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MINISTRY OF HEALTH MALAYSIA
NATIONAL INSTITUTES OF HEALTH

ABSTRACT BOOK

INTERNATIONAL MEDICAL RESEARCH JOURNAL

1ST INTERNATIONAL BIOMEDICAL CONFERENCE 2025

BRIDGING THE GAPS: TRANSLATING BIOMEDICAL RESEARCH FROM LAB TO COMMUNITY

3RD - 4TH SEPTEMBER 2025

AC HOTEL BY MARRIOTT, KUANTAN PAHANG

PENYELIDIK
PERSATUAN PENYELIDIK KKM

MyBiomed

International Medical Research Journal

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WELCOME MESSAGE FROM THE ORGANISING CHAIRPERSON

Assalamualaikum warahmatullahi wabarakatuh, Salam Malaysia Madani to all distinguished guests, esteemed speakers, dedicated researchers, brilliant students, and participants.

It is with immense pleasure and great honour that I extend my warmest welcome to each and every one of you attending the 1st International Biomedical Conference 2025 (IBC 2025), which proudly organised by the National Institutes of Health (NIH), Persatuan Pegawai Penyelidik Kementerian Kesihatan Malaysia (PENYELIDIK KKM), and Malaysia Biomedical Science Association (MyBiomed). On behalf of the Organising Committee, I am pleased to welcome you to what we anticipate will be an engaging and insightful event.

This conference marks a significant milestone in the biomedical landscape, bringing together bright minds from diverse backgrounds to explore the latest advancements, innovations, and challenges in the field. Our theme for IBC 2025, “Bridging the Gaps: Translating Biomedical Research from Lab to Community”, reflects our commitment to fostering collaborative discussions and forging new pathways for discovery that will ultimately benefit humanity.

In an era where biomedical science is rapidly evolving, platforms like IBC 2025 are crucial for knowledge exchange, networking, and the cultivation of future partnerships. We have curated a comprehensive program featuring keynote lectures from world-renowned experts, engaging parallel sessions, and stimulating poster presentations, all designed to inspire new ideas and stimulate robust discussions.

I would like to express my sincere gratitude to the Organising Committee, our generous sponsors, and all volunteers whose tireless efforts have made this conference possible. Your dedication is truly commendable.

To all participants, I encourage you to seize this opportunity to engage actively, share your insights, and connect with peers. May your time at IBC2025 be both professionally rewarding and personally enriching.

Thank you, and I wish you all a successful and memorable conference.

Yours Sincerely,

YBRS. DR. MOHD FAIRULNIZAL BIN MD NOH
Organising Chairperson (PENYELIDIK KKM)
1st International Biomedical Conference 2025 (IBC 2025)

WELCOME MESSAGE FROM THE ORGANISING CHAIRPERSON

On behalf of the Organising Committee, it is my great pleasure to welcome you to the 1st International Biomedical Conference (IBC 2025) with the theme “Bridging the Gaps: Translating Biomedical Research from Lab to Community”.

This inaugural gathering marks an exciting milestone, made possible through the collaborative effort between Persatuan Penyelidik Malaysia (PENYELIDIK) and the Malaysian Biomedical Science Association (MyBiomed), brings together researchers, academics, healthcare professionals, and industry partners to share knowledge, foster collaborations, and highlight innovations in biomedical science. The chosen theme underscores the urgent need to ensure that scientific discoveries do not remain confined within laboratories, but instead are effectively translated into real-world applications that benefit communities and improve quality of life.

Over the course of this conference, we will engage in stimulating keynote sessions, insightful oral and e-poster presentations, Rapid-Fire and Young Investigator Awards sessions, as well as meaningful discussions that reflect the diversity and dynamism of the biomedical sciences. This platform also provides valuable opportunities for networking, capacity-building, and sparking new collaborations that transcend borders and disciplines.

We would like to extend our deepest gratitude to our distinguished speakers, dedicated participants, supporting institutions, sponsors as well as our committee members, who have made this conference possible. Your contributions are vital in making this event not only a success but also a milestone in advancing biomedical science and its translation into practice.

We hope that this conference will inspire innovative thinking, encourage cross-disciplinary dialogue, and pave the way for impactful solutions that bring science closer to society.

With that, we warmly welcome you to the 1st International Biomedical Conference 2025. May your participation be enriching, rewarding, and memorable.

Yours Sincerely,

YBRS. PROF. DR. NOR FADILAH BINTI RAJAB
Organising Chairperson (MyBIOMED)
1st International Biomedical Conference 2025 (IBC 2025)

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PROGRAMME

DAY 1 : 3rd September 2025

Time	Ballroom	Meeting Room
0800-0900	Registration	
0915	Arrival of YBhg. Dato' Indera Dr. Nor Azimi binti Yunus, Deputy Director General of Health (Medical), Ministry of Health Malaysia	
0930	National Anthem "Negaraku" Doa Recital	
0935	Joint Welcome Address by **YBrs Dr. Mohd Fairulnizal Md Noh** and **YBrs Prof. Dr. Nor Fadilah Rajab**, Organising Chairpersons, 1st International Biomedical Conference 2025	
0945	Officiating Speech by YBhg. Dato' Indera Dr. Nor Azimi binti Yunus, Deputy Director General of Health (Medical), Ministry of Health Malaysia	
1000 - 1030	**KEYNOTE:** MicroRNAs: Tiny Regulators, Massive Impact - Unlocking Their Potential in Cancer Diagnosis and Therapy *Prof. Ts. Dr. Cheah Yoke Kqueen, FASc. (Universiti Putra Malaysia)* Chairperson: Prof. Dr. Fadilah Rajab (UKM)	
1030	Tea Break & Networking	
1045 -1115	**PLENARY 1:** Uncovering Novel Therapeutic Targets for Head and Neck Cancers *Prof. Dr. Cheong Sok Ching (Cancer Research Malaysia)* Chairperson: Assoc. Prof. Dr. Lim Chooi Ling (IMU University)	
Time	**Ballroom**	**Meeting Room**
1115 - 1215	**SYMPOSIUM 1:** **Precision Medicine** Chairperson: Dr. Mohd. Khairul Nizam Mohd Khalid (IMR) MyGENOM: Advancing Precision Medicine Through Inclusivity and Equity in Malaysia *Dr. Adiratna Mat Ripen (IMR)* Precision Medicine in Practice: Bridging Genomic Insights to Public Health Impact *Prof. Dr. Chee-Onn Leong (AGTC Genomics)*	**SYMPOSIUM 2:** **AI & Machine Learning** Chairperson: Dr. Mohd Kamarulariffin Kamarudin (IMR) The Future of Computational Methods in Personalised Medicine *Assoc. Prof. Dr. Ooi Ean Hin (Monash University Malaysia)* Clinician-Centric Innovation: From Smart Forms to Deep-Learning Suites in Biomedical Imaging *Prof. Dr. Mohd Zulfaezal Che Azemin (IIUM)*
1215 - 1300	RAPID-FIRE PRESENTATION 1	RAPID-FIRE PRESENTATION 2
1300 - 1400	Lunch Break	
1400 - 1530	ORAL PRESENTATION 1	ORAL PRESENTATION 2
Time	**Ballroom**	
1530 – 1630	**FORUM:** R&D to Remedy: The Pathway of Drug Discovery Moderator : Assoc. Prof. Dr. Wan Amir Nizam Wan Ahmad (USM) *Prof. Dr. Nor Fadilah Rajab (UKM)* *Dr. Zaril Zakaria (NPRA)* *Mr. Sheikh Mohamad Nor Hafiz Abdul Aziz (ROCHE (M))*	
1630	End of Day 1	

