated carbon (rGO_RHAC) composite film was fabricated on a glassy carbon electrode using an electrochemical method. Graphene oxide (GO) was first deposited on GCE and then reduced to rGO, followed by dropcasting RHAC to form the rGO-RHAC film. The resulting rGO_RHAC/GCE sensor was evaluated for paracetamol detection by cyclic voltammetry (CV) in 0.1 M PBS. The sensor's selectivity was tested against common interfering agents, and its applicability was assessed using real water samples. CV and EIS techniques in 5mM K3[Fe(CN)6] solution confirm the formation of rGO_RHAC composite. The modified sensor exhibited excellent electrocatalytic activity towards paracetamol oxidation, with a detection limit of only 0.51μM with a wide linear range 1μM to 2000μM. The enhanced performance is attributed to the synergistic effect between the high conductivity of rGO and the porous adsorption capability of RHAC. The rGO-RHAC/GCE sensor offers a cost-effective, simple, and stable platform for paracetamol detection. Its high sensitivity, selectivity, and applicability in real sample analysis make it a promising candidate for paracetamol monitoring. Further optimization could enhance its use in portable paracetamol sensors.

PP046

A NOVEL ELECTROCHEMICAL SENSOR BASED ON AMINE FUNCTIONALIZED GRAPHENE OXIDE/TUNGSTEN OXIDE NANOCOMPOSITE MODIFIED GLASSY CARBON ELECTRODE FOR THE DETECTION OF 4-AMINOPHENOL

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4-Aminophenol (4-AP) is a crucial building block for pharmaceuticals and colorants, but it has acute and chronic health risks, especially its harmful effects on human blood and kidneys. Herein, a novel electrochemical sensor was designed based on a facile, fast and sensitive electrochemical method to detect 4-aminophenol by amine functionalized graphene oxide-tungsten oxide (NH2-GO/WO3). A simple drop-casting method was utilized to fabricate the sensor. The synthesized NH2-GO/WO3 was characterized by X-ray diffraction (XRD), scanning electron microscopy (SEM), Fourier transform infrared spectroscopy (FTIR) and energy-dispersive X-ray spectroscopy (EDS). Under optimized conditions e.g. scan rate 50 mV/s, phosphate buffer (pH 7) as supporting electrolyte and potential window from -0.2 to 0.6 V, the prepared sensor showed excellent response for 4-AP. The developed sensor based on NH2-GO/WO3 exhibited a linear range from 5 μ mol L-1 to 800 μ mol L-1, a detection limit of 7x102 n mol L-1, and limit of quantification of 2.24 x103 n mol L-1. Scan rate analysis was performed to determine the charge transfer coefficient and Tafel slope. The practical application of NH2-GO/WO3 was evaluated in river water, orange juice and pharmaceutical samples. The fabricated sensor displayed remarkable stability and sensitivity, making it highly effective for monitoring 4-AP without interference. A low RSD value suggests the practical use of NH2-GO/WO3 based sensor in real life applications.

PP047

A NONENZYMATIC GLUCOSE SENSOR BASED ON GOLD NANOPARTICLES-ANTIMONY(V) OXIDE NANOCOMPOSITE MODIFIED GLASSY CARBON ELECTRODE

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Herein, a highly sensitive and selective non-enzymatic voltammetric glucose sensor was constructed by a gold nanoparticles-antimony(V) oxide nanocomposite modified glassy carbon electrode (AuNPs-Sb2O5/GCE) in an alkaline medium. A simple drop-casting method was utilized to fabricate the sensor. The synthesized AuNPs-Sb2O5 nanocomposite was characterized by scanning electron microscopy (SEM), transmission electron microscopy (TEM), fourier transform infrared spectroscopy (FTIR), energy-dispersive X-ray spectroscopy (EDS), X-ray diffraction (XRD), and selected area electron diffraction (SAED). Cyclic voltammetry (CV) and electrochemical impedance spectroscopy (EIS) were employed to assess the interfacial charge transfer properties.

The least 〖ΔG〗 _p^‡ (0.14 eV) value of AuNPs-Sb2O5/GCE further supports its favourable charge transfer environment for the oxidation of glucose. Scan rate analysis suggests the diffusion-controlled oxidation of glucose at the interface of the modified electrode with the loss of two electrons. The kinetic analysis was implemented to determine the Tafel slope (102 mV/decade) and charge transfer coefficient (0.42). Under optimized conditions, the non-enzymatic sensor exhibited three linear response ranges from 75 µM to 900 µM, 1 mM to 12 mM, and 15 mM to 50 mM with sensitivities of 0.119 µA µM-1 cm-2, 26.468 and 19.532 µA mM-1 cm-2, respectively. The prepared sensor demonstrated good stability, high selectivity, satisfactory reproducibility, low detection (21.78 µM, S/N = 3), and quantitation limit (65.99 µM). Moreover, the commonly interfering species such as AA, KCl, NH4Cl, NO2− and Na2CO3 did not cause any obvious interference. A low RSD value (< 5%) suggests the applied use of AuNPs-Sb2O5/GCE in real-life applications. Furthermore, the sensor's practical utility was demonstrated by using blood serum and mango juice sample analysis, which resulted in a reliable and robust infrastructure for next-generation point-of-care glucose monitoring and diagnostics

PP048

SATELLITE-BASED ASSESSMENT OF URBAN CO_2 ENHANCEMENT OVER VEGETATED AND BUILT-UP AREAS IN DHAKA DIVISION USING OCO-2 & 3 OBSERVATIONS

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Urban areas are major emitters to atmospheric carbon dioxide (CO_2), conducting an evaluation of urban CO_2 enhancement essential for tracking local climate trends. Satellite missions such as OCO-2 and OCO-3 provide rigorous readings of column-averaged CO_2 (XCO_2). This study aims to assess spatial variations in XCO_2 across vegetated and built-up areas in the Dhaka Division and evaluate the effect of urban forestry on atmospheric CO_2 enhancement. Bias-corrected Level 2 XCO_2 data from OCO-2 and OCO-3 (including Snapshot Area Mapping where available) were used for periods with valid observations. Land cover classification derived from Sentinel-2 imagery was used to measure vegetation fraction within satellite footprints. Meteorological parameters, including wind speed and direction, were obtained from ERA5 to account for atmospheric transport effects. Urban CO_2 enhancement was estimated by comparing XCO_2 values between up wind background regions and downwind urban areas under similar atmospheric conditions. Consistent with previous studies, urban built-up areas are expected to exhibit higher XCO_2 enhancement compared to vegetated areas, typically on the order of ~1–3 ppm depending on atmospheric conditions. Areas with higher vegetation fraction tend to demonstrate relatively lower XCO_2, suggesting localized CO_2 uptake. However, the observed differences remain modest and are strongly influenced by wind-driven transport and spatial mixing. Satellite observations can capture urban CO_2 enhancement patterns in the Dhaka Division, but interpretation requires careful consideration of atmospheric transport and spatial resolution limitations. Urban forestry contributes to localized reductions in atmospheric CO_2, though its overall impact is limited relative to anthropogenic emissions. The study highlights the importance of integrating transport-aware approaches for reliable urban carbon assessments.

PP049

HIERARCHICAL RGO@NICO-LDH/NB2C MXENE ARCHITECTURES ON NICKEL FOAM AS BIFUNCTIONAL ELECTRODES FOR HIGH-PERFORMANCE SUPERCAPACITORS AND OXYGEN EVOLUTION REACTION

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The development of high-performance composite materials for energy storage and conversion has attracted significant interest, particularly for applications in supercapacitors and electrochemical water splitting. In this study, we fabricated a novel rGO-15@NiCo-LDH(2:1)/Nb2C/NF composite to enhance both capacitive performance of supercapacitor and catalytic activity in oxygen evolution reaction (OER). To fabricate the engineered composite, NiCo-LDH and Nb2C MXene were incorporated on a nickel foam (NF) substrate via hydrothermal method and then, electrochemical method was used to deposit graphene oxide (rGO) onto the upper layer of the modified NF. The rGO-15@NiCo-LDH(2:1)/Nb2C/NF electrode exhibited a high specific capacitance of 1360 F•g-1 at 1 A•g-1 and excellent cycling stability, retaining 94.18% of its initial capacity after 10000 cycles at 10 A•g-1. It also displays superior electrocatalytic performance for OER, demonstrating a low overpotential of 126 mV at current density of 10 mA·cm-2 in 1 M KOH with a small Tafel slope of 43.3 mV·dec-1. Furthermore, it exhibited remarkable long-term stability, maintaining its performance over 112 hours. These results highlight the potential of the rGO-15@NiCo-LDH(2:1)/Nb2C/NF as an effective bifunctional material for next-generation energy storage and conversion technologies.

PP050

A HIGH-PERFORMANCE PEDOT:PSS/NICOFE/NF ELECTROCATALYST FOR EFFICIENT OXYGEN EVOLUTION REACTION

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Oxygen evolution reaction (OER) is a key kinetic process in many renewable energy applications, while high-efficiency electrocatalysts are essential to overcome substantial overpotential and sluggish reaction kinetics. Nickel foam (NF), a low-cost commercial material, has been widely used as a substrate and support for electrode materials due to its high electrical conductivity, three-dimensional porous structure, and large specific surface area. In recent years, transition metal-based composites combined with conducting polymers have attracted significant attention for OER applications owing to their enhanced conductivity, structural stability, and abundant active sites. In this study, a ternary composite of PEDOT:PSS/NiCoFe supported on NF was successfully synthesized and investigated as an efficient electrocatalyst for OER in alkaline medium. First, the NiCoFe/NF substrate was prepared via a hydrothermal method to develop a two-dimensional sheet-like structure on the porous NF surface, providing abundant active sites for electrochemical reactions. Subsequently,

PEDOT:PSS was deposited onto the NiCoFe/NF substrate through a one-step electrodeposition process, forming a uniform conductive coating. Both NiCoFe and PEDOT:PSS contribute significantly to the overall electrocatalytic performance. The porous structure of NiCoFe offers a large number of active sites, while PEDOT:PSS enhances electrical conductivity, stability, and further increases the active surface area. As a result, the PEDOT:PSS/NiCoFe/NF composite exhibits excellent electrocatalytic activity, achieving an ultra-low overpotential of 123 mV at a current density of 10 mA cm^{-2}, along with a small Tafel slope of 49 mV dec^{-1} and remarkable stability for up to 100 hours. These results are comparable to those of reported noble metal-based electrocatalysts.

PP051

FABRICATION OF POLYPYRROLE AND MO2TIC2 MXENE BASE EFFECTIVE ELECTROCATALYST FOR OXYGEN EVOLUTION REACTION

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Oxygen evolution reaction (OER) is an essential kinetic process in many important renewable energy applications. At the same time, high-efficiency electrocatalysts are necessary to overcome OER's substantial overpotential and sluggish kinetics. Nickel foam (NF), a cheap commercial material, has been widely used as a substrate and support for electrode materials because of its high electronic conductivity, desirable 3D open-pore structure, and high specific surface area. Numerous studies have found that transition metal carbide MXenes are ideal candidates for OER catalysts. MXenes has a unique 2D layered structure similar to graphene, with a large specific surface area, good hydrophilicity, conductivity, and stability. In combination with conducting polymers, MXenes offers exceptional reinforcing properties due to the surface terminal group present in its structure. In this study, we develop a new composite PPy@Mo2TiC2/NF for oxygen evolution reaction (OER). Firstly, the Mo2TiC2/NF substrate is prepared using the solvothermal method. The motivation was to develop the 2D sheet-like structure of Mo2TiC2 on Ni foam porous substrate to provide the essential active sites for electrochemical reactions. Then, one Stape electrodeposition loads the PPy on Mo2TiC2/NF substrate. The PPy agglomerated along the 2D Mo2TiC2/NF pours sheets and make a layer along the Mo2TiC2/NF substrate. Both of these materials i.e. Mo2TiC2 and PPy contributed in overall electrocatalytic performance. Because Mo2TiC2 has a porous structure, it provides additional active sites, and on the other hand, PPy increases the conductivity and stability of the composite matrix and active sites. Because of magnificent electrocatalytic performance, the PPy@Mo2TiC2/NF composite shows an ultralow overpotential of 129 mV of OER against 10 mAcm-2 current density, a fast OER kinetics (45 mV dec−1) with high stability of 125 hr which are reasonably close to reported Nobel electrocatalysts.

PP052

ELECTROCHEMICAL SENSOR FOR DETECTION OF TOXIC METALS IN FOODSTUFFS

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Heavy metal contamination in foodstuffs poses a serious threat to public health because of its toxicity, persistence, and bioaccumulation in biological systems. In this study, a highly sensitive electrochemical sensing platform was developed for the simultaneous detection of toxic heavy metals in food samples using a PEDOT:PSS and AuNPs modified screen-printed electrode (SPE). The synergistic effect of the conductive polymer matrix and gold nanoparticles significantly enhanced the electron transfer capability and electroactive surface area of the sensing interface, leading to improved analytical performance. The fabricated PEDOT:PSS@AuNPs/SPE sensor enabled simultaneous determination of cadmium, lead, and mercury with excellent sensitivity over a wide linear concentration range from 1 ppb to 10 ppm. The limit of detection for Cd2+, Pb2+, and Hg2+ was achieved at 1 ppb for each analyte, demonstrating remarkable trace-level detection capability suitable for food safety monitoring. Surface morphology and successful electrode modification were confirmed by scanning electron microscopy (SEM), revealing uniform nanostructured distribution on the electrode surface, while Fourier-transform infrared spectroscopy (FTIR) verified the presence of characteristic functional groups associated with the composite modifier. The developed sensor exhibited strong selectivity, rapid response, and reliable analytical performance for heavy metal analysis in food matrices. Owing to its low cost, portability, and high sensitivity, the proposed electrochemical platform presents significant potential for routine food quality assessment and on-site environmental monitoring applications.

PP053

COMPUTATIONAL INVESTIGATION OF ANODIC CHLORINE EVOLUTION REACTION OVER SIN4-CODOPED GRAPHENE ELECTROCATALYST

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Chlorine is an industrially crucial chemical with diverse applications predominantly produced via the chlor-alkali process, where dimensionally stable anodes (DSAs; RuO2, IrO2, TiO2) are conventionally employed. However, their high cost, limited selectivity, scarcity, and environmental issues accentuate the necessity for alternative electrocatalysts for the chlorine evolution reaction (CER). Carbon nanomaterials have recently grown attention to design promising electrocatalysts for their superb electrical conductivity, conjugated sp2 π-electron framework, and structural stability. In this work, we have computationally investigated anodic CER over oxygen-anchored silicon-nitrogen-incorporated graphene (Gr-N4Si-O) using density functional theory (DFT). All computations have been performed employing B3LYP functional and 6-31 basis set in Gaussian 16w software. Structural optimization reveals moderate geometric distortion upon Cl adsorption at the O site, accompanied by a slight decrease in Si–O bond order. The Si–O bond length increases from 1.624 to 1.792 Å after adsorption, indicating displacement of the O and Si atoms due to O–Cl interaction. The calculated positive

adsorption energy of 0.410 eV implies a slightly endothermic yet feasible adsorption step, allowing easy desorption of Cl in the subsequent step of Volmer–Heyrovsky pathway. The Gibbs free energy of adsorbed Cl* is 0.206 eV at the equilibrium potential of 1.36 V, corresponding to a thermodynamic overpotential of 206 mV, which aligns with the reported related literatures. Electronic structure analyses, such as frontier molecular orbitals, Egap, NBO and DOS analyses confirm the auspicious electronic characteristics of the substrate. Notably, NBO charges on N, Si, and O shift from −0.644 to 2.121, and −1.139 to −0.697, 2.199, and −0.797, respectively, upon Cl adsorption, while Cl acquires a charge of 0.061, indicating charge transfer toward the substrate. Further the studied substrate exhibits excellent selectivity toward CER regarding the parasitic OER. These findings highlight the potential of Si-doped graphene as efficient electrocatalysts toward CER.

PP054

MICROBIAL SIGNATURES AND FUNCTIONAL SHIFTS IN UPPER GASTROINTESTINAL CARCINOMA: A METAGENOMIC ANALYSIS

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Upper gastrointestinal (UGI) carcinoma remains one of the leading contributors to global cancer mortality, where the human microbiome plays a crucial role in immune regulation and inflammatory processes. While earlier studies primarily analyzed taxonomic differences associated with UGI cancer, the functional landscape of microbial communities—particularly in biopsy versus mucosal swab specimens-remains insufficiently characterized. This study aims to investigate microbial richness, compositional shifts, and functional pathway alterations associated with UGI carcinoma using high-resolution 16S rRNA metagenomic profiling. Publicly available 16S rRNA sequencing datasets were processed using the DADA2 denoising pipeline, including stringent quality control, chimera removal, and rarefaction. A total of 2461 high-quality amplicon sequence variants (ASVs) and 282 samples met rarefaction thresholds. Alpha and beta diversity analyses were conducted using standard ecological indices, while taxonomic profiling was performed through established 16S classification workflows. Functional predictions were obtained via MetaCyc pathway inference, followed by linear discriminant analysis (LDA) to identify differentially enriched pathways between sample types. Carcinoma tissues exhibited higher microbial richness and marked compositional divergence from adjacent normal tissues, whereas carcinoma swabs showed increased evenness but lacked strong beta-diversity separation. Normal tissues were dominated by Streptococcus and Rhodanobacter, while carcinoma tissues were enriched with Fusobacteria, Veillonella, Capnocytophaga, Fusobacterium, Treponema, and Campylobacter. Across 43 predicted MetaCyc pathways, 24 were enriched in tissue biopsy samples and 19 in mucosal swabs. Heme b biosynthesis II and L-tryptophan biosynthesis dominated normal tissues, while carcinoma tissues showed enrichment for the incomplete reductive TCA cycle and dTDP-β-L-rhamnose biosynthesis. This study provides comprehensive insights into taxonomic and functional microbial signatures associated with UGI carcinoma. The observed tissue- and swab-specific functional pathways highlight distinct microbial shifts linked to malignant transformation. Future work will extend these findings by identifying key bacterial genes underlying these pathways and conducting molecular docking analyses to explore candidate drug interactions.

PP055

COMPUTATIONAL STUDY ON POLYENE CAROTENOIDS FOR APPLICATIONS IN DYE-SENSITIZED SOLAR CELLS: DFT AND TD-DFT METHOD

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Carotenoids are promising natural sensitizers for dye-sensitized solar cells (DSSCs) due to their abundance, nontoxicity, and strong visible-light absorption. The suitability of four carotenoids-α-carotene, β-carotene, γ-carotene, and lycopene-as DSSC sensitizers was investigated using Density Functional Theory (DFT) together with Time-Dependent Density Functional Theory (TD-DFT). The calculations were used to examine frontier molecular orbitals, absorption properties, and several key photovoltaic parameters, including the HOMO–LUMO energy gap, light-harvesting efficiency (LHE), Gibbs free energy of electron injection (ΔG_inject), and open-circuit voltage (Voc). The analysis indicates that the length of the conjugated chain plays an important role in determining the optoelectronic behavior of these molecules. Among the studied dyes, lycopene shows the smallest HOMO–LUMO gap (2.101 eV) and the most noticeable red-shift in the absorption spectrum, suggesting improved visible-light harvesting. All dyes exhibit very high light-harvesting efficiencies (0.999–1.000), sufficiently negative electron-injection free energies (−2.203 to −2.234 eV), and favorable open-circuit voltages ranging from 1.796 to 1.873 V, indicating efficient electron transfer from the excited dye to the semiconductor. These results highlight the pivotal role of conjugation length and electronic structure in optimizing carotenoid-based DSSCs and identify lycopene as the most promising sensitizer among those studied.

PP056

EARLY SEPSIS ONSET PREDICTION FROM ROUTINE EHR DATA: AN XGBOOST MODEL WITH DEMOGRAPHIC FAIRNESS EVALUATION ACROSS AGE AND GENDER

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Sepsis is an infectious condition which arises when the body's immune system goes into overdrive, setting off a chain reaction that begins to damage its own tissues and organs. If Sepsis goes undetected or fails detection, it drastically escalates mortality risks. Although conventionally the clinical scores are incapable of providing adequate discrimination in many instances, furthermore in very few cases age and gender specific performance or demographic fairness is not evaluated distinctly. We incorporated routine Electronic Health Record (EHR) data for the purpose of constructing more than one machine learning model to execute early sepsis onset prediction. We performed final scaling subsequent to imputing residual missing data and eliminating zero-variance features. Following this, we trained Logistic Regression (LR), XGBoost (XGB), and LightGBM (LGBM) classifiers and subsequently performed threshold tuning, wherein a threshold of 0.4 was specifically emphasized, taking into account the trade-off between recall and specificity. The models were assessed on the held-out test set based on their AUROC, recall, and specificity; Moreover, the predicted risk's reliability was evaluated

through calibration curve analysis. In order to increase the model interpretability, we assessed XGBoost feature importance and SHAP based explainations. Additionally, on the basis of predicted probability multiple layers were fixed through risk satisfaction. Based on the predetermined threshold, model performance was distinctly measured across age (<60 vs. ≥60 years old) and gender subgroups. Comprehensively, the XGBoost model has achieved high discrimination (test AUROC ≈ 0.93) as well as strong recall and specificity, which outperformed LR and demonstrated comparable performance to other gradient-boosting baselines. In the age- and gender-stratified analyses, the AUROC, recall, and specificity were found to be highly comparable, which indicates that the model is demographically stable, with no notable performance degradation observed across various subgroups. Calibration analysis revealed a strong alignment between the predicted probabilities and the observed sepsis incidence across the different risk strata. Utilizing the trained XGBoost-based model by routine EHR data, early sepsis onset prediction can yield more accurate, reasonably calibrated and clinically interpretable outcomes. Simultaneously, the age and gender subgroups demonstrated consistent performance. As a result, this approach proves highly applicable for providing fair, clinically meaningful risk stratification and could effectively be utilized as serving as a viable potential clinical decision support system for patients with sepsis.

PP057

AI GUIDED OPTIMIZATION OF MICROBIAL DEGRADATION OF TEXTILE DYES

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The textile industry is a major contributor to environmental pollution due to the discharge of harmful dye-containing wastewater into the natural ecosystem, endangering aquatic life, worsening air pollution, and adversely affecting agricultural soils. Commonly used dyes, such as acid dyes, reactive dyes, sulfur dyes, basic dyes, and azo dyes, are chemically stable and mostly resistant to conventional wastewater treatment methods. Microbial degradation has emerged as a promising and sustainable alternative, as certain bacteria, fungi, and actinomycetes possess enzymatic systems capable of breaking down complex dye molecules through oxidative and reductive pathways. Enzymes such as laccases, azoreductases, and peroxidases play key roles in the biotransformation of these pollutants. However, the identification of the most efficient microbial strains and optimization of degradation conditions require a lot of time, energy, and can be cost-prohibitive. This project develops an AI-guided approach to optimize microbial degradation of textile dyes. Databases containing information on microbial species, various strains, their enzyme activity, metabolic pathways, the structure of dyes, and reaction parameters such as pH, temperature, nutrient concentrations, oxygen availability, and salinity levels will be used to train machine learning models. Our AI system will analyze such variables and predict the optimal microbial strains, the most appropriate consortium combination, and reaction conditions that maximize dye degradation efficiency, while minimizing energy and resources. Predicted outcomes will be validated through controlled biodegradation assays. By integrating microbial biotechnology with AI-driven predictive modeling, this research aims to accelerate the identification and optimization of microbial systems for textile wastewater treatment. In the future, this framework could be expanded to develop intelligent bioremediation platforms capable of predicting microbial solutions for a wide range of industrial pollutants, enabling more efficient wastewater treatment systems and supporting sustainable environmental management.

PP058

HANDWRITTEN BENGALI NUMERAL RECOGNITION USING DEEP LEARNING: ANALYSIS OF AN EFFECTIVE AND ACCURATE METHOD.

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Currently building a Digital Bangladesh, the use of information technology is increasing. However, the automatic processing of handwritten Bangla scripts and numerals remains a major challenge. This issue is especially important areas such as postal services or cheque reading in banking systems, where human errors are so common. In this study, we propose a simple yet powerful Artificial Neural Network (ANN) model that can recognize accurately handwritten Bangla digits (0-9). We used an architecture of Convolutional Neural Network (CNN) and trained the model using locally collected handwritten data from Bangladesh. Testing results shows that, our model achieved more than 98% accuracy and can even recognize unclear or distorted handwriting digits. The results of this study can directly support in both government and private organizations process data faster and more accurately. Therefore, it represents a simple yet impactful AI-Based solution for Bangladesh.

