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Poster ID 1A001

Neuroprotective Effects of Centella asiatica and Asiatic Acid in a Scopolamine-Induced Amnesia ModelPoster ID

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Background: Cognitive impairment is closely associated with cholinergic dysfunction, oxidative stress, and altered monoaminergic activity. Scopolamine-induced amnesia is a well-established experimental model that mimics memory deficits and redox imbalance1. Centella asiatica extract (CAE) and its bioactive constituent, Asiatic acid (AA), possess potential neuroprotective properties2.
Objective: This study aimed to evaluate the neuroprotective effects of CAE (25, 50, and 100 mg/kg) and AA (30 and 60 mg/kg) against scopolamine-induced cognitive impairment using behavioural and biochemical parameters.
Methods: Amnesia was induced by scopolamine administration. Animals were treated with CAE (25, 50, and 100 mg/kg), AA (30 and 60 mg/kg), or donepezil (DPZ) as the standard drug. Behavioural performance was assessed using the Y-maze test. Biochemical estimations included acetylcholinesterase (AChE), superoxide dismutase (SOD), reduced glutathione (GSH), reactive oxygen species (ROS), nitric oxide (NO), malondialdehyde (MDA), and monoamine oxidase-B (MAO-B). Data were analyzed using one-way ANOVA followed by the Newman–Keuls multiple comparison test3.

Results: Scopolamine significantly impaired Y-maze performance and induced marked oxidative imbalance, as evidenced by increased AChE, ROS, NO, MDA, MAO-B, and SOD levels, along with a significant reduction in GSH. Treatment with CAE and AA significantly ameliorated these alterations in a dose-dependent manner. Both CAE and AA normalized elevated SOD levels, indicating attenuation of oxidative burden. The higher dose of AA (60 mg/kg) exhibited the most prominent neuroprotective effect, comparable to donepezil[1].
Conclusion: CAE and AA effectively counteract scopolamine-induced cognitive deficits by modulating cholinergic activity, restoring redox homeostasis, and normalizing MAO-B levels. Thus, AA may serve as a promising therapeutic candidate for memory-related neurodegenerative disorders.

References:

1. Mahdi, O. *et al.* Chemicals used for the induction of Alzheimer's disease-like cognitive dysfunctions in rodents. *Biomedical Research and Therapy* **6**, 3460–3484 (2019).
2. Firdaus, Z., Singh, N., Prajapati, S. K., Krishnamurthy, S. & Singh, T. D. Centella asiatica prevents D-galactose-Induced cognitive deficits, oxidative stress and neurodegeneration in the adult rat brain. *Drug and Chemical Toxicology* **45**, 1417–1426 (2022).
3. Firdaus, Z., Kumar, D., Singh, S. K. & Singh, T. D. Centella asiatica Alleviates AlCl3-induced Cognitive Impairment, Oxidative Stress, and Neurodegeneration by Modulating Cholinergic Activity and Oxidative Burden in Rat Brain. *Biological Trace Element Research* **200**, 5115–5126 (2022).

Poster ID 1A002

Correlation of Rheumatoid Arthritis (RA) Factor and Anti-CCP (Anti-Cyclic Citrullinated Peptide) Antibody in Patients of Rheumatoid Arthritis

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Introduction: Rheumatoid arthritis (RA) is a chronic autoimmune inflammatory disorder affecting synovial joints, leading to progressive biomarkers joint damage and disability. Anti-cyclic citrullinated peptide (Anti-CCP) antibodies are highly specific for RA and are important in early diagnosis and prognosis. We also measured Rheumatoid factor (RF) which is commonly used as prognostic marker for RA diagnosis. The correlation between Anti-CCP and RF can help in understanding disease severity and progression.
Objective: The objective of this study was to measure serum RF and Anti-CCP antibody levels in RA patients and to assess the correlation between these two markers.
Method: The present cross-sectional study includes total of 30 patients were clinically diagnosed with RA, from Orthopedic OPD, MGM Hospital, Kamothe, Navi Mumbai. The age group was 18 to 60 years with known for RA were included and other autoimmune diseases, such as SLE, chronic infections were excluded. Blood samples were collected under aseptic condition. Serum RF and Anti-CCP antibody levels were estimated using standard immunoassay methods. Statistical analysis was performed

to evaluate the correlation between RF and Anti-CCP levels by using SPSS version 25.

Result: We found Mean value of RF 40 ± 36 U/mL and Anti-CCP was 92 ± 62 U/mL and found positive correlation between RF and Anti-CCP levels in RA patients (r= 0.6, p <0.01).

Conclusion: We observed elevated levels of both RF and Anti-CCP antibodies in RA patients with a significant positive correlation between them, due to immune response against citrullinated joint proteins formed during chronic inflammation in RA patients. Anti-CCP antibodies, being highly specific, serve as a reliable marker for early diagnosis and prognosis of RA, and combined estimation of RF and Anti-CCP improves clinical assessment of disease severity in RA.

Keywords: Rheumatoid Arthritis, Rheumatoid Factor, Anti-CCP.

References:

1. Bugatti S, Vitolo B, Manzo A, Montecucco C, Caporali R. Anti-citrullinated protein antibodies and rheumatoid factor in rheumatoid arthritis: clinical and pathogenic associations. Autoimmun Rev. 2023;22(2):103270.
2. Smolen JS, Aletaha D, McInnes IB. Rheumatoid arthritis: immunopathogenesis and biomarkers. Nat Rev Dis Primers. 2023;9(1):45.
3. Wang M, Liu Y, Zhang X. Diagnostic and prognostic value of anti-CCP antibodies and rheumatoid factor in rheumatoid arthritis. Front Immunol. 2025;16:1298456.

Poster ID 1A003

Study of Urinary Vanillylmandelic Acid (VMA) level in Patients of Anxiety Spectrum Disorder.

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Introduction: Anxiety is a typical stress response. Studies have indicated that anxiety spectrum disorder (ASD) can change the amounts of catecholamines in the blood, and prevalence of anxiety disorders is rising worldwide. VMA (Vanillyl Mandelic Acid) is a primary metabolite of norepinephrine & epinephrine, secreted in response to anxiety through hypothalamus. It is a marker of sympathetic nervous system. Elevated VMA may indicate future risk of CVD. Therefore, we aim to estimate urinary VMA and find its association with anxiety level.

Methods: The present case control study comprised total 70 participants (18-60 years), of which 35 pre-diagnosed anxiety spectrum disorder and 35 healthy controls. Individual with other psychiatric disorders and those are on medication that could alter catecholamine metabolism were excluded. The subjects with pre-diagnosed ASD were further divided into three categories based on diagnostic and statistical manual of mental disorders (DSM-5) criteria as: anxiety disorder, panic disorder, and generalized anxiety disorder. HAM-A scale was used to check severity of anxiety. Urine samples were processed on same day for VMA analysis using ELISA. Statistical analysis was done at SPSS version 25.

Result: We found mean urinary VMA level (ng/ml) was 44.8 ±4.9 in Anxiety Spectrum Disorder, which is significantly higher as compared to healthy control group (5.4 ±1.89, p: <0.001). Increase urinary VMA indicates chronic stress induced excess catecholamine activity, leading to sympathetic overactivation, hypertension, endothelial dysfunction, and increased cardiovascular disease risk.

Conclusion: Due to physiological alterations in patients with ASD, particularly those with anxiety disorder, may be at a higher risk of developing thrombotic and other cardiovascular diseases.

Keywords: Anxiety Spectrum Disorder, Vanillyl Mandelic Acid, cardiovascular diseases

References:

1. F. Mukta, Q. Akhter, et al. "The evaluation of urinary vanillylmandelic acid level in patients with generalized anxiety disorder." World journal of advanced research and reviews. 2021;12(1):001-005.
2. M.J. Garvey, R Jr. Noyes, C. et al. The association of urinary 5-Hydroxyindoleacetic acid and vanillylmandelic acid in patients with generalized anxiety Neuropsychobiology. 1995;31(1):6-9.
3. M.J. Garvey, R Jr. Noyes, C. et al. Relationship of generalized anxiety symptoms to urinary 5-Hydroxyindoleacetic acid and vanillylmandelic acid psychiatry Research. 1995;57(1):1-5

Poster ID 1A004

Correlation of vitamin D level and Glycemic control in type 2 Diabetes Mellitus

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Keywords: Type 2 diabetes mellitus, Vitamin D, Glycemic control, HBA1c.

Introduction: Type 2 diabetes mellitus (T2DM) is a common metabolic disorder characterized by chronic hyperglycemia and insulin resistance. Recent evidence suggests that vitamin D plays an important role in glucose metabolism, insulin secretion, and insulin sensitivity. Vitamin D deficiency is highly prevalent in individuals with T2DM,

Aim & Objectives:

- To study the correlation between serum vitamin D levels and glycemic control in patients with type 2 diabetes mellitus.
- To analyse FBS, PPBS, HbA1c and Vitamin D.

Materials and Methods: This cross-sectional observational study was conducted on 30 patients diagnosed with type 2 diabetes mellitus. Fasting blood sugar (FBS), Postparandial blood sugar (PPBS) glycated hemoglobin (HbA1c), and serum 25-hydroxyvitamin D [25(OH)D] levels were estimated using standard laboratory methods. Glycemic control was assessed based on FBS, PPBS and HbA1c values.

Statistical analysis was performed to evaluate the correlation between vitamin D levels and glycemic parameters.

Results: Vitamin D deficiency was commonly in type 2 diabetes mellitus and showed an inverse association with glycemic parameters, where lower vitamin D levels correlated with higher FBS, PPBS, and HbA1c, indicating poor glycemic control.

Conclusion: The study suggests that decreased serum vitamin D levels are associated with poor glycemic control in patients with type 2 diabetes mellitus. Assessment and management of vitamin D deficiency may be beneficial.

References:

1. Organization WH. World Health Organization. Global Report on Diabetes. 2016;
2. Association AD. Diagnosis and classification of diabetes mellitus. Diabetes Care. 2010;33
3. Siu AL, on behalf of the U.S. Preventive Services Task Force*. Screening for abnormal blood glucose and type 2 diabetes mellitus: U.s. preventive services task force recommendation statement. Ann Intern Med [Internet]. 2015;163(11):861–8

Poster ID 1A005

Neurotoxicity effect of 2.4 GHz Electromagnetic Radiation on inducing oxidative stress causing Parkinson Disease: An in vitro study using SH-SY5Y cell line

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Background: The ubiquity of wireless devices emitting 2.4 GHz electromagnetic radiation (EMR) has raised concerns regarding its biological impact. Oxidative stress is a known driver of Parkinson's disease (PD), yet the specific role of EMR in inducing PD-like neurodegeneration remains under active investigation. Methods: SH-SY5Y neuroblastoma cells were divided into control, Rotenone-treated (positive PD control), and EMR-exposed groups (8, 12, 24, and 48 hours). Neurotoxicity was measured via electrochemical detection of dopamine. Cellular health was evaluated through intracellular calcium (Ca2+), Reactive Oxygen Species (ROS), Mitochondrial Membrane Potential (MMP), and lipid peroxidation. Cell death mechanisms were analyzed using Annexin V/PI flow cytometry, while genotoxicity was assessed via COMET assay. Results: EMR exposure and mimicking the rotenone-induced phenotype resulted in reducing dopamine levels. Oxidative stress markers (ROS and lipid peroxidation) peaked at 8 hours before shifting toward irreversible cellular damage. Conversely, Ca2+ accumulation and mitochondrial dysfunction with prolonged exposure (12–48 hours). Flowcytometry results have shown that early apoptosis at 8 hours to late apoptosis and necrosis at later stages. Genotoxicity, evidenced by DNA fragmentation in the COMET assay, increased significantly with exposure duration. Conclusion: 2.4 GHz EMR exposure induces neuronal integrity by inducing oxidative stress, calcium overload, and mitochondrial failure. The observed progression to necrosis and loss of dopamine highlight the potential effect of EMR posing it as a risk factor for neurodegenerative conditions such as Parkinson's disease.

Poster ID 1A006

Exploring a Natural Meroterpenoid as an HSP90-Targeting Lead Against Triple-Negative Breast Cancer: *in vitro and in slico approaches*

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Psoralea corylifolia holds a prominent position in traditional herbal medicine. Bakuchiol, the principal phytoconstituent present in the seeds of P. corylifolia, significantly contributes to the medicinal properties of the plant. The present study aims to investigate the potential of bakuchiol in mitigating triple-negative breast cancer (TNBC) by targeting heat shock protein 90 (HSP90), a pivotal molecular chaperone implicated in cancer cell growth and progression. The study has employed a multi-approach strategy, by combining in-silico (Network pharmacology, molecular docking, molecular dynamics simulation), cell-free assay (N-terminal HSP90 binding activity assay), and in-vitro methodologies, to explore its anticancer activities against TNBC and to elucidate HSP90 as a target of bakuchiol, using a HSP90-inhibitor radicicol as a reference. The Chou-Talalay combination index method was employed for determining its synergistic potential. Bakuchiol showed preferential cytotoxicity on MDA-MB-231 cells, with minimal impact on non-cancerous cells HEK-293, demonstrating a favourable selectivity index. In-silico studies identified HSP90 as a prime target via which bakuchiol exhibits its anticancer activity, and the competitive binding assay established it as an N-terminal HSP90 inhibitor. Detailed in-vitro studies further highlighted the anti-proliferative, pro-apoptotic, and anti-metastatic role of bakuchiol, with radicicol serving as a control to verify HSP90-mediated activity. Moreover, bakuchiol was also found to exhibit a synergistic effect against TNBC cells in association with the standard chemotherapeutic drug doxorubicin, thereby enhancing its therapeutic efficacy. These findings highlight bakuchiol as a promising HSP90-targeting natural compound with potential therapeutic benefit against TNBC, therefore making it a crucial lead for further research.

Poster ID 1A007

Ongoing Randomized Controlled Trial Comparing Effectiveness, Safety, Hepatic Outcomes, Renal outcomes and Cost-Effectiveness of Dapagliflozin versus Empagliflozin in Patients with Type 2 Diabetes Mellitus and High Body Mass Index: A Study Protocol

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Background

India bears a substantial burden of Type 2 Diabetes Mellitus (T2DM), frequently associated with increased visceral adiposity and early cardiometabolic complications. Patients with high body mass index (BMI) are at heightened risk of metabolic dysfunction–associated steatotic liver disease (MASLD), cardiovascular disease, and renal impairment. Sodium–glucose cotransporter-2 (SGLT2) inhibitors offer glycaemic control alongside weight reduction and cardio-renal benefits. However, direct head-to-head randomized comparative evidence between dapagliflozin and empagliflozin in Indian patients with high BMI—particularly integrating hepatic and cost-effectiveness outcomes—remains limited.

Objective

To compare the effectiveness, safety, hepatic Outcomes, renal outcomes and cost-effectiveness of dapagliflozin versus empagliflozin in adults with T2DM and high BMI.

Methodology:

This ongoing prospective, randomized, open-label, parallel-group clinical trial (CTRI/2025/11/097341) is being conducted at AIIMS Bhopal, India. A total of 112 adults (HbA1c 7–10%; BMI ≥25 kg/m^2) are being randomized in a 1:1 ratio using computer-generated block randomization stratified by baseline HbA1c. Participants receive either dapagliflozin 10 mg once daily or empagliflozin 25 mg once daily in addition to stable background therapy (metformin ± other oral hypoglycaemic agents) for 24 weeks.

Primary outcomes include change in HbA1c and body weight at 6 months. Secondary outcomes comprise changes in fasting blood glucose, blood pressure, lipid profile, hepatic enzymes (ALT, AST, GGT), liver steatosis and fibrosis assessed using controlled attenuation parameter (CAP) and liver stiffness measurement (LSM), renal function (serum creatinine, eGFR, UACR), safety, and treatment adherence (SDSCA tool).

A concurrent pharmacoeconomic evaluation will assess direct and indirect costs. Cost-effectiveness will be calculated using Average Cost-Effectiveness Ratio (ACER) and Incremental Cost-Effectiveness Ratio (ICER) based

on weighted clinical effectiveness measures. Data will be analysed using intention-to-treat principles with ANCOVA for primary outcomes.

Expected Outcome

This trial is designed to generate India-specific comparative evidence on metabolic, hepatic, safety, and economic outcomes of two widely prescribed SGLT2 inhibitors. The findings aim to inform rational, patient-centred, and economically sustainable diabetes management strategies in real-world clinical practice.

References:

1. Zinman B, Wanner C, Lachin JM, et al. Empagliflozin, cardiovascular outcomes, and mortality in type 2 diabetes. *N Engl J Med*. 2015;373(22):2117–2128.
2. Wiviott SD, Raz I, Bonaca MP, et al. Dapagliflozin and cardiovascular outcomes in type 2 diabetes. *N Engl J Med*. 2019;380(4):347–357.
3. Kuchay MS, Krishan S, Mishra SK, et al. Effect of empagliflozin on liver fat in patients with type 2 diabetes and non-alcoholic fatty liver disease: a randomized controlled trial. *Diabetes Care*. 2018;41(8):1801–1808.

Poster ID 1A008

Viruses in Adult Chronic Diarrhoea: A Study from North India

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Background: Chronic diarrhoea is the "persistent alteration from the norm with stool consistency between Types 5 to 7 on Bristol stool chart and increased frequency >4 weeks" according to the British Society of Gastroenterology.1 Various causes include colonic neoplasia, inflammation, malabsorption, and motility disorders, while infections remain less explored.2,3 Our study, conducted at a tertiary care teaching hospital in North India, aimed to evaluate viral causes of chronic diarrhoea.
Methods: Adults with chronic diarrhoea were recruited for between 1st December 2022 to 31st May 2024 and assigned into 4 groups - IBD in remission (Group A, n=40), Acute severe ulcerative colitis (ASUC) (Group B, n=40), non-IBD chronic diarrhoea (Group C, n=35) and healthy controls (Group D, n=35). After obtaining consent, a small amount of stool sample was collected in 7 ml phosphate buffer saline (PBS), vortexed, centrifuged, and the supernatant used for automated nucleic acid extraction. FlexStar® RT-PCR Detection Mix 1.5 (Altona Diagnostics GmbH, Germany), an in-vitro real-time PCR-based diagnostic test, was used to detect Astro, Adeno, Noro group 1 and 2, Rota and Sapoviruses.
Results: Mean age of study population was 36.63 ± 13.72 years, with 51.3% males. Viruses were detected in 8% cases, with 4 cases in each patient group, including Adenovirus (3.3%), Norovirus Group 2 (3.3%), and Sapovirus (2.7%). No viral aetiologies were detected in controls. Mixed infection with adeno and sapovirus was noted in 2 patients.
Conclusion: More priority should be given to gastrointestinal viruses in those with chronic diarrhoea, to streamline management and give targeted therapy.
Words count: 245 words

References:

1. Arasaradnam RP, Brown S, Forbes A, Fox MR, Hungin P, Kelman L, et al. Guidelines for the investigation of chronic diarrhoea in adults: British Society of Gastroenterology, 3rd edition. Gut. 2018;67:1380–99.
2. Schiller LR, Pardi DS, Spiller R, Semrad CE, Surawicz CM, Giannella RA, et al. Gastro 2013 APDW/WCOG Shanghai Working Party Report: Chronic diarrhea: Definition, classification, diagnosis: Chronic diarrhea. J Gastroenterol Hepatol. 2014;29:6–25.
3. Kaiser L, Surawicz CM. Infectious causes of chronic diarrhoea. Best Pract Res Clin Gastroenterol. 2012;26:563–71.

Poster ID 1A009

From Selection to Sensing: One-Step Aptamer Selection and Continuous Stress Monitoring

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Aptamers are gaining attention for their versatility and cost-effectiveness in theranostics, offering a competitive alternative to antibodies. However, their selection process is complex. To streamline this, we developed the Hydrogel-based Aptamer Selection (HAS) method, which utilizes a diffusion-binding process in a non-fouling porous hydrogel with immobilized targets. HAS simplifies the process by reducing PCR rounds, skipping negative selection, and preserving the target's native 3D conformation. This method allows for easy synthesis and customization of

aptamers, advancing medical research, personalized medicine, and biotechnological innovations. Additionally, we address the need for precise stress monitoring with a non-invasive, wearable sensor that measures cortisol levels in sweat using conformation switching pseudoknot aptamer. Using a pseudoknot-assisted aptamer and a flexible microfluidic system, this sensor provides real-time, continuous monitoring of cortisol, offering a more specific alternative to traditional methods like heart rate variability. These advancements highlight the critical role of molecular recognition agents in modern healthcare and analytical sciences.

References:

1. Naveen K Singh et al., One-step Aptamer Selection in a Three-dimensional Non-fouling Porous Hydrogel, Published in Nature Biotechnology, 42, 1224-1231 (2024)
2. Naveen K. Singh et al., A non-invasive wearable stress patch for real-time cortisol monitoring using a pseudoknot-assisted aptamer. 2023. Biosensors and Bioelectronics, 227, 115097.

Poster ID 1A010

Serum Nitrite and Endothelial Dysfunction in Angiographycally-Proven Coronary Artery Disease

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Endothelial dysfunction is characterized by a reduction in endothelium-derived vasodilators and/or an increase in opposing vasoconstrictive factors. Nitric oxide (NO), a biologically active free radical, plays a crucial role in maintaining vascular tone, regulating immune responses, and facilitating neurotransmission. It is synthesized from L-arginine by the enzyme nitric oxide synthase (NOS) in vascular endothelial cells.
Aims & Objectives: The present study aimed to evaluate endothelial dysfunction in angiographically confirmed cases of coronary artery disease (CAD) by measuring serum nitrite levels as an indicator of nitric oxide availability.
Method: A total of 231 patients with angiographically proven CAD, aged between 18 and 75 years, were included. The control group comprised 40 healthy individuals (26 males and 25 females). Serum nitrite levels were determined using a simple, cost-effective, and precise High-Performance Liquid Chromatography (HPLC) method performed on the ULTIMATE 3000 (Dionex, USA) system.
Result: The findings revealed a statistically significant reduction in serum nitrite levels among CAD patients (8.98 ± 4.45 µmol/L) compared to healthy controls (18.86 ± 4.04 µmol/L) ($p < 0.0001$).
Conclusion: The decreased bioavailability of nitric oxide may contribute to endothelial injury and atherosclerosis through enhanced leukocyte and platelet adhesion, increased vasoconstriction, and proliferation of vascular smooth muscle cells.
Keywords: Serum nitrite, Endothelial dysfunction, HPLC, Coronary Artery Disease.

Poster ID 1A011

Ongoing Ambispective Observational Study Evaluating Real-World Safety and Lipid-Lowering Effectiveness of Statins at a Tertiary Care Centre in Central India- A study Protocol

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BACKGROUND

Statins are first-line therapy for dyslipidaemia and atherosclerotic cardiovascular disease (ASCVD) prevention. Although randomized trials demonstrate substantial LDL-C reduction and cardiovascular risk benefit, real-world data on safety, tolerability, and adherence in Indian populations remain limited. Patient-reported statin-associated muscle symptoms (SAMS) and perceived intolerance often contribute to discontinuation despite low rates of objective biochemical toxicity.

OBJECTIVE

To evaluate the real-world safety and lipid-lowering effectiveness of statins in patients receiving statin therapy at a tertiary care centre in Central India.

METHODOLOGY

This ongoing ambispective observational study is being conducted at AIIMS Bhopal across Medicine, Cardiology, and CTVS departments. Patients initiated on or receiving statins are enrolled after consent. Estimated sample size ranges from 117–188 participants. Safety assessment includes structured evaluation of SAMS using the validated SAMS-Clinical Index (SAMS-CI), gastrointestinal adverse effects using the Gastrointestinal Symptom Rating Scale (GSRS), and monitoring of hepatic enzymes (ALT, AST) to estimate hepatic adverse effects. Adverse events are categorized using WHO-UMC causality criteria. Effectiveness is assessed by change in total cholesterol and LDL-C from baseline to 1 and 3 months. Medication adherence is evaluated using the 8-item Morisky Medication Adherence Scale (MMAS-8). Multivariable analyses using ANOVA and Chi square tests as required will identify predictors of adverse effects and lipid response.

EXPECTED OUTCOME

This study will generate India-specific real-world evidence on statin safety, tolerability, adherence, and effectiveness, supporting rational prescribing and improved cardiovascular risk management.

References:

1. Grundy SM, Stone NJ, Bailey AL, et al.2018 AHA/ACC/AACVPR/AAPA/ABC/ACPM/ADA/AGS/APhA/ASPC/NLA/PCNA Guideline on the Management of Blood Cholesterol. *J Am Coll Cardiol.* 2019;73(24):e285–e350.
2. Li W, Wang D, Lin C, et al. A Meta-Analysis of the Incidence of Adverse Reactions of Statins in Various Diseases. *Cardiovasc Ther.* 2025;2025:6684099.
3. Cannon CP. Statin intolerance: how common is it and how do we work with patients to overcome it? *Eur Heart J.* 2022;43(34):3224–3226.

Poster ID 1A012

Salivary Uric Acid as a Non-Invasive Predictor of Pregnancy Complications: Findings from a Nested Case–Control Study

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Keywords: Salivary biomarkers; uric acid; pregnancy complications; preeclampsia; gestational diabetes mellitus; non-invasive diagnostics; maternal health

Background:

Pregnancy-related complications such as preeclampsia, gestational diabetes mellitus (GDM), and miscarriage remain major contributors to adverse maternal and fetal outcomes. Early identification of women at risk is essential, yet current screening approaches rely largely on invasive blood-based investigations. Salivary biomarkers offer a non-invasive, easily accessible alternative for early risk assessment. Uric acid (UA), a marker of oxidative stress and metabolic dysregulation, has been implicated in several pregnancy complications, but its utility in saliva remains underexplored.

Objective:

To evaluate the potential of salivary uric acid as a predictive biomarker for pregnancy complications and associated adverse outcomes.

Methods:

This exploratory nested case–control study was conducted among 132 healthy pregnant women enrolled at ≤20 weeks of gestation. Saliva and serum samples were collected at recruitment and stored for subsequent analysis. Participants were prospectively followed for the development of pregnancy-related complications. For biomarker evaluation, 24 women were selected—12 who developed complications (cases) and 12 who had uncomplicated pregnancies (controls). Salivary uric acid levels were quantified using the uricase-based spectrophotometric method on the Cobas 8000 platform.

Results:

Mean salivary uric acid levels were significantly higher in cases compared to controls (1.1 ± 0.4 mg/dL vs. 0.5 ± 0.3 mg/dL; p = 0.004). Although salivary cortisol levels were higher in cases than controls (0.125 ± 0.03 µg/mL vs. 0.10 ± 0.05

µg/mL), this difference was not statistically significant (p = 0.4). These findings suggest that salivary uric acid may be a useful biomarker for predicting pregnancy complications, though further validation is needed.

Conclusion:

Salivary uric acid demonstrates potential as a non-invasive biomarker for the early prediction of pregnancy complications, including preeclampsia, miscarriage, and GDM. While salivary cortisol did not show significant discriminatory ability in this cohort, the findings support further investigation of salivary biomarkers in maternal risk stratification. Larger, prospective studies are required to validate the clinical applicability of salivary uric acid in routine antenatal screening.

References:

1. Püschl I.C. Salivary uric acid as a non-invasive biomarker predictive of preeclampsia. Eur J Obstet Gynecol Reprod Biol. 2024.
2. Chmielewska B. Validation of salivary uric acid remote self-monitoring for early detection of hypertensive disorders of pregnancy. BMJ Open. 2025.
3. Deepashree P.G., Madhushankari G.S., Nandini D.B., et al. Saliva as an alternative non-invasive biomarker for uric acid in pregnancy. J Oral Maxillofac Pathol. 2021.

Poster ID 1A013

Utility of the MPT64 Antigen Assay for Rapid Differentiation of Non-Tuberculous Mycobacteria from Mycobacterium tuberculosis Complex

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Background: Differentiation between Mycobacterium tuberculosis complex (MTBC) and non-tuberculous mycobacteria (NTM) is essential for appropriate clinical management. Conventional diagnostic algorithms that rely on smear microscopy and molecular testing may miss NTM infections in routine diagnostics. The MPT64 antigen detection assay is widely used for rapid confirmation of MTBC and may aid in the presumptive identification of NTM (1).

Objective: To evaluate the utility of the MPT64 antigen test for presumptive identification of NTM in routine diagnostic workflows.

Methods: Clinical specimens from patients suspected of mycobacterial infection were screened by Ziehl–Neelsen staining. AFB-positive samples were subjected to nucleic acid amplification testing (NAAT) for MTBC detection. NAAT-negative samples were cultured. Culture-positive isolates were confirmed by ZN staining and tested using the MPT64 antigen assay. MPT64-negative isolates were considered presumptive NTM and further characterised using molecular methods. (2)

Results: Of the 7,984 clinical specimens screened, 627 (7.85%) were AFB positive, and all were confirmed as MTBC by NAAT. The remaining 7,357 samples were subjected to culture, of which 1,540 (20.9%) were positive in the BACTEC MGIT 960 system. Among these culture-positive isolates, 387 (25.1%) were AFB positive. Of these, 367 (94.8%) were MPT64-positive and identified as MTBC, while 20 (5.2%) were MPT64-negative and considered presumptive NTM. A high level of concordance was observed between MPT64 results and confirmatory methods.

Conclusion: Integration of MPT64 antigen testing into routine diagnostic workflows provides a rapid and reliable approach for presumptive differentiation of MTBC and NTM, facilitating timely clinical management. Confirmatory molecular techniques remain essential for definitive species identification.

References:

1. Arora J, Kumar G, Verma AK, Bhalla M, Sarin R, Myneedu VP. Utility of MPT64 Antigen Detection for Rapid Confirmation of Mycobacterium tuberculosis Complex. *J Glob Infect Dis*. 2015;7(2):66-69.
2. Maurya AK, Nag VL, Kant S, et al. Evaluation of an immunochromatographic test for discrimination between Mycobacterium tuberculosis complex & non-tuberculous mycobacteria in clinical isolates from extra-pulmonary tuberculosis. *Indian J Med Res*. 2012;135(6):901-906.

Poster ID 1A014

Study of serum calcium, vitamin D3 and vitamin B12 in backache patients

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Keywords: Serum calcium, vitamin D3, vitamin B12, musculoskeletal, bone health

Introduction: Backache is a common musculoskeletal problem and may be associated with deficiencies of calcium, vitamin D3 and vitamin B12. This study aims to evaluate serum levels of these micronutrients in patients with backache to understand their possible role in adult population with back ache and which will support appropriate management.

Objectives: The objectives of this study were to find the association between serum calcium, vitamin D3 and vitamin B12 backache patients.

Methods: The present cross-sectional study were included 30 patients (30-60 Years) diagnosed with backache attending orthopedic OPD, MGM Hospital, Kamothe, Navi Mumbai in 2025. Patients with H/O chronic kidney disease, endocrine disorders, or those actively taking calcium and vitamin supplementation were excluded.

The blood samples are collected under aseptic condition and processed for Serum calcium, and Vitamin D, and B12 by CLIA technique. Statistical analysis done by SPSS version 25.

Results: The mean age of the study population is 43.07 ± 10.96 years. The mean serum calcium level is 8.26 ± 0.60 mg/dl. The mean serum Vitamin D3 level is 25.47 ± 2.33 ng/ml. The mean serum Vitamin B12 level is 473.95 ± 264.39 pg/ml. Conclusion: This study highlights the importance of assessing serum calcium, vitamin D3 and vitamin B12 in patients with backache. We found serum calcium and vitamin D3 levels were insufficient, indicates impaired bone-muscle metabolism leading to musculoskeletal pain. Identification of deficiencies of these micronutrients may aid in early intervention and contribute to improve clinical management and prevention of backache related complications.

References:

1. N. Krishnamurthy, Serum vitamin D levels in patients with chronic low back pain, International Journal of Clinical Biochemistry and Research, 2019, 6, 118–120.
2. Pishgahi, Association of serum 25-hydroxyvitamin D_3 with pain severity and disability in low back pain patients, BMC Research Notes, 2019, 12, 738.
3. S. Nasir, Correlation between vitamin D_3 deficiency and back pain in adult patients, Journal of Advances in Medicine and Medical Research, 2024, 36, 134–141.