PROGRAMME

DAY 2 : 4th September 2025

Time	Ballroom	
0800-0830	Registration	
0830-0900	**PLENARY 2:** Effects of Environmental Changes on the Transmission Dynamics of Aedes-borne Diseases *Assoc. Prof. Dr. Pratap Singhasivanon (SEAMEO TROPMED Network)* Chairperson: Dr. Nor Aziyah Mat Rahim (IMR)	
Time	**Ballroom**	**Meeting Room 5**
0900 - 1000	**SYMPOSIUM 3:** **Non Communicable Diseases** Chairperson: Assoc. Prof. Dr. Adeline Chia Yoke Yin (Taylor's University) Decoding the Lung Immune Ecosystem: From Fundamental Insights to Biomedical Impact. *Dr. Megat Hafizzuddin Abd Hamid (UM)* Lipoprotein (a): The new target in CV risk reduction? *Assoc. Prof. Dr. Ahmad Syadi Mahmood Zuhdi (UM)*	**SYMPOSIUM 4:** **Molecular Biology & Immunology** Chairperson: Dr. Ibrahim Adham Taib (IIUM) Exploration Of Protoemic Biomarker Discovery For Precision Medicine. *Asst. Prof. Dr. Norbaiyah Mohamed Bakrim (IIUM)* Human-induced pluripotent stem cell-derived neural models to understand neuropathogenesis in Down syndrome. *Prof. Dr. Ling King Hwa (UPM)*
1000	Breakfast Talks & Tea Break	
1030 - 1130	**SYMPOSIUM 5:** **Drug discovery & regulatory** Chairperson: Assoc. Prof. Dr. Suvik Assaw (UMT) From Bench to Bedside: Incorporating Herbal Therapies in Treatment of Diabetic Nephropathy *Assoc. Prof. Dr. Wan Amir Nizam Bin Wan Ahmad (USM)* Cancer Chemopreventive Activity of Terpenoid Rich Canarium odontophyllum MIQ. Leaf Extract (TRCO) in UVB-Induced Skin Cancer Models In Vitro and In Vivo *Prof. Dr. Ahmad Rohi Ghazali (UKM)*	**SYMPOSIUM 6:** **Planetary Health** Chairperson: Assoc. Prof. Dr. Suzita Mohd Noor (UM) Planetary Health in Focus: Redefining Human Well-being in a Changing World *Prof. Ts. Dr. Muhammad Lokman Md Isa (IIUM)* Planetary Boundaries and Child Health *Prof. Dr. Amir Hamzah Abdul Latiff (Sunway University)*
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44	**RF_24** **UNCOVERING HEALTH VULNERABILITIES TO CLIMATE CHANGE: AN INDEX-BASED HOUSEHOLD ASSESSMENT IN REDANG ISLAND, MALAYSIA** Raheel Nazakat, Nik Muhammad Nizam Nik Hassan, Noraishah Mohammad Sham, Mohd Faiz Ibrahim, Siti Aishah Rashid, Nadia Mohamad, Fadly Syah Arsad, Thahirahtul Asma' Zakaria, Wan Rozita Wan Mahiyuddin, Rohaida Ismail

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60	**EP_046** **FROM MYSTERY TO MOLECULAR CLARITY: METAGENOMICS SEQUENCING IDENTIFIES UNSEROTYPEABLE DENGUE VIRUS** Jeyanthi Suppiah, Nur Ain Zahidah Zainudin, Murni Maya Sari Zulkifli, Amir Hussin Adiee, Mazrul Effendy Dukut Soeharto, Nuraisyah Ramli, Rozainanee Mohd Zain
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WOUND HEALING EFFICACY OF *Kyllinga nemoralis* CREAM IN A DIABETIC RAT MODEL

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ABSTRACT

INTRODUCTION: Diabetic wound healing is a complex biological process that is often delayed due to impaired angiogenesis, inflammation, and oxidative stress. Natural-based therapies have gained growing interest in their potential to support and accelerate healing, particularly those derived from medicinal plants. *Kyllinga nemoralis*, traditionally used in folk medicine, is rich in bioactive compounds that may contribute to wound repair.

OBJECTIVE(S): The main objective of this study was to evaluate the effectiveness of cream formulations containing *K. nemoralis* extract at different concentrations

MATERIALS & METHODS: The crude extract of *K. nemoralis* was obtained via methanol extraction and analysed using Gas Chromatography-Mass Spectrometry (GC-MS) to identify phytochemicals. Cream formulations were prepared and assessed for quality. Diabetes was induced in rats using streptozotocin, followed by creation of standardised excision wounds. Wound healing progress was monitored following topical application of treatments. Each rat received four treatments: 5% cream, 10% cream, a placebo, and a commercial control.

RESULTS: Preliminary findings suggest that the 10% *K. nemoralis* cream demonstrated promising wound healing activity in diabetic rats, with observable improvements compared to other groups. Statistical differences were noted among the treatment groups; however, further analysis is ongoing.

CONCLUSION: The study highlights the therapeutic potential of *K. nemoralis* as a wound healing agent. These findings support its further development in diabetic wound care and contribute to the exploration of underutilised medicinal plants in complementary medicine.

KEYWORDS: *Kyllinga nemoralis*, Diabetic wound, Medicinal plant, Rat model

YIA_02

SYNERGISTIC CYTOSTATIC EFFECT OF *Scenedesmus parvus* EXTRACT WITH 5-FU AGAINST COLORECTAL CANCER CELL LINE

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ABSTRACT

INTRODUCTION: Colorectal cancer (CRC) remains a leading cause of global cancer mortality. Overcoming limitations of current therapies like 5-fluorouracil (5-Fu) necessitates the development of novel, complementary therapeutic strategies. Bioactive compound-rich microalgae, such as *Scenedesmus parvus* (*S. parvus*) (high in fatty acids, flavonoids, and carotenoids), represent a promising source for such agents.