PP059

RATIONAL DESIGN OF PHENOLIC ANTIOXIDANTS: A DFT STUDY ON SUBSTITUENT-DRIVEN MODULATION OF O–H BOND DISSOCIATION ENERGIES

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The antioxidant activity of phenolic compounds is closely associated with their ability to donate a hydrogen atom from the hydroxyl (O–H) group, which is largely determined by the O–H bond dissociation energy (BDE). In this work, a systematic density functional theory (DFT) study was performed to investigate the influence of substituent type and positional arrangement, and their number on the antioxidant properties of phenol derivatives in terms of bond dissociation energy (BDE) reported as the descriptor of hydrogen atom transfer (HAT) pathway of antioxidant mechanism. A series of methyl (–CH3), amino (–NH2), methoxy (–OCH3), and mercapto (–SH) substituted phenols at ortho-, para-, di-, and tri-substituted positions were examined. All molecular geometries were fully optimized and thermochemical parameters were calculated to determine O–H BDE values. To elucidate the electronic factors governing radical stabilization, frontier molecular orbital (FMO) analysis, spin density distributions, molecular electrostatic potential (MEP) surfaces, natural bond orbital (NBO) charge, and density of states (DOS) analyses were carried out. The results indicate that electron-donating substituents significantly decrease the O–H BDE by increasing electron density and enhancing resonance stabilization of the resulting phenoxyl radicals. Among the investigated systems, aminophenol derivatives exhibit the lowest BDE values due to the strong resonance-donating capability of the –NH2 group

.Furthermore, para- and poly-substituted systems display enhanced radical stabilization through extended π-conjugation and improved spin density delocalization. The computed electronic descriptors, including HOMO energies and HOMO–LUMO gaps, DOS, NBO charges consistently support the observed trends. Therefore, the present computational study provides molecular-level insights into substituent effects on the antioxidant activity of phenolic compounds and offers useful guidelines for the rational design of efficient antioxidants.

PP060

EMPOWERING LOCAL AGRICULTURE: A DEEP LEARNING-POWERED WEB SYSTEM FOR IDENTIFYING BANGLADESHI MANGO VARIETIES

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Bangladesh grows some of the tastiest mangoes in theworld, but telling different varieties apart just by looking at them isn't easy-even for farmers who've worked with mangoes for years. Varieties like Amrapali, Bari-4, Bari-7,Fazlee, Harivanga, Kanchon Langra, Katimon, Langra, Mollika, and Nilambori each have their own unique qualities, but misidentification happens all the time. We wanted to build something practical that could help farmers, traders, and everyday buyers identify mango varieties instantly from a simple photo. So we created a deep learning system that does exactly that, and put it online so anyone can use it for free. First, we collected over 2000 high-quality mango photos (3024×4032 pixels) from local markets and farms across Bangladesh. We grouped Bari-4 and Bari-7 together as ”Bari” since they're closely related, giving us nine distinct variety classes. After splitting the data (70% for training, 15% for validation, 15% for testing), we applied some smart augmentation tricks-flipping images, rotating them slightly, adjusting colors - to help our models learn better. We tested three different pre-trained networks: ResNet18, ResNet50, and EfficientNetB0, fine-tuning each one on our mango dataset. Once we found the best model, we built a simple web interface using Streamlit and made it live at mangoclassifier.streamlit.app. EfficientNetB0 turned out to be the clear winner. It correctly identified mango varieties 98.01% of the time on our validation set and 97.36% on the test set- way better than ResNet18 (86.47%) and ResNet50 (78.55%). Looking at individual varieties, our model performed impressively well, with F1-scores ranging from 0.93 to 1.00. The combined Bari class scored an F1 of 0.97. Best of all, EfficientNetB0 is surprisingly lightweight - only about 4 million parameters - so it runs quickly even on modest hardware. The web app is live and lets anyone upload a mango photo and get an instant prediction. What started as a simple idea - can a computer learn to recognize mango varieties? - turned into a working tool that people can actually use. Our systemis accurate, fast, and freely available online. Whether you're a farmer checking your harvest, a seller labeling your products, or just someone curious about what kind of mango you're about to eat, this tool can help. We're already thinking about next steps: gathering more photos, adding new varieties, and maybe building a mobile app so it works even better in rural areas with limited internet.

PP061

FROM CO2 TO CH4: MECHANISTIC INSIGHTS FROM GAUSSIAN-BASED DFT CALCULATIONS ON NI CATALYSTS

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Converting CO_2 into valuable fuels through catalytic hydrogenation is considered a promising strategy for both greenhouse gas mitigation and sustainable energy production. Nickel-based catalysts are particularly attractive due to their high activity and economic viability. Previously, we presented a prototype experimental project entitled “Conversion of CO2 to CH4 by Ni-based Nano-Catalyst” in the Science and Technology fair organized by Bangladesh Council of Science and Industrial Research (BCSIR) in 2025. However, the detailed reaction mechanisms remain unresolved. This study aims to elucidate the mechanistic pathways of CO2 methanation on Ni-based systems and identify the most energetically favorable route using Gaussian-based density functional theory (DFT) calculations. All DFT calculations were performed using Gaussian software. Geometry optimizations, frequency analyses, and transition state calculations were conducted using appropriate exchange-correlation functional and basis sets. Model Ni-based catalytic systems were employed to evaluate adsorption energies, activation barriers, and reaction energetics. Three mechanistic pathways-two involving CO intermediates and one CO-free route-were systematically investigated. Transition states were confirmed by vibrational frequency analysis. Key intermediates, including *CO, *COOH, *CHx (x = 1–4), and *CHO, were successfully characterized. Among the proposed pathways, the CO-mediated mechanism involving CO2 dissociation followed by CO decomposition emerged as the most energetically favorable. The rate-determining step was identified as CO → C + O, exhibiting a comparatively lower activation barrier than competing pathways. Subsequent hydrogenation steps leading to CH4 formation were found to be thermodynamically and kinetically feasible, confirming the viability of this pathway. This study provides clear mechanistic insight into CO2 methanation, highlighting the dominance of the CO-mediated pathway on Ni-based catalysts. The findings demonstrate the effectiveness of Gaussian-based DFT calculations in resolving catalytic mechanisms and offer valuable guidance for the rational design of efficient catalysts for CO2 utilization and sustainable energy applications

PP062

INVESTIGATING IMAGERY AND CONTEXT-BASED LEARNING ON METACOGNITIVE AWARENESS OF SEMANTIC PROCESSING

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Metacognitive awareness plays a vital role in semantic processing by enabling individuals to monitor, regulate, and evaluate their understanding of linguistic meaning. Although prior research highlights the benefits of imagery and contextual support for semantic learning, their independent and interactive contributions to metacognitive awareness have received limited empirical attention. The present study examined how imagery and context-based

learning influence metacognitive awareness during semantic processing, with a specific focus on differences between living and nonliving word categories. 56 participants completed a learning task in which 16 novel lexical items were presented with or without contextual support, followed by a semantic categorization task and metacognitive awareness judgments. Phonological and visuospatial working memory were assessed to examine individual differences in cognitive capacity. The study employed a 2 × 2 mixed-design, with learning condition as the between-subjects factor and word category as the within-subjects factor. A significant main effect of word category, $F(1, 53) = 6.04$, $p = .017$, partial $\eta^2 = .102$, with higher metacognitive awareness for living ($M = 16.48$, $SE = 0.37$) than nonliving words ($M = 14.39$, $SE = 0.43$). In contrast, the main effect of learning conditions was not significant, indicating that contextual support did not influence overall metacognitive awareness. The interaction between learning condition and word category was also not significant. Recall accuracy was a significant covariate, $F(1, 53) = 12.34$, $p = .001$, suggesting consistency between performance and metacognitive awareness. These findings suggest that intrinsic semantic properties, particularly animacy, have a stronger influence on metacognitive awareness than external contextual support. The study offers new insights into the interaction between semantic representation and metacognitive monitoring during novel word learning.

PP063

IMPROVING MEDICATION SAFETY THROUGH BRAND-NAME–BASED DRUG INTERACTION DETECTION IN BANGLADESH

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Drug–drug interactions (DDIs) are a major cause of adverse drug events and pose significant patient safety risks, particularly in settings with widespread polypharmacy. Most existing DDI detection tools rely exclusively on generic drug names, which creates an accessibility barrier for patients and caregivers in Bangladesh who are more familiar with locally marketed brand names. Furthermore, currently available systems rarely contextualize interactions with prevalent regional health conditions such as diabetes, hypertension, and chronic kidney disease. The aim of this study is to develop a brand-name–based drug interaction detection system that maps locally used pharmaceutical brand names to their corresponding generic drugs and identifies potential DDIs using internationally recognized pharmacological databases. A dataset of commonly used Bangladeshi drug brand names and their corresponding generic compositions will be compiled from publicly available pharmaceutical sources, including the Directorate General of Drug Administration (DGDA) database. These brand names will be mapped to standardized generic drug entries in pharmacological datasets such as DrugBank and OpenFDA. A relational database system will be developed to support brand-name queries and automatically resolve them to generic drug names for DDI detection. The system will also incorporate structured information on common comorbid conditions to identify elevated interaction risks in relevant patient profiles. In addition, a medication guidance module will summarize key information, including intake timing, potential food interactions, and adherence recommendations. The study is currently ongoing. Preliminary work involves compiling a curated dataset of commonly prescribed Bangladeshi brand-name medications and

establishing the mapping pipeline to their generic equivalents using DrugBank and OpenFDA datasets. Expected outcomes include the development of a validated brand-to-generic mapping database and successful retrieval of drug–drug interaction information through brand-name queries. Integration of interaction risk alerts based on common health conditions is also anticipated. The system will further explore machine learning-based drug interaction prediction using existing DDI datasets. This study aims to bridge the gap between locally recognized pharmaceutical brand names and generic-based DDI databases. By enabling interaction detection through brand-name inputs and providing patient-oriented medication guidance, the proposed system may improve medication safety, enhance patient awareness, and support clinical decision-making in resource-limited settings.

PP064

ARTIFICIAL INTELLIGENCE IN BANGLADESHI HEALTHCARE: PERSPECTIVES OF PROFESSIONALS AND STUDENTS

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Artificial Intelligence (AI) is transforming global healthcare by enhancing diagnostics and system efficiency. However, its integration in Bangladesh remains limited. Assessing the awareness and readiness of healthcare professionals and students is crucial for informed policy and sustainable implementation. To assess AI knowledge, attitudes, barriers, ethical concerns, and future expectations among healthcare professionals and students in Bangladesh. A nationwide cross-sectional survey was conducted among 677 healthcare students and professionals using a structured questionnaire covering demographics, AI awareness, perception, implementation barriers, ethics, and future perspectives. Data were analyzed using descriptive statistics and chi-square tests to determine significant associations. Among 677 respondents, 50.4% were students and 49.6% were job holders; 58.3% were male and 41.7% female. Most participants were aged 18–25 years (51.3%) and 96.5% were from urban institutions. Regarding AI familiarity, 58.2% were somewhat familiar, 17.6% were quite familiar/expert, and 8.1% had no knowledge. Online learning was the primary source of AI knowledge (77.8%). Attitudes were largely positive, with 58.8% somewhat positive and only 4.7% negative. Trust in AI was highest for administrative tasks (69.1%), and 88.9% agreed that AI should require human oversight. Major barriers included lack of funding (80.8%), poor technological infrastructure (75.3%), and organizational resistance (61.4%). Data protection (88.5%) and algorithm transparency (72.2%) were the leading ethical concerns. Although 76.1% reported no AI implementation plans in their institutions, 68.2% expressed willingness to participate confidently in AI-assisted care. Profession was significantly associated with AI familiarity ($\chi^2=163.62$, $p<0.001$), and gender was significantly associated with AI attitude ($\chi^2=13.81$, $p=0.007$). Healthcare stakeholders in Bangladesh demonstrate positive attitudes toward AI but limited institutional adoption. Strengthened infrastructure, funding, regulation, and structured training are essential for effective and equitable AI integration

PP065

METALLO BETA LACTAMASE (MBL) GENES AND THEIR CO-LOCALIZATION WITH MOBILE GENETIC ELEMENTS AND VIRULENCE FACTORS IN HOSPITAL EFFLUENTS

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Hospital effluents are recognized as environmental reservoirs of antimicrobial resistance (AMR), particularly against last-resort carbapenems. Metallo-β- lactamases (MBLs), including blaNDM and blaVIM, confer resistance to nearly all β-lactam antibiotics and are frequently associated with mobile genetic elements (MGEs), facilitating horizontal gene transfer (HGT). This study aimed to investigate the occurrence of carbapenem resistance genes in hospital effluents in Bangladesh and to characterize their genomic context using integrated culture-based and shotgun metagenomic approaches, with emphasis on ARG abundance, virulence determinants, and ARG-MGE co-localization. Forty-three effluent samples from tertiary hospitals in Dhaka were analyzed. Isolates were cultured, identified by 16S rDNA sequencing, and tested against imipenem and meropenem using disk diffusion and MIC assays. PCR detected blaNDM-1, blaVIM, and class-1 integrons. Shotgun metagenomics of four samples identified ARGs, virulence factors, and mobile genetic elements. Distance-based analysis assessed ARG–MGE co-localization, focusing on carbapenemase genes. Among 294 bacterial isolates, blaNDM-1, blaVIM, and class-1 integron genes were detected in 15%, 16.3%, and 36.7% of isolates, respectively. blaNDM-1 and integron-positive isolates exhibited significantly elevated phenotypic resistance and higher meropenem MIC values. Metagenomic analysis revealed high abundance of carbapenemase genes, including blaNDM, blaVIM, and blaOXA variants, across all sequenced samples. Carbapenem resistance genes were frequently embedded within contigs harboring insertion sequences, composite transposons, and integron-associated elements. ARG–MGE co-localization analyses demonstrated close genomic proximity between carbapenemase genes and mobilizable elements, indicating strong dissemination potential. Virulence-associated genes were also detected within ARG-rich assemblies. Hospital effluents in Bangladesh harbor mobilizable carbapenem resistance genes enriched with virulence factors. Frequent co-localization of blaNDM, blaVIM, and other carbapenemases with mobile genetic elements increases the risk of horizontal transfer to pathogens. Genomic wastewater surveillance and integrated One Health strategies are essential to limit environmental spread of carbapenem-resistant organisms.

PP066

DETERMINANTS OF METABOLIC SYNDROME CONTROL AMONG ADULTS PEOPLE WITH NON-COMMUNICABLE DISEASES RECEIVING SERVICES AT NCD CORNER IN BANGLADESHI HOSPITALS: MULTILEVEL ANALYSIS

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Metabolic syndrome (MetS) is a cluster of risk factors, including low HDL cholesterol,high blood pressure, elevated blood sugar, high triglycerides, and abdominal obesity.Uncontrolled MetS significantly raises the risk of ischemic heart disease, heart failure and stroke, leading to increased hospital admissions and higher healthcare costs. This study aimed to investigate the multilevel relationship between health service system factors and individual level factors influencing the control of MetS among adults with NCDs receiving healthcare services at NCD corner in hospitals across Bangladesh over 1-year period. The study was conducted in a cross-sectional manner with a descriptive and analytical approach from February to March 2025. Data were collected from primary, secondary and tertiary government hospitals in Bangladesh using a multistage stratified random sampling technique. A total of 14 hospitals (6 primary, 4 secondary, and 4 tertiary) were selected. 472 valid patients questionnaires and 14 doctor/nurses questionnaire were used. Data were analyzed using multilevel logistic regression analysis. In this study, 51% participants successfully controlled MetS within 1 year. In secondary hospitals are the most effective in controlling MetS with 62.3% of patients having controlled MetS compared to 37.7% with uncontrolled MetS. This contrasts with primary hospitals, where 59.9% of participants had uncontrolled MetS and only 40.1% had controlled MetS. Tertiary hospitals showed a nearly equal distribution with 50.3% of patients having uncontrolled MetS and 49.7% controlling their condition. Individual-level factors significantly influenced MetS control. Adults with a BMI >30 had an 83% lower chance of controlling MetS compared to those with BMI <18 (OR = 0.17, 95% CI: 0.05-0.53, p = 0.001). Regular physical exercise increased the odds of control by 2.83 times (OR = 2.83, 95% CI: 1.73–4.62, $p < 0.001$). Participants using ≥5 medications had a 70% lower chance of controlling MetS (OR = 0.30, 95% CI: 0.18–0.52, $p < 0.001$). High medication adherence increased the odds of control by 3.78 times (OR = 3.78, 95% CI: 1.93–7.36, $p < 0.001$). At the hospital level, comprehensive health behavior monitoring was associated with a 3.42 fold increase in MetS control compared to partial monitoring (OR = 3.42, 95% CI: 1.47–7.96, $p < 0.05$). This study highlights the critical role of individual factors such as BMI, physical activity, polypharmacy and medication adherence in controlling MetS. It also underscores the importance of comprehensive health behavior monitoring at the hospital level. These findings provide valuable insights for healthcare providers and policymakers to improve MetS management strategies in Bangladesh.

PP067

RIFAMPICIN-LOADED SOLID SNEDDS WITH EXALTED BIOAVAILABILITY: AN IN VITRO AND IN VIVO EVALUATION

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Rifampicin (RF) is a key first-line anti-tuberculosis drug commonly administered orally; however, it has low bioavailability and high hepatotoxicity due to its biopharmaceutical properties. Therefore, the objective of our study was to overcome these issues by enhancing solubility using natural carriers. In this tune, we previously formulated a coconut oil-based RIF-loaded self-nanoemulsifying drug delivery system (RFL). Here, this RFL was solidified by adsorbing onto solid lactose monohydrate, followed by physicochemical characterisation using Fourier transform infrared spectroscopy (FTIR), x-ray diffraction (XRD), differential scanning calorimetry (DSC), and scanning electron microscopy (SEM). The in vitro drug release of this solid SNEEDS (RFS) was assessed by the USP II method. Finally, the pharmacokinetics and safety of the formulation were evaluated using a rat model. The physicochemical characterisations demonstrated the absence of any unusual chemical

interactions between raw RIF and additives of formulation. The in vitro dissolution study showed that RFS released 100% of RIF within 30 min, which was significantly ($p<0.05$) higher than pure RIF (only 49.8%). The pharmacokinetics study revealed 2-fold greater bioavailability by RFS than that of pure RIF. Moreover, the in vivo safety evaluation showed no significant deterioration in liver and kidney tissues compared with raw RIF, as demonstrated by biochemical and histological examinations, despite the higher bioavailability. Thus, rifampicin-loaded solidified-SNEDDS could be offered as a promising therapeutic alternative to raw rifampicin for combating tuberculosis.

PP068

ROLE OF NIGELLA SATIVA (BLACK CUMIN SEEDS) AS AN ADJUNCT THERAPY IN TREATING SEVERE AND CRITICAL COVID -19 INFECTION COMPARED TO THOSE WITH STANDARD THERAPY: AN OPEN LABEL RANDOMIZED CLINICAL TRIAL

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During recent COVID-19 pandemic (2019-2021) clinician-researchers had been looking for effective treatment of Covid-19 infection. Nigella sativa (NS), a well-known herbal medicine, has been used as anti-viral, anti-inflammatory, immune modulatory, anti-oxidant, broncho-dilatory, anti-histaminic, anti-tussive activities for patients with mild to moderate COVID-19 infection. Our study aimed to determine the efficacy of NS for treatment of severe and critically ill Covid-19 patients as an adjunct therapy with conventional treatment. This was an open label randomized clinical trial conducted in severely and critically ill COVID-19 patients admitted into COVID ICU of United Hospital, Dhaka, Bangladesh. The study subjects were randomly divided into two equal groups: NS group in which subjects received NS orally in addition to the conventional treatment, and Control group, who received conventional treatment only. Primary outcome focused mainly on duration of ICU stay, use of mechanical ventilation (MV)/noninvasive ventilation (NIV)/ High-flow nasal cannula (HFNC) oxygen (HFNO) and mortality. The secondary outcomes were based on comparison of those above - mentioned parameters between the groups (NS and Control). A total of 150 subjects were enrolled according to eligibility criteria. There were 60 deaths (29 NS + 31 Cont.) and 90 survivals (46 NS + 44 Cont.). Among the survivals 16 NS subjects as opposed to 6 Cont. subjects stayed in ICU for 8 to 14 days ($P = 0.043$). Twenty - one subjects of NS group as opposed to 8 subjects of Cont. group stayed in ICU for less than 7 days to 14 days. Whereas among subjects who died there was no significant difference in length of stay among majority of NS and Cont. subjects. NS group required significantly lower number of O_2 delivery methods like mechanical ventilation (MV), noninvasive ventilation (NIV), high-flow nasal oxygen (HFNO) compared to their counterparts on Day 7 and Day 14 of stay in ICU. NS as an adjunct therapy with severe and critical COVID 19 infection was associated with some reduction of duration of stay in ICU but significantly less requirement of invasive and non-invasive ventilator support, high flow nasal oxygen than standard treatment group. Establishing accurately therapeutic efficacy of NS in critically ill COVID-19 patients requires placebo controlled double blind studies.

PP069

INVESTIGATION OF CHOLINESTERASE INHIBITION, ANTIOXIDANT AND MEMORY ENHANCING POTENTIAL OF SMILAX PERFOLIATA: IDENTIFICATION OF ACTIVE CONSTITUENTS

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Alzheimer's disease (AD) is a progressive neurodegenerative disorder characterized by impairment of memory and cognition. Cholinergic dysfunction and oxidative stress have been identified to be closely associated with AD. There are no drugs that can completely cure the disease. Smilax perfoliata has been traditionally used in the treatment of different ailments. This study aimed to evaluate the anticholinesterase, antioxidant, and memory-enhancing potential of Smilax perfoliata and to isolate bioactive compounds that may serve as lead candidates for AD management. Crude methanol extract (CME) of the plant was fractionated into n-hexane (NHF), chloroform (CHF), ethyl acetate (EAF), and aqueous (AQF) fractions. Total phenolic and flavonoid contents were quantified. In vitro anticholinesterase activity was assessed using the modified Ellman's method, while antioxidant activity was evaluated in several in vitro models. The most active fraction was tested in a scopolamine-induced memory-impaired mouse model using the Y-maze test, followed by biochemical estimations of acetylcholinesterase (AChE), glutathione (GSH), and malondialdehyde (MDA). Bioactivity-guided isolation were conducted to isolate the active compounds and identified by spectroscopic analyses. EAF contained the highest phenolic (61.861 mg GAE/g) and flavonoid (193.79 mg CE/g) contents. It exhibited significant AChE (IC_{50} 19.89 μg/ml) and butyrylcholinesterase inhibition (IC_{50} 169.53 μg/ml), along with strong antioxidant activity (DPPH IC_{50} 8.33 μg/ml). In vivo, EAF significantly improved scopolamine-induced memory deficits, reduced AChE activity, elevated GSH levels, and decreased MDA levels in mouse brain tissue. Three compounds were isolated: 3,4-dihydroxybenzoic acid, secoisolariciresinol, and 3-methyl glutaric anhydride. Among them, 3,4-dihydroxybenzoic acid showed the strongest AChE inhibitory (IC_{50} 14.81 μg/ml) and antioxidant activity. These findings suggest that the EAF fraction of S. perfoliata possesses significant neuroprotective properties mediated through cholinesterase inhibition and antioxidant mechanisms, highlighting its potential as a natural source of bioactive molecules for AD management.