Poster ID 1A015

NOTUM, a WNT Signaling Antagonist, Drives Cell-Autonomous Progression of Colorectal Cancer and Serves as a Potential Diagnostic Biomarker

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Colorectal cancer (CRC) is driven by early hyperactivation of WNT signalling, most commonly caused by loss-of-function mutations in the APC gene. NOTUM, a secreted WNT feedback antagonist, is induced under these conditions, but its diagnostic and functional relevance in human CRC remains poorly understood. We hypothesized that NOTUM is selectively upregulated in CRC, contributes to tumor progression in a cell-autonomous manner, and can serve as a circulating biomarker. Analysis of surgically resected human samples revealed significantly elevated NOTUM mRNA and protein expression in CRC tumors compared with matched peritumoral tissues across all disease stages, whereas no differential expression was observed in inflammatory bowel disease, indicating CRC-specific upregulation. Importantly, serum ELISA demonstrated markedly increased circulating NOTUM levels in CRC patients relative to healthy controls and IBD patients, supporting its potential as a non-invasive diagnostic biomarker. Functional studies using colorectal cancer cell lines showed that doxycycline-inducible NOTUM overexpression significantly enhanced cell proliferation, while shRNA-mediated knockdown suppressed proliferation and clonogenic survival. Consistently, pharmacological inhibition of NOTUM using the selective inhibitor ABC99 resulted in a dose-dependent reduction in CRC cell growth and long-term clonogenic potential, phenocopying genetic depletion. These effects were observed in APC/β-catenin–mutant cells and therefore were independent of extracellular WNT ligand availability, demonstrating a cell-autonomous pro-tumorigenic role for NOTUM. Collectively, our findings identify NOTUM as a CRC-specific biomarker detectable in patient serum and establish it as a functional driver of colorectal cancer progression, highlighting its promise as both a diagnostic and therapeutic target.

Poster ID 1A016

Gut-Derived Metabolites Trigger

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Oxidative Stress in Kidney Cells: A Protective Intervention Using Sorghum bicolor Seed extract

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Background- Diabetic kidney disease is a leading cause of end-stage renal disease, with limited tools for early detection. Gut microbiota-derived metabolites may contribute to disease progression; however, their diagnostic potential and mechanistic impact on renal cells remain unclear. This study aims to identify GC–MS-derived microbial metabolites, evaluate their role in inducing oxidative stress, and assess the protective effects of Sorghum bicolor extract.
Methodology- A total of 30 Urine and 30 stool samples from healthy, T2DM, and DKD groups were analyzed using GC–MS to identify differential metabolites. Statistical analysis, including ANOVA and ROC curve analysis, was performed to assess diagnostic potential, while box plots were used to visualize group-wise variations. Selected metabolites (HIVA, HPA, ICAL, SA, and PA) were evaluated in HEK-293 cells. Cytotoxicity was assessed using the MTT assay to determine IC_{50} values, while Sorghum bicolor extract was evaluated for EC_{50}. An IC_{30} dose of metabolites was used to induce sub-lethal stress, followed by co-treatment with EC_{50} of Sorghum bicolor. Intracellular ROS levels were measured using the DCFH-DA assay.
Results- GC–MS analysis revealed distinct metabolite profiles across study groups. Selected metabolites showed significant differences with strong discriminatory ability in ROC analysis, supported by box plot distributions. In vitro studies demonstrated that metabolites significantly reduced cell viability and increased ROS levels in HEK-293 cells. Co-treatment with Sorghum bicolor extract significantly restored cell viability and reduced ROS generation.
Conclusion GC–MS-identified microbial metabolites may serve as potential biomarkers for DKD and contribute to oxidative stress–mediated renal damage. Sorghum bicolor exhibits protective effects by attenuating ROS, highlighting its potential as a natural therapeutic strategy.

References:

1. Pereira, P. R., Carrageta, D. F., Oliveira, P. F., Rodrigues, A., Alves, M. G., & Monteiro, M. P. (2022). Metabolomics as a tool for the early diagnosis and prognosis of diabetic kidney disease. Medicinal research reviews, 42(4), 1518-1544.

Poster ID 1A017

Potential Association of Sickle Cell Disease Genotypes (SS, AS, SB Thalassemia) with ABO Blood Groups: In Indian Population

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Keywords: Sickle cell disease, ABO blood group, hemoglobinopathies, RDW, anemia, India

Sickle cell disease (SCD) exhibits marked clinical and hematological heterogeneity influenced by genetic and biological modifiers. The ABO blood group system has been implicated in vascular and thrombotic pathways relevant to SCD pathophysiology; however, data exploring its association with SCD genotypes and hematological severity in the Indian population remains limited.
The association between SCD genotypes (HbSS, HbAS, and sickle β-thalassemia), ABO blood group distribution, demographic variables, and hematological parameters in patients attending a tertiary care center in central India was evaluated. This hospital-based cross-sectional study included 53 confirmed hemoglobinopathy patients identified from 500 screened individuals. Diagnosis and genotype classification were performed using high-performance liquid chromatography (HPLC). ABO and Rh blood grouping was determined by standard serological methods. Complete blood count parameters were analyzed, and correlations between hematological indices, blood groups, and disease phenotypes were assessed using Pearson's and Spearman's correlation tests.
HbSS was the predominant genotype (54.7%), followed by HbAS (30.1%) and compound heterozygous states (13.2%). Blood group O was most prevalent (37.7%) and significantly overrepresented among SCD patients compared to the general population. Individuals with blood group O demonstrated the lowest mean hemoglobin levels and highest red cell distribution width (RDW), indicating more severe anemia and greater anisocytosis. A strong inverse

correlation was observed between RDW and hemoglobin ($r = -0.548$, $p < 0.001$), particularly pronounced in blood group O patients ($r = -0.723$, $p < 0.001$). Hematological indices such as MCV, MCH, and PCV varied significantly across genotypes, reflecting phenotype-specific disease severity. ABO blood group, particularly blood group O, is associated with greater hematological severity in sickle cell disease within this Indian cohort. Integration of ABO phenotype with routine hematological parameters may aid in risk stratification and personalized management of SCD. Larger population-based studies are warranted to validate these findings and elucidate underlying mechanisms.

Poster ID 1A018

Dual Drug Delivery for Augmenting Bacterial Wound Complications via Tailored Ultradeformable Carriers

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Addressing the complex challenge of bacterial-infected wound healing, this study investigates the therapeutic potential of lipid nanomaterials, particularly advanced ultradeformable particles (UDPs), in modulating the wound microenvironment. A dual-drug delivery system comprising silver sulfadiazine (SSD) and vitamin E (VE) was developed using UDPs (ethosomes, transferosomes, and transethosomes) for synergistic antibacterial and regenerative action. Comparative physicochemical characterization revealed superior stability of transethosomes with a zeta potential of −36.5 mV. These vesicles exhibited sustained and pH-responsive release, achieving approximately 90% SSD and 72% VE release under wound-like conditions, while minimizing the side effects associated with conventional topical formulations. Cytotoxicity assays demonstrated 60% cell viability even at 175 µg/mL, and hemolysis remained below 5% at 250 µg/mL, confirming excellent biocompatibility. Vitamin E–SSD-loaded transethosomes (VSTEs) significantly enhanced cellular migration and proliferation, resulting in ~95% wound closure within 24 hours and an 80% reduction in E. coli and S. aureus populations. Ongoing in vivo studies using a rat model of third-degree burn wounds include temporal evaluation of wound contraction, histological analysis of granulation and re-epithelialization, and immunohistochemical assessment of angiogenic and inflammatory markers. Preliminary findings indicate accelerated fibroblast migration, enhanced tissue regeneration, and pronounced antibacterial effects. Collectively, these results highlight the VSTE-based nanocarrier as a multifunctional, biocompatible, and efficient therapeutic platform for managing complex burn wounds, integrating antimicrobial defense with enhanced tissue repair mechanisms.

References:

1. Arora K, Dhruw B, Pm S, Madhukar P, Sundar S, Mudavath SL. Dual Drug Delivery for Augmenting Bacterial Wound Complications via Tailored Ultradeformable Carriers. Bioconjugate Chemistry. 2024 Apr 16.
2. Holzer-Geissler JC, Schwingenschuh S, Zacharias M, Einsiedler J, Kainz S, Reisenegger P, Holecek C, Hofmann E, Wolff-Winiski B, Fahrngruber H, Birngruber T. The impact of prolonged inflammation on wound healing. Biomedicines. 2022 Apr 6;10(4):856.
3. Liang Y, Liang Y, Zhang H, Guo B. Antibacterial biomaterials for skin wound dressing. Asian Journal of Pharmaceutical Sciences. 2022 May 1;17(3):353-84.

Poster ID 1A019

Association Between Metformin and Vitamin B 12 Levels in Patients Newly Diagnosed With Type 2 Diabetes in Tertiary Care Hospital Ratlam

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Keywords: Type 2 Diabetes Mellitus, Metformin, Vitamin B12, Drug-nutrient interaction.

Metformin is the first-line pharmacological therapy for type 2 diabetes mellitus (T2DM) and is used by over 120 million patients worldwide. Although long-term metformin use is known to impair vitamin B12 absorption, early changes in vitamin B12 levels after treatment initiation are less well documented. This report highlights a newly

diagnosed T2DM patient at a tertiary care hospital in Ratlam who demonstrated an early reduction in serum vitamin B12 levels after starting metformin treatment. This study highlights the importance of early monitoring of vitamin B12 levels in patients initiated on metformin.

References:

1. Sayedali, E. D., Yalin, A. E., Yalin, S., *World Journal of Diabetes,* 2023, 14, 585–593
2. Fujita, Y. D., Inagaki, N., *Diabetology International,* 2017, 8, 4–6.
3. Bell, D. S. H., *Diabetes, Obesity and Metabolism, 2022*, 24, 1423–1428.
4. Parsonage, I. D., Wainwright, D., Barratt, J., *BMJ Open,* 2025, 15, e101016.

Poster ID 1A020

Title: Serum and urinary proteins as early predictive biomarkers of acute kidney injury in patients with acute respiratory distress syndrome

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Introduction:

Acute respiratory distress syndrome (ARDS), is a life-threatening lung condition in ICUs, characterized by severe hypoxemia and increased lung permeability. Acute kidney injury (AKI) is the abrupt loss of kidney function resulting from tissue damage. The mortality rate with ARDS is approximately 27.9%, which can increase up to 42.3% in the presence of AKI. Current diagnostic approach for AKI includes measuring of serum creatinine and urine output, the levels of both won't increase until significant kidney damage. Therefore, there is need to evaluate more sophisticated molecules that would enable early diagnosis and a better prognosis. Cystatin C, KIM-1, NGAL, TIMP-2, IGFBP-7 and IL-18 are promising molecules to be act as early predictive biomarkers of AKI in ARDS patients.

Method:

Blood and urine samples from ARDS patients with or without AKI (disease groups) and non-ARDS or non-AKI (control group) patients were collected, processed and stored at -80˚C. The sandwich ELISA was performed to determine the concentration of the proteins. The cumulative result was plotted in graph using GraphPad Prism software.

Result:

The concentration of proteins varies corresponding to the groups. In case of ARDS patients with or without AKI, there is an elevated concentration of the proteins as compared to non-ARDS or non-AKI.

Conclusion:

Cystatin C, KIM-1, NGAL, TIMP-2, IGFBP-7 and IL-18 effectively demonstrate higher concentrations than usual in cases therefore, can act as early predictive biomarkers of AKI in ARDS patients.

References:

1. Michael Darmon et al. "Acute respiratory distress syndrome and risk of AKI among critically ill patients." Clinical journal of the American Society of Nephrology: CJASN vol. 9,8 (2014): 1347-53.
2. Won K. Han et al. "Kidney Injury Molecule-1 (KIM-1): a novel biomarker for human renal proximal tubule injury." Kidney international vol. 62,1 (2002): 237-44.
3. Carolyn M. Hendrickson et al. "Higher plasma cystatin C is associated with mortality after acute respiratory distress syndrome: findings from a Fluid and Catheter Treatment Trial (FACTT) substudy." Critical care (London, England) vol. 24,1 416. 11 Jul. 2020.

Poster ID 1A021

Influence of oncogene ZNF726 on glycolytic metabolic changes and lipid accumulation in breast cancer cells

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Keywords: Breast Cancer, ZNF726, KEGG pathway, Warburg effect, lipid accumulation

Zinc finger proteins are critical regulators of gene expression and are involved in several cellular processes, including proliferation, differentiation, and metabolic reprogramming in cancer cells [1]. Our study recently demonstrated that unexplored zinc finger Protein 726 (ZNF726) displayed oncogenic activity in breast cancer by modulating cholesterol metabolism [2]. However, its

role in metabolic alterations and lipid reprogramming remains obscure. Breast cancer progression is closely linked to metabolic plasticity, particularly the Warburg effect, characterised by enhanced aerobic glycolysis and increased lactate production that supports rapid tumour growth and survival [3]. In addition, lipid biosynthesis and adipogenic differentiation contribute to energy storage, providing fuel for cancer cell growth and metastasis [4]. In the present study, the functional role of ZNF726 was investigated using overexpression and knockdown approaches in MDAMB231 and MCF-7 breast cancer cells. Transcriptomic analysis followed by KEGG pathway enrichment revealed that a large proportion of differentially expressed genes were associated with metabolic pathways, indicating a potential role of ZNF726 in metabolic regulation. Real-time PCR analysis demonstrated that overexpression of ZNF726 increased the expression of glycolysis-associated genes, including hexokinase II, GLUT1 and GLUT4, suggesting enhancement of Warburg effect in breast cancer cells. Furthermore, Oil Red and Nile red staining confirmed increased lipid droplet accumulation in ZNF726 overexpressing cells and reduced lipid deposition in knockdown cells in both MDAMB231 and MCF-7 cells. Collectively, these findings indicate that ZNF726 promotes metabolic glycolysis and lipid accumulation, highlighting its potential as a therapeutic target.

References

1. Bandyopadhayaya, S., et al., Oncogenic role of an uncharacterized cold-induced zinc finger protein 726 in breast cancer. *J Cell Biochem*, 2023. 124(6): p. 889-906.
2. Bandyopadhayaya, S., et al., Multifaceted In Silico Screening Strategies Identifies Potent Inhibitors Facilitating Inhibition of ZNF726 *Activity in Breast Cancer. Chem Biol Drug Des*, 2025. 106(1): p. e70144.
3. Qiao, Y., et al., Lactate metabolism and lactylation in breast cancer: mechanisms and implications. *Cancer Metastasis Rev,* 2025. 44(2): p. 48.
4. Soni, S., et al., Lipid metabolism associated PLPP4 gene drives oncogenic and adipogenic potential in breast cancer cells. *Biochim Biophys Acta Mol Cell Biol Lipids*, 2025. 1870(5): p. 159609.

Poster ID 1A022

A Comparison of Accuracy and Precision of Glucose Values Measured By Glucometer and Autoanalyser in Type 2 Diabetes Mellitus

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Keywords: Type 2 Diabetes Mellitus, glucometer, autoanalyser.

Regular and reliable measurement of blood glucose is crucial for effective management of Type 2 Diabetes Mellitus (T2DM). Glucometers are widely used as point-of-care devices due to their rapid results and ease of use, whereas laboratory-based autoanalyser's are regarded as the reference method for glucose estimation. Differences in accuracy and precision between these two methods may have important clinical implications. In this study we found glucometer readings demonstrated a strong positive correlation with autoanalyser values, indicating good precision. However, glucometer measurements showed a slight overestimation of glucose levels compared to autoanalyser results, despite this difference being statistically significant, most values remained within clinically acceptable limits.

References:

5. Kermani S.K., Najafpour Boushehri S., Salari A., Sadeghi A., Baradaran A., *Journal of Diabetes & Metabolic Disorders,* 2017, 16, 8.
6. Sharma S.P., Anjankar A.P., Kale A., *International Journal of Clinical Biochemistry Research,* 2017, 4(1), 6–10.
7. International Organization for Standardization, *ISO 15197: In vitro diagnostic test systems—Requirements for blood-glucose monitoring systems for self-testing in managing diabetes mellitus,* 2013.

Poster ID 1A023

Clinical pharmacist intervention among the infectious disease patients in tertiary care hospital setting.

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Keywords: infectious diseases, pharmacist intervention, DRPs

Background: Infectious diseases impose a severe global health burden, causing high mortality and significant economic costs. Clinical pharmacists possess essential expertise to optimize pharmacotherapy and improve patient outcomes in this area. However, their impact remains underutilized, necessitating focused research to quantify their value in enhancing treatment efficacy and curbing resistance.
Aim: To assess the Clinical pharmacist intervention among the infectious disease patients in tertiary care hospital setting.
Methodology: A prospective study was conducted over 6 months at JSS Hospital, Mysuru, involving 35 infectious disease patients. Data were collected systematically after informed consent. Drug-Related Problems (DRPs) were identified using the Hepler and Strand classification through detailed medication chart reviews. Interventions were tailored for each DRP. Prescribing patterns were evaluated using WHO indicators and compared to institutional policy. Causality, severity, and preventability were assessed using WHO-UMC and Naranjo's scales. Data analysis employed descriptive and inferential statistics (Chi-square test, Z-test). Results: The study identified 39 DRPs, including 28 drug interactions and 11 other drug-related issues. Interventions were highly successful, with physicians accepting 35 recommendations (89.7%). Among these, 22 drug interactions (78.6%) were addressed, all overdose cases (100%) and improper drug selections (100%) were corrected, and 9 adverse drug reactions were documented. Only one recommendation (Pantoprazole dosing frequency) was rejected. Statistical analysis confirmed the significance of the findings.
Conclusion: Clinical pharmacist interventions effectively optimized drug therapy and improved patient safety by identifying and resolving drug-related problems in infectious disease care.

Poster ID 1A024

One Scaffold, Two Battles: Benzothiazole Derivatives Targeting Breast Cancer and Resistant Bacteria

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The urgent need for therapeutics capable of addressing cancer and microbial resistance simultaneously has directed attention toward privileged heterocyclic scaffolds such as benzothiazole. In the present study, a series of structurally diverse benzothiazole derivatives was rationally designed and synthesized to explore their potential as multifunctional bioactive agents. The synthesized compounds were structurally confirmed using FT-IR, NMR, and mass spectrometric techniques, ensuring their chemical integrity and purity. Biological evaluation commenced with screening against human breast cancer cell lines MCF-7 and MDA-MB-231, representing estrogen receptor-positive and triple-negative breast cancer models, respectively. From the library of best analogues, two molecules emerged as lead candidates, exhibiting pronounced antiproliferative activity against both cell lines. To elucidate the molecular basis of this activity, in silico molecular docking studies were performed against key breast cancer targets, estrogen receptor alpha (ERα) and human epidermal growth factor receptor 2 (HER2). The lead compounds demonstrated stable binding conformations and favorable interactions within the active sites of both targets. These findings were further supported by mechanistic investigations, which revealed that the lead compound induces apoptosis and cell-cycle arrest, confirming a target-driven anticancer mechanism. In parallel, the synthesized derivatives were evaluated for antimicrobial activity, where two compounds from the series showed significant inhibitory effects against Gram-negative bacterial strains, highlighting their potential to address intrinsically resistant pathogens. Based on these encouraging outcomes, the lead compounds were further assessed for anti-inflammatory, analgesic, and antioxidant activities, demonstrating significant efficacy in established experimental models. In conclusion, this integrated in silico, in vitro, and in vivo investigation identifies benzothiazole derivatives as promising multifunctional lead candidates for future anticancer and anti-infective drug development.

References:

1. S.K. Singh, M. Singh, S.K. Singh, M. Gangwar, G. Nath, Design, synthesis and mode of action of some benzothiazole derivatives bearing an amide moiety as antibacterial agents, RSC Adv. 4 (2014) 19013–19023. https://doi.org/10.1039/c4ra02649g.
2. M. Singh, S.K. Singh, M. Gangwar, G. Nath, S.K. Singh, Design, synthesis and mode of action of novel 2-(4-aminophenyl)benzothiazole derivatives bearing semicarbazone and thiosemicarbazone moiety as potent antimicrobial agents, Med. Chem. Res. 25 (2016) 263–282. https://doi.org/10.1007/s00044-015-1479-5.

Poster ID 1A025

Cellular and Molecular insights into silica-induced lung tissue calcification

in pathogenesis of silicosis

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Keywords: Silicosis, silica, lung fibrosis, calcification, EMT, alizarin red staining, osteogenic markers

A progressive irreversible occupational lung disease silicosis, is highly prevalent in mining and stone processing regions of India, particularly in Rajasthan belt. Government implemented policies for its diagnosis, financial compensation and preventive measures for affected workers. However, the molecular mechanisms driving silica-induced lung fibrosis remain poorly understood [1]. This study focuses on investigating the underlying molecular mechanism driving silica-induced cellular plasticity in lung epithelial cells [2]. In vitro experiments were conducted to evaluate cytotoxicity using cell viability MTT assay. Cellular differentiation and lung tissue calcification were examined through ALP assay and alizarin red S (ARS) staining, respectively. Furthermore, gene expression-associated changes were analysed using RT- PCR and RT-qPCR. Various epithelial cancer cells, including lung A549 cells, were exposed to varying concentrations of silica to assess cell viability. Silica exposure resulted in a noticeable modulation of epithelial to mesenchymal transition (EMT) marker genes with simultaneous changes of silicosis marker in A549 cells, suggesting a shift from epithelial towards a mesenchymal phenotype. A prolonged exposure of silica induces calcification as revealed by ARS staining. RT-qPCR analysis found elevated expressions of various osteoblast markers RUNX2 and OSTERIX with concomitant induction of osteo-inducer BMP-2 and ALP activity in response to silica treatment. Collectively, these findings suggest that silica induces EMT and subsequent calcification through BMP2 dependent pathway by inducing cellular plasticity of epithelial cells. Further study is required to develop molecular markers for early detection and targeted therapeutic intervention in silicosis.

References

1. Sellamuthu, R., et al., *Mechanisms of crystalline silica-induced pulmonary toxicity revealed by global gene expression profiling.* Inhal Toxicol, 2011. 23(14): p. 927-37.
2. Sun, J., et al., *Metabolic landscape of human alveolar type II epithelial cells undergoing epithelial-mesenchymal transition induced directly by silica exposure.* J Environ Sci (China), 2025. 149: p. 676-687.

Poster ID 1A026

ASSOCIATION OF RISK ALLELE BURDEN WITH CLINICAL MANIFESTATIONS AND OXIDATIVE STRESS IN AGE-RELATED MACULAR DEGENERATION

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Purpose: Age-related macular degeneration (AMD), a leading cause of vision loss, has a strong genetic basis, accounting for 46–71% of individual susceptibility. Genome-wide association studies have identified ARMS2, HTRA1, CFH, C3, and SKIV2L as key risk loci. This study aimed to determine how cumulative genetic risk translates into clinical phenotypes and disease severity, and its association with oxidative stress, to improve genetic risk assessment in AMD.

Methods: A total of 210 participants (112 AMD patients and 100 controls) were genotyped for SNPs in ARMS2 (rs10490924, rs3750846), HTRA1(rs11200638), CFH(rs1061170, rs10922109),
C3(rs2230199), and SKIV2L(rs429608). AMD patients were stratified based on cumulative risk allele load into high-risk (8–14 alleles) and low-risk (0–6 alleles) groups, and associations with clinical phenotypes and oxidative stress parameters were evaluated.

Results: Overall, 95.45% of AMD patients carried more than four risk alleles. Among AMD patients, 75.45% harboured high-risk allele load (8-14 alleles), presenting larger drusen (82%), PED (38%), atrophy(45.70%), and disciform scars (23.90%). Conversely, patients with low-risk allele load (0-6 alleles) comprised 12.7% of cases and showed milder clinical features (e.g., larger drusen (78.60%), pigmentary alterations(38.40%), PED(21%), atrophy (38.50%), and disciform scars(0%)). Additionally, high-risk allele carriers demonstrated significantly elevated oxidative stress levels compared to controls ($p < 0.05$).

Conclusion: AMD patients with a high genetic risk allele burden (8–14 alleles) exhibited more severe disease, strongly associated with pigment epithelial detachment ($p<0.01$), disciform scar formation ($p<0.041$), and elevated oxidative stress, underscoring the clinical relevance of genetic risk profiling in AMD progression.

References

1. Thee EF, Colijn JM, Cougnard-Grégoire A, Meester-Smoor MA, Verzijden T, Hoyng CB, Fauser S, Hense HW, Silva R, Creuzot-Garcher C, Ueffing M. The phenotypic course of age-related macular degeneration for ARMS2/HTRA1: the EYE-RISK consortium. Ophthalmology. 2022 Jul 1;129(7):752-64.
2. Matušková V, Zeman T, Ewerlingová L, Hlinomazová Z, Souček J, Vlková E, Goswami N, Balcar VJ, Šerý O. An association of neovascular age-related macular degeneration with polymorphisms of CFH, ARMS2, HTRA1 and C3 genes in Czech population. Acta ophthalmologica. 2020 Sep;98(6):e691-9.
3. Heesterbeek TJ, de Jong EK, Acar IE, Groenewoud JM, Liefers B, Sánchez CI, Peto T, Hoyng CB, Pauleikhoff D, Hense HW, den Hollander AI. Genetic risk score has added value over initial clinical grading stage in predicting disease progression in age-related macular degeneration. Scientific reports. 2019 Apr 29;9(1):6611.

Poster ID 1A027

Neuroprotective Potential of *Crocus sativus* Against Cold Stress Induced Brain Injury in Aged Rodent Model

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Chronic exposure to low temperatures is an underexplored physiological stressor that adversely affects brain function, especially during aging through mechanisms involving neuroinflammation and oxidative imbalance. The study aimed to evaluate the neuroprotective potential of Crocus sativus against cold stress induced behavioral and molecular alterations in an aged rodent model. Aged Wistar male rats (18–20 months) were subjected to cold stress at 4 °C for 30 minutes per day for four weeks. Animals received oral administration of Crocus sativus extract (150 mg/kg). Anxiety-like behavior and cognitive performance were assessed using the Elevated Plus Maze, Open Field Test, Novel Object Recognition (NOR) and Y-maze following stress exposure. Inflammatory targets were shortlisted using in silico target disease network analysis, and expression of selected genes was quantified in brain tissue using real-time polymerase chain reaction. Cold stress produced consistent anxiety-like behavior and impaired spatial working memory across behavioral paradigms. Treatment with Crocus sativus resulted in partial but significant improvement in cognitive performance and anxiety-related parameters, indicating attenuation rather than complete reversal of behavioral deficits. In silico analysis identified key neuroinflammatory regulators associated with cold stress pathology. Quantitative PCR demonstrated stress-induced upregulation of inflammatory markers, which was moderately normalized following saffron treatment. These findings demonstrate the potential role of Crocus sativus in moderating neuroprotection against cold stress induced brain injury through regulation of behavioral and inflammation. Saffron may represent a promising multi-target therapeutic candidate for mitigating environmental stress associated neurological dysfunction in the aging brain models.

Keywords: Cold stress, Crocus sativus, Behavior, Neuroinflammation

References:

1. Y. Liu, Y. Liu, H. Jin, P. Cong, Y. Zhang, C. Tong, M. Hou, Brain Research, 2017, 1670, 201–207.
2. C.-Y. Kim, K. Ko, S.-H. Choi, M. Jo, J. Kim, S. Yoon, S.-S. Yi, Nutrients, 2023, 15, 4855.
3. N. A. Salem, M. A. Ahmed, E. M. El-Sayed, M. M. El-Shafey, Scientific Reports, 2022, 12, 6237.

Poster ID 1A028

Blinded Trial of Multiplex Serodiagnostic Test in India for Diverse Forms of Active Tuberculosis

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Tuberculosis (TB) is generally curable when diagnosed and treated promptly. However, gaps in TB diagnosis continue to be a major limitation in controlling TB. TB diagnosis still depends largely on sputum-based tests: smear microscopy has poor sensitivity, liquid culture, while the gold standard, is slow and only ~80–86% sensitive. Molecular assays still require sputum and are benchmarked against liquid culture. Moreover, all sputum-based diagnostic tests have serious limitations for diagnosing extrapulmonary TB (EPTB) and pediatric TB (PEDTB), where sputum is either of limited use or difficult to obtain. We developed a non-sputum multiplex serodiagnostic test that enables the simultaneous detection of antibodies to multiple Mycobacterium tuberculosis (Mt. tb.) antigens, capturing immune responses across diverse groups of active TB patients. We conducted a blinded trial of the test in India. Sensitivity was 93.8% for smear+/culture+/Xpert+ adult pulmonary TB and 85.7% for smear−/culture+/Xpert+ (90.8% combined). Sensitivity was 64.5% for EPTB,

87.0% for PEDTB, 52.2% for microbiologically negative adult pulmonary TB, and 75.0% for HIV-associated TB. Specificity was 90.3% in healthy controls (IGRA+ 88.5%, IGRA– 91.3%) and 78.4% in disease controls with TB ruled out by liquid culture. This non-sputum-based test detects diverse forms of TB with sensitivity and specificity better than the WHO Target Product Profile for a triage test. It is technology-platform agnostic and amenable to high-throughput and point-of-care applications.

Poster ID 1A029

Appetite modulator Quercetin enhances antioxidant defence and neuroprotection in induced aging Rat model

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This study investigated the neuroprotective and antioxidant effects of a potent appetite modulator Quercetin in a d-galactose-induced accelerated aging model using male Wistar rats. Animals were assigned to four groups: control, Quercetin-treated, d-galactose-induced aging, and d-galactose and Quercetin treatment. Quercetin was administered orally (100 mg/kg) and d-galactose subcutaneously (300 mg/kg) for 28 days. Biochemical analyses included measurement of ferric reducing antioxidant power (FRAP), glutathione (GSH) content, malondialdehyde (MDA), protein carbonyl (PCO) formation, and activities of superoxide dismutase (SOD) and catalase in brain tissue homogenates. Levels of appetite regulatory hormones leptin, ghrelin and insulin were also measure in serum. Gene expression of Beclin-1, ULK-1, SIRT1, NSE, TNF-α, IL-6, GSHR, and GLP-1 was assessed by RT-PCR. Histopathological evaluation of hippocampal architecture was performed, and statistical significance was determined by ANOVA with Bonferroni post-hoc analysis. D-galactose significantly reduced FRAP, GSH, SOD, and catalase activities while increasing MDA and PCO levels, alongside downregulation of autophagy and neuroprotection-related genes and elevation of inflammatory cytokines. Quercetin treatment effectively restored antioxidant markers, reduced oxidative stress indices, improved enzymatic activity, upregulated neuroprotective and autophagy-associated genes, and attenuated inflammation. Histopathological assessment confirmed preservation of neuronal structure in treated rats. Quercetin supplementation robustly enhances cerebral antioxidant defenses, mitigates oxidative damage, modulates gene expression related to neuron survival and inflammation, and confers histological neuroprotection in experimental aging.

References:

1. Friedman, J.M., Halaas, J.L., 1998. Leptin and the regulation of body weight in mammals. Nature 395, 763–770. https://doi.org/10.1038/27376
2. Barzilai, N., Ferrucci, L., 2012. Insulin resistance and aging: a cause or a protective response? J. Gerontol. A. Biol. Sci. Med. Sci. 67, 1329–1331. https://doi.org/10.1093/gerona/gls145
1. Boots, A.W., Haenen, G.R.M.M., Bast, A., 2008. Health effects of quercetin: from antioxidant to nutraceutical. Eur. J. Pharmacol. 585, 325–337. https://doi.org/10.1016/j.ejphar.2008.03.008

Poster ID 1A030

Utility of Multicopy RLEP and Single-Copy Resistance Markers for Molecular Confirmation of Type II Reaction in Leprosy: A Clinical–Translational Study

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Keywords: Mycobacterium leprae , Type II Lepra Reaction, RLEP PCR, Drug Resistance Markers, Molecular Diagnostics

Background: The acute inflammatory phase of multibacillary leprosy is represented by the type II lepra reaction (T2R). The use of targets with different genomic copy numbers in molecular detection of Mycobacterium leprae may affect test sensitivity in reactional conditions when the bacillary burden fluctuates.
Objective: To evaluate the detectability of multicopy (RLEP) and single-copy drug-resistance–associated gene targets in

clinically diagnosed Type II reaction leprosy cases.

Methods: Eighty-six slit skin smear specimens were subjected to AFB microscopy, clinical categorization, DNA extraction, and RLEP PCR. Sixteen cases were clinically categorised as Type II reaction and further analysed. Drug-resistance gene regions (single-copy targets) were amplified in RLEP-positive samples, and sequencing was initiated for mutation analysis.

Results: Among 86 specimens, 16 (18.6%) were identified as Type II reaction cases based on clinical presentation, including erythematous tender nodules, systemic inflammatory features, and neuritic involvement. RLEP positivity (multicopy target) was observed in 7 cases (43.75%). However, amplification of single-copy resistance-associated gene regions was detected only in a subset, suggesting differential sensitivity between multicopy and single-copy targets. Notably, several clinically evident reaction cases were RLEP-positive but negative for single-copy amplification.

Conclusion: Type II lepra reaction demonstrates differential molecular detectability based on genomic target copy number. Single-copy resistance genes require more template availability, while multicopy targets, such as RLEP, are more sensitive. Multicopy RLEP improves molecular confirmation of ENL, while single-copy resistance targets inform drug susceptibility. Combining both enhances diagnostic accuracy and guides personalized therapy.