OBJECTIVE(S): This study aimed to investigate the *in vitro* anticancer potential of *S. parvus* extract, both alone and in combination with 5-Fu, against HT29 colorectal cancer cells. Specifically, it assessed cytotoxicity, cytostatic effects, and impacts on apoptosis, cell cycle progression, DNA synthesis, clonogenic survival, and cell migration, while evaluating selectivity towards normal colon cells.

MATERIALS & METHODS: Cytotoxicity and cytostatic activity of *S. parvus* extract (alone and combined with 5-Fu) on HT29 cells were evaluated using viability assays. Mechanisms were probed using: 1) Annexin V-FITC/PI staining and flow cytometry for apoptosis detection; 2) Propidium iodide DNA staining and flow cytometry for cell cycle analysis; 3) BrdU incorporation assays for DNA synthesis quantification; 4) Colony formation assays for long-term clonogenic survival; and 5) Scratch assays for cell migration. Selectivity was assessed using normal colon cells.

RESULTS: Treatment with *S. parvus* extract alone caused a significant, dose-dependent reduction in HT29 cell viability. The combination with 5-Fu synergistically enhanced this anticancer effect. Crucially: 1) Annexin V/PI staining confirmed no significant induction of early or late apoptosis; 2) Cell cycle analysis revealed that the combination treatment induced profound G0/G1 phase arrest; 3) BrdU assays demonstrated significant suppression of DNA synthesis. Furthermore, the *S. parvus*-5-Fu combination effectively suppressed long-term clonogenic survival and significantly inhibited HT29 cell migration. The extract showed selectivity, preserving normal colon cell viability.

CONCLUSION: *S. parvus* extract combats HT29 cancer cells by stopping their growth and division (G0/G1 arrest), not by killing them. It significantly boosts 5-Fu's effectiveness while sparing healthy cells, making it a promising add-on therapy for colorectal cancer.

KEYWORDS: *Scenedesmus parvus*, Colorectal Cancer (CRC), Cytotoxicity, 5-FU Synergy, HT29

YIA_03

MNAZYME PAN-FUNGAL ASSAY: AN ISOTHERMAL PLATFORM FOR BROAD-RANGE FUNGAL DETECTION

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ABSTRACT

INTRODUCTION: Fungal infections affect more than one billion individuals worldwide and are responsible for an estimated 1.5 million deaths each year. Delays in diagnosis, particularly in healthcare settings with limited resources, contribute to the severity of these outcomes. This study describes the development of a molecular assay using Multi-component Nucleic Acid Enzymes (MNAzymes) designed to detect conserved fungal ribosomal DNA sequences under isothermal conditions.

OBJECTIVE(S): This study aimed to develop and evaluate a catalytic MNAzyme assay for universal detection of fungal DNA targeting conserved ribosomal regions.

MATERIALS & METHODS: The assay targeted a conserved fungal sequence (AF-ITS4LR1) identified through multiple alignments of ITS and LSU regions. Custom Partzymes and a fluorogenic substrate (Sub3-JB) were designed to assemble on this target. Optimisation was performed for temperature (30–64 °C), Partzyme concentration (0.005–0.2 µM), and magnesium chloride (6–50 mM). Specificity was assessed using bacterial and non-target fungal controls. The limit of detection was determined via serial dilutions of the synthetic target sequence and fluorescence monitoring.

RESULTS: The assay performed best at 50 °C, with 0.05 µM of each Partzyme, and 10 mM magnesium chloride. No fluorescence was detected in negative controls, indicating high specificity. The lowest detectable concentration of the synthetic target was 0.0025 µM, equivalent to approximately 3.76 x 1010 copies of the nucleic acid sequence.

CONCLUSION: The developed MNAzyme assay enables specific, sensitive detection of fungal DNA under isothermal conditions and shows strong potential as a rapid, amplification-free diagnostic tool for fungal infections.

KEYWORDS: MNAzyme, Pan-fungal Detection, ITS–LSU Region, Isothermal Assay, Molecular Diagnostics

YIA_04

BRIDGING THE GENE-DIET GAP: A CROSS-SECTIONAL STUDY ON PERSONALIZED CARDIOVASCULAR RISK MANAGEMENT IN TYPE 2 DIABETES USING DIETARY PATTERNS AND A POLYGENIC RISK SCORE

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ABSTRACT

INTRODUCTION: Cardiovascular disease (CVD) remains the leading cause of death among individuals with type 2 diabetes (T2D). While both genetic and dietary factors contribute to CVD risk, their interaction (GxD) and clinical relevance remain underexplored, particularly in Asian populations.

OBJECTIVE(S): This study addresses this gap by exploring GxD in Malaysian adults with T2D and developing a diet-targeted polygenic risk score (dt-PRS) to guide personalised dietary strategies.

MATERIALS & METHODS: This cross-sectional study involved 186 Malaysian adults with T2D. The 10-year CVD risk was estimated using the validated diabetes-specific UKPDS calculator. Reduced-rank regression (RRR) derived dietary pattern (DP) from 3-day diet records using 10-year CVD risk as the response variable. Participants in the highest and lowest DP tertiles were matched via propensity score matching and compared in the downstream analysis. Genotyping was conducted using the Illumina Infinium Asian Screening Array, covering 657,490 genetic markers (Single Nucleotide Polymorphisms, SNPs). After quality control and literature curation, 461 SNPs were selected to

compute the CVD-PRS using GWAS-derived effect sizes. GxD was examined using a General Linear Model. SNPs with significant GxD were used to construct the dt-PRS, which was subsequently dichotomised into diet-sensitive and diet-resistant groups.

RESULTS: RRR established 'Refined Grain-Red Meat-Tea & Coffee-SSB' (ReGReTS) pattern. Both the CVD-PRS (b=2.057, p=0.012) and ReGReTS dietary pattern (b=2.688, p<0.001) were positively associated with 10-year CVD risk. Notably, their interaction was also significant (p=0.040). Further analysis identified 37 SNPs with significant GxD. Of these, 23 were diet-resistant while 14 were diet-sensitive. The protective effect of low ReGReTS adherence on 10-year CVD risk was observed only in the diet-sensitive group (p<0.001), not in the diet-resistant group (p=0.927).

CONCLUSION: Although both genetic and dietary factors independently influence 10-year CVD risk in Malaysian adults with T2D, their interaction modifies this risk. This underscores the importance of personalised nutrition strategies using the dt-PRS equation to combat CVD in T2D.