PP070

AUTOPHAGY RECONSTITUTION AND CANCER DRUG DISCOVERY

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Autophagy is a lysosomal degradation system that involves de novo autophagosome formation through several steps. To regenerate each step of this phenomenon in vitro, we have started to elaborate on the molecular mechanisms of such a complicated process by in vitro reconstitution and validated in vivo. The structural biological, biochemical, biophysical and cell biological approaches applied throughout the experiments using HS-AFM, NMR, diffraction, Cryo-EM and Confocal Laser Scanning Microscope. Here we show that the PAS is a liquid-like condensate of Atg proteins. The autophagy-initiating Atg1 complex undergoes phase separation to form liquid droplets in vitro and point mutations or phosphorylation that inhibit phase separation impair

PA formation in vivo (Nature, 2020). The isolation membrane (IM) is generated from the PAS and bent by the membrane perturbation of lapidated-Atg8 (Nature Structural and Molecular Biology, 2021). For the lipidation of Atg8, Atg7 (E1), Atg3 (E2), and Atg12–Atg5–Atg16 (E3) are essential, and this complete set of Atg8-E1-E2-E3 forms an interaction web that triggers the formation of the cup shape of IM before closing to form an autophagosome (Nature Structural and Molecular Biology, 2024). In another trial, we have also observed that Atg proteins coated membrane bending occur when it interplays with protein liquid droplets, and it depends on the wetting of droplets (Molecular Cell, 2020 & 2023). From these experiments, we have successfully reconstituted and revealed the molecular mechanism of autophagosomal initiation site, bending of IM, and formation of cup shape of IM which are crucial steps for the formation of autophagosomes. In the future, this reconstitution information may be used for the development of regulators for selective recycling of the P62 protein from breast and liver tissues, which are commonly associated with cancer development. Thereby, we can discover drugs against cancer through the regulation of autophagy.

PP071

A COMPLEX POLYSACCHARIDE-RICH SULPHATED EXTRACT (CPSE) FROM THE MARINE RED ALGAE GRACILARIA TENUISTIPITATA ATTENUATES LIVER FIBROSIS AND RESTORES HEPATIC FUNCTION IN A MOUSE MODEL

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Liver fibrosis, a precursor to cirrhosis and hepatocellular carcinoma, represents a major global health challenge with a pressing need for effective therapeutic agents. This study investigates the therapeutic potential of a complex phytochemical extract derived from the red alga G. tenuistipitata, a promising yet largely uncharacterized species, in a preclinical model of liver fibrosis in mice. Comprehensive structural characterization using FTIR, 1H NMR, and GC-MS revealed that the extract is not a simple sulfated polysaccharides (SPs) but a complex entity. It comprises a characteristic agar-type polysaccharide backbone (alternating β-D-galactose and 3,6-α-L-anhydrogalactose units) that is co-purified with a significant suite of bioactive lipids, including the anti-inflammatory agent hexadecanoic acid methyl ester and the neuromodulatory fatty acid amide, erucamide. While exhibiting a favorable safety profile with no toxicity observed up to 2000 mg/kg in Swiss albino mice, the extract demonstrated potent, dose-dependent antifibrotic activity in a carbon tetrachloride (CCl_4)-induced liver fibrosis model. Administration of the G. tenuistipitata complex extract resulted in the significant normalization of key serum biomarkers of liver injury (ALT, AST) and function (albumin, bilirubin), alongside a striking restoration of normal hepatic architecture, mitigating the extensive hepatocellular damage, necrosis, and inflammatory infiltration induced by CCl_4. Interestingly, the profound in-vivo efficacy contrasted with moderate in-vitro antioxidant activity, suggesting that the extract's hepatoprotective mechanism extends beyond direct radical scavenging and is likely driven by a multi-target, synergistic action of its polysaccharide and lipid constituents. These findings establish the SP-rich extract from G. tenuistipitata as a powerful multi-component therapeutic agent.

PP072

BIOASSAY-GUIDED ISOLATION AND CHARACTERIZATION OF NOVEL PHYTOCHEMICALS WITH POTENT CYTOTOXIC ACTIVITY AGAINST HUMAN CANCERS

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The burgeoning field of natural product research has highlighted the need for sustainable and effective approaches to cancer treatment. Our study focuses on the screening of various plant materials as a resource for potential anticancer agents. A number of medicinal plants, known for their traditional uses in folk medicine, were systematically evaluated for their cytotoxic properties against a panel of cancer cell lines, including breast, prostate, and colorectal carcinomas, using in vitro and in vivo functional assays. Analytical, chromatographic, and spectrometric methods were used to isolate, purified and characterize the phytochemical. Also, fluorescence microscopy and RT-qPCR analyses were used to identify the mechanisms of action of the bioactive compounds. Our results demonstrated significant anticancer activity in several plant extracts, correlating with the presence of specific bioactive phytochemicals through the induction of apoptosis. The isolated phytochemical significantly inhibited cancer cells' proliferation, tumor weight, and increased the survival of tumour-bearing animals. Identified bioactive compounds also improved the hematological parameters in tumor-bearing mice, indicating protective effects against tumor induced anemia in experimental animals. Most of the tested bioactive compounds induce intrinsic apoptotic pathways followed by activation of pro-apoptotic genes such as p53, Bax, caspase-9, -3, along with inactivation of antiapoptotic gene such as Bcl-2. Notably, the purified compounds exhibited no cytotoxicity and tissue damage in control animals, which underscores their therapeutic potential. These findings support the hypothesis that plant materials are a valuable resource for anticancer drug discovery, providing a foundation for the development of novel therapeutic agents that could complement existing cancer treatments. Altogether, the natural bioactive compounds showed anticancer activity and can be regarded as an effective phytotherapeutic agent. However, more preclinical and clinical research is essential for further development.

PP073

EFFECTS OF GSTP1 GENE POLYMORPHISMS ON THE DRUG INDUCED ALLERGY OF ANTIRETROVIRAL THERAPY ON BANGLADESHI HIV PATIENTS

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Antiretroviral therapy (ART) has greatly improved the survival and quality of life of HIV-infected patients. However, drug-induced hypersensitivity reactions remain a major challenge in ART management. Genetic polymorphisms in drug-metabolizing enzymes, particularly Glutathione S-transferase P1 (GSTP1), may influence individual susceptibility to adverse drug reactions. The GSTP1 rs1695 polymorphism may alter enzyme activity and affect the detoxification of antiretroviral drugs such as Lamivudine, Tenofovir, and Efavirenz, potentially leading to allergic reactions. The objective of this study was to investigate the association between GSTP1 gene polymorphism (rs1695) and antiretroviral drug-induced hypersensitivity reactions among Bangladeshi HIV patients receiving ART. A total of 414 HIV-infected patients undergoing antiretroviral therapy were enrolled in this study. Patients were recruited from Bangabandhu Sheikh Mujib Medical University (BSMMU/BMU) Hospital and Infectious Disease Hospital (IDH), Mohakhali, Dhaka, Bangladesh. The patients were treated with common antiretroviral drugs including Lamivudine, Tenofovir, and Efavirenz. Participants were categorized into groups based on the presence or absence of drug-induced allergic (hypersensitivity) reactions. Genomic DNA was collected and GSTP1 rs1695 gene polymorphism was analyzed to determine genotype and allele frequencies. Statistical analyses were performed to evaluate the association between GSTP1 polymorphism and hypersensitivity reactions. Among the 414 HIV patients, variations in the GSTP1 rs1695 genotype distribution were observed between patients who experienced allergic reactions and those who did not. Certain GSTP1 genotypes showed a higher frequency in patients with hypersensitivity reactions following treatment with Lamivudine, Tenofovir, and Efavirenz. The results suggest a significant association between GSTP1 gene polymorphism and susceptibility to ART-induced allergic reactions. The findings indicate that GSTP1 rs1695 polymorphism may influence the risk of drug-induced hypersensitivity reactions in Bangladeshi HIV patients receiving antiretroviral therapy. Understanding genetic susceptibility may contribute to personalized treatment approaches and improved safety of ART. Further large-scale pharmacogenetic studies are recommended to validate these findings and facilitate the integration of genetic screening into clinical practice.

PP074

ONE HEALTH SURVEILLANCE OF BIOFILM-FORMING MULTIDRUG-RESISTANT ENTEROCOCCUS FAECALIS AT THE HUMAN–ANIMAL–ENVIRONMENT INTERFACE IN A BANGLADESHI SLUM COMMUNITY

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Enterococcus faecalis is an opportunistic pathogen of increasing concern for its ability to form biofilms and develop antibiotic resistance. From a One Health perspective, this poses a significant public health risk. This study aimed to determine the prevalence, antibiotic resistance, and biofilm-forming capacity of E. faecalis isolated from a densely populated slum region (Duldul Camp, Mymensingh) in Bangladesh. 51 samples were collected from the environment (n = 21), humans (n = 17), and animals (n = 13). Detection of E. faecalis was based on culture on Enterococcus agar media followed by and PCR targeting the ddl gene. Antibiogram was determined by disc diffusion method against multiple antibiotics. Biofilm formation was evaluated using Congo red agar. Out of the 51 samples, 21 (41.2%) tested positive for E. faecalis. Among the 21 PCR-positive samples, 15 were randomly chosen (5 from each source) for testing biofilm formation and antibiotic resistance. In the biofilm assay, 40% of the tested samples were identified as strong biofilm formers, 26.7% as intermediate, 26.7% as weak, and 6.7% as non-biofilm formers. In the antibiogram study, result showed that 93.3% of isolates were

resistant to nitrofurantoin and 66.7% to tetracycline, followed by vancomycin, linezolid, and teicoplanin (46.7%), erythromycin and fosfomycin (40%), chloramphenicol (26.7%), and ciprofloxacin (13.3%). Isolates with stronger biofilm-forming ability showed higher resistance scores, suggesting a correlation between biofilm formation and antibiotic resistance. Comparative investigation of different sources showed that human, animal, and environmental isolates had similar resistance profiles. This indicates possible cross-sector transmission routes for AMR. Findings of this ongoing study underscore the presence of multidrug-resistant, biofilm-forming E. faecalis in interconnected ecological niches in vulnerable urban environments, emphasizing the need for integrated One Health surveillance and targeted antimicrobial interventions to limit the spread of resistant enterococci.

PP075

TIME-DEPENDENT RECOVERY AFTER ARSENIC EXPOSURE ATTENUATES ARSENIC-INDUCED NEUROBEHAVIORAL AND BIOCHEMICAL CHANGES IN MICE

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Arsenic (As) is a highly toxic, naturally occurring metalloid widely distributed in the environment. Prolonged exposure to As can cause behavioral and biochemical changes in both humans and laboratory animals. However, the potential for self-recovery after long-term As exposure remains unclear. The aim of this study was to evaluate the effects of behavioral and biochemical changes induced by As (50 ppm) exposure via drinking water for 60 days in a mouse model, and to assess spontaneous recovery at 30, 45, and 60 days post-exposure. Mice exposed to As exhibited elevated anxiety-like behavior, impaired memory, and diminished motor coordination compared to control mice. Additionally, significant cholinergic dysfunction and oxidative imbalance, accompanied by increased inflammation, were observed in the brains of As-exposed mice compared with control mice. Furthermore, nuclear factor erythroid 2-related factor 2 (Nrf2), a key regulator of oxidative stress-responsive proteins, was significantly reduced in mice exposed to As. However, after withdrawal of As-contaminated drinking water, the recovered groups showed reduced anxiety as well as improved memory deficits and motor coordination compared to the mice exposed to As. The 45- and 60-day recovery groups showed significant upregulation of Nrf2 levels compared with the As-exposed group. In addition, these groups markedly improved behavioral performance, restored acetylcholinesterase (AChE) and butyrylcholinesterase (BChE) activities, enhanced antioxidant capacity by increasing heme oxygenase-1 (HO-1) and reduced glutathione (GSH) levels, and increased superoxide dismutase (SOD) activity in the brains compared to the As-exposed group. These findings suggest that cessation of As intake facilitates the amelioration of oxidative stress-mediated anxiety, cognitive impairment, and disturbances of motor coordination in As-exposed mice.

PP076

ANTIOXIDANT AND HEPATOTOXICITY AMELIORATIVE POTENTIAL OF MENTHA CANADENSIS LEAVES AGAINST PARACETAMOL-INDUCED HEPATIC DAMAGE IN MICE

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Mentha canadensis (wild Mint), a member of the Lamiaceae family, is traditionally used in herbal medicine, teas, and as a food additive in various regions, including Bangladesh. This research is designed to evaluate the hepatoprotective activity of M. canadensis leaf methanolic extract (MCLME) along with its antioxidant and anti-inflammatory potential. The in vitro antioxidant potential was evaluated through free radical scavenging assays such as ABTS and DPPH, as well as by a lipid peroxidation test. The anti-inflammatory property of MCLME was examined using albumin denaturation and RBC membrane stabilization assays. Furthermore, qualitative and quantitative analyses of phytochemicals were carried out. A paracetamol-induced hepatotoxicity Swiss-albino mice model was used to assess the hepatoprotective activity. Phytochemical analysis confirmed the presence of alkaloids, flavonoids, triterpenoids, coumarins, saponins, and steroids. The extract exhibited antioxidant and anti-inflammatory activity. In the hepatotoxicity model, MCLME showed a significant ($p < 0.0001$) reduction in SGPT, SGOT, ALP, total bilirubin, and IL-6. Histopathological analysis confirmed protective effects on hepatic architecture. MCLME also restored hepatic glutathione (GSH) levels. The effect was comparable to Silymarin (50 mg/kg). M. canadensis demonstrates hepatoprotective, antioxidative, and anti-inflammatory characteristics and may serve as a natural therapeutic agent for liver injury.

PP077

PLANT-BASED ALTERNATIVES TO ANTIBIOTICS: ASSESSING THE ANTIMICROBIAL ACTIVITY OF LOCAL AND THAI GINGER (ZINGIBER OFFICINALE) EXTRACTS AGAINST MULTIDRUG-RESISTANT SHIGELLA SPP AND SERRATIA MARCESCENS.

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As Antimicrobial resistance (AMR) has soared into a multifaceted global concern, repeated failures in treating illnesses caused by gram-negative bacteria like Shigella spp and Serratia marcescens have become evident. This study investigated the antimicrobial efficacy of methanolic extracts of Local and Thai ginger against antibiotic-resistant strains (Shigella spp. and Serratia marcescens), comparing their inhibitory effects with those of standard antibiotics. Ginger extracts from both Local and Thai cultivars were processed through Soxhlet extraction, followed by rotary evaporation, and the extracts' efficacy was assessed via the well diffusion method at different concentrations, such as 50-400mg/ml. Furthermore, antibiotic susceptibility was assessed by the Kirby-Bauer

disk diffusion method using ciprofloxacin, gentamicin, levofloxacin, and amoxicillin as controls. The Local ginger extracts exhibited superior activity compared to the Thai variant and were more effective against Shigella spp. In the case of Shigella spp., the local ginger extracts formed inhibitory zones of up to 15.7 mm, while the Thai variant showed only moderate inhibition. Moreover, the local extracts showed dose-dependent inhibition against Serratia marcescens; however, the Thai extracts showed lower and inconsistent inhibition at comparable concentrations. Although Shigella spp. showed susceptibility against the antibiotics tested except amoxicillin, Serratia marcescens was susceptible to gentamicin only. The outcomes of this study reiterate ginger's role as a complementary alternative and illuminate the gravity of cultivating Local cultivars. Further research should isolate specific genes and explore their molecular mechanisms, offering insights for future antimicrobial drug development.

PP078

MECHANISTIC INSIGHTS INTO THE ANTI-INFLAMMATORY AND ANTIOXIDANT ACTIVITIES OF BOERHAVIA DIFFUSA LEAF FRACTIONS: ATTENUATION OF OXIDATIVE STRESS AND INFLAMMATION IN A CARRAGEENAN-INDUCED MICE MODEL

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Oxidative stress and chronic inflammation are closely associated with the pathogenesis of numerous diseases, including cardiovascular disorders, arthritis, diabetes, and neurodegenerative conditions. Medicinal plants are widely recognized as valuable sources of bioactive compounds with antioxidant and anti-inflammatory properties. The present study aimed to investigate the phytochemical constituents and evaluate the antioxidant and anti-inflammatory activities of Boerhavia diffusa leaf extracts using both in vitro and in vivo experimental models. Dried leaf powder was extracted with methanol to obtain a crude methanol extract (CME), which was further partitioned into n-hexane (NHF), chloroform (CHF), ethyl-acetate (EAF), and aqueous (AQF) fractions. Phytochemical screening and quantitative estimation of phenolic and flavonoid contents were performed. Antioxidant activity was assessed using DPPH radical scavenging, reducing power, and total antioxidant capacity assays. Anti-inflammatory activity was evaluated through egg albumin denaturation and erythrocyte membrane stabilization assays, along with an in vivo carrageenan-induced paw edema model. Oxidative stress markers including malondialdehyde (MDA), superoxide dismutase (SOD), catalase (CAT), and reduced glutathione (GSH) were also measured. Phytochemical analysis revealed the presence of alkaloids, flavonoids, phenolics, and terpenoids. The EAF and CHF contained the highest amount of phenolics (463.33 mg GAE/gm) and flavonoids (93.03 mg CE/gm), respectively. Among the tested fractions, the EAF demonstrated the strongest antioxidant activity with a DPPH IC50 value of 12.95 µg/ml and showed significant reducing power and total antioxidant capacity. In vitro anti-inflammatory assays indicated that the EAF and CHF exhibited the highest inhibition of protein denaturation and membrane stabilization, respectively. In vivo studies showed that chloroform and ethyl-acetate fractions significantly reduced carrageenan-induced paw edema, decreased MDA levels, and restored antioxidant enzymes (SOD, CAT, and GSH). The findings demonstrate that Boerhavia diffusa leaves possess significant antioxidant and anti-inflammatory activities and highlight its potential as a promising source of natural therapeutic agents for oxidative stress-related inflammatory diseases.

PP079

ISOLATION OF BIOACTIVE COMPOUNDS FROM LEUCAS ASPERA AND ITS ANTINEOPLASTIC ACTIVITY WITH MECHANISMS

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Cancer remains one of the leading causes of mortality worldwide, with current chemotherapeutic agents limited because of the high cost, toxicity, and drug resistance. Due to the anticancer properties, medicinal plants offer diverse bioactive compounds. Leucas aspera (Lamiaceae), widely used in traditional medicine in South Asia, has shown various pharmacological activities; however, its active compounds and in vivo anticancer potential remain underexplored. The aim of the study is to isolate, characterize, and evaluate anticancer compounds from the methanolic leaf extract of L. aspera. The methanolic leaf extract of L. aspera was subjected to column chromatography and preparative thin-layer chromatography, yielding a compound designated LA-1. Structural characterization was carried out using FT-IR, 1H and 13C NMR, DEPT-135, COSY, HSQC, HMBC, and LC-MS analyses. The in vivo antineoplastic activity of LA-1 was evaluated using the Ehrlich Ascites Carcinoma (EAC) model in Swiss albino mice, followed by hematological and gene expression analyses. The isolated compound was identified as methyl 2-octyloxybenzoate ($C_{16}H_{24}O_3$; molecular weight 264.36 g/mol), which is reported here for the first time from L. aspera. In the in vivo study, LA-1 demonstrated significant dose-dependent tumor growth inhibition of 34.52% ($p < 0.01$), 63.07% ($p < 0.01$), and 75.69% ($p < 0.001$) at doses of 3.5, 5.0, and 10.0 mg/kg, respectively. Treatment also reduced tumor weight by 54.78%, increased mean survival time and lifespan by 45.24% at the 10.0 mg/kg dose, and restored altered hematological parameters. Furthermore, the upregulation of pro-apoptotic genes, including p53, Bax, caspase-3, and caspase-9, along with the modulation reduction of BCL2, suggests that the anticancer effect may be mediated through apoptosis. Methyl 2-octyloxybenzoate isolated from L. aspera showed mild cytotoxicity and promising in vivo anticancer activity, suggesting its potential as a lead compound for anticancer drug development and permitting further pharmacokinetic and toxicological studies.

PP080

ANTIBACTERIAL ACTIVITY OF SECONDARY METABOLITES OF AN ISOLATED, PURIFIED AND CHARACTERIZED SUNDARBANS MANGROVE FOREST SOIL-BACTERIA

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Soil and mangrove sediments are complex ecological habitats and important sources of bioactive secondary metabolites. The hydro-biogeochemical conditions of the Sundarbans mangrove ecosystem-including fluctuating salinity, tidal inundation, hypoxic sediments, and high organic matter-create selective pressure on native microbiota, favoring stress-adapted bacteria with antimicrobial potential. Bacteria were isolated from Sundarbans soil samples using the plate spread dilution method. A promising isolate was selected based on morphological characteristics and identified through 16S rRNA gene sequencing and phylogenetic analysis. Crude secondary metabolites were extracted from cell-free culture supernatant using ethyl acetate. Antibacterial activity was evaluated against pathogenic bacteria using disc diffusion and broth dilution methods. The isolate was identified as Acinetobacter baumannii. The crude extract exhibited concentration-dependent antibacterial activity against both Gram-positive and Gram-negative bacteria, with inhibition zones ranging from 9.83 to 22.67 mm (0.20–0.50 mg/disc). MIC values ranged from 0.642 to 1.276 mg/mL for reference pathogenic strains. These findings suggest that bacteria from Sundarbans mangrove soil are promising sources of antibacterial compounds. The study highlights the mangrove ecosystem as a valuable bioresource for antimicrobial discovery and provides a foundation for future purification, structural characterization, and mechanistic studies of bioactive secondary metabolites.

PP081

MENTHA CANADENSIS LEAVES INDUCE ANTITUMOR ACTIVITY IN EAC-BEARING MICE BY INDUCING APOPTOSIS

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Mentha canadensis is an aromatic plant commonly used in herbal tea, folk medicine, and food additives in manparts of the world, including Bangladesh. Recently, researchers have focused on medicinal plants due to their significant impact on human health. This study aimed to evaluate the in vivo antineoplastic activity of the M. canadensis leaves methanolic extract (MCLME) against Ehrlich ascites carcinoma (EAC) in Swiss albino mice, supported by in silico studies. Antineoplastic efficacy was assessed by analyzing EAC cell growth inhibition, survival time, and tumor burden in tumor-bearing mice, hematological parameters, apoptotic morphology, and expression of apoptosis-related genes. Molecular docking and dynamics simulations were performed to investigate interactions between MCLME-derived phytochemicals and the anti-apoptotic protein Bcl-2. MCLME significantly inhibited EAC cell growth by 62.95% ($p<0.001$) and 45.655% ($p<0.001$) at doses of 200 mg/kg and 100 mg/kg, respectively. At 200 mg/kg, it increased lifespan by 50.66% and reduced tumor burden by 34.7% ($p<0.001$). Furthermore, MCLME restored blood parameters in EAC-bearing animals, suggesting potential resistance to tumor burden. MCLME-treated EAC cells exhibited apoptotic features under microscopy. The DNA profile in agarose gel electrophoresis also demonstrated that MCLME caused EAC cell death via apoptosis. Moreover, in the treated animals, the anti-apoptotic gene Bcl-2 was suppressed while important pro-apoptotic genes (p53, Bax, caspase-9, and caspase-3) were upregulated. Bcl-2 protein suppression was further supported by the energetically favorable interactions of MCLME-derived compounds within the protein's binding site. Among the identified compounds, CID 60157539 and CID 576686 exhibited the highest binding affinities for Bcl-2, respectively. Molecular dynamics simulations demonstrated stable protein–ligand complexes with energetically favorable conformations, supporting their potential role as Bcl-2 inhibitors. The results of the present study show that M. canadensis might be a potential resource for cancer chemotherapy, exhibiting promising anticancer activity through a caspase-

PP082

PAN-CANCER ANALYSIS IDENTIFIES ELEVATED RNF20 EXPRESSION IS ASSOCIATED WITH METASTATIC PROGRESSION AND PROGNOSTIC SIGNIFICANCE IN SKIN CUTANEOUS MELANOMA

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RNF20 (Ring Finger Protein 20) is a protein-coding gene that encodes an E3 ubiquitin ligase, part of the RNF20/40 ubiquitin ligase complex. RNF20 conducts H2B monoubiquitination, forms a complex with RNF40, and mediates the transfer of a single ubiquitin molecule to histone H2B at lysine 120 (H2BK120ub1), resulting in chromatin relaxation and facilitating the access of DNA repair and replication machinery to the chromatin. The aim of this study is to comprehensively evaluate the epigenetic landscape of RNF20, enabling assessment of its diagnostic and prognostic significance, as well as, its therapeutic potential across multiple cancer types. A comprehensive pan-cancer analysis was performed, focusing on differential gene expression, tissue-level expression, survival (Cox proportional hazards and Kaplan-Meier), DNA methylation (CpG-based), gene alteration, immune infiltration (EPIC algorithm), drug sensitivity, and gene enrichment (GO and Reactome) using publicly available data from TCGA, UALCAN, GEPIA2.0, cBioPortal, SMART, and GSCA. RNF20 can act either as a tumor suppressor or an oncogene driver depending on its role on cellular-specific contexts as its H2Bub1-mediated chromatin regulation influences distinct transcriptional and DNA-repair pathways. Elevated RNF20 expression is found in metastatic SKCM tumors, suggesting that RNF20 promotes stress adaptation in malignant SKCM cells. Survival analysis revealed that RNF20 can act as a prognostic biomarker across various cancer types, functioning either as a risk factor or a protective factor. Uterine Corpus Endometrial Carcinoma (UCEC) from the TCGA cohort showed the highest frequency of RNF20 alterations. RNF20 gene alterations were not significantly correlated with progression-free survival across TCGA cancer types due to the underrepresentation of altered cases. Immune infiltration analysis showed that tumors with high RNF20 expression exhibit increased CD8+ T cell infiltration in the tumor microenvironment, whereas low NK cell infiltration. The study demonstrates RNF20 as a valuable molecular indicator for cancer prognosis and potential target for immunotherapy.