Reference:

1. Mohanty PS, Naaz F, Bansal AK, Kumar D, Sharma S, Arora M, Singh H, Katara P, Soni N, Patil SA, Singh M. Molecular detection of Mycobacterium leprae using RLEP-PCR in post elimination era of leprosy. Molecular biology research communications. 2020 Apr;9(1):17.
2. Sardana K, Kulhari A, Mathachan SR, Khurana A, Bansal P, Ahuja A, Lavania M, Ahuja M. Late leprosy reaction presenting as erythema multiforme-like erythema nodosum leprosum with underlying rifampicin resistance and its potential implications. The International Journal of Mycobacteriology. 2020 Apr 1;9(2):226-8.
3. Turankar RP, Pandey S, Lavania M, Singh I, Nigam A, Darlong J, Darlong F, Sengupta U. Comparative evaluation of PCR amplification of RLEP, 16S rRNA, rpoT and Sod A gene targets for detection of M. leprae DNA from clinical and environmental samples. International journal of mycobacteriology. 2015 Mar 1;4(1):54-9.
4. Luo RF, Scahill MD, Banaei N. Comparison of single-copy and multicopy real-time PCR targets for detection of Mycobacterium tuberculosis in paraffin-embedded tissue. Journal of clinical microbiology. 2010 Jul;48(7):2569-70.

Poster ID 1A031

In-Vitro Analysis of Candida albicans–Host Cell Interactions

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ABSTRACT

Candida albicans is an opportunistic fungal pathogen that can cause mucosal infections by adhering to, invading, and damaging host epithelial cells. Understanding these early and late interaction events is crucial for elucidating mechanisms of fungal pathogenesis. In the present study, in vitro fungal–host interactions between C. albicans SC5314 and human epithelial cells were investigated to characterise adhesion, invasion, and host cell damage.

Fungal adhesion to epithelial cells was assessed following short-term co-incubation, allowing quantification of surface-associated fungal cells. Invasion was evaluated by differential staining approaches to distinguish invading hyphae from non-invading fungal cells. Host cell damage was assessed using lactate dehydrogenase (LDH) release assays following prolonged exposure to the fungus. The results demonstrated efficient adhesion of C. albicans to epithelial cells, followed by active invasion and significant host cell damage at later stages of interaction.

Collectively, these findings highlight the dynamic nature of C. albicans–host cell interactions and underscore the role of fungal adhesion and invasion in epithelial damage. The study provides experimental insight into key stages of fungal pathogenesis and establishes a foundation for further investigation into virulence mechanisms and functional validation of interaction-associated genes.

References:

1. Richardson JP, Ho J, Naglik JR. Candida–epithelial interactions. Journal of fungi. 2018 Feb 8;4(1):22.
2. Wächtler B, Citiulo F, Jablonowski N, Förster S, Dalle F, Schaller M, Wilson D, Hube B. Candida albicans-epithelial interactions: dissecting the roles of active penetration, induced endocytosis and host factors on the infection process. PloS one. 2012 May 14;7(5):e36952.
3. Phan QT, Myers CL, Fu Y, Sheppard DC, Yeaman MR, Welch WH, Ibrahim AS, Edwards Jr JE, Filler SG. Als3 is a Candida albicans invasin that binds to cadherins and induces endocytosis by host cells. PLoS biology. 2007 Mar;5(3):e64.

Poster ID 1A032

"Alkaline phosphatase –Driven Breast Tumorigenicity and its Inhibition as Evidenced through Animal and Cell-

Based Study"

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Keywords: Breast cancer cell, levamisole, Alkaline phosphatase activity, Mice, Tumor growth, cellular plasticity, breast osteoblast-like potential.

Indeed, cellular plasticity and clonal variations play a crucial role in making the molecular complexity within tumor tissues. Breast density and microcalcification are risk factors for breast malignancy. A few studies, including us, proposed that osteoblast-like potential present within breast cancer cells drives calcified nodule formation within breast tumors. A few scattered studies indicated that levamisole may act as an ALP inhibitor. Our past studies evidenced the presence of elevated ALP and microcalcification levels in breast malignant tissues compared to benign tissues [1]. In this study, we have found the existence of intrinsic osteoblast-like potential within 4T1 mouse triple-negative breast cancer cells, where osteo-inducer bone morphogenetic protein (BMP-2) further enhanced this cellular plasticity towards osteoblast-like phenotype. Here, BMP-2 treatment enhanced both ALP activity and calcified nodule formation with concomitant increment of various osteoblast-differentiation markers, including RunX2 and Osterix expressions. However, treatment with levamisole showed inhibition of the ALP activity as evidenced by ALP assay and staining, and calcification as revealed by Alizarin Red S (ARS) staining in 4T1 cells. Our in vivo study in Balb/c female mice found a significant reduction in 4T1-induced tumor growth in the case of levamisole-treated mice as compared to the control. Furthermore, ALP and ARS staining displayed a significant inhibition of osteoblast-like potential and calcium deposition in tumor tissues of levamisole-treated mice as compared to control. These findings suggest that levamisole showed an anticancer role in breast cancer by blocking ALP-driven osteoblast-like activity. Thus, levamisole can be a therapeutic intervention in case of osteoblast-like activity-driven cancer.

Reference:

1. Sharma, T., et al., Docosahexaenoic Acid (DHA) Inhibits Bone Morphogenetic Protein-2 (BMP-2) Elevated Osteoblast Potential of Metastatic Breast Cancer (MDA-MB-231) Cells in Mammary Microcalcification. Nutrition and Cancer, 2020. 72(5): p. 873-883.

Poster ID 1A033

Investigating the role of bovine milk exosomes in modulating cellular responses

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Bovine milk exosomes are extracellular vesicles enriched with bioactive molecules such as proteins, lipids, and microRNAs, which have potential roles in modulating cellular functions. This study investigated the effects of these exosomes on the human embryonic kidney cell line HEK293T, a commonly used model in cellular and molecular biology research. Exosomes were isolated and characterized using differential ultracentrifugation and microscopy techniques. To assess cytoprotective effects, lead was used as a cytotoxic agent, and biochemical assays were performed to evaluate cell viability, proliferation, and oxidative stress. Data analysis was conducted using ANOVA via GraphPad Prism software. Results demonstrated that exosomes significantly enhanced cellular proliferation by mitigating lead-induced toxicity and reducing oxidative stress. These findings highlight the potential of milk-derived exosomes as bioactive modulators in cell culture systems, offering insights into their therapeutic and biotechnological applications. Further studies are needed to elucidate the underlying molecular mechanisms and to validate these effects across different cell lines and biological contexts. Understanding the influence of milk exosomes on human cells may have important implications for nutrition science and therapeutic strategies, particularly concerning redox and mitochondrial signalling pathways, which could be leveraged to treat diseases such as neurodegenerative disorders and metabolic syndromes.

Keywords: exosomes, HEK293T cell line, isolation method, oxidative stress, viability, redox signalling

References:

1. R. Munagala, F. Aqil, J. Jeyabalan, and R. C. Gupta, "Bovine milk-derived exosomes for drug delivery," Cancer Lett., vol. 371, ID 1, pp. 48–61, 2016, doi: 10.1016/j.canlet.2015.10.020.
2. Al-Ghafari A, Elmorsy E, Fikry E, Alrowaili M, Carter WG. The heavy metals lead and cadmium are cytotoxic to human bone osteoblasts via induction of redox stress. PLoS One. 2019;14(11). doi:10.1371/journal.pone.0225341
3. Meldolesi J. Exosomes and Ectosomes in Intercellular

Communication. Curr Biol. 2018;28(8):R435-R444. doi:10.1016/j.cub.2018.01.059

Poster ID 1A034

Phenotypic Characterization of Extracellular Vesicles in a MASH-Induced Mouse Model

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Metabolic dysfunction-associated steatohepatitis (MASH) involves progressive hepatic steatosis and inflammation and is linked to extracellular vesicle (EV)-mediated signaling. To investigate EV phenotypes in the murine MASH model, C57BL/6 mice were divided into control and MASH groups (n=6). The MASH group received a Western diet, while the control group was fed normal chow for 12 weeks. In addition, the MASH group received sugar solution supplementation and intraperitoneal CCl4 injections at a dose of 0.32 µg/g body weight. Body weight over time and the liver-to-body weight ratio at sacrifice were measured to monitor disease progression. Pathological changes associated with MASH were evaluated by histological characterization of the liver using hematoxylin and eosin, Oil Red O, Masson's trichrome, and periodic acid–Schiff staining. EVs were isolated by size-exclusion chromatography (SEC) and characterized by nanoparticle tracking analysis (NTA) and Western blotting.

MASH animals showed a distinct pattern of body weight over time, along with a highly significant liver-to-body weight ratio. Histopathological analyses revealed marked steatosis, inflammation, structural alterations with lipid deposition, fibrosis, and the absence of glycogen deposition.

SEC-based isolation yielded reproducible EV preparations, and NTA analysis showed a higher EV concentration in the MASH group than in controls; however, the difference was not statistically significant. EV size also did not differ significantly among the groups. Although EV size and concentration did not differ significantly with disease status, EV cargo profiling may reveal molecular signatures associated with MASH severity and progression.

References:

1. Vacca M, Kamzolas I, Harder LM, Oakley F, Trautwein C, Hatting M, et al. An unbiased ranking of murine dietary models based on their proximity to human metabolic dysfunction-associated steatotic liver disease (MASLD). Nat Metab. 2024 Jun;6(6):1178–96.
2. Tsuchida T, Lee YA, Fujiwara N, Ybanez M, Allen B, Martins S, et al. A simple diet- and chemical-induced murine NASH model with rapid progression of steatohepatitis, fibrosis, and liver cancer. J Hepatol. 2018 Aug;69(2):385–95.
3. Mohan V, Joshi S, Kant S, Shaikh A, Sreenivasa Murthy L, Saboo B, et al. Prevalence of Metabolic Dysfunction-Associated Steatotic Liver Disease: Mapping Across Different Indian Populations (MAP Study). Diabetes Ther Res Treat Educ Diabetes Relat Disord. 2025 Jul;16(7):1435–50.

Poster ID 1A035

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Thematic Area: Clinical and Therapeutic Applications (ARTH 2026)

Serum Angiopoietins, Adhesion Molecules, and Proteomic Signatures as Predictive Biomarkers of Anti-VEGF Response in Diabetic Macular Edema

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Background: Diabetic macular edema (DME) demonstrates variable responses to anti-VEGF therapy, with substantial numbers of patients experiencing suboptimal outcomes. This study integrates bead-based flow cytometry and shotgun proteomics to investigate circulating angiopoietin-1/2, adhesion molecules (ICAM-2, VCAM-1), and serum proteome remodeling as predictors of anatomical/functional outcomes, advancing precision ophthalmology.

Methods: Sixteen treatment-naïve ci-DME patients were enrolled. Ten received intravitreal ranibizumab with serum collected at baseline and clinical parameters like Best corrected visual acuity (BCVA), central retinal thickness (CRT), and macular fluid area recorded at baseline, one and two months after therapy; analyzed via multiplex flow cytometry for angiogenic cytokines/adhesion molecules (GraphPad Prism statistics). Serum from six DME patients

collected at baseline and after three aflibercept injections (n = 12) underwent LC-MS/MS analysis with protein identification via Proteome Discoverer and pathway analysis using Reactome and MetaboAnalyst 6.0.

Results: Anti-VEGF therapy significantly reduced CRT ($p<0.01$) and improved BCVA. Baseline Ang-2 strongly correlated with adhesion molecules ($r\approx0.8$) and CRT ($r \approx 0.6$; poor response), while Ang-1 negatively correlated with CRT reduction ($r \approx -0.7$; ROC AUC$\approx$0.8). Proteomics showed pre-therapy VEGF/FGFR2 dysregulation, lipid/ECM/immune activation; post-therapy normalization of VEGF, FGFR2/lipoprotein modulation, upregulated complement/laminin interactions-confirming therapeutic homeostasis restoration.

Conclusion: This study reveals DME's dual vascular-inflammatory pathophysiology, where elevated baseline Ang-2 and adhesion molecules correlate with treatment-resistant DME. Ang-2 positively correlates with CRT, indicating poor anatomical response, while Ang-1 negatively correlates with CRT reduction, suggesting favorable visual and structural outcomes. APOA2/C3 also serve as stratification biomarkers for anti-VEGF responders, enabling personalized treatment strategies and minimizing therapeutic failure in DME management.

Poster ID 1A036

Antidepressant drug as potential antifungal agent against Candida albicans: An In vitro study

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Keywords: Candida albicans, antidepressant, Drug Repositioning, antifungal, virulence, Planktonic.

Candida albicans is a major fungal pathogen causing various infections, especially in people with weakened immune systems. With growing resistance to existing antifungals, alternative treatments are urgently needed. Repurposing approved drugs like antidepressants could speed up development given their known safety profiles. This study checks antidepressants' antifungal activity against C. albicans using various in vitro tests (1). The antifungal activity of sertraline, fluvoxamine, paroxetine, fluoxetine, escitalopram, and clomipramine was assessed by determining the minimum inhibitory concentration (MIC) against planktonic growth using broth microdilution methodology. Sertraline, fluvoxamine, and paroxetine demonstrated strong antifungal activity with MIC values of 0.125 mg/mL, whereas fluoxetine and clomipramine exhibited moderate activity with MIC values of 0.25 mg/ml. Escitalopram did not show inhibitory activity under the tested conditions (2). The antidepressants reduced C. albicans virulence by inhibiting adhesion, biofilm formation, and disrupting membrane integrity. They also reduced fungal viability, altered phosphate uptake, and caused cell cycle changes and morphological damage, indicating a multifaceted antifungal mechanism (3). SEM analysis showed treated C. albicans cells had surface deformation and structural damage. These findings suggest antidepressants like sertraline, fluvoxamine, and paroxetine have antifungal effects by targeting multiple pathways. Repurposing antidepressants as antifungals looks promising and warrants further in vivo studies (4).

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References:

1. Talapko J, Juzbaši M, Matijevi T. Candida albicans — The Virulence Factors and Clinical Manifestations of Infection. 2021;
2. Ahmed EI, Alhuwaydi AM, Taha AE. Anti-Candidal Activity of Reboxetine and Sertraline Antidepressants: Effects on Pre-Formed Biofilms. 2023;1–11.
3. Neto DA, Anny R, Silva C, Rocha C, Ramos A, Campos RS, et al. Microbial Pathogenesis In vitro anti- Candida activity of selective serotonin reuptake inhibitors against fl uconazole-resistant strains and their activity against bio fi lm- forming isolates. 2017;107:341–8.
4. Serotonin S, Alım G, Tek İ, Limoncu MH, Ateş A, Eraç B, et al. Antifungal and Antibiofilm Activities of Selective Serotonin Reuptake Inhibitors Alone and in Combination with Fluconazole. 2020;17(6):667–72.

Poster ID 1A037

Polystyrene Microplastics Induce Oxidative Stress–Driven β-Cell Failure: Implications for Diabetes Pathogenesis

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Pollution has escalated into a severe global environmental crisis, with microplastics (MPs) now recognized as pervasive contaminants across all ecosystems [1]. Among the polymers constituting MPs, polystyrene (PS) is consistently detected at high frequencies in human-associated environments, including metabolically relevant tissues [2]. The pervasive and unavoidable nature of PS-MP exposure raises critical concerns regarding its long-term consequences for human health, particularly the escalating global burden of diabetes.

Recent research has begun to bridge the mechanistic gap linking PS-MP exposure to diabetes pathogenesis. In this study, we investigated the cellular and functional consequences of PS-MP exposure in pancreatic β-cells using the MIN6 cell line. We demonstrate that 1 µm PS-MPs are efficiently internalized and predominantly localize within cytoplasmic and perinuclear regions. PS-MP exposure induced a dose- and time-dependent increase in mitochondrial superoxide and intracellular reactive oxygen species [3], accompanied by marked suppression of antioxidant gene expression. This oxidative stress was associated with pronounced necrotic cell death. Furthermore, metabolic viability assays revealed a progressive decline in β-cell viability and suppression of key β-cell identity markers such as PDX1 and MAFA, consistent with established mechanisms of oxidative stress–mediated β-cell failure in diabetes. These converging defects culminated in early β-cell failure, a hallmark event in diabetes initiation.

Collectively, our findings provide mechanistic evidence that PS-MPs induce oxidative stress–driven cytotoxicity, necrosis, and functional impairment in pancreatic β-cells, highlighting a plausible environmental pathway through which chronic microplastic exposure may contribute to β-cell dysfunction, reduced insulin production, and increased susceptibility to diabetes.

References:

1. T. S. Galloway, Marine Pollution Bulletin, 2015, 92, 1–3.
2. H. A. Leslie, Environment International, 2022, 163, 107199.
3. J. Hwang, Environmental Pollution, 2020, 263, 114525.

Poster ID 1A038

Unmasking Hidden Drug Resistance: A Whole Genome Sequencing-Based Evaluation of Molecular TB Diagnostics in Central India

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Keywords: Whole Genome Sequencing, GeneXpert, Line probe Assay, Discordance, DR-TB

Background: Rapid molecular diagnostic tools such as GeneXpert and Line Probe Assays (First-Line and Second-Line LPA) are routinely used for detecting drug-resistant tuberculosis (DR-TB) in India. However, their probe-based design restricts mutation coverage and may cause discordant resistance profiles when compared with whole genome sequencing (WGS). This study evaluated diagnostic discordance between routine assays and WGS-based resistance profiling in clinical isolates from All India Institute of Medical Sciences Bhopal (AIIMS Bhopal).

Methods: Five Mycobacterium tuberculosis clinical isolates from AIIMS Bhopal underwent WGS and were compared with GeneXpert, FL-LPA, and SLPA results. Lineage classification, and resistance-associated mutations across first- and second-line anti-tubercular drugs were systematically analysed.

Results: Among the 5 isolates, rifampicin resistance was detected in one case by GeneXpert and in a different case by FL-LPA. In contrast, WGS classified 4 isolates as pre-XDR-TB and 1 as isoniazid mono-resistant. Of the 4 pre-XDR isolates, three belonged to Lineage 3 (East-African-Indian) and one to Lineage 4 (Euro-American). The isoniazid mono-resistant isolate belonged to Lineage 1 (Indo-Oceanic). All pre-XDR isolates harboured mutations in rpoB, inhA, gyrA, and katG. Additional resistance-associated mutations affecting ethambutol, pyrazinamide, ethionamide, and streptomycin were identified.

Conclusion: Substantial discordance was observed between routine molecular assays and WGS-based resistance profiling in this Central Indian cohort. These findings highlight the limitations of probe-based diagnostics in detecting complex and evolving resistance patterns, particularly within predominant regional lineages. Integration of WGS into TB diagnostic and surveillance frameworks may enhance treatment individualization, prevent inappropriate therapy, and reduce transmission of

undetected drug-resistant strains.

References:

1. D. Papaventsis, N. Casali, I. Kontsevaya, F. Drobniewski, D. M. Cirillo, V. Nikolayevskyy, Clinical Microbiology and Infection, 2017, 23, 61–68.
2. D. Sadovska, A. Nodieva, I. Pole, A. Vīksna, J. Ķimsis, I. Ozere, I. Norvaiša, I. Bogdanova, D. Bandere, R. Ranka, Infection and Drug Resistance, 2024, 17, 3289–3307.
3. M. Vogel, C. Utpatel, C. Corbett, T. A. Kohl, A. Iskakova, S. Ahmedov, U. Antonenka, V. Dreyer, A. Ibrahimova, C. Kamarli, D. Kosimova, V. Mohr, E. Sahalchyk, M. Sydykova, N. Umetalieva, A. Kadyrov, G. Kalmambetova, S. Niemann, H. Hoffmann, Scientific Reports, 2021, 11, 15333.

Poster ID 1A039

Title: Assessment of ANA IIFA Pattern: Antigen Correlation Using ENA Immunoblot in Suspected SARD Patients

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Background: Antinuclear antibody (ANA) testing by indirect immunofluorescence assay (IIFA) remains the gold-standard screening tool for systemic autoimmune rheumatic diseases (SARDs). ANA(IIFA) interpretation alone is insufficient and requires confirmation with antigen-specific assays1/2.
Objective: To evaluate the correlation between ANA-IIFA patterns and specific autoantigen reactivity on ENA immunoblot in suspected SARD patients
Methods: Laboratory-based observational study evaluated 60 SARD patients with ANA(IIFA) and ENA immunoblot (Tulip Diagnostics). IIFA pattern interpretation was performed as per International Consensus on ANA Patterns (ICAP)3, and antigenic associations were evaluated on ENA immunoblot against observed patterns. Data was managed and analyzed in Microsoft Excel.
Results: Out of 60 samples, 54 (90%) were ANA positive with predominance of nuclear fine speckled 50%, nuclear homogeneous 25.9% and nuclear dense fine speckled 13%. ENA immunoblot showed autoantibodies in 32/60(53.3%), mainly RNP, Ro-52, and dsDNA. When compared with ICAP-expected pattern–antigen, concordance was observed in 9/32 (28.1%) mainly in the centromere pattern and discordance in 23/32 (71.9%) especially nuclear coarse/large speckled pattern.
Discussion: Higher ANA positivity reflects reactivity against limited antigens not represented on the immunoblot panel4, with observer's bias, multiple autoantibodies. ICAP suggests probable targets but does not guarantee antigen identity because of antibody multiplicity and methodological variability. Low concordance in our study is consistent with study by Ouazzani et al.4 and Salman et al5.
Conclusion: These findings underscore that ANA fluorescence patterns may indicate probable antigenic targets but fails to reliably predict specific autoantigen and necessitates the use of comprehensive antigen- specific assays for characterization and management in SARD.

References:

1. J. Damoiseaux, L.E.C. Andrade, O.G. Carballo, et al., Annals of the Rheumatic Diseases, 2019, 78, 879–889.J.
2. Jang, S. Kim, H.S. Kim, K.A. Lee, J. Park, Y. Park, Journal of International Medical Research, 2021, 49, e11014390.E.K.L.
3. Chan, C. von Mühlen, M.J. Fritzler, et al., Journal of Applied Laboratory Medicine, 2022, 7, 322–330.H.
4. Ouazzani, H. Fadili, H. Filali, A. Zrara, Y. Bamou, J. El Bakkouri, Cureus, 2025, 17, e85723.E.
5. Salman, Turkish Journal of Immunology, 2025, 13, 90–98.

Poster ID 1A040

STUDY OF OXIDATIVE STRESS IN OBESE AND NON-OBESE MENOPAUSAL WOMEN

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Keywords: MDA, SOD, BMI, obese menopausal women.

Introduction: Oxidative stress, a key mediator of cardiovascular disease, among postmenopausal women, the correlation between obesity and oxidative stress is poorly examined. parameter including criteria for group A and B; Height, weight, BMI, malondialdehyde (MDA), Superoxide Dismutase (SOD), Therefore, in present study, we compared oxidative stress states in postmenopausal women with or without obesity and body mass index is assessed.
Aim: Present study is aimed to assess oxidative stress markers (MDA, SOD) & BMI
Materials and Methods: The study includes 60 post-

menopausal women, further divided into two group. Group A includes (n = 30) Obese Menopausal women and Group B (n = 30) non-obese Menopausal women. Blood sample were collected for oxidative stress marker (MDA, SOD) & Lipid Profile. SOD was estimated by Marklund and Marklund method and MDA by Thiobarbituric-acid-reactive substances (TBARS) method.

Results: We found increase in MDA and decrease in SOD and lipid profile altered in obese menopausal women on compared with non-obese. Obesity was diagnosed with BMI >25 kg/m2.

Conclusions: Menopause is associated with increased oxidative stress. Obesity increases, oxidative stress in postmenopausal women as compared with non-obese.

Poster ID 1A041

Neutrophil depletion at the early stage of Japanese encephalitis virus infection affects CD8+ T cell infiltration into the mouse brain and causes severe encephalitis

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Neutrophils have been reported to have protective and detrimental functions in viral infections. However, the role of neutrophils remains unexplored in Japanese encephalitis virus (JEV) infection. In this study, we elucidated the dynamics of neutrophils and their influence on immune cell recruitment in subclinical and severe encephalitis in mouse models. Further, we depleted neutrophils from 3-4 week-old C57BL/6 mice using mAb1A8 (anti-Ly6G) antibody and studied their association with inflammation, viral replication, immune cell infiltration and disease outcome. We observed that an increase in JEV replication is associated with increased infiltration of neutrophils in the spleen and brain. Further studies confirmed that depletion of neutrophils at an early stage of JEV infection reduced CD8 abundance in the infected brain and accelerated death in mice. We also observed that inhibition of the CXCL12-CXCR4 signalling axis by antagonist AMD3100 reduced CD8 abundance in the brain and augmented inflammasome activation, leading to fatal encephalitis. Reduced CXCR4 levels in the spleen and blood of CD8+T cells correlated with enhanced Granzyme B level, indicating CD8 cells differentiated more into effector phenotypes in neutrophil-depleted mice. Furthermore, CD8 depletion delayed the death of mice infected with a sublethal strain compared to neutrophil-depleted mice, suggesting that neutrophils play a vital role in the early restriction of viral replication, whereas CD8 is essential later in clearing the virus. Taken together, our study sheds new light on the role of neutrophils in the pathogenic mechanisms of JEV encephalitis and highlights the importance of neutrophils and CD8 cells associated with disease outcomes.

Poster ID 1A042

Understanding the role of inflammation in Glioblastoma-Astrocyte cellular crosstalk in Tumor Microenvironment

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Glioblastoma (GBM), grade 4 astrocytoma, is a central nervous system tumor with an average survival after diagnosis of less than 14 months, despite surgery, chemotherapy, and radiotherapy1. Two crucial innate immune cells of the brain, namely microglia and macrophages, promote tumor growth and progression in GBM by fostering a tumor-promoting microenvironment2. The Nucleotide-binding domain leucine-rich repeat-containing receptor (NLR) family recognizes pathogen- and damage-associated molecular patterns that induce inflammation3. NLRP12 is a cytosolic NLR protein that downregulates inflammatory responses in active immune cells by inhibiting the non-canonical and canonical NF-kB pathways4. This impacts downstream signalling, release of cytokines and chemokines responsible for inflammation. NLRP3, upon activation, initiates proteolytic cleavage of more than 70 substrates, including the conversion of pro-IL-1ß and pro-IL-18 to IL-1ß and IL-18, respectively, leading to pyroptosis. Interestingly, NLRP12 has both tumor-promoting and anti-tumor functions in various cancers5.
NLRP12 is a prognostic marker for glioblastoma, and its increased expression correlates with poor survival in GBM patients6. However, the cellular and molecular mechanisms in are largely unknown. siRNA-mediated knockdown of NLRP12 and NLRP3 in human GBM and astrocyte cell lines affects cell proliferation, migration, and viability in 2D and 3D spheroids by impacting the NF-κB pathway. Patient-derived Glioma samples exhibit differential NLRP12 and NLRP3 expression based on tumor grade, intra-tumor heterogeneity, and gene expression profiles7,8. This study

aims to understand the effects of NLRP12 and NLRP3 expression in GBM, interpret its pathophysiology, and help develop future targeted therapeutic interventions.

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References:

1. Louis, D. N. *et al.* The 2021 WHO classification of tumors of the Central Nervous System: A summary. *Neuro. Oncol.* **23**, 1231–1251 (2021).
2. Ma, J., Chen, C. C. & Li, M. Macrophages/microglia in the glioblastoma tumor microenvironment. *Int. J. Mol. Sci.* **22**, 5775 (2021).
3. Chou, W.-C., Jha, S., Linhoff, M. W. & Ting, J. P.-Y. The NLR gene family: from discovery to present day. *Nat. Rev. Immunol.* **23**, 635–654 (2023).
4. Lich, J. D. *et al.* Cutting edge: Monarch-1 suppresses non-canonical NF-κB activation and p52-dependent chemokine expression in monocytes. *J. Immunol.* **178**, 1256–1260 (2007).
5. Rajkhowa, S. & Jha, S. The role of NLRP3 and NLRP12 inflammasomes in glioblastoma. *Genes Immun* **25**, 541–551 (2024).
6. Sharma, N. *et al.* Differential expression profile of NLRs and AIM2 in glioma and implications for NLRP12 in glioblastoma. *Sci. Rep.* **9**, (2019).
7. Rajkhowa, S. *et al.* NLRP12-mediated Glioblastoma-Astrocyte Cross-talk Promotes Tumor Growth. 2025.11.13.688374 Preprint at https://doi.org/10.1101/2025.11.13.688374 (2025).
8. Rajkhowa, S. *et al.* NLRP3 Inflammasome Exhibits Context-Dependent Roles in Glioblastoma-Astrocyte Crosstalk. 2025.12.30.697027 Preprint at https://doi.org/10.64898/2025.12.30.697027 (2025).

Poster ID 2A043

Systemic Autoimmunity: An Autoantibody Perspective

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Autoantibodies are central biomarkers in systemic autoimmune diseases, providing diagnostic, prognostic, and stratification value across a broad spectrum of conditions. Autoantibody signatures defined by the presence, patterns, and combinations of autoantibodies support the differentiation of diseases such as systemic lupus erythematosus, Sjögren's syndrome, systemic sclerosis, myositis, rheumatoid arthritis, and ANCA-associated vasculitis. These signatures also have organ-specific relevance, including autoimmune liver disease and endocrine autoimmunity.

Indirect immunofluorescence on HEp-2 cells remains the first-line screening method due to its high sensitivity and ability to reveal pattern-based diagnostic clues, as illustrated by nuclear, cytoplasmic, and mitotic patterns across AC designations. Solid-phase assays, including ELISA, fluoroenzyme immunoassays, line immunoassays, and multiplex bead-based platforms, provide complementary specificity, automation, standardisation, and expanded antigen coverage. Reflex algorithms incorporating second-line testing, such as ENA panels, myositis panel blot, and Luminex-based multiplex profiling, improve diagnostic confidence, particularly in overlap syndromes and for refining phenotypes. Local laboratory trend analysis demonstrates increasing autoimmune testing demand and evolving disease patterns, emphasising the need for optimised workflows and evidence-based test utilisation. The integration of screening and confirmatory methods enhances accuracy and supports precision immunology. In conclusion, autoantibody signatures, when interpreted in the context of clinical presentation and assay methodology, are powerful tools guiding diagnosis, risk assessment, and management in systemic autoimmunity.

Poster ID 2A044

Surface-decorated Extracellular Vesicles Derived from Human Cells for Targeted Drug Delivery

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Extracellular Vesicles(EVs) have been widely explored as drug delivery systems due to their favourable biophysical and biochemical properties. However, the limited targeting ability of EVs and the lack of strategies to engineer their surfaces make the clinical translation of EV-based therapeutics more difficult. Conventionally, the surface functionalisation of EVs primarily relies on tetraspanin protein scaffolds or the chemical conjugation of

targeting moieties. However, recent efforts have been made to explore single-pass membrane proteins as a scaffold, thereby reducing the genetic payload required for parent cell modification.

Through literature screening, an ideal single-pass transmembrane protein was identified as a suitable scaffold for engineering the EV surface. Using in-silico tools, we designed a truncated protease-resistant variant of the protein to enhance its biochemical stability under proteolytic conditions. For the ligand display, Enhanced Green Fluorescent Protein (EGFP) was fused to the N-terminal domain of the single-spanning protein. For EGFP expression, a lentiviral construct encoding EGFP fused to the engineered protein in the 5′ to 3′ orientation was cloned into a pGenLenti vector and was co-transfected into Human Embryonic Kidney 293FT cells along with third-generation packaging and envelope plasmids. The HEK293 FT cells were transduced and selected using puromycin. The results demonstrated successful membrane presentation of the fusion protein, and EVs derived from these cells also display EGFP on their surface. Surface Green Fluorescent Protein–decorated EVs can be passively or actively loaded with the drug of interest and can be readily tracked within cellular systems.

References:

1. Silva AM, Lázaro-Ibáñez E, Gunnarsson A, Dhande A, Daaboul G, Peacock B, et al. Quantification of protein cargo loading into engineered extracellular vesicles at single-vesicle and single-molecule resolution. J Extracell Vesicles. 2021 Aug;10(10):e12130.
2. Meng W, Wang L, Du X, Xie M, Yang F, Li F, et al. Engineered mesenchymal stem cell-derived extracellular vesicles constitute a versatile platform for targeted drug delivery. J Controlled Release. 2023 Nov 1;363:235–52.
3. Dooley K, McConnell RE, Xu K, Lewis ND, Haupt S, Youniss MR, Martin S, Sia CL, McCoy C, Moniz RJ, Burenkova O, Sanchez-Salazar J, Jang SC, Choi B, Harrison RA, Houde D, Burzyn D, Leng C, Kirwin K, Ross NL, Finn JD, Gaidukov L, Economides KD, Estes S, Thornton JE, Kulman JD, Sathyanarayanan S, Williams DE. A versatile platform for generating engineered extracellular vesicles with defined therapeutic properties. Mol Ther. 2021 May 5;29(5):1729-1743.
4. Zhao H, Li Z, Liu D, Zhang J, You Z, Shao Y, Li H, Yang J, Liu X, Wang M, Wu C, Chen J, Wang J, Kong G, Zhao L. PlexinA1 (PLXNA1) as a novel scaffold protein for the engineering of extracellular vesicles. J Extracell Vesicles. 2024 Nov;13(11):e70012. doi: 10.1002/jev2.70012. PMID: 39508411; PMCID: PMC11541859.