KEYWORDS: Precision nutrition, Cardiovascular risk, Dietary pattern, Polygenic risk score, Type 2 diabetes

YIA_06

DATA-DRIVEN PHENOTYPING OF TYPE 2 DIABETES MELLITUS IN MALAYSIA: A NATIONAL REGISTRY CLUSTER ANALYSIS

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ABSTRACT

INTRODUCTION: The clinical heterogeneity of Type 2 Diabetes Mellitus (T2DM) challenges standardised management. Data-driven subtyping using real-world data is crucial for advancing precision medicine, yet such analyses are absent for the diverse Malaysian population, representing a critical knowledge gap.

OBJECTIVE(S): To identify and characterise distinct clinical phenotypes of T2DM using an unsupervised machine learning approach on data from the Malaysian National Diabetes Registry.

MATERIALS & METHODS: This cross-sectional study analysed 123,137 adults with T2DM. Six routinely collected variables were used: age at diagnosis, diabetes duration, body mass index, HbA1c, triglyceride-glucose index, and triglyceride-to-HDL ratio. Following rigorous preprocessing including clinically informed outlier handling and random forest-based imputation, data were standardised and partitioned using K-means clustering. A comprehensive validation framework, incorporating statistical metrics, bootstrap analysis for stability, and confirmation with hierarchical clustering and Gaussian mixture models, was employed to ensure the robustness of the final cluster solution.

RESULTS: Four clinically distinct and robust T2DM phenotypes were identified. These were: Severe Insulin-Resistant Diabetes (SIRD, 24%) with high insulin resistance and long disease duration; Severe Insulin-Deficient Diabetes (SIDD, 18%) with the poorest glycaemic control (mean HbA1c 10.4%); Mild Age-Related Diabetes (MARD, 29%) characterised by late onset and the best metabolic profile; and a large Obesity-Related Diabetes group (ORD, 30%) with the highest BMI and severe insulin resistance. All patient characteristics differed significantly across clusters ($p < 0.001$).

CONCLUSION: This first national-level cluster analysis reveals four distinct T2DM phenotypes within the Malaysian population. The identification of these subgroups, particularly a severe obesity-related phenotype, provides a foundational evidence base for developing targeted screening, prevention, and treatment strategies. This work represents a critical first step towards implementing precision diabetology in Malaysia.

KEYWORDS: Diabetes Clustering, Machine Learning, Malaysia, Precision Medicine, Registry Data

OP_01

HCD1: A NEW PLANT-BASED ALKALOID ANTIBIOTIC AGAINST MRSA

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ABSTRACT

INTRODUCTION: Methicillin-resistant *Staphylococcus aureus* (MRSA) has been known to display multidrug-resistance properties towards a wide range of structurally unrelated antimicrobial agents. Currently, only a handful of antibiotics can inhibit this dangerous nosocomial pathogen. Thus, a dire need for an alternative source of antimicrobials is crucial to reduce MRSA infections worldwide. Previously, HCD1 showed good antibacterial activity with minimum inhibitory concentration (MIC) values of < 8 µg/mL against 90 MRSA and 20 methicillin-susceptible *Staphylococcus aureus* (MSSA) isolates.

OBJECTIVE(S): This study was carried out to determine the antibacterial, safety, and efficacy properties of HCD1 using *in vitro* and *in vivo* models.

MATERIALS & METHODS: *In vitro* time-kill, single-step FOR assay and cytotoxicity studies were carried out against HCD1. Next, in vivo acute and sub-acute toxicity using Sprague-Dawley (SD) rats was conducted as per the Organisation for Economic Co-operation and Development (OECD) 420 and 407 guidelines, respectively. Additionally, the survival rate and mean effective dose (ED_{50}) of HCD1 against MRSA systemic infection in ICR mice were determined. Lastly, gene expression of an MRSA isolate exposed to HCD1 was analysed.

RESULTS: HCD1 showed a bactericidal effect in the time-kill assay and displayed a low toxicity with IC_{50} values of >300 µg/mL against two normal cell lines. No resistant MRSA mutants were detected in the FOR assay (up to 16x MIC values). No mortality or behavioural changes were observed in SD rats treated with a single dose of 2000 mg/kg and repeated doses of 125 mg/kg of HCD1 in acute and sub-acute toxicity evaluations, respectively. HCD1 provided an 83% survival rate in MRSA-infected mice with an ED_{50} calculated at 38.76 mg/kg. Transcriptomic analysis revealed that HCD1 may disrupt MRSA survival by repressing its energy production, hence abolishing the regulation of various important transmembrane transporters and the formation of biofilm in the cell.

CONCLUSION: HCD1 is highly recommended to be developed further as a safe and efficacious novel antibiotic against MRSA.

KEYWORDS: MRSA, Novel Antibiotic, Toxicity, Animal Model, Systemic Infection

OP_02

ACCEPTABILITY OF MEDICATION FOR EARLY VASCULAR AGEING IN MALAYSIA: A NATIONWIDE SURVEY

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ABSTRACT

INTRODUCTION: There has been extensive recent effort to identify potential drug candidates targeting cellular senescence to treat ageing-related comorbidities. Malaysia could particularly benefit from such therapies, given the country's high burden of cardiovascular diseases (CVDs) as 1.7 million people are currently living with three major risk factors of CVDs; diabetes, hypertension, and high cholesterol. These risk factors can induce early vascular ageing (EVA) and eventually progress to CVD in young adults.

OBJECTIVE(S): This study aimed to investigate hypothetical acceptance of medication for EVA, and to assess the determinants that influence acceptance among Malaysians aged 18 to 50 years old.

MATERIALS & METHODS: An anonymous cross-sectional survey was conducted across Malaysia among 1607 respondents from September 2023 to May 2024. The determinants of medication for EVA acceptance (knowledge, attitudinal factors and lifestyle risk behaviours) were analysed using partial least-squares structural equation modelling (PLS-SEM).

RESULTS: The majority reported "probably yes" (24.7%), and 6.7% reported "definitely yes" regarding the acceptability of medication for EVA. The PLS-SEM revealed two strong significant predictors of medication for EVA acceptance: (1) sceptical attitude (**β**=-0.328, $p< 0.0001$) and (2) perceived future risk of EVA (**β**=0.299, $p<0.0001$). There was a negative association between acceptability with perceived high current risk of EVA (**β**=-0.161, $p<0.0001$) and more frequent physical activity (**β**=-0.115, $p<0.0001$). The model showed that higher level of daily stress (**β**=0.117, $p=0.007$), being diagnosed with chronic disease (**β**=0.114, $p<0.0001$), greater body weight (**β**=0.113, $p=0.001$) and more frequent of practicing healthy eating (**β**=0.092, $p=0.002$) had a significant direct association with medication for EVA acceptability. Of the demographic characteristics, income (**β**=-0.064, $p=0.032$) and educational level (**β**=0.058, $p=0.031$) were significantly associated with acceptability.