PP083

INTEGRATED ANTIOXIDANT, ADME, AND MOLECULAR DOCKING STUDIES OF CALOPHYLLUM INOPHYLLUM FOR ALZHEIMER'S DISEASE

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Alzheimer's disease (AD) is a progressive neurodegenerative disorder associated with cholinergic dysfunction and oxidative stress. Cholinesterase inhibitors remain the primary therapeutic option; however, limited availability necessitate the search for new candidates. Calophyllum inophyllum is a multipotential medicinal plant rich in bioactive compounds with reported antioxidant potential. However, no systematic study targeting AD has been done yet on this plant. The objective of this work is to evaluate the antioxidant activity of methanolic extract . fractions of Calophyllum inophyllum and explore th potential against AD through ADME and molecular docking approaches. The crude methanol extract of stem of the plant was prepared and partitioned into n-hexane, dichloromethane, ethyl acetate and aqueous fraction. Total phenolic and flavonoid content was assayed. The antioxidant activity was determined by several in vitro assays. Compounds available in the crude methanolic extract of stem was determined by literature review. Pharmacokinetic assessment using SwissADME revealed potential compounds and molecular docking was done targeting acetylcholinesterase. Among the fractions, ethyl acetate fraction exhibited the highest antioxidant activity in DPPH radical scavenging assay with IC50 value of 6.70 followed by dichloromethane fraction. The fractions also showed good antioxidant activity in terms of iron reducing power and total antioxidant activity. Phytochemical analysis revealed the highest content of phenolics (105.67 ± 0.56 mg GAE/g) and flavonoids (32.88 ± 0.26 mg CE/g) in the ethyl acetate fraction. SwissADME profiling indicated favorable pharmacokinetic properties, including high GI absorption and BBB permeability for several compounds. Most compounds showed low P-gp interaction and acceptable metabolic profiles. Molecular docking against acetylcholinesterase showed strong binding affinities, with Inophyllum G-1 demonstrating the highest activity (-10.9 kcal/mol), comparable to Donepezil (-11.8 kcal/mol). These results suggest that Calophyllum inophyllum is an important source of antioxidant activity and cholinesterase inhibitors that may have potentiality in the treatment of AD.

PP085

RESISTOME PROFILING AND PLASMID PHYLODYNAMICS OF MULTIDRUG-RESISTANT DIARRHEAL ESCHERICHIA COLI FROM BANGLADESH

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Multidrug-resistant (MDR) Escherichia coli is a growing concern in Bangladesh, yet plasmid backbones and mobile genetic element (MGE) architectures driving resistance among clinical isolates remain poorly characterized. We aimed to characterize the resistome, plasmid phylodynamics, and genomic island landscape of MDR E. coli from diarrheal patients in a global context. Eight MDR E. coli from diarrheal patients at the icddr,b Hospital, Dhaka (2017-2025) underwent susceptibility testing and Illumina whole-genome sequencing, followed by resistome profiling, plasmid typing, genomic island detection, and phylodynamic analysis. All isolates were resistant to ≥5 antibiotic classes across five sequence types (ST44, ST131, ST354, ST381, ST648) and four phylogroups, with 7-27 resistance determinants per genome. blaCTX-M-15, present in six isolates across four sequence types, was the central resistance hub. Fluoroquinolone resistance was chromosomally mediated via gyrA (S83L, D87N) and parC/parE mutations, whereas aminoglycoside, sulfonamide, and macrolide resistance was largely plasmid-borne. A clade A ST131 isolate carried dual parC mutations (S80I + E84V) with chromosomal blaCTX-M-15 and erm(B)-a clade C2-type profile indicating horizontal acquisition. Two ST648 isolates harbored plasmid-encoded AmpC β-lactamases (DHA-1, CMY-59/CMY-146) undetectable by routine ESBL screening. Genomic island counts ranged from 66 to 152; ST381 isolate Z12641 carried two islands exceeding 460 kbp. Conjugative IncF-type plasmids (pAA324-like) co-carried blaCTX-M-15, aminoglycoside resistance genes, and the aerobactin operon (iucABCD-iutA). Phylogeny of 104 related plasmids revealed spread across 25 countries since 2006, with recent expansion into Klebsiella. An IS6100-flanked composite transposon, first reported from Bangladesh, consolidated five-class resistance on one mobile unit. CMY-146 on the pAA026 backbone represented the second global detection of this rare β-lactamase, despite the plasmid circulating in 24 countries. Conjugative IncF-type plasmids carrying linked resistance and virulence genes drive MDR in Bangladeshi clinical E. coli, providing genomic targets for AMR surveillance across South Asia.

PP-086

KNOWLEDGE, ATTITUDE, AND PRACTICE TOWARD SKIN CANCER PREVENTION AND DETECTION AMONG BANGLADESHI UNIVERSITY STUDENTS: A CROSS-SECTIONAL STUDY

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Skin cancer in Bangladesh is an emerging health issue, frequently associated with prolonged arsenic exposure from groundwater, excess ultraviolet radiation and inadequate knowledge among the population. This study aims to assess the knowledge, attitude, and practice toward skin cancer prevention and detection among Bangladeshi university students. This cross-sectional study entailed the distribution of a structured questionnaire to public university students across various locations of Bangladesh, specifically Dhaka, Noakhali and Sylhet. The questionnaire assessed socio-demographics, knowledge (15 items), attitudes (11 items), and practices (10 items) regarding skin cancer screening and prevention. A binary logistic regression was performed to assess variables associated with practice levels (high vs. low). The study had 414 participants, of which 54.3% were females, with almost 90% aged between 21 and 26 years. Results demonstrated a potential for enhanced knowledge [median = 11 (7-14) out of a maximum score of 15], negative attitudes [median = 44 (40-51) out of a maximum score of 55], and insufficient practices [median = 20 (16-28) out of a maximum score of 50]. Students with an agriculture or veterinary science background (OR = 0.34, 95% CI: 0.13-0.86), a monthly income below 20,000 BDT (OR = 0.34, 95% CI: 0.13-0.86), and less favorable attitudes (OR = 0.23, 95% CI: 0.06-0.84) showed lesser screening and prevention practices while female category (OR = 4.21, 95% CI: 2.50-7.06) was associated with better screening practices. The government and NGOs must implement both short-term and long-term emergency intervention programs to prevent skin cancer in Bangladesh. Focused online and in-person awareness efforts are essential for improving public knowledge and assumptions, thereby improving screening and prevention practices, particularly among students from varied academic backgrounds and economically disadvantaged groups.

PP-4.24

A COMPREHENSIVE ANALYSIS OF PHENOTYPIC, GENOTYPIC, SEROLOGICAL, AND PATHOGENIC CHARACTERISTICS OF POTENTIAL VACCINE CANDIDATE STRAINS FOR SHIGELLOSIS

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Shigellosis, caused by Shigella spp., remains a major global health concern, with no approved vaccine available due to challenges related to safety, immunogenicity, and broad-spectrum efficacy. This study aimed to identify environmental bacterial strains as potential live vaccine candidates by confirming their identity (API 20E, MALDI-TOF, and whole-genome sequencing), assessing cross-reactivity with Shigella-specific antisera, and evaluating safety using the Congo Red assay, Sereny test, Rabbit Ileal Loop assay, and Mouse Lethality assay. Bacterial strains were identified using API 20E, MALDI-TOF biotyping, 16S rDNA sequencing, and WGS-based phylogenetic analysis. Serological cross-reactivity was assessed using Shigella-specific antisera. Virulence and antimicrobial resistance profiles were analyzed through whole-genome sequencing. Pathogenicity was further evaluated using the Congo Red binding assay, Sereny test, Rabbit Ileal Loop assay, and Mouse Lethality assay. Morphological, biochemical (API 20E), MALDI-TOF, and phylogenetic analyses (16S rDNA and WGS) identified six bacterial strains as Escherichia coli (S12B210), Escherichia hermannii (S14D13), Klebsiella pneumoniae (S7D9, S4D11), and Citrobacter freundii (S8B11, S1A4). All strains demonstrated significant cross-reactivity with Shigella -specific antisera. WGS analysis revealed low virulence gene content across all bacterial strains .The Congo Red assay was positive for strains S14D13, S8B11, and S1A4, while others were negative. The Sereny test confirmed a non-invasive phenotype in all strains. Enterotoxin activity was observed only in strains S14D13 and S1A4; however, no neurotoxin-induced lethality was detected in any strain, indicating favorable safety profiles. This study identifies E. coli (S12B210) and K. pneumoniae (S7D9, S4D11) as promising live vaccine candidates, demonstrating strong protein & LPS-specific crossreactivity and absence of enterotoxin and neurotoxin production, supporting their potential for safe and broadly protective vaccine development.

PP088

PROFILING OF BREAST CANCER-ASSOCIATED GENES IN PATIENTS OF NORTH BENGAL REGION OF BANGLADESH

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Breast cancer is a leading cause of global cancer morbidity and mortality, with genetic abnormalities such as chromosomal and point mutations contributing to its development. Gene expression profiling reveals transcriptional differences between normal and malignant cells, offering molecular insights into breast cancer. However, data from Bangladesh remain limited. This study aimed to profile gene expression in Bangladeshi breast cancer samples with the following objectives: (i) examine expression of breast cancer-related genes, (ii) analyze copy number variations (CNV), and (iii) assess associations between gene expression, CNV, and clinicopathological parameters. The study was conducted at the Department of Biochemistry and Molecular Biology, University of Rajshahi, over a three-year period from July 2022 to June 2025. Formalin-fixed tissue samples were collected from Rajshahi Medical College Hospital and histopathologically confirmed breast cancer patients. Gene expression profiling was performed using cDNA obtained via reverse transcriptase-polymerase chain reaction (RT-PCR) from mRNA extracted from formalin-fixed tissues. Expression of p53, HER2, and TNF-α genes was assessed by quantitative PCR and correlated with clinicopathological profiles, including tumor grade, stage, lymph node involvement, lymphovascular invasion, tumor necrosis, and focality. Gene expression analysis

revealed differential expression of p53, HER2, and TNF-α in breast cancer samples compared to normal tissues. p53 expression showed a statistically significant association with tumor grade and disease stage ($p<0.001$). HER2 overexpression was significantly associated with higher tumor grade and advanced staging ($p<0.05$). TNF-α expression was significantly correlated with tumor grade and stage ($p<0.01$). No significant associations were observed between gene expression levels and age, tumor size, focality, lymphovascular invasion, or lymph node involvement. Gene expression profiling of Bangladeshi breast cancer clarifies genomic heterogeneity, improves classification, and provides prognostic value. It supports treatment decisions in early cases and identifies mutant genes for better diagnosis, management, and prognosis.

PP089

DEVELOPMENT OF MICRONEEDLE PATCHES FOR CO-DELIVERY OF LEVOFLOXACIN AND LIDOCAINE IN DIABETIC WOUND HEALING

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Microneedle patches (MNPs) offer a promising platform for local drug delivery by enabling painless, self-administered treatment and bypassing first-pass metabolism. However, many current MNP systems are limited by high production costs, inadequate mechanical strength, and poor biodegradability and bio-adhesion. This study aims to develop a cost-effective, biodegradable gelatin-based MNP using a hot-melt press deposition technique. The patch, loaded with levofloxacin and lidocaine, was designed for localized therapeutic action and full biodegradation post-application. In vivo evaluations were conducted using a diabetic wound healing mouse model and a pinch test for localized pain relief. FT-IR and EDX analyses confirmed drug incorporation, while FE-SEM imaging showed microneedle dimensions ranging from 200 to 600 μm. Mechanical testing demonstrated sufficient tensile strength for skin insertion. In vitro antimicrobial assays revealed significant zones of inhibition. Histological analysis confirmed enhanced wound healing and post-penetration effects after five days of treatment. The developed system presents a cost-effective, biodegradable MNP suitable for various biomedical applications, including vaccine delivery, insulin administration, and gene therapy. In summary, we developed a levofloxacin/lidocaine-loaded microneedle patch (MNP) for the smart care of topical wounds and pain relief. The smart MNP demonstrated bio-adhesive with dermal penetration strength, which can disappear after administration. This MNP was studied against a diabetes-induced mouse wound model that showed irritation-free complete wound recovery.

PP090

BIOFILM-FORMING MULTIDRUG-RESISTANT KLEBSIELLA PNEUMONIAE AT DAIRY CATTLE AND FARM ENVIRONMENT: A POTENTIAL THREAT TO ANIMAL AND HUMAN HEALTH IN MYMENSINGH.

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Multidrug-resistant and biofilm-forming Klebsiella pneumoniae pose a global health concern; dairy cattle and their farm environment silently harbor these pathogens. This study aims to isolate and characterize K. pneumoniae from dairy cattle (rectal swabs from healthy and diarrhoeal cattle), and environmental samples (drinking water, drainage water, feed trap, feed, feces, and soil) at Mymensingh Sadar and Trishal Upazila with their antibiotic-resistant pattern, virulence, resistance gene profiles, and biofilm formation ability. A total of 132 samples were collected and subjected to cultural and biochemical staining tests, followed by PCR-based molecular analysis. Among them, 62 tested positive for PCR; the total prevalence was 46.2%, with notable variations between healthy 24.24% (8/33) and diseased animals 42.42% (14/33), and across the farm environment 60.60% (40/66). Of the 62 isolates randomly selected, 42 samples were subjected to the Congo red biofilm formation assay, showing 54.77% strong biofilm formers, 26.20% intermediate, 11.91% weak, and 7.14% non-biofilm formers. Biofilm formation was also confirmed by microtiter plate assay. In the antibiogram study, 100% isolates were found resistant to ampicillin, then fosfomycin 62.07%, and tetracycline 31.03%. In diarrhoeal cattle, is 100% isolates are resistant to ampicillin, fosfomycin 85.71%, tetracycline 57.14%, cefotaxime 50%, ceftriaxone 42.9%, gentamicin, chloramphenicol 28.6%, and ciprofloxacin 7.14%. Class-1integron gene detected by int1 PCR in 88.70% isolates, fosA gene in 75.81%, and the virulence gene kfu in 74.20% isolates. These findings of the ongoing study indicate that dairy cattle and environments are potential sources of antibiotic-resistant biofilm-forming virulent K. pneumoniae, which could pose a risk to both animal and human health.

PP091

GENOMIC AND PHENOTYPIC CHARACTERIZATION OF KLEBSIELLA QUASIPNEUMONIAE, KLEBSIELLA VARIICOLA, AND KLEBSIELLA AEROGENES FROM CLINICAL SPECIMENS IN DHAKA, BANGLADESH

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Klebsiella species contribute to rising antimicrobial resistance (AMR) and hospital-acquired infections. While Klebsiella pneumoniae (Kpn) is well characterized, limited data are available for closely related species such as K. quasipneumoniae, K. variicola, and K. aerogenes. This study characterized these species isolated from clinical specimens in Dhaka, Bangladesh. Between February–September 2022, 98 Klebsiella isolates were collected from Dhaka Medical College Hospital. Whole-genome sequencing (Illumina) was used for species identification, sequence typing, virulence and AMR gene detection, and plasmid profiling via Bactopia, Kleborate, AMRFinderPlus, and PlasmidFinder. Phenotypic antimicrobial susceptibility testing (AST) was also performed. Among 98 isolates, 86 were identified as K. pneumoniae and previously published (DOI: 10.1016/j.jgar.2024.12.016). The remaining 12 included eight K. quasipneumoniae, three K. variicola, and one K. aerogenes. Of these, 41.7% (5/12) were multidrug-resistant (MDR), all K. quasipneumoniae. KL68 and O3/O3a were the predominant K and O types. All isolates harbored ESBL genes, most commonly blaTEM-1. A total of 114 AMR genes were detected, with efflux-associated determinants (emrD, fosA, kdeA, oqxAB) most prevalent. Eight distinct plasmid types were identified in nine isolates. ST1998 exhibited the highest AMR gene and plasmid burden but lacked virulence genes. Genotypic resistance showed strong concordance with phenotypic AST. K. quasipneumoniae demonstrated notable genetic diversity and high ESBL prevalence, indicating emerging clinical relevance and the need for continued surveillance.

PP092

EXPLORING THE ASSOCIATION BETWEEN HOUSEHOLD COOKING PRACTICES AND ACUTE RESPIRATORY INFECTION AMONG UNDER FIVE CHILDREN IN BANGLADESH

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Acute Respiratory Infections (ARIs) remain a leading cause of illness and death among children under five in low- and middle-income countries. This study access household cooking practice and ARIs risk in children od selected environmental, socioeconomic, and health-related factors, with a focus on indoor solid fuel use. Data were extracted from the Bangladesh Demographic and Health Survey conducted during 2017/18, analyzing 7412 weighted cases of children under five. Descriptive, bivariate and multivariate analyses using a series of binary logistic regression accounted for the complex survey design. Cooking practices significantly influenced ARI occurrence. Children from households cooking outdoors had 69% lower odds of ARI symptoms (AOR: 0.31; 95% CI: 0.18–0.53), while those not exposed to indoor solid fuels had 73% lower odds ((AOR: 0.27; 95% CI: 0.15–0.49). Although cooking practices were the primary focus, these models also identified other signifcant predictors, including child's age and sex, mother's age and education, household wealth status, region, and recent episodes of diarrhea. Promoting cleaner cooking practices and addressing broader health and socioeconomic factors are crucial for reducing ARI prevalence and improving child health outcomes in Bangladesh.

PP093

MULTIDRUG-RESISTANT ORAL STAPHYLOCOCCUS AUREUS ISOLATES AND ANTIMICROBIAL STEWARDSHIP GAPS IN DENTAL SETTINGS IN BANGLADESH

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Staphylococcus aureus, particularly methicillin-resistant S. aureus (MRSA), is an increasing concern in dental settings due to its involvement in periodontal infections, oral abscesses, and post-procedural complications. Frequent antibiotic exposure and aerosol-generating procedures in dental clinics may facilitate MRSA colonization among patients and healthcare workers. MRSA strains are often associated with multidrug resistance (MDR), limiting treatment options. However, data on oral MRSA and antibiotic use practices in Bangladesh remain limited. Oral swab samples were collected from patients with dental infections and processed using standard microbiological culture and identification methods. Antimicrobial susceptibility testing was performed using the Kirby-Bauer disk diffusion method following CLSI guidelines. Confirmation of resistant isolates was conducted using the Vitek automated system and molecular detection of the mecA gene. A structured questionnaire assessed antimicrobial resistance-related knowledge, attitudes, and practices (KAP) among dental staff. Whole-genome sequencing is currently ongoing. Preliminary findings confirmed the presence of S. aureus in oral samples through culture and biochemical tests. Vitek and molecular analyses identified isolates exhibiting multidrug-resistant profiles, including resistance to commonly used beta-lactams and macrolides, suggesting possible MRSA. The KAP survey revealed gaps in antibiotic stewardship, including empirical prescribing without guideline adherence and incomplete antibi-

otic courses. These findings indicate the presence of MDR S. aureus in dental patients in Bangladesh and highlight the potential role of MRSA in oral healthcare settings. Inappropriate antibiotic practices among dental professionals underscore the need for improved antimicrobial stewardship and infection control. Ongoing genomic analysis will further clarify resistance mechanisms and support evidence-based interventions.

PP094

DESIGN, SYNTHESIS, BIOLOGICAL EVALUATION AND IN SILICO DOCKING STUDIES OF NEW N-ACETYL-1,3,4-THIADIAZOLE ANALOGUES AS ANTIMICROBIAL AND ANTIOXIDANT AGENT

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The 1,3,4-thiadiazole scaffold represents a valuable structural motif in the design of biologically active compounds with antifungal, antibacterial, anti-inflammatory, antitubercular, and anticonvulsant properties. In the present study, fifteen N-acetyl-1,3,4-thiadiazole analogues (4a-o) were synthesized via cyclization of aryl thiosemicarbazones (3a-o) and characterized by FT-IR, ^{1}H NMR, and mass spectrometry. The antibacterial activity of the synthesized compounds was evaluated against two Gram-positive strains (S. aureus and B. subtilis) and four Gram-negative strains (E. coli, S. typhimurium, P. aeruginosa, and E. cloacae). Antifungal activity was assessed against A. niger and T. harzianum. Several derivatives (3a-e, 3h, 4f, 4h, 4l, and 4n) demonstrated broad-spectrum antimicrobial activity. Compounds 3n, 3o, and 4l exhibited the highest bactericidal activity against S. aureus, with inhibition zone diameters (IZD) ranging from 15 to 19 mm, whereas 4b, 4h, 4i, 4j, 4l, and 4o showed superior activity against S. typhimurium (IZD: 15-18 mm). In antioxidant assays, compounds 3n, 4a, and 4i displayed the strongest DPPH radical scavenging activity, with IC_{50} values of 0.33-0.996 µg mL^{-1}, exceeding that of ascorbic acid (IC_{50} =1.15 µg mL^{-1}). Additional compounds, including 4e, 3o, 4f, 3k, 4b, and 3m, also exhibited notable antioxidant potential. Molecular docking studies were performed using S. aureus DNA gyrase (PDB: 2XCT) and a human antioxidant enzyme receptor (PDB: 3MNG) to evaluate the binding interactions of the most active antibacterial (3b and 4l) and antioxidant (3n and 4i) compounds, respectively. In silico drug-likeness and ADME/toxicity assessments, conducted using Molinspiration and Osiris Cheminformatics, indicated favorable pharmacokinetic profiles, compliance with Lipinski's rule of five, and low predicted toxicity. Furthermore, density functional theory (DFT) calculations at the B3LYP/6-311G(d,p) level were employed to analyze frontier molecular orbitals, providing insight into the electronic properties and reactivity of the synthesized compounds. Collectively, these findings highlight the potential of aryl thiosemicarbazones and N-acetyl-1,3,4-thiadiazole derivatives as promising candidates for the development of novel antimicrobial and antioxidant agents

PP095

ANTIMICROBIAL COMPOUNDS PRODUCING ENDOPHYTIC BACTERIA ISOLATED FROM OCIMUM BASILICUM IN BANGLADESH

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Antibiotic resistance is a major threat to global health, prompting the search for new antimicrobials. Bacteria living in medicinal plants are a potential source of antimicrobial compounds. They have applications in medicine, food, agriculture, and animal husbandry. There is little research on endophytes that produce antimicrobial compounds in Bangladesh. The goal of this study is to isolate and examine bacteria from Ocimum basilicum (basil), a medicinal plant capable of producing antimicrobial compounds. A total of 12 samples were collected, including basil leaves and stems. We sterilized the samples and crushed them to obtain the bacteria. Isolate identification was based on morphological and biochemical reactions. Bacterial strains grown in synthetic media produced antimicrobial compounds, and the well-diffusion method was used to assess activity. The extracted antimicrobial compounds were tested for stability at different temperatures, pH, organic solvents, food-grade salt, and surfactants. A total of 40 bacterial strains were isolated from the collected samples. Three isolates (7.5%) showed antimicrobial activity against Staphylococcus aureus, Bacillus cereus, and Escherichia coli. The antimicrobial compounds were more effective against Gram-positive bacteria. One isolate proved stable under different temperature, pH, organic solvent, and food-grade salt conditions. Antimicrobial compound production reached its peak at 96 hours of incubation, after which it declined. The antimicrobial compounds extracted from endophytic bacteria of Ocimum basilicum (basil) showed significant activity against Gram-positive and Gram-negative pathogens. The antimicrobial compounds may serve as potential alternatives to chemical preservatives in food and can be used to treat infectious diseases.