Poster ID 2A045

Nano-Mechanical Assessment of Bone Quality for Clinical Decision-Making in Chronic Kidney Disease

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Chronic kidney disease–mineral and bone disorder (CKD-MBD) disrupts mineral homeostasis, resulting in compromised bone strength and an elevated risk of fractures, comparable to that observed in type 2 diabetes (T2D) and advanced stage 5 CKD. However, bone quality in CKD remains poorly investigated at the nanoscale. In this study, nanoindentation was conducted on human and animal bone samples using a Berkovich tip mounted on a TI-950 TriboIndenter (Hysitron Inc.). Samples were prepared by low-speed diamond sectioning, epoxy embedding, sequential polishing, and sonication. Indentation tests were performed using a 10 s loading, 10 s holding, and 5 s unloading protocol, with ten indents per sample at a peak load of 5000 μN. Hardness (H) and reduced modulus (Er) were calculated using the Oliver–Pharr method. Trabecular bone parameters were compared in stage 5 CKD patients treated with either Cinacalcet (n = 13, age = 35.8 ± 9.8) or Parathyroidectomy (n = 5, age = 35.2 ± 12.1). Despite the high fracture risk in advanced CKD, structural and mechanical bone changes remain underexplored. To address this, micro-CT and nanoindentation analyses were conducted. Structural results showed increased bone volume (BV/TV) in the parathyroidectomy group, driven by higher trabecular number (Tb.N), thickness (Tb.Th), and reduced spacing (Tb.Sp). Nanoindentation revealed significantly higher reduced modulus (Er = 7.382 ± 0.977 GPa) and hardness (H = 0.5053 ± 0.0548 GPa) in the parathyroidectomy group compared to the Cinacalcet group (Er = 6.492 ± 0.752 GPa; H = 0.4431 ± 0.0572 GPa), indicating superior bone material quality.
This study demonstrates a clear association between CKD progression and bone fragility, revealing how structural and mechanical deterioration, along with mineral alterations, heighten fracture risk across CKD stages.

Keywords: Nanoindentation, CKD-MBD, Cinacalcet, Parathyroidectomy, Reduced modulus (Er), Hardness (H), Trabecular bone, fragility fracture, and micro-CT.

Poster ID 2A046

Comprehensive Profiling of Neutrophil

Metabolism During Sepsis

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Sepsis is a life-threatening condition defined by a dysregulated host immune response to infection, in which neutrophils play a central role. Early sepsis is triggered by pathogen- and damage-associated molecular signals that drive a burst of inflammatory mediators and rapid neutrophil mobilization (1). This acute response frequently causes transient neutropenia and defective pathogen clearance. To compensate, the host initiates emergency granulopoiesis, increasing the production and release of mature and immature neutrophils with altered functions (2). These dynamic shifts in neutrophil abundance and activity strongly shape sepsis progression and outcome, however excessive or prolonged activation can worsen tissue damage, increasing mortality. Because neutrophil effector mechanisms are highly energy dependent, sepsis induces profound metabolic reprogramming. Understanding neutrophil metabolism alongside function may therefore reveal therapeutic opportunities (3,4). Using the cecal ligation and puncture model of polymicrobial sepsis in C57BL/6 mice, we identified time-dependent changes in neutrophil number, function, and metabolism. High bacterial burden and marked neutrophil activation, including sustained NETosis, coincided with neutropenia at 12 and 24 hours after sepsis. By 48 hours, neutrophil counts rebounded and bacterial clearance occurred, consistent with emergency granulopoiesis. Despite infection control, mortality rose between 48 and 54 hours. Elevated liver enzymes and persistent NETosis at this stage indicated that NET-mediated organ damage, rather than ongoing infection, drove lethality. Metabolomic profiling revealed dynamic alterations in pathways governing inflammation, reactive oxygen species production, energy metabolism, nucleotide turnover, lipid remodeling, and glutathione balance. Together, these results suggest that while neutrophil expansion is required for bacterial control, unresolved inflammatory and metabolic stress promotes immunopathology in sepsis.

References:

1. Arina P, Singer M. Pathophysiology of sepsis. Current Opinion in Anaesthesiology. 2021 Feb 4;34(2):77–84.
2. Patel JM, Sapey E, Parekh D, Scott A, Dosanjh D, Gao F, et al. Sepsis Induces a Dysregulated Neutrophil Phenotype That Is Associated with Increased Mortality. Mediators of Inflammation. 2018 Jan 1;2018:1–10.
3. Leblanc PO, Bourgoin SG, Poubelle PE, Tessier PA, Pelletier M. Metabolic regulation of neutrophil functions in homeostasis and diseases. Journal of Leukocyte Biology. 2024 Mar 7;116(3):456–68.
4. Shen X, Cao K, Zhao Y, Du J. Targeting neutrophils in Sepsis: From Mechanism to translation. Frontiers in Pharmacology. 2021 Apr 12;12:644270.

Poster ID 2A047

Rapid Biochemical Recovery Versus Delayed Immunological Reconstitution of the Transplanted Liver Graft- Unexplored Landscape for Infection Risk Stratification

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The liver serves as a dual metabolic and immunological hub, yet the relationship between these roles following living donor liver transplant remains poorly understood globally. This prospective study of 265 patients at a tertiary transplantation centre compared 134 tacrolimus/mycophenolate-treated recipients with 131 non-transplanted controls to examine metabolic-immune decoupling post-transplantation and determine whether multidrug-resistant (MDR) infection susceptibility reflects intrinsic immune dysfunction or pharmacological suppression, addressing critical knowledge gaps with worldwide clinical relevance. Serial biochemical monitoring demonstrated rapid metabolic recovery. Transient bilirubin, AST, ALT, ALP, and GGT elevations resolved by month 2 ($p< 0.001$), confirming graft metabolic competence. However, flow cytometry revealed severe innate immune deficits under immunosuppression: Reduced $CD45^+$ leukocyte density, profound monocyte depletion and near-complete $CD56^+$ NK cell absence (0.8–11.7% vs 8.7–53.6%). Despite normal liver function tests, 32.5% of transplanted patients developed MDR infections, highlighting the metabolic-immune recovery gap. To predict MDR infection risk, 134 immunosuppressed patients underwent Elastic-Net

regression (α = 0.7) with 17 clinical variables, comparing performance against LASSO regression by area-under-receiver-operating-characteristic curve. Nineteen correlations changed, and 29% reversed direction, reflecting major post-transplant metabolic-immune reorganisation. The Elastic-Net model achieved strong discrimination (AUC=0.86, Brier=0.18), retaining ALBUMIN, AST, ALT, and ALP as predictors, while immunosuppressive variables were removed during regularisation. These findings demonstrate divergent recovery kinetics, with rapid metabolic restoration and distinct immune reconstitution patterns, offering commercial potential for clinical decision-support systems. MDR susceptibility appears primarily driven by impaired innate immunity rather than pharmacological suppression. Results suggest graft optimisation and immune monitoring may reduce infection risk while decreasing costs.

References:

1. Lehmann, Christopher J et al. "Fecal metabolite profiling identifies liver transplant recipients at risk for postoperative infection." *Cell host & microbe* vol. 32,1 (2024): 117-130.e4. doi:10.1016/j.chom.2023.11.016
2. Delignette, M C et al. *"Individual mHLA-DR trajectories in the ICU as predictors of early infections following liver transplantation: a prospective observational study."* Critical care (London, England) vol. 29,1 79. 18 Feb. 2025, doi:10.1186/s13054-025-05305-x

Poster ID 2A048

Surfactant protein D Regulates Inflammatory Responses and B-Cell–Mediated Antigen Presentation via Interaction with CD23 and the High-Affinity B-Cell Receptor, CD21

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Surfactant protein D (SP-D) is a soluble pattern recognition molecule of the innate immune system with established roles in host defence and regulation of allergic inflammation. A recombinant fragment of human SP-D (rfhSP-D), consisting of the homotrimeric neck region and the C-type lectin/carbohydrate recognition domain (CRD), has been demonstrated to be equally effective as the full-length protein in modulating immunological responses. In addition to its anti-microbial properties, SP-D has emerged as an important modulator of adaptive immune responses through interactions with immune cell surface receptors. rfhSP-D significantly inhibited allergen-induced basophil responses at the single-cell level, reduced CD23-mediated facilitated allergen presentation, and suppressed Th2 cytokine production. Furthermore, rfhSP-D inhibited IgE synthesis by B cells derived from grass pollen-sensitised allergic patients when primed by CD40L/ IL-4 and IL-21. Subsequently, we have examined the interaction between rfhSP-D and the two IgE receptors, CD21 and CD23, and evaluate the functional consequences of these interactions, such as IgE production and IgE-mediated allergen presentation. rfhSP-D strongly inhibits allergen-driven Th2 cytokine production, significantly reducing IL-4, IL-5, IL-9, IL-13, and IL-10. Additionally, rfhSP-D suppressed key inflammatory mediators, including the chemokines eotaxin and MDC and the cytokines IL-6, IL-17a, and IL-27, suggesting reduced inflammatory cell infiltration and attenuationof allergic inflammation. Our results highlight the importance of SP-D in protection against allergen sensitisation by interfering at the level of CD21 and CD23 and offer a mechanistic approach to delineate its therapeutic value.

Poster ID 2A049

Ubiquitin specific peptidase 37 (USP37) facilitate Replication stress tolerance to promote prostate cancer oncogenesis.

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Several reports have suggested that the DUBs (deubiquitinating enzymes) are highly-elevated in various cancers, Reverses the process of ubiquitination and are responsible for stabilization of oncoproteins. Among DUBs, Ubiquitin-specific peptidase 37 (USP37) is one of the least studied member of the Ubiquitin specific protease family. USP37 controls numerous aspects of oncogenesis, including stabilizing many oncoproteins as reported in our recent studies. Prostate cancer (PC) is the most common cancer diagnosis made in men remains the leading cause of cancer death in men. However, the biological functions of USP37 in prostate cancer remain unclear. Analysis of TCGA data indicated that overexpression of USP37 correlated with reduced progression free survival (PFS) in prostate cancer patients. Mass spectrometry (MS) analysis of Prostate cancer cells (DU145) indicated that distinct set of genes were altered on knockdown of USP37. Survival Data indicate that USP37 overexpression confers survival advantage while its depletion enhances sensitivity for cell killing in PC cells. USP37 overexpressing cells were able to resolve DNA damage foci much more rapidly than the control cells or cells in which USP37 was depleted in response to genotoxic stress. USP37 depletion results in reduced resolution of γ H2AX and 53BP1 DNA damage foci which indicates the reduced ability of cells to carry out constitutive DNA replication. USP37 was found to interact with different replication factors as also seen in our MS analysis including many previously reported partners. We further correlated our data with archived tissue blocks of PC patients by analysing if USP37 overexpression correlated with disease progression. Present data suggests that USP37 is required for tolerance of replication stress in PC and is required to dock additional replication factors and stabilize DNA replication fork. The current data provides novel pathways regulated by USP37 in PC cells which reinforce development of targeting strategies against USP37 in context of Prostate Cancer.

Poster ID 2A050

Nanoparticle Mediated Gene Delivery for Lineage Specific Differentiation of Mouse Embryonic Stem Cells

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Keywords: Modified RHAp nanoparticles, Sox17 expression, Stem cell differentiation, Pancreatic markers, Notch pathway knockdown

Sustained gene expression is crucial for directing stem cell differentiation through defined developmental stages. Although viral vectors are widely used, their application is often limited. To address this, we explored glucose-arginine functionalized hydroxyapatite (G-RHAp) nanoparticles as an efficient, non-viral delivery platform for prolonged Sox17 expression in mouse embryonic stem cells (mESCs). A single G-RHAp transfection resulted in up to 90 ± 3% Sox17-positive cells with just 25 ng plasmid, significantly outperforming arginine-functionalized HAp (RHAp), which reached 77% only at 100 ng. While Sox17 expression was transient after a single transfection, repeated G-RHAp transfections at 72-hour intervals, five cycles (T1-T5), maintained over 90% Sox17-positive cells up to day 24, as confirmed by RT-PCR, flow cytometry, and immunofluorescence. Sustained Sox17 expression led to robust downregulation of pluripotency markers (Oct4, Nanog, Sox2, Klf4) and upregulation of endodermal and pancreatic markers, including FOXA2, GATA4, GATA6, Hnf1β, and Pdx1. Sequential activation of Pdx1 and Ptf1a, followed by amylase expression by day 18, indicated successful exocrine pancreatic differentiation. However, mature endocrine markers (NKX6.1, insulin, and glucagon) were not detected, suggesting a lineage bias. Our findings demonstrate that G-RHAp nanoparticles enable efficient, sustained gene delivery and precise control of stem cell fate, offering significant potential for nanomedicine and regenerative applications.

Poster ID 2A051

Title - Role of HnRNP D in Regulating Stem Cell Differentiation and Cell Cycle Progression in Induced Pluripotent Stem Cells

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The maintenance of induced pluripotent stem cell (iPSC) identity and the precise control of lineage commitment rely on intricate post-transcriptional and epigenetic regulatory networks. Heterogeneous nuclear ribonucleoprotein D (hnRNP D), also known as AUF1, is an RNA-binding protein that plays a key role in post-transcriptional regulation by controlling mRNA stability, alternative splicing, and translation. Although hnRNP D has been widely studied in cancer biology and cellular senescence, its role in stem cell fate decisions, including cell cycle progression, remains largely unexplored.

This study aims to determine the specific role of hnRNP D in regulating the balance between pluripotency

maintenance and differentiation toward the myogenic lineage in iPSCs. To investigate this, we engineered iPSCs with a doxycycline-inducible CRISPR-Cas9 system to enable rapid and controlled editing of the hnRNP D gene. Following induction, we quantified changes in key regulatory factors, including pluripotency markers, myogenic differentiation markers, cell cycle regulators, and RNA-binding proteins such as MBNL.

Based on our findings, we hypothesize that hnRNP D knockdown disrupts cellular proliferative control and alters RNA-binding protein expression, thereby priming cells for specialized fate acquisition. Understanding how hnRNP D modulates pluripotency and lineage commitment will help uncover novel molecular regulators involved in stem cell differentiation and regenerative potential.

Poster ID 2A052

The fate of Embryonic Stem Cells in PCOS-like Physiological Conditions

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Polycystic ovarian syndrome (PCOS) is a multifaceted endocrine disorder with significant psychological, reproductive, and metabolic implications. This condition is characterized by dysregulation of insulin and androgen levels, and its phenotypic expression exhibits considerable variability among affected individuals. Elevated levels of these hormones in reproductively aged women can profoundly influence the functional dynamics and developmental outcomes of various cellular populations.

Pregnancies in women with PCOS are associated with increased risks for complications such as preeclampsia, preterm birth, and gestational diabetes. Nevertheless, with appropriate medical interventions, favorable pregnancy outcomes can be achieved. The current literature lacks comprehensive insights into the potential implications of embryonic stem cells (ESCs) derived from mothers with PCOS who present with hyperandrogenemia and hyperinsulinemia. Notably, ESCs can express androgen and insulin receptors, suggesting responsiveness to these hormones.

This study aims to investigate the effects of elevated insulin, glucose, and androgens on the characteristics of ESCs cultured in leukaemia inhibiting factor (LIF)-containing media for 6 to 10 days under in vitro conditions. Exposure to insulin and dehydroepiandrosterone (DHEA) induced significant morphological changes in the ESCs by day four compared to controls treated solely with LIF. Furthermore, the research evaluates the impact of these hormonal conditions on the stemness properties of mouse ESCs through assessments of OCT4 expression, alkaline phosphatase activity and metabolic activity through glucose uptake assay.

Our findings indicate a reduction in OCT4 expression and alkaline phosphatase staining in ESCs under PCOS-like conditions. Additionally, glucose uptake was markedly diminished in these cells, reflecting impaired metabolic function. These results suggest that maintaining stem cell integrity and functionality in ESCs may be particularly challenging in the context of PCOS characterized by elevated insulin and androgen levels, potentially leading to adverse reproductive outcomes. A thorough investigation of this relationship is essential for elucidating the implications of metabolic disturbance on reproductive health in women with PCOS.

Poster ID 2A053

Bioengineered Marine Collagen Composite Skin Grafts for Wound Healing Applications"

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Three-dimensional collagen scaffolds are promising for skin tissue engineering, leveraging collagen's role as the primary ECM component. Marine collagen offers advantages over mammalian sources, including structural similarity to human collagen, enhanced bioactivity, improved thermal stability, reduced immunogenicity, and favourable cellular adhesion and proliferation. Derived from marine waste, it addresses ethical and safety concerns of mammalian materials while promoting sustainability. However, existing marine collagen scaffolds often lack mechanical stability for load-bearing, exhibit batch-to-batch variations in purity and yield, and require optimization for skin regeneration, particularly for wound healing and controlled degradation. Limited access to pure, characterized marine collagen in India hinders comparative research and translational studies, as it is mostly imported as dietary supplements rather than biomedical-grade materials. To bridge these gaps,

we developed novel marine collagen composite scaffolds by integrating marine collagen with natural polymers and synthetic PEG. This study advances these composites by incorporating agarose, gelatin, and PEG, each contributing uniquely to tissue engineering: agarose enhances structural integrity and biocompatibility for 3D scaffold formation; gelatin promotes cell attachment and mimics ECM elasticity; and PEG improves mechanical strength, crosslinking efficiency, and controlled degradation for load-bearing wound healing applications. Scaffolds (MCAG-PEG) were fabricated via cryogelation and freeze-drying at varying concentrations, crosslinked with 0.5% glutaraldehyde. Physicochemical characterization used SEM, ATR-FTIR, and DSC-TGA. Biological assays confirmed biocompatibility with mouse fibroblasts (L929), human keratinocytes (HaCaT), and primary human dermal fibroblasts (NHDF), demonstrating excellent cellular adhesion, proliferation, and viability. This work advances the field by harnessing marine waste-derived biomaterials, supporting both scientific innovation and eco-friendly manufacturing for next-generation skin regeneration therapies.

References:

1. Liu, S., Lau, C. S., Liang, K., Wen, F., & Teoh, S. H. (2022). Marine collagen scaffolds in tissue engineering. *Current Opinion in Biotechnology*, *74*, 92-103.
2. Coppola, A., Oliviero, M., De Cesare, N., Russo, N., Nappo, N., Buonocore, C., ... & Coppola, D. (2025). Marine Collagen from European Sea Bass (Dicentrarchus labrax) Waste for the Development of Chitosan/Collagen Scaffolds in Skin Tissue Engineering. *Marine Drugs*, *23*(10), 375.
3. Bhat, S., Tripathi, A., & Kumar, A. (2011). Supermacroprous chitosan–agarose–gelatin cryogels: in vitro characterization and in vivo assessment for cartilage tissue engineering. *Journal of the Royal Society Interface*, *8*(57), 540-554.
4. Bhende, P. P., Dias, J. D., Srivastava, H., Chauhan, R., Waigaonkar, S., Ganguly, A., & Bragança, J. M. (2024). Haloarchaeal poly[(3-hydroxybutyrate)-co-(3-hydroxyvalerate)] composite films reinforced with graphene nanoplatelets as a biomaterial for skin tissue engineering. *RSC advances*, *14*(34), 24398-24412.
5. G. Sundar, J. Joseph, C. Prabhakumari, A. John, and A. Abraham, "Natural collagen bioscaffolds for skin tissue engineering strategies in burns: a critical review," *International Journal of Polymeric Materials and Polymeric Biomaterials*, vol. 70, no. 9, pp. 593–604, 2021, doi: 10.1080/00914037.2020.1740991.

Poster ID 2A054

Non-Viral Delivery of Full-Length Dystrophin Using Lipid-Modified Gold Nanoparticles for Duchenne Muscular Dystrophy Therapy

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Duchenne Muscular Dystrophy (DMD) is a severe X-linked genetic disorder characterized by progressive muscle degeneration caused by mutations in the dystrophin gene. The absence of functional dystrophin protein leads to muscle fibre damage, gradual loss of muscle strength, and premature mortality. Delivery of the full-length dystrophin gene remains a major challenge because of its exceptionally large size, which limits efficient gene transfer using conventional vectors. Moreover, viral vectors, although widely used for gene delivery, are associated with limitations such as immunogenicity, restricted cargo capacity, and safety concerns.

In this study, we developed lipid-modified gold nanoparticles as a non-viral platform for the delivery of the full-length DMD plasmid. Transmission electron microscopy confirmed the nanoscale size of the synthesized particles. Dynamic light scattering and zeta potential analysis indicated successful lipid coating of the nanoparticles, while FT-IR spectroscopy confirmed effective interaction between the lipid and the gold nanoparticle surface. The concentration of nanoparticles was quantified using ICP-OES.

The nanoparticles efficiently bound and complexed the DMD plasmid, indicating their suitability as a gene delivery carrier. Cytocompatibility was assessed using the MTT assay in MCF-7 cells, demonstrating good biocompatibility at concentrations used for transfection. Delivery of the full-length DMD plasmid resulted in significant overexpression of the DMD gene. Successful expression at the protein level was confirmed through mCherry reporter fluorescence and flow cytometry analysis of dystrophin protein.

Overall, this nanoparticle-based system demonstrates potential as an efficient non-viral carrier for the delivery of large plasmids. The platform may be further extended to muscle cells for the development of gene-mediated therapeutic strategies for DMD.

References:

1. Farruggio, A. P., Bhakta, M. S., du Bois, H., Ma, J., & Cals, M. P. (2017). Genomic integration of the full□length dystrophin coding sequence in Duchenne muscular dystrophy induced pluripotent stem cells. *Biotechnology Journal,* 12(4), 1600477.

[2]Duan, D. (2024). Full-length dystrophin gene therapy for Duchenne muscular dystrophy. *Molecular Therapy,* 32(9), 2817-2818.

[3]Zhou, Y., Zhang, C., Xiao, W., Herzog, R. W., & Han, R. (2024). Systemic delivery of full-length dystrophin in Duchenne muscular dystrophy mice. *Nature Communications,* 15(1), 6141.

Poster ID 2A055

Effect of Spermidine in Adult Female and Polycystic Ovary Syndrome Like Hyperandrogenized Mice

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Polyamines are biogenic amines that are present and synthesized de novo in all living organisms. They can also be acquired through the diet, including meat, fish, and green vegetables. Our group's earlier research has demonstrated that putrescine can control the expression and release of hypothalamic gonadotropin-releasing hormone (GnRH). The present work focuses on one of the polyamines, Spermidine, and its effects on the Hypothalamic-Pituitary-Gonadal and gut microbial-brain axis. Studies have shown that exogenous spermidine supplementation can enhance oocyte quality in aged mice.

The effects of spermidine on adult female mice have not yet been investigated. To study the effects of polyamines, we examined interactions within the gut-brain and hypothalamic-pituitary-gonadal axis. For this study, female adult mice (C57BL/6) were used and treated with Spermidine (SPD) for 7 days with 50mg/kg body weight per day, along with a positive control group injected with HCG and PMSG, and a control mice group. To study the microbiome, we separated bacteria from vaginal swabs, gut contents, and intestinal swabs, and cultured them in complex media to assess their diversity. In case of the HPG axis, we are examining the body weight, pathological conditions, hormone analysis and gene expression.

We found that the control, positive control, and treated groups had varying microbial loads. Microorganisms from these groups also demonstrated unique colony morphology in addition to varied microbial load. Furthermore, comparing the histology of the ovaries of control, positive control, and SPD-treated mice, the treated group showed enhanced folliculogenesis. The distinct changes mentioned above need further investigation.

Poster ID 2A056

Deciphering the role of Innate Lymphoid Cells (ILCs) under "immune stress" conditions: Intestinal inflammation and Aging

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Innate lymphoid cells (ILCs) are the innate counterparts of T cells, having similar effector functions but lacking the specific antigen receptor. ILCs are highly enriched at barrier surfaces where they are essential for early host defense (1). Group 3 ILCs (ILC3s) are particularly enriched in the gut and are important for protecting the intestinal mucosa. However, under conditions of immune stress, such as intestinal inflammation, ILC3 function can become dysregulated. One such condition is inflammatory bowel disease (IBD), which includes Crohn's disease and ulcerative colitis. Recent work from our group identified a transcription factor TOX2 as a key regulator of ILC3 persistence and function in the gut (2). Our findings indicate that elevated TOX2 expression in intestinal ILC3s is driven by the hypoxic microenvironment of the gut and by IL-17 signaling. Since hypoxia and IL-17 are hallmarks of intestinal inflammation, we hypothesize that TOX2 expression is enhanced in IBD. Our preliminary data from single cell analysis suggests that Tox2 is highly expressed in Crohn's disease patients. Hence, we aim to investigate the role of TOX2 in intestinal inflammation and evaluate its potential as a biomarker in IBD. Therefore, we wish to screen tissue samples from human IBD patients.
Aging is another form of immune stress, which is associated with functional decline of the adaptive immune system. However very little is known regarding the function of ILCs in aged individuals. Our preliminary observations indicate that aged mice from different genetic backgrounds exhibit variable susceptibility to acute colitis. We further wish to study how aging and genetic background influence ILC responses in both mice and humans.

References:

1. A Das et al., Nature Immunology, 2026, vol 27, 401- 412
2. A Das et al., Immunity, 2024, vol 57, 1019- 1036

Poster ID 2A057

Structural characterization of the

Transcription Factor TOX2 to Explore Its Therapeutic and Biomarker Potential in Colorectal Cancer

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TOX (Thymocyte-associated HMG box), family of proteins comprises sequence-independent high mobility group (HMG) box transcription factors that play important role in immune system development and function. The TOX family comprises TOX1, TOX2, TOX3, and TOX4. While TOX1 has been extensively characterized and is known to regulate the development of $CD4^+$ T cells, natural killer cells, and lymphoid tissue inducer cells, studies on TOX3 and TOX4 have primarily linked them to neuronal survival and DNA damage response, respectively. In contrast, the role of TOX2 and its impact on immune cells and disease remains poorly understood.

Recent work from our group reported that TOX2 is required for the persistence of a subset of innate lymphoid cells (ILCs) in the gut, called ILC3s, which play key role in maintaining intestinal homeostasis. Our published data also show that TOX2 expression increases in hypoxic environment and is associated with increased production of interleukin-17, features commonly linked with inflammatory responses and tumor progression. In addition, analysis of publicly available cancer transcriptomic datasets using GEPIA database show that colorectal cancer (CRC) patients with higher TOX2 expression exhibit poorer survival rates. These observations suggest that higher expression of TOX2 may contribute to CRC progression.

Based on these findings, we hypothesize that TOX2 plays a functional role in colorectal cancer and could serve both as a therapeutic target and potential biomarker. n this study we aim to predict the structure of TOX2 using in-silico techniques and identify potential drug compounds against it through computational screening. Further, the potential compounds will be validated using CRC mouse models and human CRC samples.

References:

1. Das, Arundhoti et al. *"Transcription factor Tox2 is required for metabolic adaptation and tissue residency of ILC3 in the gut."* Immunity vol. 57,5 (2024): 1019-1036.e9. doi:10.1016/j.immuni.2024.04.001
2. O'Flaherty, Emmett, and Jonathan Kaye. *"TOX defines a conserved subfamily of HMG-box proteins."* BMC genomics vol. 4,1 (2003): 13. doi:10.1186/1471-2164-4-13
3. Aliahmad, Parinaz et al. *"The many roles of TOX in the immune system."* Current opinion in immunology vol. 24,2 (2012): 173-7. doi:10.1016/j.coi.2011.12.001

Poster ID 2A058

Camptothecin analogue encapsulated albumin nanoparticles for sustained release and targeted delivery

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Camptothecin analogue 1 (CA1) is a derivative of Camptothecin, a natural alkaloid that inhibits Topoisomerase. Although some of the analogue are clinically approved many others derivatives still cause significant side effects because they affect rapidly dividing healthy cells. The E-ring lactone of camptothecin analogues is chemically unstable at physiological pH. we synthesised a sustained release albumin nanoparticle (CA1-AL-NPs) for targeted cancer therapy. The NPs exhibited a uniform spherical morphology with an average hydrodynamic diameter of 147 nm, zeta potential of −24 mV, and high monodispersity (PDI < 0.1). In vitro release kinetics demonstrated pH-responsive, sustained drug release for up to nine days, with faster release under acidic (tumor-like) conditions. The NPs both exhibited excellent biodegradability and hemocompatibility, indicating favorable safety and clinical translation potential. CA1-AL-NPs displayed potent cytotoxicity in oral cancer (OSCC) and lung cancer (A549) cells, with significantly reduced toxicity in non-cancerous embryonic kidney cells (HEK293T). Intra cellular uptake assay analysed by FACS revealed preferentially higher cellular uptake in cancerous cells compared to non-cancerous cells. Overall, CA1-AL-NPs offer a promising strategy for sustained, tumor-targeted delivery of CA1-AL-NPs with improved therapeutic index and reduced systemic toxicity.

References:

1. Ulukan, H.; Swaan, P. W. *Camptothecins: A Review of Their Chemotherapeutic Potential. Drugs* 2002, 62, 2039–2057.
2. Seiter, K. *Toxicity of the Topoisomerase I Inhibitors. Expert Opin. Drug Saf.* 2005, 4, 45–53.
3. Rothenberg, M. L. *Topoisomerase I Inhibitors: Review and Update. Ann. Oncol.* 1997, 8, 837–855.

Poster ID 2A059

Exploring the Potential of

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Pharmaceutical Polymer Based Bioink for Skin Tissue Engineering

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3D Bioprinting is state-of-the-art technology used to fabricate tissues, thereby making bioink, the essential components in tissue engineering and regenerative medicine. Bioinks are made up of polymers and biological entities like cells, growth factors, drugs, crosslinkers etc. Bioinks composed of naturally derived polymers, show excellent printability, rheological behaviour, crosslinking kinetics and cytocompatibility.

In the present study, an attempt was made to develop and optimize composite skin bioinks for extrusion-based bioprinting to engineer skin tissue constructs. The bioink formulation made with sodium alginate as base polymer proved to be highly biocompatible and least cytotoxic, as revealed by MTT assay. Moreover, the long-term growth and sustenance of cells, is also shown by confocal microscopy. The ideal viscosity of the hydrogel greatly contributed to its printability. The SEM Imaging was carried out to analyze the micro-architecture of the printed scaffold. It was observed that the gel was porous in nature, which enhanced the growth and migration of the scaffolds.

Overall, alginate-based bioinks provide suitable microenvironment for the proliferation and maturation of cells. Hence, they are significantly used in engineering of soft tissues.

References:

1. Bankhede, H. K., & Ganguly, A. (2022). Pharmaceutical polymer-based hydrogel formulations as prospective bioinks for 3D bioprinting applications: A step towards clean bioprinting. *Annals of 3D Printed Medicine*, 6, 100056. https://doi.org/10.1016/j.stlm.2022.100056
2. Ramakrishnan, R., Kasoju, N., Raju, R., Geevarghese, R., Gauthaman, A., & Bhatt, A. (2022). Exploring the Potential of Alginate-Gelatin-Diethylaminoethyl Cellulose-Fibrinogen based Bioink for 3D Bioprinting of Skin Tissue Constructs. *Carbohydrate Polymer Technologies and Applications*, 3, 100184. https://doi.org/10.1016/j.carpta.2022.100184

Poster ID 2A060

Alleviating obesity using microencapsulated fucoxanthin: A safe and natural remedy to a global problem

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Obesity is chronic disease characterised by excessive adiposity and comorbidities like cardiovascular defects, diabetes, and non-alcoholic fatty liver disease. Commercial medications induce to nausea, liver failure, diarrhoea and fatality in extreme cases. Fucoxanthin(Fx), a carotenoid found in brown seaweed is known for its anti-obesity property. Applications of Fx is hindered by its low solubility, stability, and poor bioavailability. This study aims to microencapsulate fucoxanthin with inulin(IN) and gum acacia(GA) and study its bioavailability and anti-obesity effect in obese mice. Fx was extracted from Padina tetrostmatica. Purified Fx was microencapsulated with IN, and GA viz lyophilisation. Obesity(ob) was induced in C57/BL6 mice (n = 5) with 40% high fat diet (HFD) for 8-10 weeks and were orally dosed (200nM) with microencapsulated fucoxanthin (IN-Fx & GA-Fx) to study its bioavailability at 2,4,6&8h. The most bioavailable encapsulation was further evaluated for its anti-obesity effect in obese mice along with orlistat (ORL) (66mg/Kg/BW). Fx was quantified by HPLC with 98% purity. The Cmax of Fx (18.56nM) in blood plasma was detected at the 4h (Tmax) for ob-InFx. After 8 weeks of the anti-obesity study, ORL, Free Fx and INFx-treated groups saw a decrease in body weight of upto 4.9, 3.4 and 3.62%, respectively, whereas HFD group observed a 6.23% increase. A 20% mortality rate was observed in ORL-treated group. IN-Fx demonstrated significantly ($p \leq 0.05$) better glucose tolerance and lower serum cholesterol and triglyceride levels in obese mice compared to the other groups. These results demonstrate microencapsulated fucoxanthin to be a safe and effective agent for combating obesity.