CONCLUSION: Overall, Malaysian young adults indicated low acceptance of medication for EVA. Interventions to reduce negative perceptions of new therapies and improve awareness about vascular ageing may enhance acceptance of medication for EVA.

KEYWORDS: Senotherapeutic, Early Vascular Ageing, Young Adults, Cardiovascular, Premature Ageing

OP_03

CURCUMIN-LOADED PLURONIC NANOFORMULATION (NANOCUR) FOR WOUND HEALING APPLICATION

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ABSTRACT

INTRODUCTION: Wounds are defined as disruptions to normal anatomical structure and function. Wound healing is a complex biological process influenced by oxidative stress, inflammation, and cytokine activity. Current treatments are costly, inefficient, and often result in scarring. Curcumin (CUR), a bioactive phenolic compound isolated from turmeric, exhibits potent wound healing properties through its anti-inflammatory, antioxidant, and antimicrobial activities. It promotes collagen synthesis, enhances fibroblast proliferation, and accelerates re-epithelialisation, thereby supporting faster tissue regeneration and improved wound closure. However, some limiting factors, such as poor bioavailability, low aqueous solubility, and rapid metabolism, have hindered the therapeutic efficacy of CUR.

OBJECTIVE(S): This study aimed to evaluate the wound healing potential of a newly developed nanoformulation, curcumin-loaded Pluronic (PF), NanoCUR, by assessing its antioxidant capacity, cytotoxicity, and effects on inflammatory cytokines *in vitro*.

MATERIALS & METHODS: NanoCUR was synthesised using a thin-film hydration method and characterised for size, size distribution, zeta potential, morphology, drug loading, and loading efficiency. The antioxidant capacity of NanoCUR was assessed using the ferric-reducing antioxidant power (FRAP) assay, while its cytotoxicity was evaluated in 3T3-NIH murine fibroblast cells. The wound-healing property was determined through a migration assay, and its effect on tumour necrosis factor alpha (TNF-**α**) expression in lipopolysaccharide (LPS)-induced RAW 264.7 macrophage cells was analysed via polymerase chain reaction (PCR).

RESULTS: NanoCUR exhibited a drug loading of 18.89 ± 0.60 mg CUR/g, a loading efficiency of 96.39 ± 3.04%, a zeta potential of -2.11 mV, a particle size of 25.79 nm, and a size distribution of 0.236. Ultraviolet-Visible (UV-Vis) spectroscopy and Fourier Transform Infrared (FTIR) spectroscopy confirmed successful CUR encapsulation, enhancing its antioxidant activity significantly at 100 µM and 150 µM compared with CUR. Toxicity profiling showed significantly lower cytotoxicity for NanoCUR in 3T3 cells, with median lethal concentration (LC_{50}) values of 91.87 ± 0.02 µM (24h), 36.57 ± 0.05 µM (48h), and 20.63 ± 0.06 µM (72h) compared with CUR. Migration assays at 5 µM and 10 µM revealed enhanced wound closure over 72 hours. NanoCUR significantly suppressed TNF-**α** expression ($p < 0.0001$) in LPS-induced RAW 264.7 macrophage cells at 5 µM and 10 µM with increased cellular uptake.

CONCLUSION: These findings highlight the potential of NanoCUR for wound healing with improved toxicity, as well as antioxidant and anti-inflammatory properties. Further studies, particularly *in vivo*, are warranted to validate these findings.

KEYWORDS: Curcumin, NanoCUR, Pluronic, Wound Healing, Inflammation

OP_04

PHYTOCHEMICAL PROFILING AND SYNERGISTIC ANTIOXIDANT POTENTIAL OF *Anacardium occidentale* AND *Barringtonia racemosa* COMBINED ETHANOLIC LEAF EXTRACTS

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ABSTRACT

INTRODUCTION: The combination of medicinal plant extracts is an emerging strategy in pharmaceutical research, offering the potential to minimise toxicity, enhance therapeutic efficacy, and modulate multiple disease pathways. *Anacardium occidentale* (*A. occidentale*) and *Barringtonia racemosa* (*B. racemosa)* are well-documented for their bioactivities, including antioxidant, anti-inflammatory, and antimicrobial properties. However, there is currently no evidence elucidating the potential synergistic interactions that may arise from their combination.

OBJECTIVE(S): This study aimed to investigate the synergistic potential of combined ethanolic leaf extracts of *A. occidentale* and *B. racemosa* and to characterise the phytochemical profiles of both individual and combined extracts to identify bioactive constituents responsible for their activity.

MATERIALS & METHODS: The antioxidant synergism of individual and combined ethanolic leaf extracts was evaluated using the 1,1-diphenyl-2-picrylhydrazyl (DPPH) radical scavenging assay. Various combinations of ratios were tested to determine the optimal synergistic effect. High-Performance Liquid Chromatography (HPLC) and Gas Chromatography-Mass Spectrometry (GC-MS) analysis were used to profile and quantify the phytochemical constituents in both individual and combined ethanolic leaf extracts of *A. occidentale* and *B. racemosa*.

RESULTS: The combined extract at a 1:1 ratio exhibited the strongest antioxidant activity, with a combination index (CI) value of 0.5917 (CI < 1 indicates synergism) and lowest IC_{50} (19.39 ± 1.10 µg/mL), significantly surpassing the activity of *A. occidentale* (26.27 ± 2.25 µg/mL) and *B. racemosa* (43.54 ± 2.79 µg/mL) alone. Remarkably, the antioxidant capacity of the 1:1 combination was comparable to quercetin (11.48 ± 0.75 µg/mL), indicating a pronounced synergistic effect. Phytochemical profiling through HPLC and GC-MS revealed both overlapping and unique compounds within the combined extract, suggesting potential interactions between phytoconstituents that may contribute to the observed bioactivity.

CONCLUSION: The combined ethanolic leaf extracts of *A. occidentale* and *B. racemosa* demonstrated significant synergistic antioxidant activity and were rich in phytochemical diversity, underscoring their potential as a natural therapeutic strategy in managing disease conditions.

KEYWORDS: Synergistic effect, Phytochemical profiling, Antioxidant activity, *Anacardium occidentale, Barringtonia racemosa*

OP_05

THERAPEUTIC POTENTIAL OF A NOVEL TETRAPEPTIDE IN FULL-THICKNESS SKIN WOUND REPAIR

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ABSTRACT

INTRODUCTION: The treatment of full-thickness skin wounds and burns remains a major clinical hurdle. Short bioactive peptides represent a novel class of therapeutic agents capable of promoting tissue regeneration by activating intrinsic wound healing mechanisms. Accordingly, the design of peptide-based biomaterials for skin repair is gaining increasing attention in regenerative medicine research.