PP096

INVESTIGATION OF THE PHYTOCHEMICAL COMPOSITION & ANTIOXIDANT PROPERTIES OF MOMORDICA CHARANTIA

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Momordica charantia is an important medicinal plant in the Cucurbitaceae family, and its fruit is frequently eaten as a vegetable. It originated from India and Malaysia and is extensively distributed throughout tropical, subtropical, and mild temperate climates worldwide. The present study evaluated the impact of different solvents on extraction yields, phytochemical constituents and in vitro antioxidants of bitter melon fruit & seed extracts. The extracts were analyzed for the presence of saponins, alkaloids, flavonoids, anthocyanin & betacyanin, steroids, terpenoids, phenols, coumarins and phlobatannin. Their antioxidant potential was assessed using 2,2-azinobis (3-ethylbenzothiazoline-6-sulfonic acid) (ABTS) and 2,2-diphenyl-1- picrylhydrazyl (DPPH) free radical scavenging assays. The acetone and methanol extracts of bitter melon fruit & seed extracts included a diverse array of

bioactive components such as saponins, alkaloids, betacyanin, quinones, terpenoids, flavonoids, which were significantly higher compared to other solvents in different experiment. The acetone extract exhibited significant DPPH radical cation scavenging activity, with (IC50= 58.26 µg/mL, R2=0.9664). The methanol extract exhibited significant DPPH radical cation scavenging activity, with (IC50=152.04 µg/mL, R2=0.9358). Ascorbic acid has the lowest IC50 value (41.06 µg/mL, R2= 0.9629), indicating very strong µantioxidant activity. The methanolic extract exhibited significant ABTS radical cation scavenging activity, with (IC50=208.20 µg/mL, R=0.9006). The acetone extract exhibited significant ABTS radical cation scavenging activity, with (IC50=224.0 µg/mL, R2=0.8398). The ascorbic acid extract exhibited significant ABTS radical cation scavenging activity, with (IC50=59.05912 µg/mL, R2=0.9563). Ascorbic acid has the lowest (IC50=59.059 pg/mL), indicating very strong antioxidant activity. This study investigates the antioxidant properties and phytochemical composition of fruit & seed extracts from these plants to enhance understanding of their bioactive compounds. Comprehensive phytochemical screening was conducted to identify the presence of alkaloids, flavonoids, phenols, and other bioactive components. Antioxidant activity was quantified using assays such as DPPH and ABTS which demonstrated significant free radical scavenging potential in both extracts. This suggests their potential use as natural sources of antioxidants in functional foods and therapeutic formulations aimed at reducing oxidative stress and supporting metabolic health. The findings underscore the value of these extracts as nutraceuticals and provide a basis for further research into their health benefits and application in chronic disease prevention.

PP097

ISOLATION, CHARACTERIZATION, AND BIOCONTROL OF PATHOGENIC VIBRIO PARAHAEMOLYTICUS FROM DISEASED TIGER SHRIMP (PENAEUS MONODON) IN BANGLADESH

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The tiger shrimp (Penaeus monodon) is a cornerstone of Bangladesh's blue economy, significantly contributing to export earnings, rural livelihoods, and national food security. However, the sustainability of shrimp aquaculture is severely threatened by bacterial diseases, particularly Acute Hepatopancreatic Necrosis Disease (AHPND), caused by toxin-producing strains of Vibrio parahaemolyticus. This study aimed to isolate and characterize pathogenic V. parahaemolyticus from commercial shrimp farms in Satkhira, Bangladesh, and to evaluate indigenous probiotics and medicinal plant extracts as sustainable biocontrol alternatives. Diseased shrimp were collected from culture ponds in Samnagar, Satkhira. Bacterial isolates were obtained using TSBS medium and identified through morphological, biochemical, and molecular methods. 16S rRNA gene sequencing confirmed the pathogenic isolate as Vibrio parahaemolyticus. Two representative strains (GISV1-1 and GISVK-2) were subjected to whole-genome sequencing to elucidate their genetic architecture, including virulence determinants. To develop eco-friendly disease management strategies, indigenous probiotic bacteria were screened for antagonistic activity against the pathogen using in vitro inhibition assays. Seven probiotic candidates demonstrated significant inhibitory effects, including Bacillus amyloliquefaciens GIFPSR-101, B. paramycoides GIFPSR-103, B. thuringiensis GIFPSR-111, Priestia aryabhattai GIFPSR-118, and B. cereus GIFPSR-121. Concurrently, ethanolic and ethyl acetate extracts of four medicinal plants viz., garlic, amla, clove, and cinnamon were evaluated for antimicrobial activity. Ethyl acetate extracts of garlic (27 mm inhibition zone) and cinnamon (30 mm inhibition zone) exhibited the most potent activity

against V. parahaemolyticus. The integration of indigenous probiotics and plant-derived antimicrobials presents a promising alternative to conventional antibiotics, reducing the risk of antimicrobial resistance while enhancing disease resilience. These findings provide a foundation for developing practical, environmentally sustainable biocontrol strategies to support the long-term viability of Bangladesh's shrimp aquaculture sector.

PP098

EXPRESSION ANALYSIS OF CANCER STEM CELL FACTORS IN BREAST CANCER PATIENTS IN BANGLADESH

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Cancer stem cells (CSCs) are a subpopulation of tumor cells capable of self-renewal, differentiation, and tumor regeneration and are strongly implicated in cancer initiation, metastasis, treatment resistance, and disease recurrence. Key transcription factors, including Oct3/4, SOX2, and Notch2 are well-established regulators of stemness and CSC activity in breast cancer. Oct3/4 and Notch2 are critical drivers of self-renewal and tumor aggressiveness, while SOX2 cooperates in maintaining pluripotency. Despite the rising burden of breast cancer in Bangladesh, expression data on these CSC-related factors in Bangladeshi patients remain scarce. This study aimed to analyze the mRNA expression of Oct3/4, SOX2, and Notch2 in breast cancer patients from the North Bengal region of Bangladesh and to correlate their expression with clinicopathological parameters. Formalin-fixed tissue samples were collected from Rajshahi Medical College Hospital and histopathologically confirmed breast cancer patients (n=20) and matched normal breast tissue controls from the North Bengal region of Bangladesh. Total RNA was extracted, quantified, and reverse-transcribed into cDNA. mRNA expression levels of Oct3/4, SOX2, and Notch2 were quantified by quantitative real-time PCR (qRT-PCR) using SYBR Green master mix. Expression data were normalized to the GAPDH housekeeping gene, and relative fold changes were calculated using the $2^{-\Delta\Delta Ct}$ method. Statistical analysis was performed using two-way ANOVA ($p<0.05$), and associations with clinicopathological parameters, including tumor grade, stage, lymph node involvement, lymphovascular invasion, and tumor necrosis, were evaluated. Oct3/4 and Notch2 were significantly upregulated in breast cancer samples compared to normal tissue. Oct 3/4 showed a striking ΔΔCt of −6.577, corresponding to a ~95-fold upregulation in cancer versus normal tissue, indicating markedly elevated stemness activity. Notch2 demonstrated a ΔΔCt of −5.328, representing a ~40-fold upregulation, suggesting active Notch-mediated cancer stem cell signaling in this cohort. SOX2 was moderately upregulated in cancer samples compared to Oct 3/4 and Notch 2 (ΔΔCt = -3.986, fold change = 14.88×), indicating activation of this particular stemness factor. These findings highlight a differential regulation of CSC markers in Bangladeshi breast cancer patients. This study provides the first qPCR-based evidence of cancer stem cell marker upregulation in breast cancer patients from North Bengal, Bangladesh. Significant overexpression of Oct3/4 (~95-fold), Notch2 (~40-fold), and SOX2 (~15-fold) underscores the activation of stemness pathways in this cohort, with Oct3/4 emerging as the most prominently dysregulated factor. These findings suggest that CSC-related transcription factors may contribute to tumor aggressiveness and poor prognosis in Bangladeshi breast cancer patients. Further large-scale studies are warranted to validate these markers as potential prognostic indicators and therapeutic targets in this underrepresented population.

PP-099

PRECLINICAL TOXICITY PROFILE AND THERAPEUTIC POTENTIAL OF TERMINALIA ARJUNA IN PATIENTS WITH NON-ALCOHOLIC FATTY LIVER DISEASE

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Non-alcoholic fatty liver disease (NAFLD) is a leading cause of chronic liver disease and hepatic fibrosis in Bangladesh and worldwide. The bark of Terminalia arjuna, traditionally used for hyperlipidemia and cardiovascular disorders, exhibits hepatoprotective, antioxidant, and lipid-lowering effects incal studies. However, data on the acute/subacute toxicity of T. arjuna bark powder (TABP) and its clinical efficacy in Bangladeshi NAFLD patients are limited. To evaluate the acute/subacute toxicity of TABP in Swiss albino mice and its clinical effects in NAFLD patients. Subacute toxicity was assessed in male Swiss albino mice given oral TABP at 500, 1000, or 2000 mg/kg daily for 14 days, with monitoring of behavioral, hematological, biochemical, and histopathological parameters. Clinically, 40 NAFLD patients were randomized in a quasi-experimental study (July 2023–June 2024, Department of Hepatology, Bangladesh Medical University, Dhaka) into two groups: TABP plus lifestyle modification (n=20) or lifestyle modification alone (n=20), treated for 24 weeks. In mice, TABP caused no mortality, morbidity, behavioral changes, or histopathological abnormalities at any dose; serum ALT decreased significantly after 14 days. In patients, adverse events were mild and did not require discontinuation. The TABP group showed significant improvements in ALT (59.25 ± 51.14 to 39.18 ± 22.83 U/L), AST (41.05 ± 24.55 to 30.73 ± 12.01 U/L), hepatic fat content (311.85 ± 24.83 to 291.0 ± 33.2 dB/m), and fibrosis (6.0 ± 1.54 to 5.46 ± 1.35 kPa). However, TABP was not superior to lifestyle modification alone. TABP is safe at high doses in mice and humans, reduces ALT dose-dependently, and improves hepatic steatosis and fibrosis in NAFLD patients. These findings support its safety and potential utility, justifying multicenter trials with higher doses and longer durations.

PP100

EVALUATION OF THE SYNERGISTIC ANTIHYPERGLYCEMIC POTENTIAL OF MOMORDICA CHARANTIA AND CINNAMOMUM CASSIA IN A RAT MODEL OF PREDIABETES

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Previous studies showed that different combinations of extracts exhibit distinct modes of action, and the combination of Momordica charantia and Cinnamomum cassia is the most effective for treating pre-diabetes in a rat model. In this study, we explored the molecular mechanisms through which Momordica charantia and Cinnamomum cassia ameliorate pre-diabetic conditions in experimental rat models. A pre-diabetic rat model was developed by feeding male Wistar rats a high-fat diet for 6 months. These pre-diabetes rats were treated with extracts of M. charantia, C. cassia, or their combination at a dose of 1g/kg/day for 30 days. After the treatment periods, FBG, 2hBG, OGTT, ITT, serum insulin, and adiponectin were measured. The thiobarbituric acid-reactive substances (TBARS) and reduced glutathione (GSH) were measured in the hearts, livers, and kidneys of the experimental rats. GLUT4 mRNA was measured from the adipose tissues, and [14C]2-deoxy D-glucose (2DG) uptake was monitored in isolated adipocytes. Treatment of M. charantia and C. cassia significantly reduced FBG level comparable to pioglitazone, a standard drug used for the management of type 2 diabetes. M. charantia and C. cassia were also effective in lowering 2hBG, and the mixture of these two extracts reduced 2hBG dramatically. Neither M. charantia nor C. cassia reduced fasting serum insulin levels significantly; however, the mixture-treated group showed a significant reduction. Both M. charantia and C. cassia increased insulin sensitivity, and their mixture showed a greater effect than either component alone. TBARS concentration increased significantly in the hearts, livers, and kidneys of pre-diabetic rats compared with non-diabetic rats. M. charantia and C. cassia were found to reduce the formation of TBARS in these tissues. The reduced GSH levels in pre-diabetic rats were restored by C. cassia treatment. Serum adiponectin was increased significantly in the mixture-treated group, and the major player for this activity is M. charantia. GLUT4 mRNA was moderately up-regulated by C. cassia and strongly by M. charantia and the mixture. The C. cassia enhanced 2DG uptake in the isolated adipocytes. M. charantia and C. cassia have synergistic activity in ameliorating pre-diabetes by up-regulating GLUT4 mRNA, modulating oxidative stress, and 2DG translocation in this rat model.

PP101

IMPROVING MEDICATION SAFETY THROUGH BRAND-NAME–BASED DRUG INTERACTION DETECTION IN BANGLADESH

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Drug-drug interactions (DDIs) are a major cause of adverse drug events and pose significant patient safety risks, particularly in settings with widespread polypharmacy. Most existing DDI detection tools rely exclusively on generic drug names, which creates an accessibility barrier for patients and caregivers in Bangladesh who are more familiar with locally marketed brand names. Furthermore, currently available systems rarely contextualize interactions with prevalent regional health conditions such as diabetes, hypertension, and chronic kidney disease. The aim of this study is to develop a brand-name-based drug interaction detection system that maps locally used pharmaceutical brand names to their corresponding generic drugs and identifies potential DDIs using internationally recognized pharmacological databases. A dataset of commonly used Bangladeshi drug brand names and their corresponding generic compositions will be compiled from publicly available pharmaceutical sources, including the Directorate General of Drug Administration (DGDA) database. These brand names will be mapped to standardized generic drug entries in pharmacological datasets such as DrugBank and OpenFDA. A relational database system will be developed to support brand-name queries and automatically resolve them to generic drug names for DDI detection. The system will also incorporate structured information on common comorbid conditions to identify elevated interaction risks in relevant patient profiles. In addition, a medication guidance module will summarize key information, including intake timing, potential food interactions, and adherence recommendations. The study is currently ongoing. Preliminary work involves compiling a curated dataset of commonly prescribed Bangladeshi brand-name medications and establishing the mapping pipeline to their generic equivalents using DrugBank and OpenFDA datasets. Expected outcomes include the development of a validated brand-to-generic mapping database and successful retrieval of drug–drug interaction information through brand-name queries. Integration of interaction risk alerts based on common health conditions is also anticipated. The system will further explore machine learning-based drug interaction prediction using existing DDI datasets. This study aims to bridge the gap between locally recognized pharmaceutical brand names and generic-based DDI databases. By enabling interaction detection through brand-name inputs and providing patient-oriented medication guidance, the proposed system may improve medication safety, enhance patient awareness, and support clinical decision-making in resource-limited settings.

PP102

VKH SYNDROME: SNP ANALYSIS OF HLA-CLASS II GENES AND AUTOIMMUNE DYSREGULATION IN BANGLADESH

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Vogt- Koyanagi- Harada (VKH) is a uveitis-associated autoimmune disease, prominently affecting the melanocyte enrich tissues such as eyes, skin, ears and central nervous system (meninges), and caused by the mutations in Human Leucocyte Antigen (HLA) region of chromosome 6. The increasing prevalence of VKH in Asia including India, China and Japan, making it a growing health concern. Although the prevalence of VKH in Bangladesh has not been documented yet, we hypothesized that VKH is also evolving in Bangladesh. In our preliminary Bangladesh-based survey data, we have found 25 VKH patients, who received inappropriate treatment and/or prescribed medication due to false-positive diagnosis, and 3% of these patients lost 70-90% of their vision in one eye before they were properly diagnosed with VKH. The aim of our study is to investigate the genetic factors influencing VKH in Bangladeshi population by studying single nucleotide polymorphisms (SNPs) in HLA-class II genes. In collaboration with hospital and physician, we further aim to list appropriate symptoms to diagnose VKH at early stage and estimate the possible prevalence of this disease by conducting survey-based study in Bangladesh. b) Method: Blood DNA has been isolated from 25 healthy and VKH subjects, PCR genotyping and sanger sequencing are being carried out for finding polymorphism. c) Result: In our preliminary data, sanger sequencing revealed two mismatch mutations in HLA gene some visual differences among samples have been seen in PCR genotyping of 25 VKH patients and healthy population. d) Conclusion: This study will help us to investigate the significant polymorphism of HLA gene, Identification of these genotypic changes can help in drug designing for the specific mutation and the case study as well as the population survey on VKH will help to predict the possible prevalence of VKH disease for the first time among Bangladeshi population.

PP 103

STATUS OF INCIPIENT NEPHROPATHY-RELATED BIOMARKERS AMONG PREDIABETIC SUBJECTS: A CASE-CONTROL STUDY

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Prediabetes (PD) is an intermediate state of hyperglycemia, with glucose levels above normal but below the diabetic mellitus (DM) diagnostic cut-off values, and it is subgrouped as Impaired Fasting Glucose (IFG), Impaired Glucose Tolerance (IGT), or IFG-IGT combined. It increases the risk of micro- and macrovascular complications. The prevalence and risk factors of early nephropathic changes (incipient nephropathy or IN) inPD and its subtypes are yet to be studied among Bangladeshi subjects. The objectives of the study were to compare the proportions of PDs (and their subgroups) with IN, and also to explore the socioeconomic, anthropometric, clinical and biochemical risk factors of IN as investigated by the early nephropathy marker, estimatedGlomerular Filtration Rate (eGFR). A case-control observational study was conducted on 171 Nondiabetic (ND) and 34 prediabetic (PD) subjects recruited purposively from clinical as well as community settings. The biochemical investigations included Fasting and 2-hr serum glucose (FBG and 2hABG) (glucose-oxidase method), lipid profile (enzymatic method), and serum creatinine (kinetic method). eGFR was calculated by using the standard formula. The proportion of PD among 215 total subjects was 16% (Nondiabetic or ND, 64%, DM 20%); among the 34 PDs, the proportions were: IFG, 53%, IGT, 32% and IFG-IGT, 15%. The median value of eGFR was significantly lower (p=0.008) in the PD [eGFR, mL/min/1.73 m², median (min-max), 115(60-131)] as compared to the ND [120(76-141)] group. Higher age, higher BMI, higher hip circumference, and higher systolic blood pressure were significant (p=0.015-0.001) risk factors associated with PD, as found in the group comparison analysis using the Mann-Whitney test. The same risk factors showed significantly higher values among subjects with IFG, IGT, and IFG-IGT, as compared to their ND counterparts. On Spearman's correlation analysis, age showed a strong negative correlation with eGFR (r, -0.887; p=0.001) among the PD subjects. About one-sixth of the adult urban Bangladeshis suffer from prediabetes and more than fifty percent of these prediabetics suffer from impaired fasting glucose (IFG). A substantial proportion of prediabetics, especially in the IFG subgroup, already develop early nephropathic changes (incipient nephropathy), and traditional risk factors like aging, obesity and hypertension play important roles in the development of the early renal problem.

PP104

ASSOCIATION OF ARSENIC EXPOSURE WITH ADVERSE NEONATAL OUTCOME AND GLUCOSE INTOLERANCE IN GDM SUBJECTS OF BANGLADESH

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Exposure to arsenic has known toxic effects but the effect on pregnancy outcomes is not widely documented. Therefore, we aimed to investigate the effects of maternal arsenic exposure on mother and neonatal outcomes. Under an observational cross-sectional design, a total of 263 pregnant women (age in years, M±SD, 21±3.7) residing in an arsenic affected area of Bangladesh, were enrolled in this study. Degree of chronic arsenic exposure was assessed by the urinary arsenic level (UAs). GDM was diagnosed by World Health Organization (WHO) criteria,

and neonatal outcomes were assessed using Activity Pulse Grimace Appearance Respirations (APGAR) Score. Birth weight and sizes of the neonates were assessed by a specialist obstetrician. Serum glucose and urinary arsenic level were measured by the Glucose Oxidase method and by ultraviolet/visible spectrophotometry. A total 263 pregnant women (age in years, M±SD, 21±3.7) residing in an arsenic affected area, were subjected to a 2 sample OGTT at the third trimester of gestation. Among them 73 (28%) women developed GDM which was significantly higher from the overall prevalence of GDM (13%) in Bangladesh. UAs was significantly higher in the GDM group as compared to the non-GDM group [UAs, µg/l, M±SD (range), 204.2±67.0 (67.0-377.0) vs 77.3±38.1 (22.0-99.0), p <0.001]. Neonates of GDM mothers had significantly lower Apgar score of the neonates compared to the neonates from non-GDM mothers [Apgar score, M±SD, 4.7±0.8 vs. 6.4±0.7, p<0.001]. Pearson's correlation analysis in GDM subjects revealed that UAs levels were positively correlated with both fasting and postprandial serum glucose levels (p<0.001) and (p<0.001) respectively. Again, a significant inverse correlation of UAs with birth weight and size was observed (p< 0.001). The APGAR Score of the neonates were found to have a significant negative correlation (p<0.001) with UAs level. The effect of chronic arsenic exposure is associated with glucose intolerance during pregnancy and it also adversely affected the birth outcomes.

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AWARENESS OF THE HOSPITAL NURSES ON PREVENTION AND CONTROL OF INFECTION IN NOAKHALI DISTRICT

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Infection control is a practical, evidence-based approach to preventing patients and health workers from being harmed by avoidable infections. Infection is a significant concern for the health care system and a burden to the public health discipline. Different types of hospital-acquired infections are urinary tract infections (UTI), respiratory tract infections (RTI), bloodstream infections, surgical site infections, etc. HAIs are associated with high morbidity and mortality, prolonged hospital stays, long-term disability, and a massive financial burden for health systems. Effective infection control requires constant action at all levels of the health system, including policymakers, facility managers, health workers, and those who access health services. This study aimed to assess the awareness level of hospital nurses on the prevention and control of infection. The study was conducted between August 2024 and November 2025 in the Noakhali district of Bangladesh. A multistage sampling technique was used to select the hospitals in Noakhali Sadar, and 152 nurses were selected by using convenience sampling. Data was collected through face-to-face interviews using a semi-structured questionnaire and analyzed through SPSS software version 22.0. The results showed that 40.79% of participants have fair awareness, 11.84% participants have poor awareness, and only 47.37% of nurses have good awareness to prevent infection. Despite established infection control measures and a workforce largely composed of trained and experienced nurses, overall awareness of infection control protocols was found to be inadequate. This gap highlights the need for continuous professional development through regular refresher courses, structured training programs for newly appointed Nurses, and ongoing monitoring of infection control practices. Strengthening nurses' knowledge and adherence to infection prevention guidelines is essential to minimizing the risk of hospital-acquired infections and improving patient safety outcomes

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KNOWLEDGE, ATTITUDE AND PRACTICES REGARDING MENSTRUAL HYGIENE MANAGEMENT AMONG ADOLESCENT SCHOOL-GOING GIRLS IN A RURAL AREA OF BANGLADESH: A CROSS-SECTIONAL STUDY

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Menstrual hygiene management (MHM) remains a significant public health concern in rural areas of developing countries, including Bangladesh. Limited knowledge, cultural taboos, and inadequate facilities can adversely affect the health and education of adolescent girls. This study aimed to assess the knowledge, attitude, and practices (KAP) regarding menstrual hygiene management among adolescent school-going girls in a rural area of Bangladesh. A descriptive cross-sectional study was conducted among 285 adolescent girls from secondary schools using a structured and pretested questionnaire. Descriptive statistics summarized socio-demographic data and KAP responses, while Chi-square tests determined associations between menstrual hygiene management knowledge and selected socio-demographic factors. Among participants, 60.35% had inadequate knowledge of menstrual hygiene, although 87.4% reported having heard about menstruation. About 72.63% showed a good attitude, while 75.8% practiced good menstrual hygiene. Significant associations were found between menstrual hygiene knowledge and mother's education (p=.012), father's education (p=.007), age (p=.027), and toilet availability (p=.033). Additionally, mother's education was significantly associated with menstrual hygiene practices (p=.022). No statistically significant association was observed between knowledge and attitude (p=.601) or between knowledge and practice (p=.060). There are still information gaps among adolescent girls in rural area of Bangladesh, despite their generally positive attitudes and practices around menstrual hygiene. Enhancements to school sanitation facilities and educational initiatives aimed at students and their parents particularly mothers are crucial for promoting improved menstrual health and lowering stigma

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KNOWLEDGE, PERCEPTIONS AND PRACTICES ABOUT DEWORMING DRUG CONSUMPTION AMONG THE WOMEN OF CHAR AREA OF MUNSHIGANJ: A CROSS-SECTIONAL STUDY

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In developing nations like Bangladesh, where it is becoming more common, especially in rural areas, helminthes infection has grown to be a significant public health concern. In order to prevent transmission of helminthic infections, it is crucial for parents to have the necessary information and use practical methods.There are limited reports focusing on how best to implement control helminthes infection intervention to increase success within the community. This study aimed to assess the knowledge, practices, and perceptions related to deworming drug consumption among women residing in the char areas of Munshiganj. This was a cross-sectional study conducted in the char areas

of Munshiganj district from November to December 2023. A total of 210 women were selected using a multistage sampling technique. Data were collected through face-to-face interviews using a semi-structured questionnaire. Descriptive statistics, Chi-square tests, and Fisher's exact tests were performed. A p-value of <0.05 was considered statistically significant with a 95% confidence interval (CI). All statistical analyses were conducted using SPSS (version 22.0). Out of 210 participants, 39% were aged 26-35 years, 91% were married, and 73.3% were home-makers. Around 40% reported a history of recent helminthic infection. Study shows that women of char area's 86.2% had poor knowledge score,12.38% had fair knowledge and only 1.4% participant's had good knowledge. In addition, knowledge was significantly associated with family income, housing condition, and occupation (p=.010, .010, and <.001). Furthermore, knowledge was significantly associated with the materials used for handwashing after defecation and the pattern of deworming drug use within the family (p<.001 and p=.018). Similarly, a significant association was found between knowledge and fear of taking deworming drugs (p=.024). Moreover, the study was revealed the scenario of knowledge, perception and perceptions of helminthes infection prevention practices. Furthermore, the study will assess the factors associated with knowledge, perception and perceptions and helminthes infection. Community-based awareness programs focusing on proper handwashing practices are recommended, particularly in vulnerable char regions, to reduce the burden of helminthic infections.