References:

1. Ravi H, Baskaran V. Chitosan-glycolipid nanocarriers improve the bioavailability of fucoxanthin via up-regulation of PPARγ and SRB1 and antioxidant activity in rat model. *Journal of functional foods*, 2017, 28, pp.215-226
2. Guo B, Yang B, Pang X, Chen T, Chen F, Cheng K.

Fucoxanthin modulates cecal and fecal microbiota differently based on diet. *Food Funct.* 2019, 10:5644–5655
3. Ding L, Luo X, Wen W. Fucoxanthin-Loaded Solid Lipid Nanoparticles Exert Potent Therapeutic Efficacy in Combating High-Fat Diet Induced Obesity in Mice. *International Journal of Molecular Sciences*. 2025,26(11):5249.

Poster ID 2A061

Hypoxia Rewires Adult Stem Cell Identity toward Functional Dopaminergic Neurons through Coordinated Secretome and Signaling Remodeling

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Adult mesenchymal stem cells represent an attractive, ethically viable source for neuronal replacement therapies; however, efficient and physiologically relevant dopaminergic specification remains a major challenge. Here, we report that hypoxic preconditioning functions as a decisive biological switch that programs infrapatellar fat pad–derived stem cells (IFP-SCs) toward functional dopaminergic neuronal identity. Primary IFP-SCs displayed stable mesenchymal morphology, robust proliferative capacity, and canonical stemness marker localization. Exposure to physiological hypoxia (5% O_2) induced marked morphological remodeling, characterized by cytoplasmic elongation and neurite-like extensions, accompanied by the generation of a neurotrophin-enriched hypoxia-conditioned secretome. FTIR and ^{1}H-NMR profiling of conditioned media confirmed the presence of NGF, EGF, bFGF, BDNF, and dopaminergic metabolites, indicating functional paracrine remodeling under hypoxia. Neuronal induction under defined conditions yielded cells with characteristic neuronal architecture, including axons and dendritic spines. Immunocytochemistry demonstrated robust expression of MAP2, NF-L, NSE, SNAP25, and advanced functional markers (GAP43, SYT11, KCNA5, PACSIN1, syntabulin, dystrophin), with strongest expression observed in hypoxia-programmed groups. Semi-quantitative RT-PCR confirmed dopaminergic lineage commitment through expression of EN1 and NURR1, while pathway analysis revealed attenuation of PI3K/Akt signaling, selective activation of TGF-β signaling, and preserved Wnt signaling dynamics. Systems-level validation using STRING network analysis revealed a highly interconnected, non-random protein interaction network (PPI enrichment $p = 2.17 \times 10^{-11}$), integrating dopaminergic specification, synaptic maturation, and mitochondrial regulation. Collectively, this study demonstrates that hypoxic programming orchestrates coordinated transcriptional, secretory, and functional remodeling of adult stem cells, enabling efficient dopaminergic neuronal differentiation with translational relevance for neurodegenerative disorders.

References

1. Klaas, M., Möll, K., Mäemets-Allas, K. et al. Long-term maintenance of functional primary human hepatocytes in 3D gelatin matrices produced by solution blow spinning. Sci Rep 11, 20165 (2021). https://doi.org/10.1038/s41598-021-99659-1.
2. Radhakrishnan S, Martin CA, Dhayanithy G, Reddy MS, Rela M, Kalkura SN, Sellathamby Hypoxic Preconditioning Induces Neuronal Differentiation of Infrapatellar Fat Pad Stem Cells through Epigenetic Alteration. ACS Chem Neurosci. 2021 Feb 17;12(4):704-718. doi: 10.1021/acschemneuro.0c00728. Epub 2021 Jan 29. PMID: 33508941.

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Biomarker-Responsive Wound Dressing for Real-time Wound Infection Monitoring

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Infectious wounds are commonly colonized by pathogens (Gram positive, Gram negative and yeast). These infections present major challenges due to dynamic shifts in wound biomarkers, rapid microbial proliferation, and biofilm formation. The wound model matrix consists of agar as

a gelling agent and gelatin to mimic the collagen-rich extracellular matrix of skin. A simulated wound exudate formulation containing physiological components recreate the biochemical composition of wound fluid. Pathogen growth assays are studied for microbial proliferation and biofilm formation in exudate-supplemented matrices and exudate-free matrices, supporting the model's ability to mimic infection-like wound conditions.

The sensing platform focuses on pH and temperature monitoring as key infection-related indicators. Two types of printed sensors are fabricated: conductive-ink printed sensors and laser-printed sensors on a polyamide substrate. The pH sensor provides a generalized range of potential measurements for the possible wound pH. The temperature sensor enables monitoring of temperature variations within the wound model, providing, additional information on infection-associated changes.

This study presents an in vitro infectious wound model and a multiplexed sensing platform for monitoring wound-related biomarkers to support early infection detection.

Poster ID 2B001

Expression of Surfactant Protein D in Transgenic Lettuce and its Role in Modulation of Gut Microbiome

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Symbiotic microbiomes in gastrointestinal tract play a crucial role in maintaining homeostasis, thus any dysregulation will affect the intestinal-mucosal immune system. Surfactant protein D (SP-D), a multi-functional collagen containing C-type lectin (collectin) is well known for pathogen pattern recognition and immunomodulatory functions. Its potential role in regulating the gut microflora and mucosal immunity needs further investigation. Here, we study the impact of a recombinant fragment of SP-D (rfhSP-D) consisting of carbohydrate recognition domain on the modulation of gut microbiome. The research explores development of transgenic lettuce expressing rfhSP-D and examines its potential as an immunomodulator of mucosal immunity. The preliminary work involved optimizing bacterial expression of rfhSP-D using E. coli BL21 DE3 PLysS, purification and characterization of the proteins. rfhSP-D will be delivered sub-lingually and their effect on gut microbial alterations will be assessed using high-throughput sequencing coupled with transcriptomic analysis of fecal pellets. Gut-associated lymphoid tissues will be analyzed for mucosal immune profiling to quantify the pro-inflammatory T cell subsets. Oral delivery of SP-D has the potential to shape host-microbiome interaction and promote mucosal immunity.

Poster ID 2B002

Time-Dependent Alterations of the Gut Microbiome During Treatment of Drug-Sensitive Pulmonary Tuberculosis: A Systematic Review and Meta-analysis

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Pulmonary tuberculosis (PTB) and prolonged anti-tuberculosis treatment (ATT) are increasingly recognized to disrupt the gut microbiome. However, the extent and temporal pattern of these changes remain inconsistent across studies. This systematic review and meta-analysis quantitatively synthesized alterations in gut microbiome alpha diversity in treatment-naïve PTB patients and across different phases of ATT. A comprehensive literature search was conducted following PRISMA. Eleven studies were included in the qualitative synthesis, of which eight were eligible for meta-analysis. Human studies reporting gut microbiome alpha diversity, primarily Shannon diversity, in adults with PTB were analyzed. Standardized mean differences were calculated to compare treatment-naïve TB patients with healthy controls and to assess longitudinal changes during the intensive phase, continuous phase,

and at treatment completion. Random-effects models were applied, and heterogeneity statistics were calculated. Compared with healthy controls, treatment-naïve TB patients exhibited significantly reduced gut alpha diversity (pooled SMD = 0.74, 95% CI 0.56–0.92; I^2 = 72%). Longitudinal analyses showed a modest but significant overall decline in alpha diversity following ATT initiation (pooled SMD = −0.19, 95% CI −0.32 to −0.06; I^2 = 72%). Subgroup analyses indicated significant reductions after the intensive phase and at treatment completion, whereas changes during the continuous phase were not statistically significant. Qualitative synthesis suggested depletion of dominant commensal phyla, including Firmicutes and Bacteroidota, with transient enrichment of Proteobacteria during treatment. Overall, gut microbiome diversity is reduced in PTB and does not consistently recover during ATT. High heterogeneity highlights the need for standardized longitudinal studies and microbiome-targeted adjunctive strategies.

References

1. Hauptmann, M., Kalsdorf, B., Akoh-Arrey, J. E., Lange, C., & Schaible, U. E. (2024). Microbiota alterations in patients treated for susceptible or drug-resistant TB. *IJTLD open, 1*(8), 355-361.
2. Baral, T., Fayaz, S. M. A., Manu, M. K., Kudru, C. U., Singh, J., Mukhopadhyay, C., ... & Miraj, S. S. (2025). Gut microbiota profile in newly diagnosed pulmonary tuberculosis patients: an exploratory pilot study in southern India. *Gut Pathogens, 17*(1), 59.
3. Zhang, S., Xu, Z., Wang, Z., Fei, X., Li, Z., Zhu, L., ... & Liu, Q. (2025). Changes in gut microbiome following anti-tuberculosis treatment: a prospective cohort from eastern China. *BMC Infectious Diseases, 25*(1), 453.
4. Diallo, D., Sun, S., Somboro, A. M., Baya, B., Kone, A., Diarra, B., ... & Maiga, M. (2025). Metabolic and immune consequences of antibiotic related microbiome alterations during first-line tuberculosis treatment in Bamako, Mali. *Frontiers in immunology, 16,* 1561459.
5. Hu, Y., Yang, Q., Liu, B., Dong, J., Sun, L., Zhu, Y., ... & Jin, Q. (2019). Gut microbiota associated with pulmonary tuberculosis and dysbiosis caused by anti-tuberculosis drugs. *Journal of Infection, 78*(4), 317-322.
6. Maji, A., Misra, R., Dhakan, D. B., Gupta, V., Mahato, N. K., Saxena, R., ... & Singh, Y. (2018). Gut microbiome contributes to impairment of immunity in pulmonary tuberculosis patients by alteration of butyrate and propionate producers. *Environmental microbiology, 20*(1), 402-419.
7. Morgan, P. A., Parbie, P. K., Ntiamoah, D. O., Boadu, A. A., Asare, P., Lamptey, I. N. K., ... & Yeboah-Manu, D. (2023). Gut microbiome variation in pulmonary TB patients with diabetes or HIV comorbidities. *Frontiers in Microbiomes, 2,* 1123064.
8. Namasivayam, S., Diarra, B., Diabate, S., Sarro, Y. D. S., Kone, A., Kone, B., ... & Maiga, M. (2020). Patients infected with Mycobacterium africanum versus Mycobacterium tuberculosis possess distinct intestinal microbiota. *PLoS neglected tropical diseases, 14*(5), e0008230.

Poster ID 2B003

Epigenetic silencing of RSPO2 favors metastatic behavior in the progression of colorectal cancer

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Keywords: Colorectal cancer, RSPO2, Methylation, Expression, Pathways.

Background: RSPO2 protein is implicated in development, morphogenesis and stem cell renewal. Context-dependent expression of RSPO2 has been identified in various cancers through Wnt signaling amplification, but its role in colorectal cancer (CRC) progression remains unclear.
Aim: To elucidate the methylation-mediated tumor-suppressive activity of RSPO2 in colorectal cancer.
Methods: The study examined RSPO2 methylation and expression in CRC tumor samples and cells and further validated them using decitabine (DAC) treatment by CoBRA and RT-qPCR. Additionally, the biological function of RSPO2 was assessed by knockdown and overexpression in SW480 and SW620 cells and the effect was measured by in vitro cell viability, proliferation, migration, clone formation and invasion. At last, the molecular pathways were explored by targeting genes involved in the Wnt-connecting pathway. This work was approved by the institute's ethics committee via approval number IEC/2024-25/02.
Results: Hierarchical clustering identifies the hypermethylated RSPO2 promoter, which predicts early-stage (I+II, p=0.040) diagnosis and is associated with low mRNA expression in tissue and cell lines ($p<0.05$). Notably, treatment with DAC has significantly reversed methylation and expression in CRC cells ($p<0.05$), particularly in SW620 cells, suggesting that RSPO2 expression is likely regulated by epigenetic modification. Moreover, depletion of RSPO2 enhances cell viability, proliferation, migration, colony formation, and invasion in metastatic SW620 cells compared to SW480 ($p<0.05$), whereas overexpression compensates for these processes, confirming the tumor-suppressing action of RSPO2 in CRC. Transcriptional profiling suggested that RSPO2 acts as an agonist of Wnt and BMP signaling pathways that

might be involved in CRC progression, raising the possibility that it could become a new potential target in CRC.
Conclusion: Our research reveals the clinical significance of RSPO2 in early diagnosis and demonstrates that it functions as a tumor suppressor gene in CRC progression.

Poster ID 2B004

Plant Derived Nanovesicles: Isolation, Characterization and Biomedical Potential

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Plant derived exosome like nanovesicles have gained increasing interest as natural nanocarriers owing to their biocompatibility, stability and bioactive cargo. Medicinal plants known for their therapeutic properties, represent a valuable yet underexplored source of such nanovesicles. The present study aimed to isolate nanovesicles from a medicinal plant comprehensively characterize their physicochemical and biochemical properties, perform proteomic profiling, evaluate storage stability and assess their biomedical potential.
Nanovesicles were independently isolated from medicinal plant leaf material using polyethylene glycol precipitation and ultracentrifugation techniques. Particle size distribution and concentration were determined using nanoparticle tracking analysis (NTA) while surface charge and colloidal stability were assessed through zeta potential measurements. Morphological characterization and membrane integrity were examined using scanning electron microscopy (SEM) and transmission electron microscopy (TEM). Protein content was quantified using Nanodrop spectrophotometry and fourier transform infrared (FTIR) spectroscopy was employed to identify functional groups associated with proteins and other bioactive components. Proteomic profiling was conducted using liquid chromatography tandem mass spectrometry (LCMS/MS) to elucidate the protein cargo and functional diversity of the isolated nanovesicles.
Storage stability was evaluated under defined conditions by monitoring changes in physicochemical characteristics over time. Functional bioactivity was assessed using in vitro biochemical assays including antioxidant and antimicrobial assays. The isolated nanovesicles exhibited characteristic exosome like stable physicochemical properties and diverse proteomic profile associated with biological activity. Functional assays demonstrated notable antioxidant and antimicrobial potential.
In conclusion this study highlights medicinal plants as a promising source of stable, bioactive nanovesicles and underscores their potential as natural nanoscale platforms for future therapeutic and biomedical applications.

References:

1. Sarasati, A., Syahruddin, M. H., Nuryanti, A., Ana, I. D., Barlian, A., Wijaya, C. H., Ratnadewi, D., Wungu, T. D. K., & Takemori, H. (2023). Plant-Derived exosome-like nanoparticles for biomedical applications and regenerative therapy. *Biomedicines, 11*(4), 1053. https://doi.org/10.3390/biomedicines11041053
2. Dad, H. A., Gu, T., Zhu, A., Huang, L., & Peng, L. (2020). Plant exosome-like nanovesicles: emerging therapeutics and drug delivery nanoplatforms. Molecular Therapy, 29(1), 13–31. https://doi.org/10.1016/j.ymthe.2020.11.030
3. Kim, J., Li, S., Zhang, S., & Wang, J. (2021). Plant-derived exosome-like nanoparticles and their therapeutic activities. Asian Journal of Pharmaceutical Sciences, 17(1), 53–69. https://doi.org/10.1016/j.ajps.2021.05.006
4. Li, Y., Wang, Y., Zhao, H., Pan, Q., & Chen, G. (2024). Engineering Strategies of Plant-Derived Exosome-Like Nanovesicles: Current knowledge and Future Perspectives. International Journal of Nanomedicine, Volume 19, 12793–12815. https://doi.org/10.2147/ijn.s496664
5. Mu, J., Zhuang, X., Wang, Q., Jiang, H., Deng, Z., Wang, B., Zhang, L., Kakar, S., Jun, Y., Miller, D., & Zhang, H. (2014). Interspecies communication between plant and mouse gut host cells through edible plant derived exosome-like nanoparticles. Molecular Nutrition & Food Research, 58(7), 1561–1573. https://doi.org/10.1002/mnfr.201300729

Poster ID 2B005

Nanoceria Capped Triazine-Based Brominated COFs: ^{13}C NMR-Validated Architectures with Enhanced Antibacterial Performance Against S. aureus

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This study presents the successful synthesis and characterization of triazine-based brominated covalent organic frameworks (TbBr-COFs) and their cerium-modified hierarchical derivatives Ce-(TbBr-COF)-C and Ce-(TbBr-COF)-L. This was accomplished through a solvothermal reaction utilizing 2,4,6-tris(4-bromophenyl)-1,3,5-triazine

(TBPT) and 1,4-dibromobenzene (DBB) in mesitylene/dioxane with acetic acid as a catalyst at 120 °C for 80 hours, followed by probe sonication and homogenization processes. Comprehensive spectroscopic and microscopic analyses confirmed their structural integrity, enhanced crystallinity, porosity, and chemical stability, with SEM and HRTEM revealing distinct morphological features: rod-like structures for TbBr-COF and flower-like hierarchical assemblies for the cerium-modified derivatives. UV-Vis spectroscopy demonstrated efficient cerium loading (91.11% after 64 hours), whereas FTIR and XRD validated framework synthesis and π-π stacking interactions. ^{13}C solid-state NMR demonstrated great purity (>90%) with no residual precursors, and a downfield shift of triazine carbons (171.7 ppm) showing the electron-withdrawing influence of bromine. The cerium-modified COFs exhibited enhanced antibacterial effectiveness against Staphylococcus aureus, with inhibition zones measuring 3.5 cm (control), 2.2 ± 1.5 cm (TbBr-COF), 3.1 ± 0.5 cm (CeO2-NP), 3.5 ± 0.6 cm [Ce-(TbBr-COF)-C], and 2.9 ± 0.4 cm [Ce-(TbBr-COF)-L]. The TbBr-COFs, distinguished by tunable porosity, high surface area, and metal incorporation capability, offer a versatile platform for drug delivery, antibacterial applications, and hybrid material synthesis.

References:

1. Bhunia, S., Deo, K. A., & Gaharwar, A. K. (2020). 2D covalent organic frameworks for biomedical applications. Advanced Functional Materials, 30(27), 2002046.
2. Chandra, D. K., Kumar, A., & Mahapatra, C. (2024). Ultrasonic Synthesis of Ag@CNT-Based Metal-Organic Framework (MOF) for Enhanced Synergetic Antimicrobial Activity Against Staphylococcus aureus. JOM, 76(10), 5626-5642. https://doi.org/10.1007/s11837-024-06714-z
3. Chandra, D. K., Reis, R. L., Kundu, S. C., Kumar, A., & Mahapatra, C. (2023). Carbon nanotube hybrid materials: efficient and pertinent platforms for antifungal drug delivery. Advanced Materials Technologies, 8(23), 2301044.
4. Wang, Z., Zhang, S., Chen, Y., Zhang, Z., & Ma, S. (2020). Covalent organic frameworks for separation applications. Chemical Society Reviews, 49(3), 708-735.
5. Zhang, J., Han, X., Wu, X., Liu, Y., & Cui, Y. (2017). Multivariate chiral covalent organic frameworks with controlled crystallinity and stability for asymmetric catalysis. Journal of the American Chemical Society, 139(24), 8277-8285.

Poster ID 2B006

To Study Serum Uric Acid and Monosodium Urate Crystal in Gout Patients

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Introduction: Globally, gout is the most frequent cause of inflammatory arthritis. Soluble (serum) urate levels consistently above the saturation threshold of 6.0 mg/dl causes hyperuricemia, and monosodium urate (MSU) crystals develop. Low GFR decreases clearance, which raised serum UA level that increases risk of precipitation and supersaturation of urate crystals.

Objectives: To study serum uric acid levels, monosodium urate crystal formation, serum creatinine, urinary uric acid and glomerular filtration rate (eGFR) to assess their association in study population.

Methods: The study includes 30 participants (30-60 years) diagnosed with gout, attending orthopedic OPD, MGM hospital, kamothe, in the year 2025. Patients with other inflammatory disorders and significant renal impairment were excluded. Serum and urine samples were collected under aseptic condition and routine parameters assessed on Vitros 5600. Urine microscopy was performed to identify MSU crystals.

Results: The mean age of the study population was 47±7.52 years, with more number of male compared to female. The mean serum uric acid level was 8.7 ±1.7 mg/dl, with maximum patients showing values above the saturation threshold of 6.8 mg/dl. MSU crystals were found in 23 participants with elevated serum uric acid levels. The mean values of urinary uric acid excretion 520±199 mg/day, serum creatinine level 1.6±0.5 mg/dl and estimated eGFR was 70±09 ml/min/1.73 m^2.

Conclusion: Patients with lower eGFR tend to high serum uric acid levels and increased presence of MSU crystals in urine suggesting that impairment of renal function, that contributes to MSU crystal accumulation and deposition in soft tissue/joints. We observed positive relationship between serum uric acid levels and MSU crystal formation, and an inverse association between renal function (eGFR) and serum uric acid levels, supporting the role of renal impairment in the pathogenesis of gout.

Key Words: Gout, monosodium urate crystals

References:

1. Dalbeth N, Merriman TR, Stamp LK. Gout. Lancet. 2016;388(10055):2039–2052.
2. Neogi T. Gout. N Engl J Med. 2011;364(5):443–452.
3. Pascual E, Addadi L, Andrés M, et al. Mechanisms of crystal formation in gout: The role of monosodium urate.

Rheumatology (Oxford). 2015;54(1):16–24.

Poster ID 2B007

Detection of Quorum-Sensing Molecules Using Quartz Crystal Resonator to Infer the Presence of ESKAPE Pathogens

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ESKAPE pathogens Enterococcus faecium, Staphylococcus aureus, Klebsiella pneumoniae, Acinetobacter baumannii, Pseudomonas aeruginosa, and Enterobacter spp. represent one of the most critical global threats to human health. These organisms are the leading causes of hospital-acquired infections, including catheter-associated urinary tract infections and ventilator-associated pneumonia [1]. Rapid and reliable detection of pathogens remains a major clinical challenge, and delays in diagnosis are often associated with persistent and drug-resistant infections [2].

Quorum sensing (QS) is a bacterial cell–cell communication process mediated by signalling molecules, such as N-acyl homoserine lactones and oligopeptides, that regulate virulence, biofilm formation, and antibiotic tolerance [1]. Conventional analytical techniques, including amperometry, chromatography, and immunoblotting, have been employed for sensitive detection of QS molecules in clinical samples. However, these approaches are typically labour-intensive, costly, and time-consuming, limiting their suitability for rapid and point-of-care applications [3][4].

To address these limitations, quartz crystal resonator (QCR)-based biosensors have emerged as promising platforms for label-free and real-time sensing of QS molecules. Recently, N-hexanoyl-L-homoserine lactone (C6-HSL) was detected at nanomolar concentrations using a 5-MHz QCR functionalised with molecularly imprinted polymer (MIP) membranes. The resonance frequency shift arising from specific C6-HSL binding to the MIP-modified QCR was monitored using an oscillator circuit coupled to a frequency counter [5]. Furthermore, Guha et al. demonstrated the detection of C6-HSL using nano-MIPs-immobilised 14.3-MHz QCRs operated at fixed-frequency drive (FFD) mode. The analytical FFD approach enabled a simpler, robust detection strategy and holds significant promise for the indirect, rapid detection of ESKAPE pathogens in clinically relevant samples [6].

References:

1. S. Santajit, N. Sookrung, and N. Indrawattana, "Quorum Sensing in ESKAPE Bugs: A Target for Combating Antimicrobial Resistance and Bacterial Virulence," Oct. 01, 2022, *MDPI*. doi: 10.3390/biology11101466.
2. D. Trevas, A. M. Caliendo, K. Hanson, J. Levy, and C. C. Ginocchio, "Diagnostic Tests Can Stem the Threat of Antimicrobial Resistance: Infectious Disease Professionals Can Help," Jun. 01, 2021, Oxford University Press. doi: 10.1093/cid/ciaa1527.
3. X. Chen, C. Wang, Q. Y. Zheng, W. C. Hu, and X. H. Xia, "Emerging advances in biosensor technologies for quorum sensing signal molecules," Jan. 01, 2025, Springer Science and Business Media Deutschland GmbH. doi: 10.1007/s00216-024-05659-1.
4. C. Miller and J. Gilmore, "Detection of quorum-sensing molecules for pathogenic molecules using cell-based and cell-free biosensors," May 01, 2020, MDPI AG. doi: 10.3390/antibiotics9050259.
5. Ö. Acet and M. Odabaşı, "Detection of N-hexanoyl-L-homoserine lactone via MIP-based QCM sensor: preparation and characterization," Polymer Bulletin, vol. 80, ID 6, pp. 6657–6674, Jun. 2023, doi: 10.1007/s00289-022-04377-x.
6. A. Guha et al., "Direct detection of small molecules using a nano-molecular imprinted polymer receptor and a quartz crystal resonator driven at a fixed frequency and amplitude," *Biosens. Bioelectron.,* vol. 158, Jun. 2020, doi: 10.1016/j.bios.2020.112176.

Poster ID 2B008

Screening and Characterization of Probiotic Lactic Acid Bacteria for In Vitro Cholesterol Reduction

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Probiotics are defined as live microorganisms that confer health benefits on the host when administered in adequate amounts. Among their diverse therapeutic properties, cholesterol reduction has gained significant attention due to the increasing prevalence of hypercholesterolemia, obesity, cardiovascular diseases, and non-alcoholic fatty liver disease (NAFLD). Probiotic lactic acid bacteria (LAB) contribute to cholesterol lowering

through multiple mechanisms, including bile salt hydrolase (BSH) activity, deconjugation of bile acids, assimilation of cholesterol into the cell membrane, and biotransformation via diverse metabolic pathways. Deconjugation of bile salts reduces micelle formation, thereby decreasing intestinal cholesterol absorption and promoting its excretion.

The present study aimed to isolate and characterize LAB strains from milk samples and evaluate their probiotic potential along with their in vitro cholesterol-lowering efficacy. The isolates were subjected to morphological, biochemical, and probiotic characterization according to standard guidelines. Cholesterol assimilation was assessed in MRS broth supplemented with cholesterol and bile salts. Quantitative estimation of residual cholesterol was performed using High-Performance Liquid Chromatography (HPLC). Selected strains demonstrated significant cholesterol reduction compared to the control. Both bacterial cell pellets and cell-free supernatants were analyzed to understand the mechanism of cholesterol removal.

The findings suggest that selected LAB strains possess strong probiotic attributes and cholesterol-degrading capacity, highlighting their potential application in functional foods and nutraceutical formulations aimed at preventing obesity, reducing cardiovascular risk, and managing NAFLD. Further in vivo studies are required to validate their clinical efficacy and therapeutic potential.

References:

1. Gupta, V., & Garg, R. (2009). Probiotics. Indian journal of medical microbiology, 27(3), 202-209.
2. Polyzos, S. A., Kechagias, S., & Tsochatzis, E. A. (2021). non–alcoholic fatty liver disease and cardiovascular diseases: associations and treatment considerations. Alimentary pharmacology & therapeutics, 54(8), 1013-1025.
3. Pavlović, N., Stankov, K., & Mikov, M. (2012). Probiotics—interactions with bile acids and impact on cholesterol metabolism. Applied biochemistry and biotechnology, 168(7), 1880-1895.

Poster ID 2B009

Effect of microbiome modulation on the neurodevelopmental gene expression profile and the associated phenotypes in the Drosophila melanogaster

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The microbiome has a tremendous influence on human physiology, including nervous system development and brain function (Mayer et al., 2014; Cryan and Dinan, 2012). In this study, we show that the absence of microbiome in Drosophila melanogaster affects neurodevelopment and circadian regulation in both male and female flies (Douglas, 2018). Conventional flies with microbiome and axenic flies without microbiome were developed by rearing them on normal food and tetracycline treated food respectively.

Gene expression analysis was performed using quantitative real time PCR on head tissues of male and female flies. The results showed significant sex specific changes in the expression of neurodevelopmental and circadian related genes in axenic flies when compared to conventional flies, indicating that microbiome plays an important role in regulating brain associated genes (Mayer et al., 2014). Along with molecular changes, axenic flies also displayed behavioral defects. A significant reduction in climbing ability was observed in axenic flies, suggesting impaired motor coordination and neuronal function. In addition, axenic flies were found to be highly susceptible to seizure assay, indicating altered neuronal excitability and compromised neural stability.

To understand the relevance of these findings to humans, human orthologs of the selected Drosophila genes were identified using OrthoDB. Functional annotation revealed that these orthologs are involved in synapse development, neuronal maturation and brain function, and their dysfunction is associated with neurodevelopmental disorders (Cryan and Dinan, 2012). Overall, these findings suggest that microbiome is essential for normal brain development and function. Any alteration in microbiome through diet, antibiotics or drugs may lead to defects in neurodevelopment and increase the risk of neurological disorders during critical early developmental stages (Sharon et al., 2010).

References:

1. Mayer E. A., Knight R., Mazmanian S. K., Cryan J. F., Tillisch K., Gut microbiota and the brain: paradigm shift in neuroscience, *The Journal of Neuroscience,* 2014, 34, 15490–15496.
2. Douglas, Angela E., The Drosophila model for microbiome research, *Lab animal,*2018, vol. 47,6.
3. Sharon A., Segal D., Ringo J., Hefetz A., Zilber-Rosenberg I., Rosenberg E., Commensal bacteria play a role in mating preference of *Drosophila melanogaster, Proceedings of the National Academy of Sciences,* 2010, 107, 20051–20056.
4. Cryan J. F., Dinan T. G., Mind-altering microorganisms: the impact of the gut microbiota on brain and behaviour, *Nature Reviews Neuroscience,* 2012, 13, 701–712.

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Poster ID 2B010

Dysregulated Cellular Stress Responses and Heat Shock Proteins: Molecular Links to Non-Communicable Disease Pathogenesis Thematic area: Non-communicable diseases

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Keywords: Heat shock proteins, cellular stress response, proteostasis, non-communicable diseases, oxidative stress, molecular chaperones, chronic disease pathways

Non-communicable diseases (NCDs) such as cardiovascular disorders, diabetes, neurodegenerative diseases, autoimmune conditions, and cancers share common pathogenic pathways rooted in chronic cellular stress and impaired homeostatic regulation. Cellular stress responses are highly conserved survival mechanisms that enable cells to counteract oxidative injury, proteotoxicity, hypoxia, and inflammatory insults. Central to these responses are heat shock proteins (HSPs), a family of molecular chaperones that regulate protein folding, proteostasis, apoptotic signaling, and cytoprotective adaptation.

This review synthesizes emerging evidence demonstrating how dysregulation of HSP-mediated stress pathways contributes to disease progression across major NCDs. Persistent oxidative and metabolic stress leads to maladaptive alterations in HSP expression, mitochondrial dysfunction, chronic inflammation, telomere attrition, and cellular senescence — ultimately promoting vascular injury, neurodegeneration, immune dysregulation, and tumorigenesis. The interplay between environmental stressors, lifestyle transitions, and intrinsic molecular stress mechanisms highlights cellular stress biology as a unifying framework in NCD pathophysiology.

Furthermore, HSPs are gaining recognition as diagnostic biomarkers, prognostic indicators, and therapeutic targets. Pharmacological modulation of stress-response pathways offers promising opportunities for precision-medicine-based interventions aimed at restoring proteostasis and cellular resilience.

By integrating molecular stress biology with clinical disease mechanisms, this work underscores the need for translational research to harness HSP pathways for prevention, early detection, and therapeutic innovation in NCDs. Understanding cellular stress responses not only advances mechanistic insight but also supports the development of holistic strategies to reduce the global burden of chronic diseases.