OBJECTIVE(S): This study evaluates the *in vivo* wound healing efficacy of a novel fatty acid-conjugated tetrapeptide, Palmitoyl-GDPH (Palmitic acid–Glycine–Aspartic acid–Proline–Histidine), in a full-thickness excision wound model in rats. The selection of Palmitoyl-GDPH was guided by its previously demonstrated ability to stimulate proliferation and migration in normal human dermal fibroblasts (NHDF), indicating its potential as a therapeutic candidate for skin repair. Structurally, Palmitoyl-GDPH was rationally designed as a derivative of Palmitoyl tetrapeptide-7 (Palmitoyl-GQPR), the active peptide in the commercial product RIGIN™ (SEDERMA), with modifications intended to enhance its regenerative properties.

MATERIALS & METHODS: A 4 cm² full-thickness excisional wound was surgically created on the dorsum of Sprague Dawley rats, followed by topical application of Palmitoyl-GDPH in liquid formulation. Tetracycline was used as the standard comparator due to its recognized wound healing and antimicrobial efficacy. Healing outcomes were analyzed through histological and hematological evaluations.

RESULTS: Palmitoyl-GDPH exhibited significant wound healing activity in a Sprague Dawley rat model of full-thickness skin injury. Following 18 days of topical administration, histological assessments revealed near-complete wound closure, marked by accelerated re-epithelialization, enhanced collagen deposition, and minimal scar formation compared to controls. Importantly, the restoration of a well-defined epidermal-dermal junction, along with the induction of new hair follicle formation, indicated regeneration of structurally and functionally viable skin tissue. Hematological analyses further corroborated these findings, showing reduced inflammatory markers consistent with faster wound resolution and improved recovery in the Palmitoyl-GDPH-treated group.

CONCLUSION: The demonstrated efficacy of Palmitoyl-GDPH suggests its potential application as a next-generation wound healing agent.

KEYWORDS: Short peptide, Tetrapeptide, Wound healing, Full-thickness skin wounds

OP_06

SYNERGISTIC EFFECTS OF DIABETES AND SARS-COV-2 SPIKE PROTEIN ON IN VITRO ENDOTHELIAL DYSFUNCTION AND INFLAMMATION

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ABSTRACT

INTRODUCTION: The COVID-19 pandemic highlighted advanced age and diabetes as major risk factors, with diabetic individuals particularly vulnerable to complications such as acute respiratory distress syndrome (ARDS), excessive systemic inflammation, and increased mortality. A key mechanism involves the viral spike protein (SP) binding to angiotensin-converting enzyme 2 (ACE2) receptors on endothelial cells, triggering angiotensin II (Ang II) activation and subsequent vascular dysfunction. In diabetes, pre-existing endothelial damage may further exacerbate vascular permeability, inflammation, and tissue injury.

OBJECTIVE(S): Blood samples were obtained from healthy adults (18–40 years) and diabetic patients (≥60 years) at Hospital Sultan Abdul Aziz Shah. Nitric oxide (NO) levels were quantified using the Griess assay. Human aortic endothelial cells (HAoECs) were co-treated with serum and SP and analyzed for reactive oxygen species (ROS) production, permeability, and the expression of ACE2, Ang II, ICAM-1, and VCAM-1. ACE2-transfected human bronchial epithelial cells (BEAS2b-ACE2) were co-cultured with Human Aortic Endothelial Cells (HAoECs) to assess cell death and secretion of proinflammatory cytokines and chemokines.

MATERIALS & METHODS: Diabetic plasma showed significantly lower NO levels. HAoECs exposed to both diabetic serum and SP exhibited elevated ROS, increased trans-endothelial permeability, and upregulation of ICAM-1 and VCAM-1. SP exposure reduced ACE2 expression but increased Ang II activity in BEAS2b-ACE2 cells, an effect amplified by diabetic serum, suggesting that SP-ACE2 binding promotes Ang II-mediated inflammatory signaling. SP and diabetic serum also synergistically increased chemokine release, particularly CXCL8, and epithelial cell death.

RESULTS: Diabetic plasma showed significantly lower NO levels. HAoECs exposed to both diabetic serum and SP exhibited elevated ROS, increased trans-endothelial permeability, and upregulation of ICAM-1 and VCAM-1. SP exposure reduced ACE2 expression but increased Ang II activity in BEAS2b-ACE2 cells, an effect amplified by diabetic serum, suggesting that SP-ACE2 binding promotes Ang II-mediated inflammatory signaling. SP and diabetic serum also synergistically increased chemokine release, particularly CXCL8, and epithelial cell death.

CONCLUSION: These findings suggest that diabetes-related endothelial dysfunction synergizes with SARS-CoV-2 SP activity to intensify vascular inflammation and tissue injury. The observed molecular changes may serve as biomarkers and therapeutic targets for early intervention in diabetic COVID-19 patients.

KEYWORDS: COVID-19, SARS-CoV-2, Cytokine, Coagulopathy, Endothelial Dysfunction

OP_07

MULTIPLE ANTIBIOTIC RESISTANCE (MAR) INDEX OF DAIRY FARMS IN SELANGOR, MALAYSIA

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ABSTRACT

INTRODUCTION: The rise of antimicrobial resistance is closely linked to the misuse of antibiotics in livestock farming, which is routinely administered to maintain animal health and productivity. As dairy farming emerges as a growing industry in our country, the reliance on antibiotics is also increasing. This highlights the need for the multiple antibiotic resistance (MAR) index, a valuable tool for assessing the risk of antibiotic contamination in farm environments.

OBJECTIVE(S): This study aimed to determine the MAR index of dairy farms and identify those that represent high- and low-risk sources of antibiotic contamination.

MATERIALS & METHODS: Soil, effluent water, and cow dung samples were collected from eight dairy farms of varying scales in Selangor between January 2022 and December 2023. The VITEK 2 system was used for bacterial identification and antimicrobial susceptibility testing. Subsequently, the MAR index for each farm was calculated. The statistical analysis was conducted using the Python programming language (version 3.11.12), implemented in the Google Colab 1.0.0 environment.

RESULTS: A total of 62 enterococcal isolates were recovered from the environment of dairy farms of varying scales. Approximately 58% of the isolates exhibited resistance to at least one of the 12 antibiotics tested, predominantly from large-scale farms (n=12/16, 75%). Four isolates exhibited multidrug resistance, all originating from commercial farms. The MAR index of the isolates ranged from 0 to 0.50, while the farm-level MAR index ranged from 0.02 to 0.23. A MAR index of 0.2 or above implies a high-risk source of antibiotic contamination. Only one commercially operated farm was classified in the high MAR index category.

CONCLUSION: Larger farms are more vulnerable to antibiotic overuse, increasing microbial resistance risks. Enhanced biosecurity, regulation, and education on sustainable farming are essential for addressing antimicrobial resistance. Proactive strategies are crucial to ensure the healthy growth of dairy farming and safeguard public health.