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INVESTIGATION OF ANTIMICROBIAL RESISTANCE PROFILE OF BACTERIA ISOLATED FROM THE SUPPURATIVE WOUND IN A CAPTIVE ROYAL BENGAL TIGER (PANTHERA TIGRIS) IN THE ENVIRONMENT-HUMAN INTERFACE IN CHATTOGRAM ZOO, BANGLADESH

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Antimicrobial resistance (AMR) poses a critical threat to human and animal health, fueled by the indiscriminate and excessive antibiotic use in livestock and captive wildlife. Intensive antibiotic use in food-producing animals contributes to the emergence of resistant bacteria that may contaminate raw meat-based diets fed to zoo carnivores. Close human-animal contact in captive settings and environmental sources further increase the risk of AMR transmission. In Bangladesh, most AMR surveillance mainly emphasizes on livestock, poultry and human but in captive wildlife, especially captive felines like tigers, are often disregarded. This research aimed to isolate, identify and molecularly characterize the AMR profile of the associated bacteria, determine the prevalence and evaluate the potential impact of bacterial strains from the human-animal-environment interface at Chattogram Zoo. Swab samples were collected from multiple sites (wounds, oral cavity, nostrils, ears, paws, rectum) of affected and healthy tigers, as well as from enclosure surfaces, feed (chicken and beef), water, and nasal/hand swabs of zoo personnel. Bacterial isolation was performed using selective media, followed by molecular identification with 16S rRNA sequencing and whole genome sequencing of selected isolates. Antimicrobial susceptibility testing will be conducted using the Kirby-Bauer disk diffusion method, and resistance profiles will be interpreted according to standard clinical breakpoints. We obtained 104 bacterial isolates from different sources, comprising 69 gram-positive and 35 gram-negative bacteria. Molecular analysis will identify key antimicrobial resistance genes and possible genetic relatedness between isolates from different sources. The findings will highlight potential transmission pathways of AMR at the human-animal-environment interface and will provide evidence to guide infection control and antimicrobial stewardship in captive wildlife settings. This research will provide critical insights into the prevalence, genetic basis, and transmission pathways of AMR in captive tigers, informing future surveillance and control strategies.

PP109

ANTIMICROBIAL RESISTANCE PATTERN, VIRULENCE GENES PROFILING, AND BIOFILM FORMATION IN AVIAN PATHOGENIC ESCHERICHIA COLI ISOLATED FROM ORNAMENTAL BIRDS AND THEIR HANDLERS: A ONE HEALTH APPROACH

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Ornamental birds, having popularity as companions; nevertheless, may act as silent reservoirs for zoonotic multidrug-resistant (MDR) bacterial pathogens such as avian pathogenic Escherichia coli (APEC). This work employed a One Health approach to isolate APEC from ornamental birds, their habitat, and human handlers, assessing their antimicrobial susceptibility and biofilm-forming ability, and specific virulence and resistance genes. A total of 20 samples (hand swabs, nasal swabs, fecal litter, feed, and water) were collected. Initial E. coli identification was confirmed by Polymerase Chain Reaction (PCR) targeting the malB gene. Antimicrobial Susceptibility Testing (AST) was conducted using commonly used seven antibiotics by disk diffusion test. Additionally, isolates were phenotypically screened for biofilm formation ability by Congo red assay. Molecular characterization was carried out by PCR for class 1 integron resistance gene (int1) and APEC specific virulence markers (fimC, iucD and papC). E. coli was highly prevalent, with 90% (18/20) of the tested samples positive for malB. AST revealed alarming phenotypic resistance: 81.8% to Azithromycin, and 63.6% to Tetracycline. Genotypic analysis was strongly aligned with these observations, detection of int1 multidrug-resistance gene in 80% (16/20) of samples. Virulence genes (fimC, iucD, papC) were widely disseminated across avian, ambient and handler samples. Additionally, in case of phenotypic studies, 63.6% (7/11) of the tested isolates exhibited weak to intermediate biofilm-forming abilities, primarily isolated from feed and fecal litter and human hand swabs that increased environmental persistence. Furthermore, strong biofilm-forming ability was present in 9.1% (1/11) of the isolates. The integration of multidrug resistance, virulence genes, and biofilm production in E. coli isolates obtained from ornamental birds, their surroundings, and related handlers represents a potential zoonotic threat. These findings underscore the necessity of a One Health strategy, promoting comprehensive surveillance, effective sanitation protocols, and increased awareness among avian handlers to minimize cross-species transmission of infectious pathogenic strains.

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DEVELOPMENT OF AN OXIDATIVE PRE-TREATED PENCIL GRAPHITE ELECTRODE FOR HIGHLY SENSITIVE AND COST-EFFECTIVE ELECTROCHEMICAL DETECTION OF PARACETAMOL: FABRICATION, COMPREHENSIVE CHARACTERIZATION, KINETIC AND MECHANISTIC INVESTIGATION

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Paracetamol (PC) is widely used as an analgesic and antipyretic, but overdose can cause serious toxicity. Accurate detection is essential for pharmaceutical quality control. Conventional methods (chromatography, spectrophotometry) are costly and time-consuming. Electrochemical methods offer a cheaper, faster alternative. This study aims to develop a low-cost, sensitive electrochemical sensor using an oxidatively pretreated pencil graphite electrode (OP-PGE). The objectives include enhancing electrode surface activity, improving selectivity and sensitivity, and studying the kinetics and mechanism of PC detection. A PGE is prepared from a 6B pencil, polished, and electrochemically pretreated using cyclic voltammetry (1.5-2.0 V, ~100 cycles). The modified electrode is characterized using CV and EIS. Detection of paracetamol is performed using electrochemical techniques (CV, amperometry). Experimental parameters such as pH and scan rate are optimized. Interference studies (with other species), stability, reproducibility, and real sample (tablet) analysis are also conducted. The CV results showed enhanced peak current and improved electrochemical response after pretreatment, indicating increased electroactive surface area. EIS analysis demonstrated reduced charge transfer resistance, confirming improved electron transfer kinetics. The sensor exhibited: LOD: 0.98 µM and LOQ: 3.29 µM. Good sensitivity and selectivity .Stable and reproducible response .These results confirm successful electrode modification even without advanced surface analysis. The study demonstrates that CV and EIS are sufficient to confirm electrochemical performance of the modified PGE. Although SEM, XPS, and EDS were not performed at this stage, they are proposed for future validation. The developed sensor is low-cost, sensitive, and suitable for practical applications.

PP111

MADRAS THORN LEAF-DERIVED ACTIVATED CARBON COUPLED WITH $NICO_2S_4$ FOR HIGH-PERFORMANCE ASYMMETRIC SUPERCAPACITOR: MECHANISTIC INSIGHTS INTO HYBRID CHARGE STORAGE

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Biomass-derived carbons are promising electrode materials for supercapacitors due to their high-power density, excellent cycling stability, and rapid charge-discharge capability. However, achieving high energy density in electrochemical double-layer capacitor (EDLC) remains challenging. This work aims to develop a low-cost, sustainable, and reliable electrode material for energy storage. To address these challenges, a novel Madras Thorn leaf-derived activated carbon (MTAC) was synthesized and evaluated in a symmetric EDLC configuration. Mechanistic analysis supported by experimental evidence was used to identify key factors limiting energy density. To further enhance performance, an asymmetric hybrid supercapacitor was constructed by coupling MTAC with $NiCo_2S_4$, combining EDLC and pseudocapacitive mechanisms. MTAC was prepared via a two-step carbonization and chemical activation process, while $NiCo_2S_4$ was electrodeposited on nickel foam. Structural and surface properties were characterized using XRD, Raman spectroscopy, scanning electron microscopy, and nitrogen adsorption-desorption analysis. Electrochemical performance was evaluated in symmetric and asymmetric configurations using cyclic voltammetry, galvanostatic charge-discharge, and electrochemical impedance spectroscopy. Capacitive and diffusion-controlled intercalation contributions were analyzed using Cottrell and Dunn's equations. MTAC exhibits a high specific surface area of 2838 $m^2 g^{-1}$, pore volume of 1.50 $cm^3 g^{-1}$, and mesopores (2-10 nm). Despite these features, the symmetric EDLC delivers a moderate energy density of 14.79 Wh kg^{-1} at 0.5 A g^{-1} with a power density of 275.9 W kg^{-1} in 3 M KOH, while maintaining excellent stability over 20,000 cycles. Mechanistic analysis reveals that incomplete surface utilization limits energy density. The asymmetric hybrid device ($NiCo_2S_4$//MTAC) overcomes this limitation, achieving 35.75 Wh kg^{-1} energy density, 3693 W kg^{-1} power density, and 95% capacitance retention after 20,000 cycles. These findings reveal the cause of energy density limitation and demonstrate that ($NiCo_2S_4$//MTAC) effectively enhances energy density, durability, offering a promising strategy for next-generation high-performance supercapacitors.

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JUTE FIBER-DERIVED FLUORESCENT NANOPARTICLES FOR SUSTAINABLE ANTICANCER DRUG DELIVERY

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The development of safe and effective nanocarrier systems is essential for enhancing the systemic delivery of chemotherapeutic agents while minimizing off-target toxicity. In this study, we developed a novel, eco-friendly nanoplatform using fluorescent nanoparticles (FNPs) synthesized from natural jute fibers for the delivery of the platinum-based chemotherapeutic agent carboplatin (CBP). The FNPs were subsequently functionalized for drug loading and encapsulated forming CBP-loaded FNPs to improve stability, circulation time, and biocompatibility. Structural and chemical characterizations using FT-IR, UV-Vis, and ^{1}H-NMR analyses confirmed the successful incorporation of CBP and liposomal components, while fluorescence emission studies demonstrated excitation-dependent multicolor fluorescence, suggesting potential for imaging-guided therapy. Additionally, SEM and TEM analyses revealed well-dispersed, spherical FNPs and a distinct core-shell morphology in CBP-loaded FNPs. The enhanced colloidal stability of the nanocarriers was further supported by zeta potential measurements. Moreover, in vitro drug release studies showed sustained and controlled release of CBP from the nanoparticle's matrix, indicating prolonged therapeutic potential. Importantly, in vivo histological assessments of major organs (liver, kidney, heart, and lungs) from skin tumor-bearing mice demonstrated that CBP-loaded FNPs induced minimal tissue damage and significantly reduced systemic toxicity compared to free CBP. Collectively, these findings highlight the promise of this jute-derived, fluorescent nanocarrier as a biocompatible and efficient platform for the systemic delivery of platinum-based chemotherapeutics, offering great potential for future cancer theragnostic applications.

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A PRODUCTION-READY MFS FRAUD DETECTION SYSTEM: FLUTTER-BASED MOBILE ARCHITECTURE WITH EMBEDDED ML INFERENCE AND FEDERATED FINE-TUNING

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Despite the 9.3% risk of scamming in Bangladesh's mobile financial services sector, 110 million registered accounts are still vulnerable to SIM-swap tricks, malware stealing one-time passwords, and investment sequence

scams. Despite the lack of infrastructure, USSD usage and 80,000 agent-handled transaction locations in 43% of areas on only 3G make it difficult to identify Bangladesh's MFS transactions with clarity.The research is built upon a proven two-way process that utilizes encoding technology and an LSTM neural network, with Kaggle's credit card data as the input. Additionally, There is a small deviation of 0.61 difference between fake data and genuine fraud cases in Bangladesh, as determined by the Maximal Mean discrepancy. The mobile system's reliability in detecting fraud remains intact, even with limited resources. The Flutter application utilizes trained models as TenorFlow Lite quantized executables, which can be purchased for under-$200. Android devices. By using Monte Carlo simulations to adjust sensitivity, a multi-level alert setup with flexible thresholds has been successfully used to reduce false alarms for rural low-income users by 31%. The use of federated learning allows for the training of privacy-friendly models across devices, while also satisfying the requirement for domain shift analysis to identify 400,000 labeled transactions. This is particularly useful in this context. With the implementation of USSD backup systems and SQLite offline storage, fraud is reduced as much (43%) of connections use 3G or slower networks are prevented by implementing open data-access; this makes it an operator-actionable solution.

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DEVELOPMENT OF AN IN VITRO REGENERATION SYSTEM AND AGROBACTERIUM MEDIATED TRANSFORMATION PROTOCOL FOR LOCAL SUGARCANE VARIETIES OF BANGLADESH

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Sugarcane (Saccharum officinarum L.) is a major cash crop of the Gramineae family, cultivated globally for sugar, ethanol and byproducts. According to BBS(2025), during the 2024–2025 fiscal year, about 2.92 million tons of sugarcane were harvested from 164,761 acres of land in Bangladesh. Despite its importance, it has been facing multiple limitations. Traditional planting by stem cuttings is slow and disease prone; pests and diseases (e.g. red rot) can cut yields up to 70%. To overcome these limitations, tissue culture offers a rapid and efficient approach for mass cultivation of disease free clonal plants. Combined with Agrobacterium-mediated transformation it enables to transfer desirable genes into the plants. Therefore, the study focuses to develop an in vitro regeneration system and Agrobacterium mediated transformation protocol for local sugarcane varieties of Bangladesh. Development of an efficient tissue culture protocol for sugarcane and establishment of an efficient Agrobacterium-mediated transformation using a selectable marker gene and confirmation of the gene through PCR,qRT-PCR etc. Plant materials: Local sugarcane varieties from Bangladesh Sugar Crop Research Institute (BSRI). Agrobacterium tumefaciens strain GV3101carrying pCAMBIA1305.1. Explants from local sugarcane varieties from BSRI were cultured on MS or modified MS media supplemented with various concentrations of plant hormone. Calli were cultured on MS media with different concentrations of plant hormones for shoot differentiation, followed by rooting on half or full strength of MS medium. Finally, acclimatization was done and transferred to the field. Embryogenic Calli were inoculated with Agrobacterium and co-cultivated, then transferred to regeneration medium. Putative transformed shoots will be confirmed through DNA isolation and PCR confirmation. An efficient in vitro regeneration protocol is established for the selected sugarcane varieties, producing healthy plantlets that are successfully acclimatized under greenhouse conditions and Agrobacterium-mediated transformation procedures have recently been initiated and are currently in progress. This study seeks to improve sugarcane production in Bangladesh by combining regeneration and transformation system for local sugarcane varieties. The output of this research can encourage the sustainable farming practices and strengthen the sugar industry.

PP115

IDENTIFICATION OF POTENTIAL INHIBITORS OF AMINOGLYCOSIDE MODIFYING ENZYMES AND DETERMINATION OF THEIR ADJUVANT ROLE AGAINST AMINOGLYCOSIDES RESISTANT BACTERIA: IN-SILICO AND IN-VITRO APPROACH

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Aminoglycosides are one of the natural and semisynthetic antibiotics used to treat microbial infections. But aminoglycoside resistance has become common, occurring in multiple forms, including enzymatic modification, target site modification via an enzyme, or chromosomal mutation and efflux. Enzymatic drug modification by aminoglycoside modifying enzymes (AMEs) is reported to be the major factor of bacterial resistance to aminoglycoside antibiotics. Several studies have reported that an adjuvant can disrupt the enzymatic activity of AMEs and improve the antimicrobial activity of aminoglycoside antibiotics. The aim of this study was to investigate the effects of adjuvants on the efficacy of aminoglycoside antibiotics against resistant bacteria. Escherichia coli, Staphylococcus haemolyticus, and Pseudomonas aeruginosa are known to express AMEs and develop resistance to aminoglycoside antibiotics. Three different AMEs such as AAC(3)-Ib (aminoglycosides-3-N-acetyltransferase), AAC(6')-Ib (aminoglycosides-6-N-acetyltransferase), and Streptomycin-ATP-APH-2''-IIa (Aminoglycoside phosphotransferase) were used in the in-silico study using molecular docking to find the adjuvant. The binding affinity of some adjuvants such as Zinc pyrithione (ZnPT), Vitamin D, Vitamin E, and Vitamin K against the above AMEs was studied using bioinformatic tools. The comparative binding affinity of these adjuvants vs natural ligands such as acetyl-CoA and adenosine triphosphate (ATP) against AMEs was calculated to gauge the efficacy of adjuvants. Furthermore, the ADMET (absorption, distribution, metabolism, excretion, and toxicity) of the adjuvants was assessed using the SwissADME bioinformatics tool to gauge the properties of adjuvants as drug candidates. Guided by the in-silico study, the in-vitro study of aminoglycosides (such as Streptomycin, Kanamycin, Gentamicin, Amikacin) against the Escherichia coli, Staphylococcus haemolyticus, and Pseudomonas aeruginosa bacteria were conducted in presence of Vitamin E, Vitamin D, Zinc pyrithione (ZnPT). Our study revealed that in presence of adjuvants, aminoglycosides showed increased sensitivity in the antibiotic susceptibility test. Therefore, the combination of adjuvants with aminoglycoside antibiotics could be a promising approach to combat antibiotic resistance.

PP116

TARGETED MODIFICATION OF IPA1 AND CRN GENES FOR DEVELOPING STRESS-TOLERANT RICE VARIETY WITH IMPROVED ARCHITECTURE

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The coastal and southern regions of Bangladesh face critical salinity challenges that threaten rice production and consequently food security. High salt concentrations disrupt water uptake in plants, causing stunted growth, thus reduce rice yield potential. OsIPA1 (Ideal Plant Architecture 1) and OsCRN (Crooked Neck) genes negatively regulate grain yield and salinity tolerance, respectively in rice. The main target of this research is to perform in silico analysis of these two genes and development of new rice varieties through Agrobacterium-mediated genetic transformation. This study explores CRISPR-Cas9 technology to modify these genes in order to develop rice varieties that are high-yielding, stress-resistant with improved plant architecture. In silico analysis was performed to design sgRNAs targeting OsIPA1 and OsCRN genes. The CRISPR-Cas9 vector (pAGM8031_OsIPA1+OsCRN) was constructed with specific target sites using a modular cloning system. The construct is currently being transformed into local rice varieties through Agrobacterium-mediated and in-planta transformation techniques. Putatively edited plants are maintained in the greenhouse. Molecular analysis including PCR and sequencing will confirm successful gene editing. Through a comprehensive in silico analysis, guide RNA design and construction of the CRISPR-Cas9 vector (pAGM8031_IPA1+CRN) with precise target sites have been successfully completed. The pAGM8031_IPA1+CRN cassette is currently being introduced into rice varieties using Agrobacterium-mediated and in-planta transformation methods. The putatively transformed plants are being grown and maintained in the greenhouse. Further molecular analyses, such as PCR and DNA sequencing, will be conducted to verify targeted successful modifications in the OsIPA1 and OsCRN genes. Additionally, phenotypic characterization of the edited plants will be conducted to assess changes in plant architecture and stress response. This study depicts the application of CRISPR-Cas9 genome editing for developing resilient rice varieties, suitable for the saline-prone regions of Bangladesh. The findings will establish a framework for enhancing rice yield and stress tolerance through targeted gene modification. Further research will focus on field evaluation of edited lines to assess agronomic traits and salinity tolerance under natural salinity conditions.

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COMPARISON OF GLYCEMIC RESPONSE TO BRRI DHAN-28 BETWEEN NONDIABETIC AND DIABETIC SUBJECTS

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Qualitative and quantitative evaluation of carbohydrates, using Glycemic Index (GI) and Glycemic Load (GL) as tools, have so far been done without much consideration regarding the choice of nondiabetic and diabetic subjects and single GI tables have been generated with presumed applicability for both the groups. The present study was undertaken to investigate whether single GI and GL tables for nondiabetic and diabeteic subjects are logical to be generated by parallelly comparing the glycemic response to a carbohydrate rich food, BRRI dhan -28; between two groups. The study was conducted on 12 nondiabetic (age in years, 35±8, M±SD) and 12 diabetic (43±9) subjects who were clinically and biochemically matched except for glycemic status. After overnight fasting each subject consumed 50g carbohydrate equivalent amount of BRRI dhan -28 cooked rice (Bangladeshi origin). The same experiment was repeated with equivalent quantity of glucose. Blood (5ml) was drawn at 0, 15, 30, 45, 60, 90 and 120 minutes in case of nondiabetic and at 0, 15, 30, 45, 60, 90, 120, 150 and 180 minutes in case of diabetic subjects. GI was calculated by standard formula and GL were calculated. Among the nondiabetic subjects the iAUC for BRRI dhan -28 was less than half compared to that for glucose (iAUC, BRRI dhan -28 vs glucose, 92.45±39.60 vs 153.0±112.93 M±SD), but in diabetic subjects the response between glucose and BRRI dhan -28 were not significantly different. The GI of the BRRI dhan -28 was found to be 80±49 in the nondiabetic and 105±92 in the diabetic groups. The GL of the BRRI dhan -28 was 10 in nondiabetic and 13 in the diabetic groups. Thus glycemic response of a carbohydrate rich food may considerably vary between nondiabetic and diabetic subjects and separate GI and GL tables for the two groups should be generated. The tested BRRI dhan -28 is a high GI and medium GL food in case of both nondiabetic and diabetic subjects.

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HIDDEN RESERVOIRS: DETECTION OF BURKHOLDERIA PSEUDOMALLEI IN SOILS ACROSS BANGLADESH

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Melioidosis, caused by the soil-dwelling bacterium Burkholderia pseudomallei, is a potentially fatal but underdiagnosed tropical disease. Environmental detection of B. pseudomallei is essential for identifying infection sources, mapping risk areas, and improving clinical awareness. However, isolating the organism from soil is difficult due to the abundance of competing microorganisms. This study evaluates a double enrichment approach using Ashdown broth to dilute soil inhibitors and promote selective growth, aiming to improve detection of B. pseudomallei from soil in Bangladesh. Soil samples were collected from selected rural paddy fields across districts of all eight divisions of Bangladesh to detect Burkholderia pseudomallei. A total of 2,589 samples were obtained from rice paddy-field soil at 20-30 cm depth using sterile technique and transported promptly to the laboratory. Soil was enriched in Ashdown selective broth, followed by double enrichment and cultured on modified Ashdown selective agar media. Suspected colonies were identified by colony morphology, Gram staining, biochemical tests, and antibiotic resistance pattern, followed by confirmation utilizing latex agglutination and PCR targeting the TTS1 gene. DNA was also extracted directly from the Ashdown broth using commercial kits, and PCR was performed. Among 2,589 soil samples collected from different districts of Bangladesh, 96 B. pseudomallei isolates were detected overall, with 93 identified by culture and 69 by PCR among 2,179 tested samples; PCR for the remaining samples is pending due to reagent shortage. Positive isolates were distributed across multiple districts, with the highest numbers in Parbatipur, Gazipur, Tangail, Manikganj, Sunamganj, and Sylhet Sadar. The study confirms B. pseudomallei in soils from nine Bangladeshi districts, indicating environmental exposure risk and highlighting the need for greater clinical awareness, prevention, and accurate diagnosis of melioidosis.