References:

1. Singh MK, Shin Y, Ju S, Han S, Choe W, Yoon KS, et al. Heat shock response and heat shock proteins: current understanding and future opportunities in human diseases. *Int J Mol Sci*. 2024;25(8):4209. doi: 10.3390/ijms25084209
2. Schroeder HT, De Lemos Muller CH, Heck TG, Krause M, de Bittencourt PIH. Heat shock response during the resolution of inflammation and its progressive suppression in chronic-degenerative inflammatory diseases. *Cell Stress Chaperones*. 2024;29(1):116–142. doi: 10.1016/j.cstres.2024.01.002
3. Zuo WF, Pang Q, Zhu X, Yang QQ, Zhao Q, He G, et al. Heat shock proteins as hallmarks of cancer: insights from molecular mechanisms to therapeutic strategies. *J Hematol Oncol*. 2024;17:81. doi: 10.1186/s13045-024-01601-1

Poster ID 2B011

Development and Evaluation of a Lytic Bacteriophage Cocktail for Combating Multidrug-Resistant *Salmonella*

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Salmonella remains a leading cause of foodborne and enteric infections worldwide, with the increasing prevalence of multidrug-resistant (MDR) strains posing a serious threat to public health. The limited efficacy of antibiotics against these pathogens highlights the urgent need for alternative antimicrobial strategies. In this study, we report the development and evaluation of a lytic bacteriophage cocktail targeting clinically and environmentally relevant Salmonella spp. Individual phages were isolated from the River Ganga and selected for their broad host range, strong lytic activity, and genetic safety. Detailed characterization included plaque morphology, adsorption kinetics, latent period, burst size,

and stability under varying pH and temperature conditions. Whole-genome sequencing confirmed the absence of lysogenic genes, virulence factors, and antibiotic resistance determinants.

The optimized phage cocktail demonstrated superior antibacterial activity compared to individual phages, achieving rapid and sustained reduction of Salmonella growth in vitro. The cocktail also significantly disrupted established Salmonella biofilms and effectively delayed the emergence of phage-resistant bacterial populations. Additionally, enhanced antibacterial efficacy was observed when the phage was combined with selected antibiotics, suggesting phage–antibiotic synergy.

Overall, this study highlights the promise of a rationally designed Salmonella-specific bacteriophage cocktail as a viable therapeutic and biocontrol strategy for combating MDR Salmonella infections. These findings support further preclinical development and translational evaluation of phage-based interventions for Salmonella control.

Poster ID 2B012

Development and Application of an In-House Primer Panel Whole-Genome Sequencing Strategy for Molecular Profiling of Hepatitis B Virus in Central India

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Background: Genomic diversity of the hepatitis B virus plays a critical role in viral persistence, immune evasion, and therapeutic outcomes. Despite India's high HBV burden, comprehensive whole-genome data from Central India remain scarce, partly due to the limited availability of cost-effective sequencing platforms. To address this gap, the present study implemented an indigenously developed primer-based WGS protocol to investigate the mutation patterns of HBV circulating in Chhattisgarh.

Methods: A total of 64 HBV DNA positive specimens, with viral loads ranging from 3.11 to 9.08 $\log_{10}$IU/mL, were included. Complete HBV genome amplification was achieved using three overlapping sets of in-house designed primers. Sequencing was performed using a customized workflow adapted from the COVIDSeq WGS assay. Sequence quality metrics, genome coverage, phylogenetic clustering, serotype distribution, and mutation pattern were systematically analysed.

Results: The sequencing protocol generated consistently high-quality data, genome coverage exceeding 98.7% across samples. Phylogenetic tree demonstrated exclusive circulation of HBV genotype D and sub-genotype analysis identified D3 as the dominant lineage (53.7%), followed by D5 (23.6%), D1 (14.8%), and D2 (7.8%). Serotype distribution showed predominance of ayw2 (68.4%) and ayw3 (31.6%). Multiple mutations were observed within the surface gene, particularly in the major hydrophilic region and "a" determinant (T113S, T114S/P, K122R, N131T, F134Y/N, A159G), alongside mutations in transmembrane, core, and precore regions.

Conclusion: This study provides the first comprehensive whole-genome characterization of HBV from Chhattisgarh using an indigenously developed sequencing workflow. The dominance of genotype D and the presence of mutations in "a" determinant highlight the integrating genomic surveillance, particularly in regions with limited access to commercial sequencing solutions.

References:

4. Singh, P., Sharma, K., Bhargava, A., Negi, S.S., 2024. Scientific Reports 14, 10660.
5. Liang, J.T., 2009. Hepatitis B: The virus and disease#. Hepatology 49
6. Sant'Anna, T.B., Araujo, N.M., 2023. Microorganisms 11, 1101–1114.

Poster ID 2B013

Understanding the molecular role of R-loop in host-pathogen interaction during *Mycobacterium tuberculosis* infection **Abstract: Poster**

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Background and aim: R-loops are RNA–DNA hybrid structures with physiological roles in transcription and genome regulation. However, their aberrant accumulation induces DNA damage, genome instability, and activates innate immune signalling, thereby triggering inflammatory

responses. During viral infections, R-loop formation has been shown to influence host transcription, DNA damage response (DDR), and genome stability. I hypothesize that Mycobacterium tuberculosis (M.tb) infection similarly promotes aberrant R-loop accumulation in macrophages, driving DNA damage, dysregulated transcription, and altered immune responses. Such R-loop–mediated perturbations may provide a protective niche for bacterial persistence, contributing to both active and latent tuberculosis, and offering potential therapeutic target.

Methods: R-loop accumulation and DNA damage were analysed in macrophages and MSCs infected with M. smegmatis, H37Ra, and H37Rv using S9.6 ICC, γH2AX, COMET, FACS, qPCR for R-loop–associated genes, and RNase H validation.

Results: Infection with M. smegmatis, H37Ra, and H37Rv significantly increased R-loop signals in THP-1 macrophages, RAW cells, and MSCs compared with controls. RNase H treatment abolished these signals, confirming R-loop specificity. Transcript analysis revealed strain-specific modulation of PIWI gene family members. THP-1 macrophages infected with H37Ra exhibited significantly increased PIWIL2 expression and moderately elevated PIWIL4 compared with controls. In contrast, H37Rv infection led to decreased expression of PIWIL2, PIWIL3, and PIWIL4. Furthermore, SET, ATR, ATM, and FANCD2 transcripts were upregulated following M. smegmatis and H37Ra infection; ATM and ATR increases were statistically significant, while SET and FANCD2 showed non-significant upward trends. Collectively, these findings suggest that M. tuberculosis modulates host PIWI family expression and DNA damage response pathways to influence R-loop homeostasis and genomic stability.

Conclusions/Novelty: Our study shows that M. smegmatis, H37Ra, and virulent H37Rv induce host genomic instability via R-loop accumulation and DNA damage. PIWI modulation and ATR/ATM activation suggest a mechanism for persistence, highlighting R-loop regulation as a novel therapeutic target in tuberculosis.

Poster ID 2B014

Investigating the Role of Protein Phosphatase 5 Catalytic Subunit (PPP5C) in Vesicular Stomatitis Virus (VSV) Lifecycle through shRNA-Mediated Knockdown

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Protein phosphatase 5 catalytic subunit (PPP5C), a serine/threonine-protein phosphatase, regulates a wide range of physiological activities, including DNA damage response, cell cycle progression, apoptosis, and signal transduction pathways such as Hsp90-mediated signaling. Vesicular stomatitis virus (VSV), a prototypical rhabdovirus and oncolytic agent, requires host cellular machinery for effective replication, transcription, and assembly, making host phosphatases such as PPP5C potential proviral factors. Recent research suggests that PPP5C promotes viral replication by suppressing oxidative stress-induced apoptosis and regulating stress granule formation, hence enhancing viral survival within infected cells.

This study systematically explores PPP5C's particular contributions to the VSV lifecycle. Lentiviral-delivered shRNA constructs targeting PPP5C were transfected into baby hamster kidney (BHK-21) cells, resulting in gene suppression as validated by qRT-PCR. Silenced cells were challenged with VSV-EGFP at a multiplicity of infection (MOI) of 0.1. Fluorescence microscopy and qRT-PCR quantification of viral G and N genes were used at 12, 24, and 48 hours post-infection to assess infection progression and viral replication.

In summary, the study sheds information on the role of PPP5C in VSV replication and underlines its potential as a host-directed therapeutic target for VSV infection control and antiviral strategy improvement.

References:

1. Zhang H, Zhang Q, Tu J, You Q, Wang L. Dual function of protein phosphatase 5 (PPP5C): An emerging therapeutic target for drug discovery. *Eur J Med Chem*. 2023;254:115350. doi:10.1016/j.ejmech.2023.115350.
2. Gopinath VR, Klotz M, Sethuraman A, et al. Antagonistic effects of cellular poly(C) binding proteins on vesicular stomatitis virus gene expression. J Virol. 2011;85(17):9437-9447. doi: 10.1128/JVI.00690-11

Poster ID 2B015

Agro-Waste Derived Biochar as a Sustainable Material for Environmental and Human Health Protection

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Keywords: Agro-waste, Biochar, Environmental remediation, Human health, Sustainable material

The environment has been severely harmed by rapid industrialisation and intensive farming practices, putting ecosystem integrity and human health at risk. Biochar, which is made from agricultural waste, is a sustainable, affordable, and adaptable material that can simultaneously address multiple issues. Biochar has a variety of functional groups, a large surface area, and porosity. It is produced by pyrolysing agricultural waste, such as wheat straw, rice husk, sugarcane bagasse, maize cob etc... Heavy metals, pesticides, drugs, microplastics, and harmful bacteria can all be effectively absorbed from soil and water systems thanks to these features. Biochar not only restores the ecosystem but also indirectly improves human health by lowering greenhouse gas emissions, improving soil quality, lowering pollution in the food chain, and lowering exposure to hazardous pollutants.

Poster ID 2B016

Unlocking Minerals through Fermentation: Mechanistic Insights from Kerala Red Rice

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Keywords: Kerala red rice, fermentation, phytate degradation, mineral bioavailability, micronutrient deficiencies.

Kerala red rice (Oryza sativa L. subsp. indica) is an indigenous Indian whole-grain variety with a red pericarp, high bran retention, and relatively low glycemic index. It is rich in dietary fiber, micronutrients, and antioxidants. Like many cereals, it contains phytate, an antinutrient that chelates essential minerals—including iron, zinc, calcium, magnesium, and manganese—into insoluble complexes, limiting gastrointestinal bioavailability. Fermentation is a traditional South Asian practice enhancing digestibility and nutritional quality, yet biochemical and functional properties of fermented Kerala red rice remain largely unexplored. Microbial communities in fermented red rice broth may improve mineral accessibility through phytase-mediated phytate degradation.

To investigate this, phytate–mineral complexes of calcium, iron, zinc (1:1 molar ratio) were synthesized to model dietary chelation and incubated in 18-hour fermented red rice water. Structural and compositional changes were analyzed using Fourier-transform infrared spectroscopy (FTIR), X-ray fluorescence (XRF), and scanning electron microscopy with energy-dispersive X-ray spectroscopy (SEM-EDX). Mineral release kinetics were quantified via ICP-MS, and phytase activity was measured using the Fiske–Subbarow assay, interpreted in the context of microbial taxa identified in parallel analyses, including Bacillus and Enterobacter. Fermentation enabled enzymatic dephosphorylation of phytate, releasing minerals in patterns consistent with stability constants, with calcium mobilizing most rapidly. Elevated phytase activity highlighted the functional role of microbial communities in mineral liberation. By bridging culinary tradition with modern nutrition science, these findings validate fermentation of Kerala red rice as a strategy to improve mineral accessibility, which could help address micronutrient deficiencies in cereal-dependent populations.

References:

1. Schlemmer U, Frølich W, Jany KD. Phytate in foods and significance for humans: food sources, intake, processing, bioavailability, protective role and analysis. Mol Nutr Food Res, 2009, 53, S330-S375.
2. Marco ML, Heeney D, Binda S, et al. Health benefits of fermented foods: microbiota and beyond. Curr Opin Biotechnol, 2017, 44, 94-102.2.

Poster ID 2B017

From plant extract to wound repair: green silver nanoparticles against MDR-ESKAPE pathogens

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The escalating burden of multidrug-resistant (MDR) ESKAPE pathogens in wound infections underscores the urgent need for therapeutic strategies capable of overcoming

biofilm-mediated persistence while simultaneously promoting tissue repair. In this study, silver nanoparticles (AgNPs) were green-synthesized using Clerodendrum serratum leaf extract and further modified by polyethylene glycol to obtain PEG-AgNPs, and their antibacterial, anti-biofilm, and wound healing potential was systematically investigated. Physicochemical characterization confirmed the formation of stable, crystalline nanoparticles, with PEGylation enhancing surface functionality and colloidal stability. Antibacterial evaluation against MDR ESKAPE pathogens demonstrated markedly improved efficacy of PEG-AgNPs, exhibiting minimum inhibitory concentration (MIC) values for uncoated AgNPs. Time-kill kinetic studies revealed rapid bactericidal activity, while mechanistic investigations indicated disruption of bacterial membrane integrity leading to cytoplasmic leakage as a key mode of action. Both nanoformulations significantly inhibited biofilm formation, with pronounced effects against the Acinetobacter baumannii and Pseudomonas aeruginosa, major contributors to chronic and non-healing wound infections. LC-MS analysis of C. serratum leaf extract identified pectolinarigenin and luteolin as major bioactive phytoconstituents, and molecular docking studies supported their potential involvement in targeting biofilm-associated regulatory proteins, suggesting a synergistic role alongside silver-mediated antibacterial effects. Furthermore, topical gel formulations incorporating the nanoparticles significantly accelerated wound closure in both uninfected and MDR pathogen-infected wound models. This study highlights phytogenic silver nanoformulations as multifunctional nanotherapeutic systems with strong potential for managing MDR biofilm-associated wound infections while promoting effective tissue regeneration.

References:

1. R. R. Patel, P. A. Pandey, V. Sagar, A. Mishra, S. K. Singh, S. Singh, B. Mishra, M. Singh. A novel nanotherapeutic approach: Dual action of green-synthesized silver nanoparticles from Clerodendrum serratum against MDR-ESKAPE pathogens with wound healing potential. Journal of Drug Delivery Science and Technology, 2025, 108, 106907.
2. V. Sagar, R. R. Patel, S. K. Singh, D. Dehari, G. Nath, M. Singh. Facile green synthesis of silver nanoparticles derived from the medicinal plant Clerodendrum serratum and its biological activity against Mycobacterium species. Heliyon, 2024, 10, e31116.

Poster ID 2B018

Gut Microbiome–Brain Mechanisms in Depression: Mechanistic Pathways from Full-Text Evidence

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Introduction

Depression is a complex neuropsychiatric disorder characterized by dysregulation across immune, metabolic, and neuroendocrine systems that influence cognition, affect, and behaviour. Emerging evidence highlights the gut microbiome–brain axis as a critical interface linking peripheral microbial alterations with central nervous system function. However, mechanistic evidence remains fragmented across individual studies.

Methods:

A PRISMA-guided full-text evidence synthesis was conducted. Original research articles were systematically screened from PubMed, DOAJ, and other open-access sources. Following eligibility assessment, 205 full-text studies published between 2015 and 2024 were included, excluding reviews, case reports, and non-original articles. Full texts were mined to extract gut microbial taxa, mechanistic pathways, including immune-inflammatory signaling, short-chain fatty acid metabolism, neurotransmitter modulation, hypothalamic pituitary adrenal axis activity, and gut barrier integrity and reported directional microbial changes.

Results:

Consistent alterations were observed in microbial genera, including Bifidobacterium, Lactobacillus, Faecalibacterium, Akkermansia, and Bacteroides. Immune inflammatory and metabolic pathways were most frequently implicated, followed by neurotransmitter related and hypothalamic pituitary adrenal (HPA) axis mechanisms. Mechanistic convergence across taxa was more prominent in studies published after 2020.

Discussion:

This synthesis demonstrates that depression-associated gut dysbiosis converges on biological pathways central to brain–behaviour relationships, cognition, and affect regulation. The findings support a translational framework linking microbiome alterations to neuropsychological mechanisms, with implications for biomarker development and adjunctive therapeutic strategies. Limitations include heterogeneity in study designs and outcome measures.

References:

1. Cheung, S. G., Goldenthal, A. R., Uhlemann, A. C., Mann, J. J., Miller, J. M., & Sublette, M. E. (2019). Systematic review of gut microbiota and major depression. Frontiers in psychiatry, 10, 34.
2. Cryan, J. F., O'Riordan, K. J., Cowan, C. S., Sandhu, K. V., Bastiaanssen, T. F., Boehme, M.,... & Dinan, T. G. (2019). The microbiota-gut-brain axis. Physiological reviews, 99(4), 1877-2013.
3. Foster, J. A., & Neufeld, K. A. M. (2013). Gut–brain axis: how the microbiome influences anxiety and depression. Trends in neurosciences, 36(5), 305-312.

Poster ID 2B019

Development of a disposable electrochemical DNA biosensor for simultaneous detection of Neisseria gonorrhoeae, Mycoplasma genitalium and Chlamydia trachomatis

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Keywords: Neisseria gonorrhoeae, Mycoplasma genitalium, Chlamydia trachomatis, Electrochemical DNA sensor, Point-of-care testing (PoCT), mgpC, fitA, hctA

Neisseria gonorrhoeae (NG), Mycoplasma genitalium (MG), and Chlamydia trachomatis (CT) are major sexually transmitted infections (STIs) with overlapping clinical symptoms and increasing antibiotic resistance, emphasizing the urgent need for a rapid, affordable, and highly specific platform for their simultaneous detection. In this study, we developed a portable electrochemical DNA biosensor functionalized with amine-labeled ssDNA probes for simultaneous detection of three bacterial STI pathogens. The AuNPs@GQDs-based electrode targets the fitA gene of NG, the MXene@PPy-based electrode targets the mgpC gene of MG, and the Fe_3O_4-based electrode targets the hctA gene of CT, enabling selective and sensitive multiplex detection. The synthesized nanocomposites were thoroughly characterized using UV–Vis spectroscopy, FTIR, fluorometry, particle size analysis, zeta potential measurements, and transmission electron microscopy (TEM), confirming their successful synthesis and probe functionalization. Uniform deposition of the nanocomposites and immobilization of ssDNA probes onto the screen-printed paper electrode (SPPE) surface were further verified by scanning electron microscopy (SEM), energy-dispersive X-ray spectroscopy (EDX), and FTIR analysis. Electrochemical characterization using cyclic voltammetry (CV), differential pulse voltammetry (DPV), and electrochemical impedance spectroscopy (EIS) demonstrated excellent sensor performance. The MG reverse complementary DNA sensor exhibited a sensitivity of 4,199.8 μA/mm^2/ng with a detection limit of 11 pg/μL. The FitA based NG DNA sensor achieved a sensitivity of 16,333.9 μA/mm^2/ng and an ultralow detection limit of 0.73 fg/μL. Meanwhile, the CT-targeted DNA sensor demonstrated enhanced sensitivity and achieving the LOD of picogram range. The biosensor displayed outstanding selectivity and specificity, successfully discriminating target DNA sequences from non-target bacterial DNA and mismatched oligonucleotides. Clinical validation using cervical swab samples confirmed the sensor's diagnostic robustness and reproducibility for simultaneous detection of NG, MG, and CT. Overall, the developed biosensing platform offers a rapid, portable, and highly sensitive diagnostic solution for multiplex STI detection, exhibiting excellent stability, reproducibility, and strong potential for next-generation point-of-care diagnostics.

Poster ID 2B020

Phylogenetic Landscape of Escherichia coli in Healthy Neonates and Mothers: Trends and Hidden Threats in Early Gut Colonization

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The phylogenetic diversity of Escherichia coli across commensal (A, B1) and pathogenic (B2, D, F) lineages, coupled with its genomic plasticity, facilitates rapid acquisition of antimicrobial resistance genes (ARGs), posing a global One Health challenge. E. coli is also an early-life colonizer of the human gut microbiome, often acquired within hours of birth. Although maternal transmission is presumed to seed initial colonization, it remains unclear

whether commensals persist or if pathogenic lineages outcompete them; their distribution in healthy infants remains poorly understood. This study characterized the E. coli phylogenetic landscape and antibacterial susceptibility patterns in healthy mother–infant pairs to uncover early colonization trends. Stool specimens from healthy mother–infant pairs admitted to a hospital were processed using the VITEK® 2 Compact system for identification and susceptibility testing. Phylogroup allocation for all E. coli isolates was performed using the revised Clermont quadruplex PCR method. Among 62 E. coli isolates, 38 were from mothers and 24 from infants. In mothers, phylogroup A predominated (42.1%), followed by B1, B2 and D (each 15.7%); in infants, A (37.5%) was most frequent, followed by D (29.1%), B2 (16.6%) and C (8.3%). Across maternal and infant isolates, resistance clustered in B2, D and F, with elevated nonsusceptibility to β-lactams; multidrug resistance was restricted to these high-risk phylogroups. Notably, commensal A also showed moderate to high nonsusceptibility in both cohorts. The
non-overlapping maternal–infant phylogroup distributions and detection of pathogenic lineages in healthy infants suggest ecologically driven acquisition and "silent" transmission of high-risk resistant strains.

Keywords: Antimicrobial resistance, gut microbiome, maternal-infant health, E. coli phylogroups, virulence associated selection

References:

1. Bhattacharjee A, Sands K, Mitra S, Basu R, Saha B, Clermont O, Dutta S, Basu S. A Decade-Long Evaluation of Neonatal Septicaemic Escherichia coli: Clonal Lineages, Genomes, and New Delhi Metallo-Beta-Lactamase Variants. Microbiol Spectr. 2023 Aug 17;11(4):e0521522. doi: 10.1128/spectrum.05215-22. Epub 2023 Jun 27. PMID: 37367488; PMCID: PMC10434172.
2. Clermont O, Bonacorsi S, Bingen E. Rapid and simple determination of the Escherichia coli phylogenetic group. Appl Environ Microbiol. 2000 Oct;66(10):4555-8. doi: 10.1128/AEM.66.10.4555-4558.2000. PMID: 11010916; PMCID: PMC92342.

Poster ID 2B021

Tuberculous Meningitis in Central India: A Prospective Analysis of CSF Profiles and Diagnostic Challenges

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Background

Delayed diagnosis of TBM, driven by paucibacillary cerebrospinal fluid, worsens outcomes. Central India, with its high adult TB burden, often presents with lymphocytic pleocytosis and basal meningeal enhancement. This prospective study from AIIMS Bhopal aimed to characterize CSF and clinical profiles to improve early detection in endemic regions.

Methods

We conducted a prospective observational study of 57 patients with suspected TBM between January–May 2025. CSF samples were analyzed for cytology, Biochemistry, molecular testing and liquid culture.

Result

A total of 57 participants were recruited for our study. MTB was detected by GeneXpert in 23% cases, all with low bacillary load; rifampicin resistance was identified in one case. Clinically, fever was present in 80% of patients and headache in 60%. Cranial nerve palsies occurred in 88%. CSF analysis showed lymphocytic pleocytosis in 30% of cases, with 56–97% lymphomononuclear cells.

Neuroimaging revealed abnormalities in approximately 80% of patients, predominantly suggestive of tuberculous CNS involvement. Co-infections included HIV in four patients and bacterial infections in 12 patients. The overall case fatality rate was 12%.

Conclusion

TBM in the Central Indian cohort demonstrated heterogeneous clinical presentation, low microbiological yield, and frequent radiological abnormalities.High rates of cranial nerve involvement and co-infections underscore the need for integrated microbiological, radiological, and clinical approaches to reduce mortality.

References

1. Oo N, Agrawal DK. Epidemiology, Pathogenesis, Clinical Manifestations, and Management Strategies of Tuberculous Meningitis. Arch Intern Med Res. 2025;8(1):48-58.
2. Kaur H, Sharma K, Modi M, et al. Prospective Analysis of 55 Cases of Tuberculosis Meningitis in North India. J Clin Diagn Res. 2015;9(1):DC15-9

Poster ID 2B022

Source-Specific $PM_{2.5}$ Disrupts Pulmonary Lipid Metabolism and Membrane Integrity in Wistar Rats

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Particulate matter ($PM_{2.5}$) is a complex environmental pollutant linked with multiple respiratory and metabolic diseases. Although, the exact mechanism of toxicity is still unknown and commonly linked with oxidative stress and inflammation. The present study investigated the mechanistic impact of $PM_{2.5}$ on lipid metabolism and membrane integrity in the lungs of female Wistar rats.

$PM_{2.5}$ samples were collected from ambient air of three locations in Lucknow, Uttar Pradesh representing a residential area (L1), industrial area (L2), commercial area (L3) to account for compositional heterogeneity. $PM_{2.5}$ were collected using an ARA-N-FRM Sampler on quartz filters at a flow rate of 16.7 l/min and subsequently extracted with methanol. Wistar rats were divided into 6 different groups Normal Control, Low Dose, Mid Dose, High Dose L1, High Dose L2 and High Dose L3 and were orally exposed to $PM_{2.5}$.

Biochemical analyses revealed significant, dose-dependent alterations in total lipids, cholesterol, phospholipids, and glycolipids, indicating disruption of lipid homeostasis and membrane integrity. Changes in phospholipid and glycolipid fractions suggest perturbations in membrane fluidity, while altered cholesterol levels further imply compromised membrane rigidity and signalling microdomain stability.

Histopathological evaluation demonstrated structural disorganization and inflammatory changes in the lung tissue. Ultrastructural analysis under SEM showed alveolar wall contractions in PM 2.5 exposed group. Notably, differential effects observed among $PM_{2.5}$ samples from the three locations underscore the role of source-specific physicochemical composition in modulating lipid metabolic pathways and cellular membrane architecture.

Overall, this study provides mechanistic evidence that sub-chronic $PM_{2.5}$ exposure disrupts pulmonary lipid metabolic and compromises membrane structural integrity, thereby contributing to adverse respiratory toxicity.

Poster ID 2B023

Evaluation of marine bacterial metabolites to combat pathogenic biofilms in static and flow systems

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Biofilm based infections are challenging to treat as they pose to be a niche for emergence and dissemination of antimicrobial resistance (1). 80% of the infections are chronic and persistent as they are associated to biofilms (2). Due to the tough extracellular matrix formed by the cells in the biofilm it is difficult for the antimicrobial agents to penetrate and effectively kill the cells (3). It is need of the hour to explore novel agents which have the potential to inhibit the formation of biofilms or disperse the cells of the biofilm.

The current study focuses on exploring the western coastal bacterial metabolites for their ability to combat biofilms. It involves isolation of marine bacteria, screening for anti-quorum sensing agents, optimizing the yield of the agent using response surface methodology and its effective extraction using ethyl acetate and chloroform methanol. The producers and the anti-biofilm agents were characterized. A concentration of 500 mcg/mL of the metabolite resulted in a 92% and 95% reduction in biofilm formation of Pseudomonas aeruginosa MTCC 2453 and Staphylococcus aureus MTCC 3160 respectively, while 1000 mcg/mL led to a 37% and 43% breakdown of preformed biofilms of Pseudomonas aeruginosa MTCC 2453 and Staphylococcus aureus MTCC 3160 respectively.

The metabolite is found to be effective in reducing the viability of the cells, exopolysaccharide content and extracellular DNA content which affects the overall architecture and stability of the biofilms making it a suitable agent to inhibit biofilm formation in static and flow systems.

This study is supported by DBT- BUILDER grant, Govt. of India (BT/INF/22/SP45358/2022).

References:

1. Liu HY, Prentice EL, Webber MA. Mechanisms of antimicrobial resistance in biofilms. Npj Antimicrob Resist. 2024 Oct 1;2(1):27.
2. Grari O, Ezrari S, El Yandouzi I, Benaissa E, Ben Lahlou Y, Lahmer M, et al. A comprehensive review on biofilm-associated infections: Mechanisms, diagnostic challenges, and innovative therapeutic strategies. The Microbe. 2025 Sept 1;8:100436.

3. Harika K, Shenoy VP, Narasimhaswamy N, Chawla K. Detection of Biofilm Production and Its Impact on Antibiotic Resistance Profile of Bacterial Isolates from Chronic Wound Infections. J Glob Infect Dis. 2020 Aug 29;12(3):129–34.

Poster ID 2B024

Air Pollution Exposure and Public Health Risks in Urban Environments: A Systematic Review and Meta-analysis

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Keywords: Air pollution, Urban health, Particulate matter, Environmental exposure, Public health risk, Meta-analysis.

Rapid urbanization and industrial growth have intensified air pollution levels in many cities worldwide, raising concerns regarding their implications for population health. Urban air contains a complex mixture of pollutants, including particulate matter ($PM_{2.5}$ and PM_{10}), nitrogen oxides (NO_x), sulfur dioxide (SO_2), ozone (O_3), and volatile organic compounds, which are associated with a wide spectrum of adverse health outcomes. The present study synthesizes existing empirical evidence to quantify the relationship between urban air pollution exposure and major public health risks. A systematic literature search was conducted in major scientific databases including PubMed, Scopus, and Web of Science to identify peer-reviewed studies reporting associations between ambient air pollution and health outcomes in urban populations. Eligible studies included epidemiological investigations that provided quantitative estimates of health effects related to specific pollutants. Data extracted from selected studies were statistically integrated using meta-analytic techniques to determine pooled effect sizes and evaluate the consistency of reported associations across different geographic regions and study designs. Measures of heterogeneity and publication bias were also assessed to ensure robustness of the findings. The synthesized results indicate a significant association between elevated concentrations of fine particulate matter and increased risks of respiratory and cardiovascular morbidity and mortality. Long-term exposure to $PM_{2.5}$ and nitrogen oxides shows particularly strong correlations with chronic respiratory diseases, ischemic heart conditions, and premature mortality. Short-term exposure episodes were also linked with acute respiratory symptoms, hospital admissions, and exacerbation of asthma and chronic obstructive pulmonary disease. Variations in effect estimates were observed across regions, reflecting differences in pollution sources, demographic characteristics, and urban environmental conditions. These findings provide consolidated evidence that air pollution remains a major environmental determinant of public health in urban settings. Strengthening emission control policies, promoting cleaner energy transitions, and integrating environmental monitoring with public health planning are critical for mitigating pollution-related health burdens and supporting sustainable urban development.

Poster ID 2B025

Antibacterial activity of Cetylpyridinium Chloride functionalized hydroxyapatite nanoparticles incorporated polystyrene fiber mats against *Staphylococcus aureus*.

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Bacterial adhesion and subsequent biofilm formation onto the material surfaces remain a major challenge in maintaining hygienic surfaces in biomedical and sanitation-related applications. Biofilm formation by bacteria such as Staphylococcus aureus complicates antimicrobial activities and control strategies, as biofilms produce an extracellular polymeric substance (EPS) matrix, which acts as a protective shield, reducing antimicrobial efficacy. Consequently, biofilm-associated cells exhibit enhanced resistance, thereby promoting the persistence of antibiotic-resistant bacteria such as methicillin-resistant Staphylococcus aureus (MRSA). To address these challenges, new and alternative antimicrobial strategies are being explored. Nanomaterial-based antimicrobial agents are gaining increasing attention due to their large surface area, enhanced interaction with bacterial membranes, and ability to be functionalized with antimicrobial agents.

In this study, Hydroxyapatite (HAp) nanoparticles (NPs) were synthesized by a modified sol-gel method and

characterized using XRD, SEM, and HR-TEM. The NPs were subsequently functionalized with cetylpyridinium chloride (CPC) and confirmed via zeta potential studies. Polystyrene nanofibers were fabricated by electrospinning technique and the obtained fiber mats were
incorporated with CPC functionalized HAp NPs to investigate their antibacterial activity against S. aureus. Antimicrobial effects were evaluated using turbidity reduction, zone of inhibition, and biofilm inhibition assays, along with Scanning Electron Microscopy (SEM) to examine bacterial adhesion on the nanofibrous surfaces. The minimum inhibitory concentration (MIC) for CPC- HAp NPs was determined. SEM analysis revealed dense biofilm formation on the untreated polystyrene nanofibers, while CPC-HAp incorporated nanofibers inhibited S. aureus growth.