KEYWORDS: MAR Index, Enterococci, Dairy Farms, Antimicrobial Resistance

OP_08

PRODUCTIVE INFECTION OF PRIMARY HUMAN SKELETAL MUSCLE CELLS BY ENTEROVIRUS A71

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ABSTRACT

INTRODUCTION: Enterovirus A71 (EV-A71) is a major cause of hand, foot, and mouth disease (HFMD), a common paediatric illness that is usually mild but can lead to severe neurological complications. Although EV-A71 infects neurons, skin, and oral epithelial cells, its ability to infect natural human skeletal muscle cells remains unclear, despite frequent use of rhabdomyosarcoma cells for virus isolation and propagation. Understanding whether primary skeletal muscle cells support EV-A71 infection may reveal early viral replication sites and the mechanism of viral spread, ultimately informing improved strategies for disease management and therapeutic intervention.

OBJECTIVE(S): This study aims to evaluate the susceptibility of primary human skeletal muscle cells to EV-A71 infection.

MATERIALS & METHODS: An EV-A71 clinical isolate, obtained from the medulla oblongata of a fatal case, was used to infect commercially available primary human skeletal muscle myoblasts (HSkMM). The cells were cultured and differentiated into myotubes using manufacturer-recommended protocols. Both undifferentiated (myoblasts) and differentiated (myotubes) cells were infected at a multiplicity of infection (MOI) of 1. Viral replication kinetics were assessed using one-step growth curves, and infectious virus titres were quantified via the 50% cell culture infectious dose ($CCID_{50}$) assay. Immunocytochemistry using a rabbit polyclonal anti-EV-A71 VP1 antibody was performed to detect viral antigens, and cytopathic effects (CPE) were monitored microscopically.

RESULTS: Both myoblasts and myotubes were permissive to EV-A71 infection, as demonstrated by VP1 antigen expression and the development of cytopathic effects (CPE). However, myoblasts exhibited significantly greater susceptibility, evidenced by higher viral titres, more pronounced CPE, and a greater number of VP1-positive cells compared to myotubes.

CONCLUSION: This study provides the first evidence that primary human skeletal muscle cells are susceptible to EV-A71 infection, highlighting their potential role as early viral reservoirs that may contribute to initial viral replication and subsequent dissemination during infection.

KEYWORDS: Enterovirus A71, Human Myoblasts, Skeletal Muscle Infection, Viral Tropism, Cellular Pathogenesis

OP_09

COMPARATIVE ANTIMICROBIAL SUSCEPTIBILITY OF *Escherichia coli* FROM DIFFERENT DAIRY FARM TYPES

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ABSTRACT

INTRODUCTION: The rapid rise of antimicrobial resistance (AMR) is closely linked to the misuse and overuse of antimicrobials in livestock farming. Dairy farms are recognised reservoirs of pathogens such as *Escherichia coli* (*E.coli*), with resistance patterns often influenced by variations in management practices, farmers' level of understanding, and biosecurity standards.

OBJECTIVE(S): This study aimed to investigate the AMR profiles of *E. coli* from four types of dairy farms, categorised as small-scale, semi-commercial, commercial, and large-scale.

MATERIALS & METHODS: A cross-sectional study was conducted across eight dairy farms in Selangor, comprising three small-scale, two semi-commercial, one commercial, and two large-scale farms. Samples were collected from soil, effluent, cow dung, milk, and workers. The spread plate method was used to isolate *E. coli*, and all isolates were initially confirmed via Gram staining, followed by species confirmation and antimicrobial susceptibility testing using the Vitek® 2 system.

RESULTS: Out of 412 *E. coli* isolates, 19.9% of the isolates were resistant to at least one antimicrobial agent. Notably, 24.1% of isolates from large-scale farms exhibited resistance to at least one antimicrobial. Conversely, the highest percentage of multidrug resistance (10.8%) was observed in isolates from small-scale farms. This may be attributed to inconsistent or unsupervised antimicrobial usage, which is often more common in smaller-scale operations. Nevertheless, statistical analysis revealed no significant differences between farm categories.

CONCLUSION: The findings highlight the need for focused interventions, especially in smaller operations, to encourage the prudent use of antimicrobials. Enhancing farmer education and expanding veterinary outreach are crucial measures for reducing AMR risks and ensuring the long-term sustainability and safety of dairy production systems.

KEYWORDS: Antimicrobial Resistance, *Escherichia coli*, Dairy, Farm Types

OP_011

REPLACING ANIMAL MODELS: EXPLORING MAMMALIAN CELL CULTURES FOR *LEPTOSPIRA* VIRULENCE ASSESSMENT

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ABSTRACT

INTRODUCTION: Maintaining the virulence of pathogenic *Leptospira* in vitro remains challenging, as repeated sub-culturing often reduces pathogenicity. Traditionally, serial passage in animals is used to preserve virulence, but this is costly and ethically concerning.

OBJECTIVE(S): TThis study explores a cell culture-based approach, hypothesising that pathogenic *Leptospira* exhibit stronger binding and cytopathic effects (CPE) on mammalian cells.

MATERIALS & METHODS: Eight pre-characterised *Leptospira* isolates were examined, comprising four pathogenic and four non-pathogenic strains. Initial protein-based assays (ELISA and western blot) were hindered by serovar-specific antibody limitations, introducing bias. To overcome this, a pan-*Leptospira* PCR assay was employed, enabling unbiased detection of cell-bound leptospires

RESULTS: Results showed higher binding by pathogenic strains, though broader serovar testing is needed for validation. Interactions of leptospires with Vero E6 and HEK293T cells under dark-field microscopy revealed notable attachment behavior.

CONCLUSION: While further optimisation is necessary, these findings support the potential of mammalian cell cultures as an ethical, scalable tool for evaluating and maintaining *Leptospira* pathogenicity, with future applications in diagnostics and research.

KEYWORDS: *Leptospira*, Pathogenicity, Cell culture, pan-*Leptospira*, Virulence assay

OP_012

VASORELAXANT POTENTIAL OF ASPERGILLININE A FROM *Aspergillus* sp. HAB10R12: *IN VITRO* AND *IN SILICO* INSIGHTS

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ABSTRACT

INTRODUCTION: Hypertension remains a major contributor to global morbidity and mortality, with current therapies often limited by adverse effects and suboptimal efficacy. Endophytic fungi have emerged as a promising alternative source of bioactive compounds for vascular modulation.

OBJECTIVE(S): This study aimed to evaluate the vasorelaxant effect of *Aspergillus* sp. HAB10R12 extract and investigates the interaction of Aspergillinine A, a diketopiperazine compound isolated from the same fungus, with key vascular targets through in vitro and in silico approaches.