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NEUTROPHIL-LYMPHOCYTE RATIO IN PREGNANT WOMEN FOR THE PREDICTION OF GESTATIONAL DIABETES MELLITUS

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Prediction of Gestational Diabetes Mellitus (GDM) risk at earlier stages of pregnancy is invaluable in management as well as prevention of the disorder. Early pregnancy Neutrophil-Lymphocyte Ratio (NLR), has recently been proposed as a candidate marker; however, only a few studies have been conducted and data against the claim has also been reported. The objective of the study was to evaluate the predictive performance (sensitivity, specificity, positive predictive value, and negative predictive value) of early pregnancy (up to 16 weeks) NLR on the detection of GDM in late pregnancy. A prospective cohort study was conducted on a purposively selected group (n=126) of nondiabetic pregnant mothers, attending the OPD Clinic within 16 weeks of gestation. Data on differential blood count were recorded on predesigned Data Collection Forms. GDM was diagnosed, at 24 weeks or later periods of gestation, following the criteria of the American Diabetes Association (as followed in DMCH) after a 75 g Oral Glucose Tolerance Test (OGTT). The Sensitivity, Specificity, Positive Predictive Value (PPV) and Negative Predictive value (NPV) of the early pregnancy Neutrophil-Lymphocyte Ratio (NLR), against the actual development of GDM at later pregnancy, were calculated by McNamara Test. A number of 72 subjects out of 126 (57.14%) developed GDM at 24 weeks and later period of gestation. The best combination of sensitivity and specificity (59% and 33%, respectively) to predict NLR was found with a cut-off value of NLR 3.0. However, the best combination of

PPV and NPV (55 and 50, respectively), with balancing of sensitivity (87%) and specificity (16%), was found with a cut-off value of 2.20. The present data lead to the following conclusions: i. The Lymphocyte-Neutrophil Ratio (NLR), assessed at early (before 16) weeks of a normal pregnancy, may be considered a useful tool to predict the development of Gestational Diabetes Mellitus (GDM) during the later (after 24 weeks) periods of pregnancy; and ii. An NLR cut-off value of 2.20 seems to be the optimum one to be used during the utilization of NLR as a predictive screening marker for GDM at early pregnancy.

PP120

FACTORS SHAPING NUTRITIONAL STATUS IN THE RURAL GARO INDIGENOUS OF BANGLADESH

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Adequate nutrition is a cornerstone of good health, higher quality of life, and increased national productivity. Ethnic groups often follow distinct lifestyles and cultural practices, which can significantly impact their nutritional needs and health outcomes. As a result, understanding the nutritional status of these populations is crucial. This study aimed to evaluate the nutritional status of the Garo ethnic community residing in Modhupur Upazila, located in the Tangail District of Dhaka, Bangladesh. Methodology: A cross-sectional study design was employed, and simple random sampling was used to select 289 adults aged between 18 and 70 years. Data collection was done through face-to face interviews, and verbal consent was obtained from a community leader prior to the interviews. Nutritional status was assessed using the body mass index (BMI) cutoff value for the Asian population. Of the total 289 subjects (36% male, 64% female), 14.9% of participants were underweight, 35.3% had a normal weight, 33.2% were overweight, and 16.6% were classified as obese. Statistical analysis showed significant associations between nutritional status and demographic factors, including age and occupation. The nutritional status of the Garo community was depicted in this study in a negative light. These results emphasize the need for a better understanding of the nutritional challenges faced by the Garo community and suggest that targeted nutrition education and intervention programs could help improve their nutritional status. By addressing these challenges, it is possible to improve health outcomes, promote a better quality of life, and contribute to the overall well-being of the Garo people.

PP121

PHYTOCHEMICAL SCREENING, ANTIMICROBIAL, AND ALLELOPATHIC POTENTIAL OF PRAXELIS CLEMATIDEA (GRISEB.) R.M. KING & H. ROB. FROM BANGLADESH

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Praxelis clematidea (Griseb.) R.M. King & H. Rob. belonging to the family Asteraceae, an invasive plant species recently recorded from Bangladesh. This study focused on identifies the phytochemical properties, allelopathy and antimicrobial activity of P. clematidea. Phytochemical screening analysis showed it contains several essential compounds, such as alkaloids, flavonoids, tannins, saponins, and terpenoids but did not detect any steroids and glycosides. Thin Layer Chromatography (TLC) confirmed the chemical diversity of the sample, revealing four distinct compound groups. These were represented by major bands with Rf values of 0.43, 0.50, 0.65, and 0.85, respectively, suggesting the presence of different phytochemical classes. The antimicrobial activity was tested using the agar well diffusion technique against three bacterial strains (Staphylococcus aureus, Escherichia coli,

Pseudomonas aeruginosa) and two fungal pathogens (Aspergillus niger, Candida albicans). The extract exhibited broad spectrum antimicrobial effects, showing the strongest inhibition zone against A. niger (21.45 mm), followed by E. coli (17.71 mm), and C. albicans (12.55 mm). These findings indicate that P. clematidea contains bioactive compounds with significant antimicrobial potential, supporting its traditional medicinal use and its relevance in new drug development. From in vitro study, P. clematidea also exhibits significant allelopathic potential that inhibit the germination rate and seedling growth of Cenchrus purpureus and Amaranthus tricolor. In the present study, alkaloids, flavonoids, tannins, saponins, and terpenoids were isolated from Praxelis clematidea for the first time in Bangladesh, highlighting the plant's rich bioactive profile and its potential relevance in antimicrobial research.

PP 122

IMPROVING DIAGNOSIS & CASE MANAGEMENT OF CHILDHOOD PNEUMONIA IN LIMITED RESOURCE SETTINGS

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The Forcibly Displaced Myanmar Nationals (FDMNs) in Cox's Bazar, Bangladesh, faces a significant burden of communicable diseases, particularly childhood pneumonia, which contributes to 14-19% of annual morbidity and mortality. Factors such as overcrowding, malnutrition, poor sanitation, and limited diagnostic resources impede effective case management and timely diagnosis in the humanitarian context. This study aims to evaluate whether strengthening pneumonia diagnostic capacity can improve clinical assessment and case management among Rohingya children under five years of age. A quasi-experimental study in Cox's Bazar investigates children aged ≤59 months with moderate to severe pneumonia, dividing them into intervention and non-intervention groups. The intervention included pulse oximeters, automated respiratory rate counters, and healthcare provider training, while the control group received routine assessments. Healthy children without respiratory symptoms served as controls for Streptococcus pneumoniae surveillance. To date, 207 pneumonia cases and 132 healthy controls were enrolled from 1000 cases (600 pneumonia, 400 control). Preliminary data suggests that children using pulse oximeters and automated respiratory rate counters demonstrated improved identification of abnormal vital signs. Pneumonia cases showed higher respiratory rates, heart rates, and body temperatures, as well as lower oxygen saturation compared to healthy controls. The intervention improved age-specific differentiation of vital signs, enhancing severity classification and hypoxaemia detection. All pneumonia cases were treated with antibiotics, mainly amoxicillin. Seasonal trends indicated a peak in pneumonia cases during the monsoon, particularly in August. Many children had incomplete pneumococcal vaccination schedules, which may influence pneumonia prevalence in the Rohingya population. Further analyses will assess the interventions' effect on clinical outcomes and pneumonia serotype distribution. Childhood pneumonia remains a critical public health concern among Rohingya refugees. Strengthening point-of-care diagnostic capacity and healthcare provider training, alongside improved immunization coverage, may substantially enhance pneumonia management and reduce preventable child morbidity and mortality in humanitarian settings.

PP 123

DECIPHERING THE MECHANISMS BY WHICH ASPERGILLUS WELWITSCHIAE OCSTREB1 (AWOCSTREB1) ENHANCES PLANT SURVIVAL AND RESILIENCE UNDER SALINITY STRESS THROUGH INTEGRATED TRANSCRIPTOMIC AND METABOLOMIC ANALYSES.

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Endophytic microorganisms can enhance the growth and tolerance of their host plants to several stresses by triggering metabolic and transcriptional reprogramming. The endophytic fungus Aspergillus welwitschiae Ocstreb1 (AwOcstreb1), isolated from the roots of the wild halophytic rice Oryza coarctata, has been shown to enhance the growth and salt tolerance of the commercial BD-28 rice plants. To understand how this interaction works, metabolomics and transcriptomic analyses were performed on BD-28 plant roots and shoots, respectively, after inoculation with AwOcstreb1 under control and salt stress conditions. Germinating seeds were inoculated with the AwOcstreb1 spore suspension prior to planting, while control seeds were treated with distilled water. At the three leaf stage, 120mM salt stress was applied and shoot and root tissues were collected after 48 h of exposure. Comparative analyses showed that AwOcstreb1 inoculation under non-stress conditions promoted growth by modulating phenylpropanoids, antioxidant systems, and cell wall alteration-related pathways, along with upregulation of genes involved in nutrient uptake and development. In contrast, salt stress in uninoculated plants led to metabolic disruption, increased lipid peroxidation, impaired photosynthesis, and activation of stress and senescence-related genes, resulting in growth inhibition. Under salt stress, however, AwOcstreb1-inoculated plants displayed distinct adaptive responses, including accumulation of protective metabolites, reduced oxidative damage, stabilization of membrane lipids, suppression of programmed cell death, and stabilization of chloroplast and photosynthetic metabolism. These changes were supported by activation of stress-responsive transcription factors, ion transporters, osmoprotective and antioxidant pathways, alongside downregulation of senescence and growth-inhibitory genes. Notably, key salt tolerance genes such as OsHKT1;5, OsSTL2, and OsMIR408 were upregulated, indicating improved ion homeostasis and enhanced stress resilience in AwOcstreb1 inoculated plants. Collectively, these findings demonstrate that AwOcstreb1 enhances salinity tolerance in BD-28 rice by promoting phenylpropanoid accumulation, reduced oxidative damage, and maintenance of photosynthetic efficiency under stress conditions.

PP124

MULTIVARIATE STATISTICAL AND AI-BASED MODELING OF ROUTINE LABORATORY DATA FOR SCREENING INBORN ERRORS OF METABOLISM IN BANGLADESH

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Inborn Errors of Metabolism (IEM) are rare diseases caused by mutations in the genes that encode enzymes of the metabolic pathways. The incidence generally ranges from 1 in every 800 to 2,500 births, where the prevalence of IEM among suspected patients is 2.6% in Bangladesh. Liquid Chromatography-Tandem Mass Spectrometry (LC-MS/MS) is an accurate and reliable approach for diagnosing IEMs, and in resource-limited settings, LC-MS/MS is not readily available. In this study, common laboratory tests with AI-Guided Statistical Modeling

have been tried to set up to provide accurate data on different presumptive metabolic disorders. A total of 1028 suspected patients with IEMs were enrolled in the first phase of the study. For every individual, complete blood count, arterial blood gas (ABG) parameters, and different biochemical tests such as ammonia, lactic acid, uric acid, urea, and glucose were measured. Among suspected patients, 5.14% showed hyperammonemia, 8.75% hypoammonemia, 44.07% lactic acidosis, 10.70% hyperuricemia, and 15.37% hypouricemia. Multivariate regression models demonstrated strong predictive relationships among laboratory parameters, with correlation coefficients ranging from R = 0.78 to 0.99, indicating strong to very strong associations. For example, models predicting pH from ABG variables and base excess and HCT from hematological parameters (HGB, RBC, MCHC) showed high predictive accuracy across several metabolic conditions. These findings suggest that AI-assisted statistical approaches can identify hidden patterns within routine laboratory data that correspond to metabolic abnormalities. Machine learning–guided statistical analysis of routine laboratory tests can reveal strong predictive relationships among metabolic and hematological parameters associated with suspected IEM conditions. We hope that this set of techniques may play a vital role in the initial screening and diagnosis of IEMs in newborns, and this may help facilitate timely therapy of treatable IEMs.

PP125

GENOMIC AND PHYLOGENETIC INSIGHTS OF THE 2023-2024 DENGUE OUTBREAK IN BANGLADESH

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With frequent outbreaks in recent years, dengue fever remains a serious mosquito-borne viral disease in Bangladesh. Although serotype 3 (DENV-3) predominated until 2019, recent epidemiological patterns suggest changing serotype dynamics. In 2023, Bangladesh reported the highest dengue-related mortality (n=1,705) globally and the second-highest number of cases (n=321,179). This study aimed to identify the predominant dengue virus serotype within the 2023–2024 outbreak and to investigate the spatial and temporal genomic dynamics of circulating strains. Blood samples collected between 2023 and 2024 were serotyped by RT-PCR. Whole-genome sequencing was performed on the Oxford Nanopore MinION platform using a modified ARTIC multiplex PCR approach. The phylogenetictrewas constructed using the polyprotein gene (10,171 bp) with other South Asian sequences, and gene-wise nucleotide diversity (π), Tajima's D, and dN/dS ratios were calculated to assess genetic variation and selection pressures. Among 395 samples, DENV-2 predominated (282; 71.4%), followed by DENV-3 (105; 26.6%), with few DENV-4 (7; 1.8%) and DENV-1 (1; 0.2%), indicating a major shift from previously dominant DENV-3. Phylogenetic analysis showed contemporary Bangladeshi DENV-2 viruses form a distinct regional lineage, sharing a recent common ancestor with few Indian sequences. Within Bangladesh, DENV-2 sequences exhibited clear temporal structuring, with a dominant 2023 clade and multiple closely related lineages co-circulating in 2024. Gene-wise analyses revealed strongly negative Tajima's D (-1.41 to -2.50), low dN/dS (<0.18), and comparatively higher nucleotide diversity (π) in the NS1, NS3, and prM genes, indicating population expansion with strong purifying selection. The recent dengue outbreak in Bangladesh showed a major serotype shift to DENV-2 and was dominated by a distinct regional lineage with limited external introductions and multiple co-circulating lineages under strong purifying selection. These results provide critical insights into the outbreak dynamics and molecular evolution of DENV2 in a regional context.

PP126

IN SILICO PREDICTION OF A CONSERVED MULTI-EPITOPE VACCINE FOR HUMAN METAPNEUMOVIRUS USING PAN-GENOMIC REVERSE VACCINOLOGY

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Human metapneumovirus (HMPV) causes significant respiratory infections globally, particularly in vulnerable populations, yet lacks an approved vaccine. This study computationally designed and evaluated a multi-epitope HMPV vaccine candidate using integrated immunoinformatics, reverse vaccinology, and pan-genomic approaches. Sixty-five HMPV genomes were analyzed for virulence, antigenicity, toxicity, and solubility, leading to three promising vaccine constructs (HMPV_V1, HMPV_V2, HMPV_V3). Fifteen conserved B-cell, MHC-I, and MHC-II T-cell epitopes were identified and linked with AAY, GPGPG, and KK linkers, plus a 50S ribosomal protein L7/L12 adjuvant. Physicochemical and immunological profiling confirmed antigenicity, non-allergenicity, and non-toxicity. High-quality 3D models were generated and validated. Molecular docking to the TLR4 immune receptor and molecular dynamics (MD) simulations assessed binding and structural stability. In silico immune simulations predicted adaptive responses, and codon optimization for HMPV_V2 was performed. Molecular docking showed strong TLR4 binding, with HMPV_V1 exhibiting the lowest binding energy (-1141.9). MD simulations revealed HMPV_V2's superior structural stability, with minimal RMSD and RMSF fluctuations over 100 ns, supporting its selection as the optimal candidate. Immune simulations predicted a robust adaptive response, including early antigen clearance, antibody class switching (IgM, IgG), memory B-cell formation, T-helper and cytotoxic T-cell activation, and IFN-γ and IL-2 production. Codon optimization indicated high expression feasibility for HMPV_V2 in E. coli K-12. These computational findings strongly support HMPV_V2 as a safe and effective preventative vaccine candidate against HMPV. However, Experimental validation through in vitro and in vivo studies is essential to confirm its immunogenicity and protective efficacy in clinical settings.

PP127

PROSPECT OF ARTIFICIAL INTELLIGENCE IN PROGNOSIS AND TREATMENT OF NEURODEGENERATIVE DISEASES

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Neurodegenerative diseases (NDs) pose a grave threat towards the humanity. Usually, the progress rate of NDs is slow. This characteristic beacon excellent in thwarting NDs progression with the aid of artificial intelligence (AI). Current presentation reveals the feasibility of AI in understanding the progression and diagnosis as well as treatment of the most common NDs. This presentation is based on the most recent outcomes of AI based studies in the field of NDs. AI-generated tricks, techniques, software, online and offline-based experimental paradigm has critically been demonstrated here. Data presented here are reflections of the published research articles. AI quickens the prognosis and diagnosis of NDs. Prediction of ND-associated physiological, biochemical and molecular biological alterations could easily be demonstrated through AI. However, extensive precaution and modulatory strategy must receive considerable attention in driving AI in the research and treatment strategy of NDs. AI seems to be an alternative tool both in diagnosing and in formulating therapeutic approaches against NDs. Anthropometric and demographic features impact AI-driven ND treatment strategies immensely.

PP128

MORPHO-ANATOMOCAL, HEMATOLOGICAL, HISTOPATHOLOGICAL AND RADIOGRAPHIC OBSERVATIONS OF SPINAL DEFORMITIES IN CULTURED STINGING CATFISH, HETEROPNEUSTES FOSSILIS

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Spinal deformities in fish are the abnormal modifications of bony and/or cartilaginous structures that differ anatomically from the normal skeletal pattern and adversely affect growth, health, market value, and overall fish welfare. The present study aimed to investigate the occurrence, characteristics, and the extent of spinal deformities in cultured Heteropneustes fossilis. A total of 100 morphologically deformed and 100 healthy uniform sized H. fossilis of were collected from commercial catfish farms and marketplaces of Mymensingh district. A questionnaire survey was conducted in 15 catfish hatcheries and 15 catfish farms to assess the deformity status and to identify causative factors. Morphological assessments included length-weight relationship (LWR), truss network analysis, and meristic counts. Hematological parameters including RBC, WBC, hemoglobin, MCH, MCV, MCHC, PCV, and blood glucose were analyzed. Histopathological examinations were performed usning muscle, liver, kidney, and intestinal tissues. Spinal abnormalities were further evaluated using dry skeletal preparation and radiographic (X-ray) analyses. The survey revealed several causes responsible for skeletal deformities, although water quality parameters remained within suitable ranges. Significant morphological variations were observed in deformed fish based on LWR and truss network analyses. Hematological parameters of deformed H. fossilis differed significantly. Histopathological examination revealed notable alterations in muscle, liver, kidney, and intestinal tissues. Radiographic observations and dry skeletons identified the deformities including vertebral fusion and, bending of neural and hemal spines. These abnormalities showed region-specific distribution along the vertebral column, with scoliosis, lordosis, and occasional kyphosis. The study demonstrates that spinal deformities in H. fossilis are associated with significant morphometric, hematological, histopathological, and meristic disruptions. This in-detailed investigation suggests for accurate clinic-pathological diagnosis, improved culture practices viz., water quality control, optimal stocking density, and careful use of chemotherapeutics, to ensure fish welfare and sustainable catfish production.

PP129

ANALYSIS AND MODELING OF THE EFFECT OF FIBER CONTENT ON 28-DAY TENSILE STRENGTH OF CONCRETE

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This study explores the relationship between fiber content and the 28-day tensile strength of concrete using a provided dataset. The analysis involved loading and exploring the experimental data. Descriptive statistics were computed for the 28-day tensile strength, revealing an average of 2.54 MPa and a standard deviation of 0.56 MPa. The data was further analyzed by grouping the 28-day tensile strength by fiber content. Visualizations, including scatter plots and line plots of averaged values, were generated to illustrate the effect of fiber content on tensile strength. A linear regression model was developed to predict the 28-day tensile strength based on fiber content, achieving an R-squared value of 0.76. Using this model, the predicted tensile strength for a fiber content of 2 kg/m^3 was found to be approximately 2.79 MPa. Initial calculations comparing plain concrete to fiber-reinforced concrete indicated an average decrease in tensile strength of 15.62% with fiber inclusion in this specific dataset. The study concludes by demonstrating how statistical analysis and linear regression can be applied to understand and model the impact of fiber content on concrete's tensile properties, highlighting the observed trends and the predictive capability of the developed model.

PP130

METAGENOMIC ANALYSIS OF SUGARCANE (SACCHARUM OFFICINARUM L.) MICROBIOME DURING RED ROT DISEASE PROGRESSION

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The most common disease affecting sugarcane is red rot, which can cause up to 29% loss of cane weight and 31% loss of sugar recovery. It causes financial ruin for the farmers and businesses who depend on this crop. The objectives of this study are to predict microbial interactions linked to disease resistance or susceptibility, identify changes in the types and functions of the sugarcane endophytic microbiomes during Colletotrichum falcatum infection, and identify core microbial taxa enriched in red rot-resistant sugarcane genotypes. Different plant parts of both resistant and affected varieties of sugarcane from 8 different plots belonging to 4 districts was performed along with soil sample collected from individual plots. A total of 16 unique samples are being subjected to DNA extraction. and isolate separation. The extracted DNA will be further purified and quantified by fluorometric quantification. Fragments of DNA will be created for library preparation, followed by tagging. Reads will be preprocessed before shotgun whole metagenomic sequencing and Shotgun WMS data will be analyzed. ITS-region and 16s rRNA amplification have been used to successfully isolate microbial DNA from some of the samples, and DNA quality has been evaluated molecularly. Alpha and beta diversity comparison, taxonomic profiling, mapping-based and assembly-based diversity analysis, differential abundance, and optional resistance will all be interpreted from the Shotgun WMS data. To find connections with the metagenomics data, a number of soil characteristics, including TDS, salinity, EC, chloride, TKN, sulfur, and phosphorus content, have been measured.This study will offer a multifaceted approach to comprehend metabolic pathways responsible for disease progression, phylogenetic relationships, dynamics, and interaction among various microbial communities associated with healthy and diseased sugarcane, as well as to better understand the dynamics of the C. falcatum pathotype, since the microbial mechanism of sugarcane has not yet been thoroughly investigated in the context of red rot. The method using metagenomic analysis will reveal how our regions' endophytic microbiota affects productivity.

PP131

INVESTIGATION OF PUBLIC HEALTH IMPORTANT ZOONOTIC DISEASES IN RUMINANTS AT SLAUGHTERED HOUSES IN CENTRAL-NORTHERN AREAS OF BANGLADESH

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Developing nations like Bangladesh. slaughterhouses represent major public health risks and zoonotic diseases are transmitted from animals to human through unsafe meat. This study examined ruminants at slaughterhouses through pathological study and molecular detection. Overall, 2,600 cattle and goats were screened during study period. Suspected lesions (liver, lungs, and mesenteric lymph nodes) from 128 cattle and 157 goats were collected across slaughterhouses in the City Corporation areas of Dhaka, Gazipur and Mymensingh districts. Grossly, interstitial pneumonia in lungs (35.6%), liver cirrhosis (38.5%), and greenish caseation in mesenteric

lymph nodes (20.3%) were noticed. In goat, cysts appeared in mesentery (46.5%). Histopathologically, tubercle featured lymphocyte infiltration, giant cells, and macrophages. Conventional PCR targeting Mycobacterium genus (16S rRNA gene) in 13 cattle samples (10.16%) and 31 goat samples (19.7%). Of these, 12 cattle (9.37%) and 29 goats (18.5%) belonged to the M. tuberculosis complex. M. bovis was confirmed in 8 cattle (6.25%) using the MPB83 gene. Corynebacterium pseudotuberculosis (16S rRNA) was detected in 57 cattle (44.5%) and 75 goats (47.7%). 16S-23S rRNA gene of Brucella species identified in 9 cattle (7.03%). Toxoplasma gondi's B1 gene was positive in 4 cattle (3.12%) and 9 goats (5.7%). Q fever's IS1111 gene was detected in 3 cattle (2.34%) and 7 goats (4.45%). Campylobacter jejuni's MapA gene was detected in 3 cattle (2.3%) and 3 goats (1.9%), while its HipO gene found in 2 cattle (1.5%) and 6 goats (3.82%). No cases of listeriosis or leptospirosis were detected. Using 12S rRNA and Cox-1 genes, 9 goats (15.51%) were detected for hydatidosis. Gene accession no. for M. tuberculosis complex (PZ096135), Corynebacterium pseudotuberculosis (PZ072331), and Cox1 of Taenia hydatigena (PZ008538, PZ008539, PZ008540, PZ008541). These findings reveal multiple zoonotic pathogens in goats and cattle posing transmission risks via direct or indirect contact, and need One Health initiatives for control measures.