References:

1. Amariei, G., Kokol, V., Boltes, K., Letón, P., & Rosal, R. (2018). Incorporation of antimicrobial peptides on electrospun nanofibres for biomedical applications. RSC Advances, 8(49), 28013–28023. https://doi.org/10.1039/c8ra03861a
2. Kadu, K., Kowshik, M., & Ramanan, S. R. (2023). Tailoring of hydroxyapatite nanoparticle surfaces of varying morphologies to facilitate counterion diffusion and subsequent protein denaturation. Biophysical Chemistry, 296, 106979. https://doi.org/10.1016/j.bpc.2023.106979
3. Munir, M. U., Salman, S., Ihsan, A., & Elsaman, T. (2022). Synthesis, Characterization, Functionalization and Bio-Applications of Hydroxyapatite Nanomaterials: An Overview. In International Journal of Nanomedicine (Vol. 17, pp. 1903–1925). Dove Medical Press Ltd. https://doi.org/10.2147/IJN.S360670

Poster ID 2B026

On-demand sweat stimulation and visual quantification of chloride via a wearable integrated paperfluidic sensor for resource-limited cystic fibrosis screening

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Keywords: Wearable sensor, Paper-fluidic device, Sweat stimulation and collection, Colorimetric analysis

The quantification of chloride ion concentration in sweat is recognized as the gold standard for the early diagnosis of cystic fibrosis, underscoring the diagnostic significance and clinical relevance of sweat as a biofluid.[1] Sweat-based diagnostics offer a non-invasive, clinically valuable approach to continuous health monitoring, enabling real-time analysis of physiological and biochemical markers directly from the skin without complex or uncomfortable sampling.[2] In this study, we present a wearable paper-based sensor that enables colorimetric detection of chloride ions (Cl^-) in sweat for cystic fibrosis (CF) screening. Unlike conventional wearable CF sensors that require complex fabrication and sophisticated instrumentation, our low-cost, disposable device integrates a hydrophobically patterned paper substrate with an overlaid paper-fluidic channel impregnated with a chloride-sensitive reagent for direct, and visual quantification of Cl^- levels. To facilitate efficient and consistent sweat collection, we developed an iontophoresis system that delivers a controlled electrical current to stimulate localized sweat secretion, with an Arduino-based module integrated for real-time monitoring of output current and elapsed time. The device was validated using artificial sweat samples for chloride quantification and further tested on human volunteers to demonstrate its effectiveness in stimulating sweat production. The sensor exhibited a clinically relevant detection range, with a strong correlation between color intensity and chloride concentration, confirming its accuracy and reliability for CF diagnostics. By combining low-cost fabrication, on-demand sweat stimulation, and colorimetric analysis, this instrument-free, user-friendly wearable platform presents a promising alternative to traditional sweat testing methods, particularly for point-of-care diagnostics in resource-constrained healthcare settings.

References:

1. P. M. Farrell, T. B. White, C. L. Ren, S. E. Hempstead, F. Accurso, N. Derichs, M. Howenstine, S. A. McColley, M. Rock, M. Rosenfeld, I. Sermet-Gaudelus, K. W. Southern,
2. B. C. Marshall, P. R. Sosnay, The Journal of Pediatrics, 2017, 181, S4–S15.e1.
3. T. Saha, R. Del Caño, E. De la Paz, S. S. Sandhu, J. Wang, Small, 2023, 19, 2206064

Poster ID 2B027

Chemoproteomics in Live Bacteria Identifies Covalent Interactome of EGCG Underlying Its Multimodal Antibacterial Mechanism

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Epigallocatechin-3-gallate (EGCG), the most bioactive catechin of green tea, exhibits remarkable antibacterial activity against a wide range of bacteria, including multidrug-resistant strains. However, its precise molecular targets and mechanisms of action remain poorly understood. Herein, we have designed YnEGCG, a clickable and cell-permeable activity-based probe of EGCG, to comprehensively investigate its molecular targets through in situ chemoproteomics. YnEGCG enabled the fluorescence visualization and mass-spectrometric identification of covalently interacting proteins from live E. coli. Quantitative proteomics identified over 600 proteins, with approximately 10% exhibiting remarkably high enrichment (H:L > 50). These included critical bacterial enzymes such as DNA gyrase, DNA polymerase, ATP synthase, ribosomal proteins, etc., and several
previously unidentified targets. Further, we experimentally validated that EGCG inhibits DNA gyrase activity as well as de novo protein synthesis. Taken together, our in situ chemoproteomics studies revealed that EGCG binds to critical bacterial enzymes, uncovering previously unknown antibacterial targets and providing insights into its broad-spectrum action.

Keywords: Epigallocatechin-3-gallate (EGCG); YnEGCG; chemoproteomics; Click reaction; antibacterial activity; mode of action; de novo protein synthesis; DNA gyrase.

Poster ID 2B028

Utility of GenoType® Mycobacterium AS Panel for detection of additional non-tuberculous mycobacterial species in a TB-endemic setting.

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Keywords: Non-tuberculous mycobacteria, Mycobacterium simiae, Line Probe Assay

Background:
In TB-endemic regions, non-tuberculous mycobacteria are clinically significant organisms. The clinical and radiological features of these organisms overlap with those of tuberculosis. The Additional Species (AS) panel of the GenoType® Mycobacterium CM/AS Line Probe Assay allows expanded identification beyond commonly detected NTM species.
Aim: To evaluate the utility of the GenoType® Mycobacterium AS Panel for the detection and identification of additional non-tuberculous mycobacterial (NTM) species in clinical specimens from a high TB-endemic setting

Methods:
A total of 624 clinical samples were inoculated for NTM culture at a tertiary care centre in Central India. Culture-positive isolates suspected as NTM were subjected to molecular identification using the GenoType® Mycobacterium CM assay, followed by further characterisation with the GenoType® Mycobacterium AS panel for detection of additional NTM species.

Results:
Out of 624 cultures inoculated for NTM, 19 isolates (19/624, 3.0%) were identified as non-tuberculous mycobacteria. Application of the AS panel enabled the detection of additional NTM species not resolved by the CM assay alone. Among the 19 NTM isolates, Mycobacterium simiae was identified in 3 isolates (3/19, 15.8%) by the GenoType Mycobacterium AS Panel.

Conclusion:
The GenoType Mycobacterium AS panel detected additional NTM species, including Mycobacterium simiae, in isolates from a TB-endemic setting. The use of these molecular assays for routine diagnostics can improve additional species identification, support treatment decisions, and assist regional NTM surveillance.

Poster ID 2B029

Title: Breaking the Amyloid Fortress: Phytochemical Disruption of Functional Amyloids Strengthening Staphylococcal Biofilms

Staphylococcus aureus is one of the leading causes of implant-associated infections, forming persistent, antibiotic-resistant biofilms on medical devices due to adhesion proteins and a self-produced matrix. Antimicrobial resistance triggered by staphylococcal biofilms is an

escalating global health crisis. Biofilm development is linked to obstinate recurrent infections, including hospital acquired infections, infections of indwelling medical devices, wounds, the urinary tract etc. Functional amyloids formed by aggregation prone proteins/peptides govern the virulence and biofilms of Staphylococcus aureus. These aggregates reinforce the staphylococcal biofilms by developing an extracellular fibrillar amyloid scaffold. Our study puts forward novel insights on the amyloid modulatory and anti-biofilm potential of some phytochemicals and bioactive flavonoids from Murraya koenigii (MK-LE) and Psoralea corylifolia (Isobavachalcone, IBC). The screened phytochemicals have shown a promising fibril remodelling effect against the virulent peptides, phenol soluble modulins (PSMs). Comprehensive analysis using thioflavin T kinetics, high-end microscopy, dynamic light scattering and circular dichroism studies has validated the amyloid modulatory potency of these phytochemicals. Collectively, our data proposes a novel activity of IBC and MK-LE that specifically targets the staphylococcal functional amyloids derived from the PSMα family. The phytochemicals used in the present study can inhibit the fibrillation of biofilm strengthening amyloids and can also disaggregate the pre-formed fibrillar species which provide architecture to the staphylococcal biofilms.

Our study underscores that these phytochemicals can be used as a scaffold for the rational discovery of potent anti-biofilm agents which can further help in combating the antibiotic-resistant, healthcare associated infections.

Poster ID 2B030

Lipidsight Cyan and Lipidsight Lime – Single Benzene Push-Pull Fluorophores for Lipid Droplet Imaging in Live Cells

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Lipid droplets (LDs) are dynamic organelles that play central roles in lipid metabolism, cellular stress response, and metabolic diseases.[1] Reliable fluorescent probes for selective LD visualization remain essential for studying these processes in live cells, since many existing probes suffer from extensive background staining, limited photostability under laser irradiation and small Stokes shifts or low compatibility with multiplexed imaging experiments.[2] In this study, we report the chemical preparation and biological validation of one cyan emissive and another green-yellow emissive lipophilic fluorescent dye created out of a single benzene unit. These molecules were found to selectively localize to lipid droplets in live HeLa cells. Confocal laser scanning microscopic imaging experiments revealed bright punctate cytoplasmic staining patterns that were characteristic of LD localization. We established the intracellular targets of these dyes through colocalization experiments with the established lipid droplet marker Nile Red,3 where we found strong spatial overlap with the positive control. Both dyes provided high-contrast lipid droplet staining with minimal cytoplasmic background and could be efficiently excited using the widely available 405 nm laser line, facilitating straightforward integration into standard confocal imaging workflows. To further evaluate their utility in biological assays, Lipidsight Cyan was tested in a live–dead dual staining experiment in 5-fluorouracil treated lung cancer cells together with propidium iodide (PI). Dual-color imaging produced clearly segregated fluorescence signals corresponding to lipid droplet staining in viable cells and nuclear PI staining in dead cells, demonstrating compatibility of Lipidsight Cyan with viability assays. Based on their imaging performance, reliable synthesis and reproducible nature of the results, we have set out to commercialize these two derivatives as practical LD probes for bioimaging workflows. The probes are available for procurement through our startup venture Fluoresight Bioprobes Private Limited.

References:

1. Tobias C. Walther, Robert V. Farese Jr, Annual Review of Biochemistry. 2012, 81, 687–714.
2. Yanyan Zhao, Wen Shi, Xiaohua Li, Huimin Ma, Chemical Communications, 2022, 58, 1495-1509.
3. P Greenspan, E P Mayer, S D Fowler, Journal of Cell Biology. 1985, 100, 965–973.

Poster ID 2B031

Smart Fluorophores for Monitoring Health Hazards: Indolizine for Selective and Sensitive Sensing of Hydrazine and Cyanide ions

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Chemodosimeters are molecular probes that utilize specific, irreversible chemical reactions to achieve distinct changes in fluorescence signaling. These platforms are critical for health and environmental monitoring as they provide the high selectivity and sensitivity required for the trace-level detection of systemic toxins, offering a robust alternative to complex analytical instrumentation. Hydrazine (N_2H_4) is widely used as an intermediate in various industrial sectors, including chemical manufacturing, cosmetics, pharmaceuticals, and textiles. Besides its utility, hydrazine poses significant health risks such as systemic and organ toxicity, carcinogenicity, and environmental risks due to its toxic, corrosive nature. On the other hand, cyanide is a potent and rapidly acting chemical asphyxiant that interferes with the body's ability to utilize oxygen, and is significantly more lethal and fast-acting than other industrial toxins. Health hazards caused by exposure to traces of cyanide include CNS damage, cardiovascular toxicity, and cytotoxic hypoxia. In the current study, we developed a novel ratiometric fluorescent probe featuring an indolizine ring and a cleavable sensing moiety. The probe showed an increase in blue emission at 443 nm, accompanied by a concurrent reduction in NIR emission at 560 nm, upon exposure to hydrazine. The system achieved an ultra-low detection limit and showed exceptional selectivity over common interfering ions. The rapid response time and color change allow detection of hydrazine at trace levels without sophisticated instrumentation. Furthermore, the sensing platform was successfully transitioned to solid-state detection using paper-strip assays and validated for real-sample analysis across diverse water sources. The sensing studies were further carried out in the cubosomal environment. This detection system can be further utilized for a portable sensing kit.

References:

1. Amanda Ana Pinheiro, Ankit Thakuri, Soumik Saha, Mainak Banerjee, Amrita Chatterjee, Analyst, 2025, 150, 3208-3216
2. Akhil A Bhosle, Mainak Banerjee, Soumik Saha, Shubham Garg, Surajit Ghosh, Amrita Chatterjee, Sensors and Actuators B: Chemical, 2023, 397, 134661
3. Soumik Saha, Shravya B, Shaurya Aneja, Amrita Chatterjee, Mainak Banerjee, Chemistry–An Asian Journal, 2025, 20, e202500113

Poster ID 2B032

Targeted Silencing of Notch1 via siRNA Using Hydroxyapatite Nanoparticle-Delivered for Cancer Cells

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One of the major contributors to Cancer treatment failure is the presence of cancer stem cells (CSCs), which possess self-renewal capacity, high proliferative potential, and the ability to drive tumor progression. The Notch signaling pathway, often dysregulated in CSCs, is associated with epithelial–mesenchymal transition (EMT) and stemness. RNA interference using small interfering RNA (siRNA) offers a targeted strategy to silence oncogenic pathways; however, efficient delivery and stability remain key challenges. Hydroxyapatite nanoparticles (HAp-NPs), due to their biocompatibility, have emerged as promising non-viral carriers for gene delivery. In this study, modified HAp-NPs were evaluated as delivery vehicles for Notch1-targeting siRNA in cancer cells. The Nanoparticle-siRNA complexes were characterized through XRD, FTIR,binding assays, and uptake studies after which the nanoparticle siRNA complex was transfected to cancer cells. FTIR and XRD results confirmed presence of characteristic Hydroxyapatite and uptake of modified HAp nanoparticles by cancer cells, with optimal uptake observed at 12 hr and 24 hr. After treatment of cancer cells with notch siRNA, the gene expression analysis revealed similar reduction for modified HAp as compared with commercially used transfection agent JetPrime. These findings highlight the potential of HAp-NP-mediated RNA interference as a promising strategy for targeted gene silencing and provide insights into the role of Notch signaling in cancer and cancer stem cells.

Poster ID 2B033

Bacteriophage φ11 encoding endolysin: A targeted approach to combat Staphylococcus aureus

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Keywords: Bacteriophage, Endolysin, Antimicrobial resistance (AMR), Staphylococcus aureus, Methicillin-resistant Staphylococcus aureus (MRSA)

The rise of antimicrobial resistance (AMR), particularly methicillin-resistant Staphylococcus aureus (MRSA) and vancomycin-resistant Staphylococcus aureus (VRSA), poses a significant challenge in the management of hospital-acquired infection. Bacteriophage lytic proteins such as endolysin, are peptidoglycan hydrolases produced at the end of the bacteriophage replication cycle to lyse the host cell. Endolysins derived from Gram-positive phages frequently possess multi-modular architectures, integrating diverse catalytic domains with specific cell wall-

binding domains. Here, we cloned the Gp_53 gene which encoded putative endolysin from Phi11 Staphylococcus phage genome. The recombinant Gp_53 expressed in BL-21 by a pET-based system. The recombinant Gp_53 purified by affinity chromatography, followed by dialysis. Turbidity reduction assays quantitatively demonstrated a time-dependent decrease in optical density, indicative of rapid bacteriolysis. Zymography validated enzymatic functionality, showing distinct lytic bands corresponding to peptidoglycan degradation. Scanning electron microscopy (SEM) provided ultrastructural confirmation, revealing extensive cell wall damage, membrane disruption, and leakage of intracellular contents following treatment. The convergence of these results confirms the potent bactericidal activity of the endolysin against S. aureus. Given their specificity, rapid killing kinetics, and low likelihood of resistance development, endolysins hold significant therapeutic potential as protein-based antimicrobials. These findings highlight their applicability as promising alternatives to conventional antibiotics for the treatment of MRSA infections.

References:

1. Kumar M, Sarma DK, Shubham S, Kumawat M, Verma V, Nina PB, Devraj JP, Kumar S, Singh B and Tiwari RR (2021) Futuristic Non-antibiotic Therapies to Combat Antibiotic Resistance: A Review. Front. Microbiol. 12:609459. doi: 10.3389/fmicb.2021.609459
2. Michael J Love, Renwick C J Dobson, Craig Billington; Stemming the tide of antibiotic resistance by exploiting bacteriophages. Biochem (Lond) 11 December 2020; 42 (6): 6–11. doi: https://doi.org/10.1042/BIO20200074

Poster ID 2B034

A REACTION BASED AMINO-SUBSTITUTED SINGLE BENZENE-BASED FLUOROPHORE FOR SELECTIVE BIOTHIOL SENSING VIA FLUOROSCENCE

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Biological thiols (Cys, Hcy, GSH) are crucial for maintaining redox homeostasis, detoxification, and signaling, and their dysregulation is associated with cardiovascular disease, neurodegeneration, and cancer, making accurate monitoring essential [1]. Conventional assays such as chromatography, electrochemistry, and immunoassays provide sensitivity but remain costly, laborious, and unsuitable for real-time studies [2]. Fluorescence-based sensing has emerged as the most effective strategy, offering high sensitivity, rapid response, and compatibility with live-cell imaging [3]. Single-benzene-based fluorophores (SBBFs) overcome these issues through a compact donor–acceptor framework that ensures tunable, stable, and biocompatible emission [3,4]. A novel subclass, amino-substituted SBBFs (ASBBFs), further enhances charge transfer, yielding broad emission ranges, large Stokes shifts, and organelle-specific imaging. Their modularity allows incorporation of thiol-reactive groups, enabling highly selective biothiol detection [1,4]. These advances establish ASBBFs as emerging fluorophores with significant promise for biomedical diagnostics and redox biology [1].

Refrences:

1. J. H. Jin, J. M. An, D. Kim, S. Lee, M. Kim, D. Kim, *Dyes Pigments,* 2024, 221, 111811.
2. P. Saha, P. Moitra, U. Bhattacharjee, S. Bhattacharya, *Adv. Mater. Interfaces,* 2022, 9, 2101874.
3. J. Kim, J. H. Oh, D. Kim, *Org. Biomol. Chem.,* 2021, 19, 933–946.
4. H. Liu, S. Yan, R. Huang, Z. Gao, G. Wang, L. Ding, J. Xie, *Chem.–Eur. J.,* 2019, 25, 16732–16739

Poster ID 2B035

Anti-Coagulant Activity from Kokum (Garcinia indica)

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Kokum (Garcinia indica), a tropical fruit of India and has been part of India's Ayurvedic medicine and traditional cuisine, not just because it enhances flavours but also for of its health benefits. Yet its bioactive components are poorly explored. In this study, we aim to isolate the bioactive

component(s) from aqueous extract of kokum prepared using dried rinds of kokum fruit. The extract was fractionated by size-exclusion HPLC and anticoagulant effects of the fractions were evaluated. One of the fractions (KP8) exhibited significant anti-platelet activity and anticoagulant effects through fibrinolysis. Structural characterisation studies of KP8 were performed using LCMS, NMR, ATR-FTIR. The results provide the functional and structural insights to KP8 and its potential in developing novel natural therapeutics for thrombosis and haemostatic disorders.

References:

1. Lim, S. H., Lee, H. S., Lee, C. H., & Choi, C. I. (2021a). Pharmacological Activity of Garcinia indica (Kokum): An Updated Review. In *Pharmaceuticals* Vol. 14, Number 12. MDPI. https://doi.org/10.3390/ph14121338
2. Hsia, C. W., Huang, W. C., Jayakumar, T., Hsia, C. H., Hou, S. M., Chang, C. C., Yen, T. L., & Sheu, J. R. (2023). Garcinol acts as a novel integrin αIIbβ3 inhibitor in human platelets. Life Sciences, 326. https://doi.org/10.1016/j.lfs.2023.121791
3. Cao, H., Bhuyan, A. A. M., Umbach, A. T., Ma, K., Borst, O., Gawaz, M., Zhang, S., Nürnberg, B., & Lang, F. (2019). Garcinol a novel inhibitor of platelet activation and apoptosis. *Toxins,* 11(7). https://doi.org/10.3390/toxins11070382
4. Bhattacharya, N., Kolvekar, N., Mondal, S., Sarkar, A., & Chakrabarty, D. (2023). Daboialipase, a phospholipase A2 from Vipera russelli russelli venom posesses anti-platelet, anti-thrombin and anti-cancer properties. *Toxicon, 239.* https://doi.org/10.1016/j.toxicon.2024.107632
5. Kolvekar, N., Bhattacharya, N., Mondal, S., Sarkar, A., & Chakrabarty, D. (2024). Daboialipase, a phospholipase A2 from Vipera russelli russelli venom posesses anti-platelet, anti-thrombin and anti-cancer properties. *Toxicon, 239.* https://doi.org/10.1016/j.toxicon.2024.107632

Poster ID 2B036

Lipid-Modified Gold Nanoparticles as a Delivery Platform for Nucleic Acid–Based Vaccines

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Vaccination remains one of the most effective strategies for preventing infectious diseases and improving global health outcomes. In recent years, nucleic acid–based vaccines, including DNA and mRNA vaccines, have gained significant attention due to their ability to induce both humoral and cellular immune responses by enabling host cells to produce target antigens. Nanoparticle-based delivery systems have emerged as promising tools to enhance the stability, cellular internalization, and intracellular trafficking of nucleic acids. Among these, lipid-modified gold nanoparticles (AuNPs) offer advantages such as biocompatibility, tunable surface properties, and improved interaction with cell membranes, making them attractive candidates for vaccine delivery.

In this study, lipid-modified gold nanoparticles (AuNPs) were developed and evaluated as a potential vaccine delivery candidate. The physicochemical properties of the nanoparticles were characterized using zeta potential analysis, dynamic light scattering (DLS), Fourier transform infrared spectroscopy (FTIR), and ICP-OES to determine particle size distribution, surface charge, chemical interactions, and concentration respectively. Binding studies were performed to evaluate the interaction between the lipid-modified AuNPs and nucleic acid cargo. The cellular uptake of the nanoparticle cargo complexes was investigated in macrophages and dendritic cells, which play key roles in antigen presentation and immune activation. To understand the mechanism of internalization,

energy-dependency studies and endocytic inhibitor assays were conducted to identify the uptake pathways involved.

The functional delivery capability of the system was assessed by analyzing mRNA expression levels following transfection. Furthermore, antigen presentation efficiency was evaluated using flow cytometry (FACS) by detecting the SIINFEKL–MHC class I complex, indicating successful antigen processing and presentation. Overall, this study evaluates the physicochemical characteristics, cellular uptake mechanisms, and antigen presentation potential of lipid-modified gold nanoparticles, highlighting their promise as a delivery platform for nucleic acid–based vaccines.

References:

1. Ferrando, R. M., Lay, L., & Polito, L. (2020). Gold nanoparticle-based platforms for vaccine development. Drug Discovery Today: Technologies, 38, 57-67

Poster ID 2B037

Incorporating Bioactive molecules into Biomimetic scaffolds for enhancing chronic wound healing in Type 2 Diabetes Mellitus

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Keywords: Diabetic wound, scaffolds, growth factors, bilayer scaffolds, wound healing

Chronic wounds related to Type 2 Diabetes Mellitus (T2DM) pose a significant clinical challenge. This is due to ongoing microbial colonization, oxidative stress, and poor blood vessel formation. In this study, we created multifunctional biopolymer scaffolds made of nanocellulose (NC) and silk fibroin (SF). We used a meltdown neutralization technique to develop these scaffolds and added silver (Ag) nanoparticles, the antioxidant silymarin (SM), and the growth factors vascular endothelial growth factor (VEGF) and transforming growth factor-β1 (TGF-β1) to improve diabetic wound healing. the scaffolds were assessed for their swelling behavior and the release rates of silver and antioxidant components over a 7-day period, showing a steady release profile. SEM, XRD and FTIR were performed for structural and physicochemical characterization of scaffolds. Antibacterial activity through zone of inhibition and bactericidal assays against Escherichia coli, Staphylococcus aureus, and Pseudomonas aeruginosa. The results confirmed the antimicrobial effectiveness of the silver incorporated scaffold. Growth factors, VEGF and TGF-β1were included in a bilayer scaffold design to support blood vessel growth and tissue repair. Biocompatibility was tested using MTT assays on L929 fibroblast cells for up to 72 hours; the results showed very low toxicity. Moreover, a scratch wound assay indicated increased cell growth and movement when silymarin and growth factors were present. In vivo wound healing studies performed in Rattus norvegicus, with skin samples taken on days 4, 7, and 10 for further analysis. Overall, these bioengineered scaffolds offer a multifunctional solution that combines antimicrobial, antioxidant, and regenerative properties. They show significant promise for treating and managing diabetic wounds.

References:

1. Ma, Guangrui, et al. "A novel multifunctional self-assembled nanocellulose based scaffold for the healing of diabetic wounds." *Carbohydrate Polymers* 361 (2025): 123643.
2. Sharifi, Roya, et al. "The effect of silymarin (Silybum marianum) on human skin fibroblasts in an in vitro wound healing model." *Pharmaceutical Biology* 51.3 (2013): 298-303.
3. Singla, Rubbel, et al. "In vivo diabetic wound healing potential of nanobiocomposites containing bamboo cellulose nanocrystals impregnated with silver nanoparticles." *International journal of biological macromolecules* 105 (2017): 45-55.
4. Shaik, M. Monsoor, and Meenal Kowshik. "Novel melt-down neutralization method for synthesis of chitosan–silver scaffolds for tissue engineering applications." Polymer Bulletin 73.3 (2016): 841-858.

Poster ID 2B038

Mangrove-Derived Phytochemicals as Potential Anticancer Agents: Cytotoxic and Metabolomic Investigations

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Mangroves are a rich source of bioactive phytochemicals having substantial pharmacological potential, especially for cancer treatment. While several mangrove species have been investigated for their therapeutic properties, many members of the Rhizophoraceae family remain relatively unexplored. This study investigates the anticancer activities, antimigratory potential and phytochemical constituents of methanolic leaf extracts from Rhizophora mucronata, Rhizophora apiculata, Bruguiera gymnorhiza, Bruguiera cylindrica, Kandelia candel and Ceriops tagal, representing four genera of the Rhizophoraceae family. Among the species studied, B. cylindrica exhibited the most prominent anticancer activity, with IC_{50} levels of 323.965 ± 1.417 µg/mL, 287.062 ± 1.127 µg/mL and 25.942 ± 2.048 µg/mL against A549, AW 13516, and HeLa cells, respectively. Importantly, no cytotoxicity was observed against HaCaT cells, indicating selective anticancer activity. In addition, the results of the scratch wound healing assay on A549 cells underscored the anti-migratory potential of mangrove-derived extracts. LC-HRMS analysis showed the presence of

107 metabolites. Compounds with well-documented anticancer properties, such as chlorogenic acid, esculetin, phloroglucinol, caffeic acid, rutin, quercetin, naringenin, kaempferol, nobiletin, and luteolin, were detected. Our study lays down a groundwork for B. cylindrica as a promising candidate for exploring mangrove-derived bioactive compounds as potential oncological drugs,

having combined cytotoxic and anti-migratory effects.

References:

1. J.H. Primavera, D.A. Friess, H. Van Lavieren, S.Y. Lee, The mangrove ecosystem. In: Sheppard C, editor. World seas: an environmental evaluation. 2nd ed. London: Elsevier; 2019. p. 1–34.
2. N.L. Dahibhate, A. Saddhe, K. Kumar, Mangrove plants as a source of bioactive compounds: a review, The Natural Products Journal, 2018, 8(2), 86–97.
3. M. Greenwell, P.K. Rahman, Medicinal plants: their use in anticancer treatment, International Journal of Pharmaceutical Sciences and Research, 2015, 6(10), 4103–4112.
4. N.L. Dahibhate, K. Kumar, Metabolite profiling of Bruguiera cylindrica reveals presence of potential bioactive compounds, PeerJ Analytical Chemistry, 2022, 4, e16.
5. G. Indrayanto, G.S. Putra, F. Suhud, Validation of in-vitro bioassay methods: application in herbal drug research, Profiles of Drug Substances, Excipients and Related Methodology, 2021, 46, 273–307.

Poster ID 2B039

Analysis of a Glycolytic Protein of Staphylococcus aureus and Exploring its Role in Pathogenesis

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Antimicrobial resistance in Staphylococcus aureus has been the cause of many deaths worldwide. The opportunistic pathogen which colonizes the skin and nasal passage, uses a plethora of virulence strategies to invade the host system. The accelerating emergence of antibiotic resistance necessitates a shift in focus towards better understanding of its diverse virulence mechanisms and exploring alternative therapeutic approaches. Our research focuses on understanding the role of Phosphoglycerate kinase (PGK))(EC 2.7.2.3), a glycolytic protein of S. aureus in pathogenesis. These proteins while canonically involved in the central metabolism, have additional moonlighting functions like host cell adhesion or immune evasion. Our study is aimed at identifying the localization of PGK and studying its interaction with host plasminogen. Our results demonstrate that the glycolytic protein localizes to the surface and interacts with human plasminogen. The results of this work suggest that PGK might be a putative moonlighting protein having a role in Staphylococcus aureus pathogenesis .

Poster ID 2B040

Disrupting Biofilm-Driven Antimicrobial Resistance: Therapeutic Potential of Murraya koenigii's leaves extract against Staphylococcus aureus and Enterococcus faecalis

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Keywords: Biofilm, Antimicrobial resistance, Murraya koenigii, Staphylococcus aureus, and Enterococcus faecalis.

Biofilm-driven infections represent a major global health concern due to their strong association with antimicrobial resistance (AMR). Staphylococcus aureus and Enterococcus faecalis are gram-positive, hospital-acquired, opportunistic bacteria that are well known for their ability to form biofilms on both biotic and abiotic surfaces. Bacterial colonies within biofilms are protected by a self-produced extracellular polymeric substance (EPS) that promotes survival, enables persistent colonization, and markedly reduces susceptibility to conventional antibiotics, thereby enhancing pathogenicity by facilitating chronic infections, evading the immune response, and enabling horizontal gene transfer, thereby expanding the dissemination of AMR. These attributes make biofilm-forming pathogens very challenging to eradicate in clinical settings.

In this study, we investigated the in vitro and in silico antibiofilm potential of Murraya koenigii's methanolic (MKM) leaf extract and its compounds against S. aureus and E. faecalis. The minimum inhibitory concentrations (MICs) against the bacterial strains were 39 and 48.8 µg/mL for S. aureus and E. faecalis, respectively, which significantly inhibited the biofilm formation, highlighting its potential as a natural antimicrobial alternative. Moreover, flow cytometry and confocal imaging revealed significant membrane damage in MKM-treated cells compared with controls and also

significantly reduced EPS production. The biofilm-disrupted structure can be further visualized by SEM after treating the cells with MKM extract. The bioactive compounds in the extract were identified by HR-LC/MS analysis, and ADME analysis was used to further assess their drug-likeness. The strong binding affinities of the identified compounds against the key biofilm adhesion proteins, SpA in S. aureus and Esp in E. faecalis, were confirmed by in silico molecular

docking and molecular dynamics simulations, suggesting possible interference with the bacterial adhesion and biofilm formation. The purified compound from the extract was also evaluated for biocompatibility with C2C12 cell lines and showed significant cell viability even at higher concentrations.

Overall, the results indicate the therapeutic potential of the MKM extract in inhibiting the growth, biofilm formation, and EPS production of S. aureus and E. faecalis, and the importance of plant-derived bioactive compounds as potential antibiofilm agents to combat AMR-associated infections.

References:

Kashyap, S., Rathod, Y. & Biswas, S. Murraya koenigii methanolic extract inhibits bacterial growth and biofilm of Staphylococcus aureus and Enterococcus faecalis. Sci Rep 15, 34056 (2025). https://doi.org/10.1038/s41598-025-14396-z.

Poster ID 2B041

Scoping Review of Biomarkers for Early Detection & Phenotype-Specific Progression of Knee Osteoarthritis

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Knee osteoarthritis (KOA) is a progressive disorder in which molecular alterations occur before definitive structural changes and clinical symptoms become apparent. This has sustained interest in the biomarkers as minimally invasive tools for early detection. However, despite extensive investigation, no biomarker panel has achieved robust clinical utility for early KOA diagnosis [1-2]. Although several serum biomarkers demonstrate significant association with KOA, their clinical applicability remains limited because osteoarthritis progresses through multiple biological phenotypes rather than a single uniform pathogenic mechanism [2-3]. Current evidence indicates that different KOA phenotypes are variably influenced by inflammatory signaling, cartilage extracellular matrix degradation, metabolic dysregulation, adipokine activity, and systemic low-grade immune activation [4-5]. Biomarkers such as CRTAC1, COMP, CTX-II, hyaluronic acid, CRP, IL-6, TNF-α, MMPs, YKL-40, adipokines, and emerging proteomic candidates reflect key osteoarthritic pathways, but their standalone clinical utility remains inconsistent across cohorts [2].

This scoping review aims to systematically map the biomarkers reported in KOA, classify them according to major biological pathways and disease phenotypes, and identify the key translational gaps limiting their utility in early clinical detection. It specifically examines how phenotype-dependent variation in inflammatory, metabolic, and matrix-remodelling pathways affects biomarker interpretation, reproducibility, and diagnostic validity, and why strong biomarker associations have not yet translated into reliable early diagnostic tools. The outcome of this review is a pathway-based, phenotype-sensitive framework to guide future biomarker prioritisation, longitudinal validation, and development of clinically relevant strategies for early KOA detection and risk stratification.

References:

1. V. B. Kraus, S. Sun, A. Reed, E. J. Soderblom, M. A. Moseley, K. Zhou, V. Jain, N. Arden, Y.-J. Li, Science Advances, 2024, 10, eadj6814.
2. M. Ostojic, J. P. Oliveira, D. Kordic, C. Mouton, R. Prill, R. Becker, Journal of Experimental Orthopaedics, 2024, 11, e12105.
3. A. Mobasheri, W. E. van Spil, E. Budd, I. Uzieliene, E. Bernotiene, A.-C. Bay-Jensen, J. Larkin, M. C. Levesque, O. Gualillo, Y. Henrotin, Current Opinion in Rheumatology, 2019, 31, 80-89.
4. J. Calvet, M. García-Manrique, A. Berenguer-Llergo, C. Orellana, S. Garcia Cirera, M. Llop, C. Galisteo Lencastre, M. Arévalo, C. Aymerich, R. Gómez, N. Albiñana Giménez, J. Gratacós, Rheumatology, 2023, 62, 3875-3885.
5. J. Calvet, A. Berenguer-Llergo, C. Orellana, M. García-Manrique, M. Rusiñol, S. Garcia-Cirera, M. Llop, M. Arévalo, A. Garcia-Pinilla, C. Galisteo, C. Aymerich, R. Gómez, A. Serrano, A. Carreras, J. Gratacós, Arthritis Research & Therapy, 2024, 26, 19.

Poster ID 2B042

Are probiotic supplements truly what they claim?

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Probiotic supplements in this decade have gained widespread popularity and are widely used due to their reported potential health benefits. However, questions

and concerns regarding their efficacy, quality, reliability and scientific validation remain insignificant. Probiotics are defined as live viable microorganisms that confer benefits to the host when consumed in an appropriate amount, yet maintaining the microbial viability and functional stability in commercial formulation presents a major challenge. Many probiotic strains commonly used in supplements, including species of Lactobacillus and Bifidobacteria, are sensitive to oxygen exposure, temperature fluctuations and storage conditions, which compromise their viability over time. Furthermore, increasing trends in combining probiotics in herbal nutraceutical compounds and other bioactive ingredients may negatively influence microbial survival and functional properties.

As part of this review, preliminary experimental attempts were conducted to isolate probiotic strains and assess their probiotic potential from available commercial capsules. This review will also discuss key considerations for selecting a reliable probiotic product for consumer awareness, taking into consideration of viability loss.

Poster ID 2B043

Flexible Laser Induced Graphene Based Electrochemical Biosensor for Glucose Detection

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Laser-induced graphene (LIG) is a promising electrochemical sensing material with excellent conductivity, porous structure, and large surface area. In this work a flexible electrochemical glucose biosensor is fabricated using LIG electrodes via a simple and cost-effective laser-based fabrication approach. Using a CO2 laser engraver, patterns of conductive graphene are generated on a polyimide sheet, through a photothermal conversion process. The fabricated sensor consisted of an integrated three-electrode system with working, reference, and counter electrodes (Figure 1a).

The laser parameters were optimized to develop a highly conductive and mechanically stable graphene structure with resistance values ranging from approximately 0.349 kΩ to 0.463 kΩ. Ag/AgCl ink was used for the fabrication of the reference electrode, and silver conductive ink was applied on contact pads to enhance electrical connectivity. To allow enzymatic detection of glucose, glucose oxidase (GOx) was immobilized on the LIG working electrode.

Raman spectrum shows the G, D and 2D bands which confirms the structural characteristics of LIG electrodes. FESEM images confirm porous structures of graphene electrodes. The electrochemicalcharacterization was performed using cyclic voltammetry and chronoamperometry in phosphate-buffered saline (PBS) solution. The biosensor shows sensitivity for glucose concentration as low as 2mM with increasing current as the glucose concentration is increased.

These results indicate that the fabricated LIG-based biosensor provides a simple, low-cost, and efficient platform for glucose sensing and has potential applications in biomedical diagnostics and wearable biosensing technologies

References:

1. Settu, Kalpana, Pin-Tzu Chiu, and Yu-Ming Huang. "Laser-induced graphene-based enzymatic biosensor for glucose detection." *Polymers* 13.16 (2021): 2795.
2. Lei, Yongjiu, et al. "Laser-scribed graphene electrodes derived from lignin for biochemical sensing." *ACS Applied Nano Materials* 3.2 (2019): 1166-1174.
3. Yoon, Hyosang, et al. "A chemically modified laser-induced porous graphene based flexible and ultrasensitive electrochemical biosensor for sweat glucose detection." *Sensors and Actuators B: Chemical* 311 (2020): 127866.

Poster ID 2C001

Emotion Awareness Speech-to-Speech System: A Cognitive AI Approach for Indian Multilingual Contexts

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Keywords- Speech-to-Speech Emotion Awareness, Deep Learning, Multilingual Emotion Recognition, Speech Synthesis, Human-Computer Interaction, Indian Speech Corpus.

Speech-to-speech emotion awareness is a new direction in human machine communication interface, combining emotional intelligence, with live speech generation and recognition. In the given study, an emotion-sensitive speech-to-speech application with the support of AI is created that can recognise, decode, and express feelings of

a speaker based on the tone of his/her voice and transmit them as natural in synthesised speech. Its main objective is to promote naturalness, empathy and communicative awareness within the automated systems particularly in multilingual Indian setting where linguistic and tonal diversity is a critical problem. The suggested framework implies combining speech emotion recognition (SER) with deep learning, speech synthesis with neural vocoders based on transformers, and inter-speaker contextual transfer of emotion. In this paper, the architecture, algorithms, consideration of dataset and comparison of performance of the developed model with Indian emotional speech corpora are presented. The system attains an average accuracy of 92.4 percent in classifying emotions in the seven classes of emotion and is also robust in generalising Hindi and English bilingual data sets. This has a translation to human-robot interaction, assistive technologies, call-center analytics, and mental health assessment.

Poster ID 2C002

Metabopsy of Inherited Metabolic Disorders (IMDs): Discard to Diagnosis Approaches

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Background: Inherited Metabolic Disorders (IMDs) are genetic disorders caused by deficient enzymes leading to defective metabolism. Recently, notable forms of IMDs, including organic acidurias and amino acidurias has grown substantially, highlighting the need for timely diagnosis, as many IMDs are treatable. However, the approach to detecting IMDs using non-invasive, affordable methods in children is limited. Also, an in-silico approach that can alleviate clinical implications due to different IMDs is not emphasized.

Methods: We have developed a novel methodology for detecting IMDs using non-invasive biological samples by employing an in-house designed Vertical Tube Gel Electrophoresis (VTGE) system and 96-well plate colorimetric assays. LC-HRMS analysis was used for the metabolic profiling and validation. Further, we extended our research to develop mimetics of metabolites computationally against the pathway-associated enzymes by using molecular docking and MD simulations.

Results: IMD suspected samples showed three folds elevated levels of methylmalonic acid in tears, 2-3 fold increased hydroxyglutaric acid in nail, urine and 4-5 folds increased hydroxyproline in milk teeth, compared to the healthy controls, after performing 96-well plate colorimetric assays. LCHRMS analysis validated these findings. Furthermore, we designed the mimetics of metabolites as potential inhibitors of respective enzymes and studied their interactions using docking and MD simulation.

Conclusion: This research provides the first and novel method to use non-invasive samples for early detection of IMDs such as organic aciduria and amino acidurias by employing VTGE and 96-well plate colorimetric assays. Also, development of mimetics is a beneficial approach to overcome metabolic conditions in patients.

References:

1. Ijaz, S. Abbas, M. Shabbir, Y. Badshah, F. Abid, T. Afsar, S. Razak, Orphanet Journal of Rare Diseases, 2025, 20, 422.
2. H. Liu, J. Zhu, Q. Li, D. Wang, K. Wan, Z. Yuan, J. Zhang, L. Zou, X. He, J. Miao, *Functional & Integrative Genomics,* 2021, 21, 645–653.
3. D. Dumitriu, E. Baldwin, R. J. Coenen, L. A. Hammond, D. S. Peterka, L. Heilbrun, M. Arora, iScience, 2023, 26, 3.
4. S. Jaramillo Ortiz, M. Howsam, E. H. van Aken, J. R. Delanghe, E. Boulanger, F. J. Tessier,
5. Critical Reviews in Clinical Laboratory Sciences, 2022, 59, 125–141.
6. S. Zaib, N. Rana, N. Hussain, H. A. Ogaly, A. A. Dera, I. Khan, *Molecules,* 2023, 28, 2623.

Poster ID 2C003

Investigating histone post-translational modification towards epigenetic therapeutics of AD

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Post-translational modification and epigenetic changes can cause long-term gene silencing or over-expression in a context-dependent manner and are related to various disease conditions, including major Neurological Disorders such as Alzheimer's Disease (AD). Due to high complexities in chromatin architecture and dynamic context-specific cross-talks between chromatin and modifying protein partners, many of these areas are still largely unaddressed due to the difficulty in constructing appropriate experimental protocols.

Our target, the G9a, is a Lysine Methyltransferase that mainly dimethylates the H3K9 of chromatin, triggering the repression of genes epigenetically, leading to Alzheimer's disease (AD). Over the last few decades, considerable G9a inhibitors were reported, such as BIX-01294, UNCO224, UNC0321, UNCO638, UNC0642, E72, as potential anti-cancer agents. However, these inhibitors were troubled in clinical trials, and the involvement of G9a in neurological disease was overlooked (gap area).

Therefore, we have ventured to bridge the gap by exploring the role of G9a in neurological disorders and to find novel leads against G9a as potential epigenetic therapeutics of Alzheimer's disease (AD). Purposefully, we used an interdisciplinary chemical biology approach in combination of AI/ML-based design, medicinal chemistry, and pharmaceutical science. Our G9a inhibitors reduced the Aβ aggregates, an important hallmark in AD, in the C elegans CL2006 worms up to 47% in a concentration-dependent manner, highlighting their potential in AD treatment.1-2

References:

1. Bellver-Sanchis, A.; Ribalta-Vilella, M.; Irisarri, A.; Gehlot, P.; Choudhary, B. S.; Jana, A.; Vyas, V. K.; Banerjee, D. R.; Pallàs, M.; Guerrero, A.; Griñán-Ferré, C. G9a an Epigenetic Therapeutic Strategy for Neurodegenerative Conditions: From Target Discovery to Clinical Trials. Medicinal Research Reviews, 2025, 1-31.
2. Jana, A.; Bellver-Sanchis, A.; Griñán-Ferré, C.; Banerjee, D. R. Repurposing of Raltitrexed as an Effective G9a/EHMT2 Inhibitor and Promising Anti-Alzheimer's Agent, ACS Medicinal Chemistry Letters, 2023, 14 (11), 1531–1536

Poster ID 2C004

Total Laboratory Automation: Transforming Clinical Laboratories through Integrated, Intelligent, and Standardized Workflows

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Background:

Modern clinical laboratories face increasing test volumes, demand for rapid turnaround time, and stringent quality and accreditation requirements. Total Laboratory Automation (TLA) has emerged as a comprehensive technological solution that integrates pre-analytical, analytical, and post-analytical processes into a single, continuous workflow, enabling reliable and efficient diagnostic services.

Description:

Total Laboratory Automation encompasses automated sample reception, barcode-based identification, centrifugation, decapping, aliquoting, analytical processing, storage, and retrieval, all connected through conveyor-based systems and middleware. Integration with laboratory information systems enables real-time sample tracking, auto-verification, and intelligent rule-based result validation. Artificial intelligence and data-driven algorithms further enhance decision support, anomaly detection, workload balancing, and predictive maintenance of analyzers.

Quality and Compliance:

TLA supports compliance with NABL and ISO 15189 standards by minimizing manual interventions, reducing pre-analytical errors, ensuring traceability, and standardizing processes. Automated documentation, quality indicator monitoring, and audit-ready data improve laboratory governance and accreditation preparedness.

Sustainability and Workforce Optimization:

Automation contributes to sustainable laboratory practices by optimizing reagent usage, reducing repeat testing, minimizing sample wastage, and improving energy-efficient operations. TLA also enables optimal utilization of skilled laboratory personnel by shifting focus from manual tasks to quality assurance, data interpretation, and clinical consultation.

Conclusion:

Total Laboratory Automation represents a paradigm shift in laboratory medicine, offering an integrated, intelligent, and sustainable approach to diagnostics. Its adoption is essential for future-ready laboratories aiming to deliver high-quality, standardized, and patient-centric services in evolving healthcare systems.

Keywords: Total laboratory automation, Laboratory workflow, Artificial intelligence, ISO 15189, Sustainable diagnostics

References:

1. Nam Y. Revolutionizing laboratory practices: pioneering trends in total laboratory automation. Ann Lab Med, 2025, 45, 472-483.
2. Plebani M. Total laboratory automation: fit for its intended purposes? Clin Chem Lab Med, 2025, Aug 8;64(1):22-26

3. Genzen J.R., Burnham C.A.D., Felder R.A., et al. Challenges and opportunities in implementing total laboratory automation. Clin Chem, 2018 Feb;64(2):259-264.

Poster ID 2C005

Ferroptosis in Heart Failure with Preserved Ejection Fraction: Identifying Biomarkers for Clinical Stratification

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Keywords: Ferroptosis, HFpEF, Biomarkers, Lipid Peroxidation, Clinical Stratification

Background: Heart failure with preserved ejection fraction (HFpEF) accounts for half of heart failure cases, but its pathophysiology is unclear. Ferroptosis, an iron-dependent, lipid peroxidation-driven cell death, is implicated in cardiovascular disease but unexplored in HFpEF. This study aimed to investigate the association between ferroptosis-related biomarkers and clinical severity in HFpEF patients.

Methods: A comparative, cross-sectional study was conducted involving 93 participants divided into three groups: HFpEF patients (n=31), non-HFpEF heart disease patients (n=31), and healthy controls (n=31). Fasting blood samples were analyzed for biomarkers including glutathione (GSH), glutathione peroxidase 4 (GPX4), solute carrier family 7 member 11 (SLC7A11), and lipid peroxidation markers (malondialdehyde (MDA) and 4-hydroxynonenal (4-HNE)). Clinical parameters such as left ventricular ejection fraction (LVEF), global longitudinal strain (GLS), and troponin levels were assessed. Statistical analysis was performed using ANOVA, Pearson/Spearman correlation, and multivariable regression.

Results: HFpEF patients demonstrated significantly altered ferroptosis marker profiles compared to control groups, including reduced GSH and GPX4 levels and elevated MDA and 4-HNE ($p<0.01$ for all). A strong inverse correlation was observed between ferroptosis activity (composite score) and LVEF ($r = -0.67$, $p<0.001$). Similarly, elevated ferroptosis markers were associated with impaired GLS ($r = 0.71$, $p<0.001$) and higher serum troponin ($r = 0.61$, $p<0.01$). The ferroptosis signature remained a significant predictor of clinical severity after adjustment for age, sex, and comorbidities.

Conclusion: A distinct ferroptosis biomarker profile is associated with HFpEF severity, indicating a pathogenic role. These biomarkers offer potential for risk stratification and therapeutic targeting in HFpEF.

References:

1. Fang X, Ardehali H, Min J, Wang F. The molecular and metabolic landscape of iron and ferroptosis in cardiovascular disease. Nat Rev Cardiol. 2023 Jan;20(1):7-23. doi: 10.1038/s41569-022-00735-4. Epub 2022 Jul 4.
2. Li Q, Zhao Z, Zhou X, Yan Y, Shi L, Chen J, Fu B, Mao J. Ferroptosis: The Potential Target in Heart Failure with Preserved Ejection Fraction. Cells. 2022 Sep 12;11(18):2842. doi: 10.3390/cells11182842.
3. Doll S, Proneth B, Tyurina YY, Panzilius E, Kobayashi S, Ingold I, Irmler M, Beckers J, Aichler M, Walch A, Prokisch H, Trümbach D, Mao G, Qu F, Bayir H, Füllekrug J, Scheel CH, Wurst W, Schick JA, Kagan VE, Angeli JP, Conrad M. ACSL4 dictates ferroptosis sensitivity by shaping cellular lipid composition. Nat Chem Biol. 2017 Jan;13(1):91-98. doi: 10.1038/nchembio.2239.

Poster ID 2C006

Deciphering the Transcriptomic Landscape of Paclitaxel Resistance in Triple-Negative Breast Cancer

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Keywords: TNBC, Chemoresistance, RNA sequencing, Non-Coding RNA

Triple-negative breast cancer (TNBC) remains a clinical challenge due to the lack of estrogen, progesterone, and HER2 receptors, leaving systemic chemotherapy as the primary treatment. However, the rapid emergence of drug resistance frequently leads to treatment failure and poor prognosis. This resistance is driven by a complex network of biological adaptations, including immune escape, metabolic rewiring, and dysregulated DNA repair.

Identifying the molecular determinants of survival under chemotherapy—specifically the interplay between coding and non-coding RNAs is essential for developing targeted strategies to overcome resistance and improve patient survival. Therefore, drug resistance serving as a critical barrier to successful clinical outcomes. To decode the mechanisms underlying this therapeutic failure, we executed an integrative transcriptomic analysis drug-resistant cancer datasets. Pathway enrichment analysis was conducted to evaluate the biological function of commonly expressed genes. In this report, we identified 169 common gene in sensitive and drug-resistant cancer dataset that primarily enriched in complement
system, pathways in cancer, inflammation. Further survival analysis revealed that nine genes (SDR16C5, PROSER-AS1, SOX21-AS1, LINC002608, CLDN1, CD82, CA3-AS1, NEURL1, AC010735.2) were significantly associated with the prognosis of TNBC patients.
Our investigation found that expression of DEGs is show similar trend in Paclitaxel resistant TNBC cells by preforming RT-PCR. Among these we found that Gene X highly expressed in resistant cells, and it's reported as part of complement system. Therefore, Functional evaluation of these Gene
X was performed using CRISPR-Cas9-mediated knockout in Paclitaxel resistant TNBC. These findings uncover the regulatory landscape of therapeutic failure and provide a roadmap for re-sensitizing TNBC to chemotherapy.

Poster ID 2C007

Advancements in Artificial Intelligence and Emerging Technologies for Early Detection and Management of Major Human Diseases

Background:

Non-communicable and infectious diseases remain a major global health burden. Conditions such as Alzheimer's disease, Parkinson's disease, cardiovascular disorders, cancer, diabetes mellitus, tuberculosis, and COVID-19 continue to challenge healthcare systems worldwide. Recent advancements in artificial intelligence (AI), machine learning (ML), wearable biosensors, telemedicine, and precision medicine have transformed disease diagnosis, monitoring, and treatment strategies.

Objective:

This study aims to highlight the role of AI-driven models and emerging health technologies in the early detection, classification, and management of multiple major diseases.

Methodology:

A comprehensive review and comparative evaluation of deep learning models (CNN, RNN, EfficientNet, and hybrid architectures) were performed across various disease datasets including MRI, CT scans, ECG signals, retinal images, and clinical laboratory parameters. Performance metrics such as accuracy, sensitivity, specificity, and AUC were analyzed to assess diagnostic efficiency.

Results:

AI-based models demonstrated high predictive accuracy in early-stage Alzheimer's and Parkinson's detection using neuroimaging data. In cardiovascular diseases, ECG-based deep learning algorithms improved arrhythmia detection. For cancer diagnosis, CNN models enhanced tumor classification in radiological imaging.

AI-supported retinal imaging effectively detected diabetic retinopathy. Additionally, AI-assisted screening models improved rapid detection of tuberculosis and COVID-19 from chest X-rays.

Conclusion:

The integration of artificial intelligence and emerging digital health technologies offers a transformative approach in early diagnosis, personalized treatment, and disease monitoring. These advancements can significantly reduce diagnostic delays, improve clinical decision-making, and enhance patient outcomes. Continued interdisciplinary research and large-scale validation studies are essential for translating these technologies into routine clinical practice.

Poster ID 2C008

Deep Learning–Based Early Detection of Alzheimer's Disease Using EfficientNet Architecture

Keywords: Alzheimer's disease, Deep Learning, EfficientNet, MRI, Artificial Intelligence, Early Diagnosis

Background:

Alzheimer's disease (AD) is a progressive neurodegenerative disorder and a leading cause of dementia worldwide. Early diagnosis remains a major clinical challenge due to subtle structural changes in the brain during initial stages.

Recent advancements in artificial intelligence (AI) and deep learning have demonstrated promising potential in medical image analysis and early disease prediction.

Objective:

This study aims to develop and evaluate a deep learning–based diagnostic model using the EfficientNet architecture for early detection and classification of Alzheimer's disease from neuroimaging data.

Methodology:

A convolutional neural network model based on EfficientNet was implemented and trained on preprocessed MRI datasets. Image augmentation and normalization techniques were applied to enhance model generalization. The dataset was categorized into four classes: Non-Demented, Very Mild Demented, Mild Demented, and Moderate Demented. Model performance was evaluated using accuracy, precision, recall, F1-score, and confusion matrix analysis.

Results:

The proposed EfficientNet-based model demonstrated high classification accuracy with improved sensitivity in detecting early-stage Alzheimer's disease compared to conventional CNN models. The model showed robust performance in distinguishing between mild and moderate dementia stages.

Conclusion:

The integration of deep learning models such as EfficientNet in neuroimaging analysis offers a reliable and efficient approach for early Alzheimer's detection. This technology-driven strategy can support clinicians in timely diagnosis and improve patient management outcomes. Further research with larger multi-center datasets is recommended to enhance model validation and clinical applicability.

Poster ID 2C009

Predictive Analytics in Diabetes Care: A 12-Week Study of AI-Driven CGM in Type 2 Diabetes Mellitus

Keywords: Type 2 Diabetes Mellitus, Artificial Intelligence, Continuous Glucose Monitoring, Digital Health, Personalized Medicine.

Background:

Type 2 Diabetes Mellitus (T2DM) is a chronic metabolic disorder characterized by insulin resistance and persistent hyperglycemia. Poor glycemic control increases the risk of cardiovascular disease, nephropathy, neuropathy, and retinopathy. Recent advancements in Artificial Intelligence (AI) and wearable biosensors provide opportunities for real-time glucose monitoring and predictive analytics.

Objective:

To evaluate the effectiveness of AI-integrated Continuous Glucose Monitoring (CGM) systems in improving glycemic control and predicting hyperglycemic events in patients with T2DM.

Methods:

A 12-week prospective interventional study was conducted among 100 patients aged 35–65 years diagnosed with T2DM. Participants were monitored using AI-enabled CGM devices that continuously recorded glucose levels and generated predictive alerts. Primary outcomes included change in HbA1c levels and Time-in-Range (70–180 mg/dL). Secondary outcomes included patient adherence and system usability.

Results:

After 12 weeks, mean HbA1c levels reduced from 8.9% to 7.4% ($p < 0.05$). Time-in-Range improved by 28%. The AI algorithm predicted hyperglycemic episodes with 85% accuracy. Patient satisfaction scores indicated high acceptability and improved treatment adherence.

Conclusion:

AI-integrated CGM significantly enhances glycemic control and supports personalized diabetes management. This approach demonstrates strong potential for scalable digital health solutions in chronic disease care.

Poster ID 2C010

A Network-based framework connecting cancer cell lines and patients for personalized drug response prediction in lung cancer

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Cancer treatment remains challenging due to the strong molecular heterogeneity observed across patients, which often leads to variable drug responses and resistance. To improve the translation of experimental findings into clinical applications, it is essential to better connect cancer cell lines with real patient tumour data. In this study, we present a network-based framework that integrates lung cancer gene expression profiles from both GDSC cell lines and TCGA patient samples to support personalized drug response prediction. To do this, we minimize batch effects

between datasets, data homogenization was performed using the ComBat algorithm. Next, patient-specific and cell line-specific gene interaction networks were constructed for every individual sample using the LIONESS algorithm, incorporating protein-protein interaction (PPI) information to generate personalized gene-gene correlation networks. This approach captures unique molecular network signatures for each patient and each cell line, reflecting their distinct biological states. To quantify the similarity between patient tumours and cell lines, we computed the Jaccard similarity index between each patient-specific network and all cell line networks. This resulted in a comprehensive patient-cell line similarity matrix across all combinations. Notably, the highest similarity score reached 0.45, indicating a meaningful level of similarity between cancer cell lines and patient tumours. By identifying the most similar cell line counterparts for each patient, this framework provides a meaningful basis for transferring drug sensitivity knowledge from cell lines to patients and improving drug response prediction in clinical settings. Overall, this study offers a systematic strategy for selecting patient-relevant cancer cell lines, advancing precision oncology and enabling more accurate personalized cancer treatment.

Poster ID 2C011

C-Phycocyanin as a Precision Therapeutic Modulator of Epoxide Hydrolase Variants in Type 2 Diabetes and Cardiovascular Disease

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Keywords: C-Phycocyanin, epoxide hydrolase polymorphism, oxidative stress, Type 2 diabetes mellitus, cardiovascular disease

Oxidative stress is a central pathogenic mechanism contributing to the development and progression of Type 2 Diabetes Mellitus (T2DM) and cardiovascular disease (CVD), particularly in individuals carrying functional polymorphisms in the epoxide hydrolase (EPHX) gene that impair epoxide detoxification and redox balance. Despite advances in clinical management, therapeutic strategies addressing genotype-dependent oxidative damage remain limited. The present study evaluates C-Phycocyanin, a natural bioactive compound with potent antioxidant properties, as a precision therapeutic modulator of EPHX variants using an integrated in-silico and in-vitro translational approach. Molecular docking, molecular dynamics simulations, and binding free-energy calculations were employed to investigate the interaction stability and affinity of C-Phycocyanin with wild-type and polymorphic EPHX proteins. These computational analyses were complemented by in-vitro validation under hyperglycaemic conditions using relevant cellular models to assess reactive oxygen species generation, lipid peroxidation, and antioxidant enzyme activities, including superoxide dismutase, catalase, and glutathione peroxidase. In-silico results demonstrated stable and energetically favourable binding of C-Phycocyanin to wild-type EPHX, whereas polymorphic variants exhibited reduced binding affinity and increased structural fluctuations. Consistently, in-vitro findings revealed a significant reduction in oxidative stress markers and restoration of antioxidant defences following C-Phycocyanin treatment. Overall, this study highlights the genotype-dependent therapeutic potential of C-Phycocyanin and underscores the value of integrating computational modeling with experimental validation. The findings support the development of precision, natural compound-based interventions for managing metabolic and cardiovascular diseases.

References

1. Morisseau, C., Hammock, B. D., *Annual Review of Pharmacology and Toxicology,* 2013, 53, 37–58.
2. Zhang, Y., Chen, M., Zhou, Y., *Journal of Functional Foods,* 2019, 58, 1–10.
3. Wang, B., Li, X., Liu, S., *Gene*, 2018, 673, 215–222.

Poster ID 2C012

Title Missing

In bioinformatics, the complex interactions between thousands of genes, along with the typically small number of available samples, form a classic challenge referred to as the curse of dimensionality. This reduces the statistical power and robustness of predictive models in identifying the imbalance, which complicates the task of confidently identifying the biologically meaningful gene signatures. Development of data augmentation strategies to combat such problems has become crucial. Generative models such as Diffusion models, Variational Autoencoders (VAEs), and Generative Adversarial Networks (GANs) have shown promise for augmenting image-based datasets; their potential for generating omics data
remains to be realized. Application of generative approaches in omics data demands a more nuanced approach as there are differences in data structure and distribution. In single-

cell studies, the generative methods are still popular, and it can be partly attributed to the relatively higher cellular resolution offered by these datasets. In this work, we introduce a computational pipeline specifically designed for gene expression signature discovery in studies constrained by small sample sizes. This work integrates methods of data augmentation with a validation module that leverages a comprehensive knowledge base incorporating evidence from the scientific literature, established molecular signature databases such as KEGG pathways, and the Therapeutic Drug Target Information database. We performed a rigorous and systematic benchmarking of this pipeline across multiple microarray datasets to report that when statistical robustness is considered, Gaussian Mixture Models (GMMs) consistently outperform complex generative architectures, such as CTGAN and transformer-based Real TabFormer. We demonstrate the result of this pipeline across five diseases, namely, breast cancer, tuberculosis, ovarian cancer, sepsis, and diabetes, to highlight the strength of a sophisticated data augmentation pipeline in extracting meaningful patterns from limited data.

Poster ID 2C013

Beyond availability: An integrated access framework for cancer care pathways

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In the discourse on access to cancer care, it has conventionally been understood and assessed through the lens of availability and affordability, often overlooking the broader relational processes that shape
care utilization mediated through dimensions of availability, accessibility, affordability, acceptability, and coordination. This paper presents the framework developed as part of an original empirical study examining access to cancer care in two states of northeast India. Central to the framework are the roles of family decision-making, inter-organizational relationships, and non-governmental actors in influencing care-seeking pathways, treatment initiation, and continuity of care. The existing models of access in cancer care are insufficient; hence, this integrated framework encapsulates the dynamic insights in examining access. The framework captures that delays and disruptions in care are often due to misalignment across dimensions rather than a single barrier. The framework brings together interconnected processes through which patients engage with the health systems for cancer services. This framework illustrates the incorporation of perspectives from patients, providers, and intra- and inter-organisational coordination. A nuanced understanding of access, shaped by this framework, can be transferable and help inform and guide the effectiveness of care delivery, health systems strengthening, policy design, and intervention planning for cancer and other non-communicable diseases. Its application can help identify leverage points to improve coordination, reduce inequities, and strengthen the effectiveness of cancer care delivery.

References:

1. A. Alkhawaldeh, M. Albashtawy, A. Rayan, A. Abdalrahim, et.al. Iranian Journal of Public Health. 2023. 52(7):1346–1354.
2. R. Bolton, C. Logan & J.H. Gittell. The Journal of Applied Behavioural Science. 2021. 57(3), 290-322.
3. A.T. Romero, V. Del, J. Señarís, L. Heredero, C. D. P. & Nuijten, M. World Journal of Clinical Cases. 2014. 2(12), 757–769.
4. D. A. Haggstrom, S. H. Taplin, P. Monahan, & S. Clauser. Journal of Health Care for the Poor and Underserved. 2012. 23(3 SUPPL), 49–66.
5. R. M. Andersen. Journal of Health and Social Behavior. 1995. 36(1):1–10.
6. S. Graham. (Ed.). Routledge. 1987. 1, 1-272.
7. J.W.T. Penchansky and R.W. Thomas. Medical Care. 1984. 22(6):553-568.
8. R. Andersen, J.F. Newman. Milbank Mem Fund Q Health Soc. 1973;51(1):95–124.
9. R.M. Andersen. Journal of Health and Social Behavior. 1995;36(1):1–10.
10. I.M. Rosenstock. Health Education Monographs. 1974. 2(4), 328–335.

Poster ID 2C014

Dynamic Modeling, Analysis of Tuberculosis Infection among Diabetic Patients and Parameters Estimation Using Physics Informed Neural Networks

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Keywords: Diabetes Mellitus (DM), Tuberculosis (TB), Stability Analysis, Parameter Estimation, Physics Informed Neural Networks (PINNs), Deep Learning, Numerical Experiments.

In this work, we discuss a compartmental dynamic model of tuberculosis infection among dia betic patients. We perform the mathematical analysis on the model and discuss the existence and uniqueness of the solution. We also show the endemic equilibrium point and disease free equilib rium point of the proposed model. We establish the nonnegativity and boundedness of the solu tion. We discuss the stability analysis of the endemic equilibrium point. Next we apply a modified physics informed neural networks (PINNs) based on a deep neural network architecture, to forecast the disease transmission pattern and estimate the key model parameters. The essence of this PINNs algorithm is that it can utilize the differential equation and efficiently estimate the parameters even with small dataset. We show that our modified PINNs can forecast the tuberculosis transmission pattern competently and estimate the key model parameters effectively.
MSC: 92-08, 92-10, 92B20, 34AXX, 68T07

Poster ID 2C015

"A Comprehensive *In-Silico* Analysis Reveals Acylsulfonamide-Based FDA Drugs to be Potential Pan Flavivirus Antivirals Targeting NS3 Protease"

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Keywords: Pan Flaviviral antivirals, NS2B-NS3 protease, Virtual screening, Molecular dynamics simulations, MMPBSA, Drug repurposing, FDA approved drugs

The Orthoflavivirus genus has 70 arthropod-borne viruses causing epidemics globally. The mosquito-borne flavivirus cluster harbors fatal Human pathogens. Despite decades of research, no effective vaccines or broad-spectrum antivirals are available against these viruses. Small-molecule drug discovery efforts have achieved limited success, often targeting a single strain. Many of these viruses have serological differences and genotypic variation within the serotypes. The structural architecture of the mosquito-borne flaviviruses is similar at both the genomic and proteomic levels. This allows for developing drugs or vaccines with multivariate potency. In this study, using sequence and structure-based alignment, we found conserved and druggable allosteric sites in the NS3 protease of nine flaviviruses. Using a library of FDA-approved small molecule anti-viral drugs, we found five, all derivatives of acylsulfonamide scaffold, approved against HCV NS3/4A protease, to have comparable binding affinities across the NS3 protease of all the nine flaviviruses. The interaction profiles have revealed the same atoms of the drugs involved in interactions in both HCV and the flaviviruses, albeit at the allosteric site in the later's case. In-depth MD simulation analysis has revealed simeprevir and paritaprevir as the most potential candidates with pan-flaviviral activity, targeting the flaviviral NS3 protease.