PP132

ADDRESSING SALINITY AND DROUGHT CHALLENGES IN RICE THROUGH CRISPR-CAS9-MEDIATED GENOME EDITING OF HELICASE GENE

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Rice (Oryza sativa L.) is the staple food for millions in Bangladesh and across South Asia, yet its production faces severe threats from abiotic stresses, particularly salinity and drought. OsRH53, a DEAD-box RNA helicase gene, has been identified as a negative regulator of abiotic stress tolerance, making it a promising target for genome editing. This study aimed to develop stress-tolerant rice varieties through CRISPR-Cas9-mediated knockout of OsRH53 in both indica and japonica genotypes. Following thorough in silico analysis for guide RNA design, a CRISPR-Cas9 vector (pAGM8031_RH53) harboring three sgRNAs was constructed and transferred to Agrobacterium strain GV3101.3. Two rice genotypes were targeted: BR-29 (indica) and Nipponbare (japonica). For Nipponbare, surface sterilization (1 min 70% alcohol, 20 min 30% Clorox) and callus induction using 2 mg/L 2,4-D in CHU (N6) medium under continuous darkness were systematically optimized. Agrobacterium-mediated transformation was performed at bacterial OD_{600} of 0.5–0.6, followed by three successive rounds of hygromycin selection (50 mg/L). For the recalcitrant BR-29 variety, an in planta transformation approach was developed, incorporating a 48-hour incubation window and 3-day co-cultivation period. Nipponbare protocols yielded 96.30% seed germination, 91.67% callus induction with superior embryogenic callus morphology, and 63.66% callus survival following hygromycin selection, resulting in successful regeneration of eleven putative transgenic plants. For BR-29, the optimized in planta approach achieved 83% germination success, and following greenhouse acclimatization at 30°C and 60–70% relative humidity, 21.98% of putative transformants survived through to maturity. Efficient and reproducible transformation protocols were successfully established for both indica and japonica rice genotypes. These optimized systems provide a strong foundation for CRISPR-Cas9-based functional genomics in rice. Molecular confirmation via PCR and sequencing, alongside phenotypic stress tolerance evaluation, are currently underway to verify successful OsRH53 editing and its downstream effects on salinity and drought resilience.

PP133

AGRICULTURAL TRANSFORMATION UNDER DROUGHT: A STUDY OF SAPAHAR UPAZILA, NAOGAON DISTRICT, BANGLADESH

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In Bangladesh, agriculture is highly sensitive to climatic variability, particularly in the drought-prone Barind Tract of the northwestern region. Sapahar Upazila in Naogaon district, characterized by low rainfall, undulating topography, and declining groundwater levels, has traditionally relied on wet-season rice cultivation. However, due to recurrent droughts and reduced rice yields, a significant shift toward commercial mango cultivation began after 2010. This study aims to assess how drought has influenced agricultural transformation in Sapahar, focusing on the shift from rice to mango cultivation and the resulting impacts on farmer livelihoods and agricultural shipment systems. Key objectives include identifying the extent to which agricultural land has been converted into mango orchards and dense vegetation, and evaluating how these changes have affected local farmers and agri-markets. Land use/land cover (LULC) changes were analyzed using supervised classification of satellite imagery from 2014 and 2024. NDVI time-series analysis was used to detect vegetation health and density changes, providing quantitative evidence of agricultural land conversion into mango orchards. In addition, field visits, focus group discussions (FGDs), and key informant interviews (KIIs) were conducted to gather primary insights from the study area. The results reveal a dramatic decrease in agricultural land from 15,158 hectares in 2014 to 5,134 hectares in 2024, alongside a sharp increase in dense vegetation primarily mango orchards from 6,601 to 17,358 hectares. Among the six unions, Sapahar union experienced the highest concentration of such agricultural transformation. Since around 1995, rice was the dominant monsoon crop, but by 2005, farmers began recognizing the unsuitability of the region's soil and climate for rice cultivation. Mango plantations began to expand gradually, accelerating rapidly after 2015 and becoming a dominant commercial activity post-2019. However, farmers now face increasing challenges in maintaining supply chains and dealing with price volatility in local markets, especially as mango yields have declined since 2023 due to shifting seasonal patterns. The study concludes that integrating geospatial techniques with field data provides a comprehensive approach to understanding drought-induced agricultural changes and supports the development of adaptive policies for ensuring food security and supply chain resilience in drought-affected regions.

PP134

EVALUATION OF IN PLANTA AND TISSUE CULTURE-BASED AGROBACTERIUM-MEDIATED GENETIC TRANSFORMATION FOR GENOME EDITING IN BRASSICA SPP.

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Brassica rapa and B. juncea are important oilseed crops and industrial resources in Bangladesh; however, seed oil's high erucic acid concentration limits its human intake. Reducing erucic acid while maintaining high yield and oil quality is a national agricultural priority. Advances in genome editing, particularly the CRISPR-Cas9 system, offer a precise, efficient, and versatile approach for targeted gene modification compared to conventional breeding and earlier transgenic methods. Both species need genetic improvement, but B. rapa's high tissue culture and transformation resistance make it difficult. This study aims to establish both in planta and tissue culture-based Agrobacterium-mediated transformation protocols for comparative genetic transformation and genome editing

studies in B. rapa and B. juncea. During this investigation, two different approaches of transformation were employed—tissue culture-based method and in planta technique—using two vectors, pBI121 and pAGM8031_-fae1, and molecular confirmation was performed using PCR technique. In planta transformation using vacuum infiltration of targeted flowers was optimized based on GUS expression at OD_{600} 0.7-1.0, 10-15 min of vacuuming, 2 days of co-cultivation and for tissue culture OD_{600} 0.5, 2-3 days of co-cultivation, and 40 mM acetosyringone in both varieties. Tori-7 variety of B. rapa was transformed with pAGM8031_fae1 vector using the optimized protocol of tissue culture. In tested shoots, molecular analysis verified Cas9 cassette integration with a 0.87% transformation efficiency. Some transgenic plants showed altered leaf dimorphism, reduced stigma length, delayed anther maturity, but high pollen viability and T1 seed germination rate. The in planta approach offered a faster, regeneration-free method but with poor silique development efficiency, whereas the optimized tissue culture method achieved stable transformation and regeneration with confirmed Cas9 integration. These findings provide a foundation for advancing genome editing in recalcitrant Brassica genotypes, with implications for breeding low-erucic acid mustard varieties in our country.

PP135

MULTIPLE ADVANTAGES OF CARBON SEQUESTRATION: CLIMATE MITIGATION AND PLANT IMMUNITY ENHANCEMENT

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Global food security has been suffering from the emerging climate crisis caused by rising atmospheric CO_2. Carbon sequestration is an implicit climate mitigation strategy. Its potentiality to develop plant disease resistance remains under several experiments. This review gathers evidence on these dual benefits, investigating the direct and indirect effect of carbon sequestration on environment and plant immunity. A robust review of Web of Science, Scopus, PubMed, and CAB Abstracts (2000-2024) was conducted. The findings found two key mechanisms. Firstly, elevated CO_2 (eCO_2) directly guides plant defenses by enhancing carbon fixation, thereby the carbon enters into photosynthesis to accumulate the sugar which alters redox balance and stimulates salicylic acid (SA) signaling while suppressing jasmonic acid (JA). Pathogens exhibit resistance due to this shift in hormonal balance. The infestation of tomato Yellow Leaf Curl Virus (TYLCV), mainly transmitted by whiteflies, was reduced by up to 14.6% and severity by 20.0%. Secondly, proper sequestration practices based on soil passively manage disease occurrence through enhancing soil organic matter and providing compatible habitat for beneficial microorganisms. This review showed that carbon sequestration is a synergistic, climate-smart strategy. Moreover, a solution to a sustainable pathway to mitigate atmospheric CO_2 and reduce overuse of chemical pesticides which fosters the climate to combat the dramatic rise of Green House Gases (GHG). More emphasis should be given in this regard by the responsible authorities.

PP136

ARTIFICIAL INTELLIGENCE-DRIVEN EARLY DETECTION OF CROP PESTS USING SMARTPHONE-BASED IMAGE ANALYSIS

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Early detection of insect infestations in rice (Oryza sativa) is essential for ensuring crop health and minimizing yield loss. This study aims to develop an AI-driven, smartphone-integrated framework for real-time pest detection using leaf imagery. Specifically, the objectives are to design a deep learning model for accurate pest identification, and integrate a decision-support system to provide actionable pest management recommendations. The approach involves systematic image acquisition followed by preprocessing techniques to enhance feature visibility and reduce noise. A deep learning model, RicePestNet, is designed to analyze approximately 1,200 rice leaf images collected from publicly available datasets (Kaggle). Data augmentation is applied to improve dataset diversity. Additionally, a decision-support module, PestCare Advisor, is integrated to generate pest management recommendations. The RicePestNet model demonstrates strong performance in detecting early-stage pest infestations, achieving high precision and recall. It effectively identifies subtle signatures in leaf images that are often overlooked during manual inspection. Preliminary testing indicates that the system can process images in near real-time, enabling rapid and reliable diagnostics. Furthermore, the integration of the PestCare Advisor provides automated, data-driven management recommendations, effectively bridging the gap between detection and timely intervention in precision agriculture. This framework demonstrates significant potential to mitigate excessive pesticide use and enhance crop management efficiency through automated diagnostics. However, rigorous validation under diverse field conditions is essential to ensure its practical reliability and seamless integration into real-world agricultural workflows.

PP137

EFFECTS OF MERCURY AND SUMITHION ON GROWTH PERFORMANCE, INTESTINAL STRUCTURE, AND GH-IGF AXIS IN NILE TILAPIA (OREOCHROMIS NILOTICUS)

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Aquatic ecosystems are increasingly contaminated by mixtures of heavy metals and pesticides, which often interact to intensify toxic outcomes. Mercury and sumithion are two pollutants commonly detected in freshwater habitats. This study assessed their individual and combined effects on growth performance, intestinal histology, and growth hormone (GH) axis regulation in Nile tilapia (Oreochromis niloticus). After acclimatization, fish were distributed into four groups in triplicate: Control, Mercury (0.03 mg/L), Sumithion (0.6 µg/L), and Combined (Mercury+Sumithion). A 42 day static renewal exposure was conducted in 100 L tanks, with sumithion replenished every other day and mercury reintroduced during water changes. Fish were fed a 32% protein diet at 5% body weight twice daily. Growth indices, survival, intestinal histomorphology, and GH axis markers (GH, IGF 1, IGF 2) were evaluated. Co exposed fish showed the greatest impairment in growth, with significantly reduced final body weight (20.09±1.73 g), weight gain (9.68±1.73 g), and specific growth rate (0.68±0.10% /day). Feed conversion ratio was highest (2.37±0.61), and survival lowest (82.5±2.74%). Histological analysis revealed severe intestinal alterations, including shortened villi (247.88±17.15 µm), disrupted mucosal folds (69.63±6.96 µm), and depletion of goblet cells (14.17±3.54). Mercury alone produced marked thinning of the intestinal wall and muscularis layer. Endocrine assessment demonstrated significant suppression of GH, IGF 1, and IGF 2 in the combined treatment, confirming disruption of the GH axis. The combined exposure to mercury and sumithion exerts synergistic toxicity in Oreochromis niloticus, resulting in impaired growth, intestinal pathology, and suppression of the GH axis. The parallel disruption of intestinal morphology and endocrine regulation provides mechanistic insight into mixture induced toxicity and underscores the necessity of incorporating multi contaminant scenarios into ecological risk assessment.

PP138

INCREASED MYOSTATIN BY ARSENIC EXPOSURE AND ITS CARDIOMETABOLIC RISK

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Arsenic exposure increases risk of insulin resistance (IR), leading to cardiometabolic diseases (CMDs). Skeletal muscle health is a critical factor in the development and progression of CMDs. Myostatin is a master negative regulator of skeletal muscle mass and causes sarcopenia (loss of muscle strength and mass) by inhibiting muscle regeneration and protein synthesis. Elevated myostatin levels are implicated in the impairment of glucose metabolism and increased risk of sarcopenia, leading to IR. In our previous study, we found that arsenic exposure was associated with the reduction of muscle mass (sarcopenia), which is linked to IR. However, the underlying mechanisms of arsenic-induced sarcopenia and IR have been poorly understood. This pilot study aimed to investigate the relationship between arsenic exposure and serum myostatin levels, particularly with regard to IR in the participants who were recruited from low- and high-arsenic exposure areas in rural Bangladesh. In this pilot study, participandrinking water, hair, and nail arsenic concentrations were measured by inductively coupled plasma mass spectroscopy (ICP-MS). Serum myostatin levels were assessed by enzyme-linked immunosorbent assay (ELISA). In the current study, we found that the median serum myostatin levels of the participants in the high-exposure area were significantly higher than those of the participants in the low-exposure area. Serum myostatin levels were significantly increased with the increasing exposure to arsenic. Serum myostatin levels were negatively associated with arsenic-related decreased muscle mass markers-serum creatinine levels and lean body mass (LBM) and positively associated with HOMA-IR. The results of this pilot study suggest that increased myostatin may be an underlying mechanism of arsenic exposure-related sarcopenia leading to IR and cardiometabolic diseases.

PP139

ASSOCIATION OF ARSENIC EXPOSURE WITH NEUTROPHIL GELATINASE-ASSOCIATED LIPOCALIN AND ITS IMPLICATION IN CARDIOVASCULAR DISEASES: A CROSS SECTIONAL PILOT STUDY

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Cardiovascular diseases (CVDs), the leading causes of arsenic-related morbidity and mortality, are a major public health concern worldwide, including in Bangladesh. However, the underlying mechanism of arsenic-induced CVDs have not yet been clearly understood. Neutrophil gelatinase-associated lipocalin (NGAL) is a protein that is mainly recognized as a marker for acute kidney injury, but it is also highly expressed in damaged heart tissue and atherosclerotic plaque and thus plays a critical role in inflammatory processes and atherosclerosis. We designed this pilot study to investigate the association of arsenic exposure with serum NGAL levels as well as its implications in CVDs. The study participants (n=120) were recruited from low- and high-arsenic exposure rural areas in Bangladesh. Participants' drinking water, hair, and nail arsenic concentrations were measured by inductively coupled plasma mass spectroscopy (ICP-MS). NGAL levels in serum were determined by immunoassay. Serum HDL-C level as a CVDs risk and creatinine levels as marker of kidney dysfunctions were measured by colorimetric methods. In this current study, we found that median serum NGAL levels of the participants in high-exposure areas were significantly higher than that of the participants from low-exposure area. Serum NGAL levels were increased with increasing concentrations of arsenic even after adjusting for several covariates. Intriguingly, NGAL levels were inversely associated with serum creatinine levels. Increased serum NGAL levels are linked to decreased HDL-C. Taken together, the results of this pilot study suggested that increased NGAL levels might be implicated in the pathogenesis of arsenic-promoted CVDs.

PP140

HPLC PROFILING, ANTHELMINTIC, AND ANTI-INFLAMMATORY ACTIVITIES OF POLYGONUM PERSICARIA L.: IN VITRO AND IN SILICO INSIGHTS

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Polygonum persicaria L. is a medicinal herb renowned for its traditional applications in treating inflammation, rheumatism, diarrhea and fungal infactions. This study aims to evaluate the anthelmintic and anti-inflammation properties of the methanolic leaf extract of polygonum persicaria(MLPP) and to identify potential lead compounds using in silico moleculer docking techniques. High-performance liquid chromatography (HPLC) was employed to identify bioactive compounds in MLPP. The anthelmintic activity was assessed in vitro against paramphistomum cervi, determining paralysis and mortality times at various concentrations. The anti-inflammatory potential was evaluated via a protein denaturation assay, measuring inhibition rates at different extract concentrations. In silico molecular docking was conducted to assess the binding affinities of identified compounds against relevant targets.. HPLC analysis identified six bioactive compounds: 3,4-dihydroxybenzoic acid, Kaempferol, myricetin, p-coumaric acid, quercetin and trans-ferulic acid.In vitro tests revealed a dose-dependent anthelmintic effect with paralysis occurring at 10.3±0.3 min and death at 16.3±0.3 min at a concentration of 200 mg/ml, comparable to the standard drug albendazole. The anti-inflammatory assay showed a maximum inhibition of 98% at 800 µg/ml. In silico docking suggested strong binding affinities of kaempferol, myricetin and quercetin against key anthelmintic and anti-inflammatory targets. The findings indicate that MLPP exhibits significant therapeutic potential, supporting its traditional uses. The identified compounds may serve as promising leads for the development of matural anthelmintic and anti-inflammatory drugs, bolstering the role of polygonum persicaria in contemporary phytotherapy.

PP142

NUTRITIONAL STATUS AND DIETARY BEHAVIOR AMONG HOSPITALIZED FEMALE CANCER PATIENTS IN BANGLADESH: A CROSS-SECTIONAL STUDY

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In Bangladesh, cancer (Ca) remains an increasingly difficult public health issue, particularly, in women facing triple threat of late-stage-diagnosis: heavy treatment, socio-economic burden and malnutrition. While good-nutrition leads to quality-of-life during treatment, there is still lack of data on ‘quality of food’ and eating-behavior in women suffering with Ca towards maintaining health and nutrition. To gain clear scenario of nutritional status and eating-habits of hospitalized female Ca-patients, we tried to determine if nutritional factors relate their clinical backgrounds and personal-demographics. This cross-sectionally designed observational study was conducted among 182 female suffering from patients at the National Institute of Cancer Research and Hospital (NICRH) in Dhaka, encompassing both in- and- out patients. Information was gathered through one-on-one personal interviews using a pre-structured questionnaire. To gauge their health status, we measured Body Mass Index (BMI) as a predictor for nutritional status with a combined food frequency based on some pertinent questions using a 24-hour-dietary recall method to understand eating pattern of these Ca-patients. Findings revealed that breast-Ca as the most commonly diagnosis among these patients by 37.4%, followed by gynecological cancers by 29.7%. Socio-demographically, most of their education levels were low, with nearly half (47.8%) having no formal schooling. Nearly 15.5% yielded underweight, >34% had overweight or were obese. While mostly struggling with eating, >81% lost their appetite, and >80% lost weight in last 6 months, mostly yielding their nutritional status associated with patient's age ($p<0.01$), but specific Ca-type didn't impact significantly on BMI, >92.3% were less aware on Ca-treatment reflecting poor diet with less fruits, vegetables, or protein-rich foods. Female-Ca patients in Bangladesh facing a "perfect-storm" of malnutrition, appetite-loss, and lacks nutritional-knowledge. To improve Ca-treatment-outcome, it isn't enough to just treat cancer; BD health system must integrate nutritional-screening/personalized dietary-counseling into standard oncology treatment and care.

PP143

A COMPARATIVE STUDY ON SOCIO-DEMOGRAPHIC, ENVIRONMENTAL, AND NUTRITIONAL DETERMINANTS OF SCABIES AMONG ADOLESCENT GIRLS IN URBAN AND RURAL MADRASAHS OF BANGLADESH

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Scabies, a contagious parasitic skin-infection with the infestation of Sarcoptes scabiei var. hominis, prevalent especially in low-resource settings of densely populated adolescent-girls living in densely populated urban & rural female-madrasahs threatening public health burden. Reportedly, adolescent girls living in madrasahs infested with scabies mites due to risky communal living, poor hygiene, and limited health facilities and sustain longer in human skins. We thus conducted this study to compare socio-demographic, behavioral and environmental determinants of scabies in adolescent-girls between urban and rural Madrasahs. This cross-sectional comparative study was conducted from June-Oct 2025 among 174 adolescent girls (n=54 urban; n=121 rural). Data was collected employing face-to-face interviews and clinical examination (by doctors/nutritionists) were confirmed based on signs /symptoms. Recoded data were analyzed on SPSS, V.25 using required statistical tools ($x2$ & FET) and the urban-rural differences were studied (a $p<0.05$ was taken as significant). A higher linkage was identified between low-education and infection-rates; parents of 92% respondent (adolescent-girls) had low-education (<SSC). Residential vulnerability was higher in rural areas (47%) than urban (16%) areas. Significant environmental risks included use of communal bathrooms (65%), frequent sharing of inner clothing/shared beds (46%). Clinical assessments revealed 74% recurrence rate, with vesicle/blisters (68%) and circular erythematous patches (27%). Rural Madrasahs were significantly poorer with dormitory-ventilation (40%) than urban ones. Lower mineral intake, specifically zinc (57% consumption) compared to urban counterparts were obvious. These factors, combined with systemic poverty, were the primary drivers of persistent infestation. Findings highlighted a disparity with rural-Madrasahs facing higher scabies prevalence, living in unhealthy bizarre and unhygienic conditions than urban Madrasa-students. Effective control requires improving Madrasah-infrastructure, enhancing ventilation, maintaining health & hygiene and addressing nutritional deficiencies properly to boost physical resilience of adolescent girls infestations with scabies- so as to prevent serious infections like nephritis.

PP0145

EVALUATING THE ROLE OF ARTIFICIAL INTELLIGENCE IN ENHANCING LEARNING OUTCOMES AND CRITICAL THINKING AMONG UNIVERSITY STUDENTS

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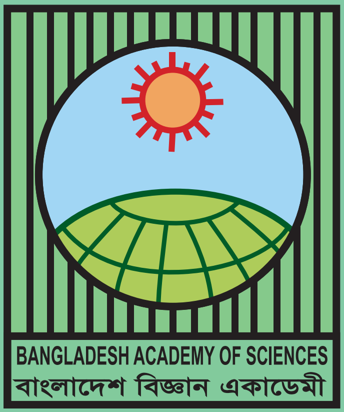
Young minds are always curious to learn new thing. Now a days the universities students commonly uses many smart technologies such as Artificial Intelligence (AI) for quick learning. However, there isa concern a regarding the data accuracy and authenticity derived from AI. This study aims to explore how students view the application of Artificial Intelligence (AI) in their academic lives and its long-term effects on the field of education. As AI tools become more accessible worldwide, understanding the primary user's viewpoint is essential for effective integration. Data was collected through an online survey using Google Forms, resulting in a total of 71 NSU university student responses. The survey consisted of a mix of quantitative and qualitative questions to assess current usage patterns, helpfulness level, and the outlook on AI-based education. Preliminary findings indicate that 39.4% of 71 respondents currently use AI tools for their studies. While 90%of participants found it much easier to understand complex concepts, concerns were raised regarding accuracy, over-resilience, and loss of human interaction. A total of 43.7% of students have expressed that they often fact-check information provided by AI. Even though 35.2% of students have rated "4" on a scale of 1-5 regarding how positively AI affects their learning outcomes, most respondents believe relying on AI will negatively affect their critical thinking skills over time. Regarding the future, 80.3% of students prefer a combination of both AI and teachers for their education, showing how quickly AI has become a permanent fixture in the academic scene. The results suggest that while students are largely optimistic about AI's role in increasing learning productivity, there is a clear demand for guidance on its responsible use. These findings highlight the need for educational institutions to develop clear AI policies that balance technological benefits with academic integrity.

JOURNAL OF

BANGLADESH ACADEMY OF SCIENCES

Volume 50 Supplement 1 April 2026

ISSN: 2224-7270 (Online), 0378-8121 (Print)



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