MATERIALS & METHODS: Thoracic aortic rings from Sprague-Dawley rats (220–250 g, n ≥ 6) were mounted in a multichannel myograph and equilibrated in Krebs–Henseleit solution. Rings were precontracted with phenylephrine before being exposed to cumulative concentrations of HAB10R12 extract (1 nM–300 µM). Methylene blue (10 µM), indomethacin (10 µM), and N-ω-nitro-L-arginine methyl ester (L-NAME, 100 µM) were used to assess involvement of nitric oxide (NO), prostacyclin, and endothelium-derived pathways. Molecular docking was conducted using AutoDock Vina and UCSF Chimera to study Aspergillinine A interactions with vascular targets—ETA, CaV1.2, and AT1R (PDB ID: 4AYA). Losartan was included as a standard reference. Pharmacokinetic and toxicity predictions were performed using SwissADME and ProTox-II.

RESULTS: HAB10R12 extract induced dose-dependent vasorelaxation with an IC_{50} of 21.8 nM. The presence of methylene blue, indomethacin, or L-NAME did not attenuate the response, indicating a non-endothelium-dependent mechanism. Aspergillinine A exhibited stable binding to all three vascular targets via hydrogen bonding and hydrophobic interactions. Pharmacokinetic analysis using SwissADME predicted high gastrointestinal absorption and good oral bioavailability. The compound complied with Lipinski's rule of five and other drug-likeness criteria. Toxicological predictions from ProTox-II classified Aspergillinine A as low-risk, with no strong evidence of hepatotoxicity, mutagenicity, or carcinogenicity.

CONCLUSION: The findings support the vasorelaxant potential of *Aspergillus* sp. HAB10R12 and its diketopiperazine derivative, Aspergillinine A, highlight their promise as candidates for novel antihypertensive drug development.

KEYWORDS: Vasorelaxation, Aspergillinine A, *In silico*, Pharmacokinetics, HAB10R12

OP_013

CONTROLLED-STIRRING SYNTHESIS OF MESALAMINE-LOADED NANO-ZIF-8 FOR EFFICIENT CANCER THERAPEUTIC

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ABSTRACT

INTRODUCTION: Mesalamine (MES), a non-steroidal anti-inflammatory drug (NSAID), is widely prescribed for inflammatory bowel disease (IBD) and is increasingly explored for its potential in cancer therapy. However, limitations in drug stability and targeted delivery prompt the need for efficient carrier systems. Zeolitic imidazolate framework-8 (ZIF-8), a metal-organic framework (MOF), offers ease of synthesis, high porosity, and suitability for drug delivery.

OBJECTIVE(S): This study aimed to synthesize mesalamine-loaded ZIF-8 nanoparticles (MES@nZIF-8) via a controlled-stirring approach and to assess the effect of reaction time on their physicochemical properties and MES loading.

MATERIALS & METHODS: MES@nZIF-8 was synthesized using different reaction time (15 min, 24 h, 48 h, 72 h). Characterization included visual observations, Powder X-Ray Diffraction (PXRD), Fourier Transform Infrared (FTIR) spectroscopy, Field Emission Scanning Electron Microscopy (FESEM), and Thermal Gravimetric Analysis (TGA). Encapsulation efficiency (EE%) and MES loading (DL%) were quantified via UV-Vis Spectroscopy.

RESULTS: A color change from milky white to yellow was observed with longer stirring, suggesting progressive oxidation of MES. PXRD confirmed structural integrity of ZIF-8, while FTIR spectra showed enhanced drug–framework interaction at 48 h. FESEM revealed increased particle size and aggregation over time and TGA demonstrated reduced thermal stability with prolonged stirring. The highest EE (95.35%) and DL (10.17%) were achieved at 48 h, with a slight decline at 72 h.

CONCLUSION: These findings suggest that reaction time significantly influences the physicochemical characteristics and stability of MES@nZIF-8, offering insight into the design of NSAID-loaded MOFs for drug delivery applications.

KEYWORDS: Mesalamine, ZIF-8, Nanoparticle, Cancer, NSAID, Drug Delivery

OP_014

EVALUATING THE OPTIMAL GLICLAZIDE LOADING INTO nZIF-8 FOR ANTICANCER APPLICATIONS

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ABSTRACT

INTRODUCTION: This study examined the encapsulation of gliclazide (GLI) into nano-sized Zeolitic Imidazolate Framework-8 (nZIF-8) as a technique for drug repurposing in targeted anticancer therapy.

OBJECTIVE(S): The objective of this study was to encapsulate GLI into nZIF-8 and evaluate its potential as a targeted nanocarrier for repurposed anticancer drug delivery.

MATERIALS & METHODS: GLI was loaded at doses of 5, 10, and 15 mg/mL using a pot solvothermal method.

RESULTS: UV–Vis spectrometry analysis demonstrated high encapsulation efficiency (≥98%) at concentrations of 5 and 10 mg/mL, declining to below 83% at 15 mg/mL. Dynamic Light Scattering (DLS) demonstrated an increase in particle size with GLI loading, validating effective encapsulation and the expansion of nanocarriers. Powder x-ray diffraction (PXRD) verified that nZIF-8 preserved its crystalline structure after loading. Current analyses (FTIR, BET, SEM, TGA) aim to further elucidate chemical interactions, porosity, and shape.

CONCLUSION: The findings indicate that nZIF-8 is a stable, pH-responsive nanocarrier with significant promise for regulated drug delivery, especially at 10 mg/mL GLI concentrations. The platform shows potential for enhancing repurposed medication techniques in cancer therapy.

KEYWORDS: Gliclazide, Zeolitic Imidazolate Framework-8 (ZIF-8), Nanocarrier, Targeted Anticancer Drug Delivery, Encapsulation-efficiency

OP_015

NEUROPROTECTIVE EFFECTS OF CHRONO-TAILORED COMBINED EXERCISE MODALITIES IN AN ALUMINIUM CHLORIDE-INDUCED MODEL OF COGNITIVE IMPAIRMENT

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ABSTRACT

INTRODUCTION: Neurodegenerative diseases such as Alzheimer's and Parkinson's are marked by progressive cognitive decline and neuronal loss posing a growing global health challenge. Exercise has emerged as a promising non-pharmacological strategy to promote neuroplasticity and attenuate neurodegeneration with both aerobic and resistance exercise offering distinct neuroprotective effects. Recent evidence suggests that aligning the timing of exercise with circadian rhythms may further modulate these benefits, yet this factor remains underexplored.

OBJECTIVE(S): This study aimed to investigate how combining aerobic and resistance exercise at different times of day affects behaviour and cognition in rats with $AlCl_3$-induced neurodegeneration

MATERIALS & METHODS: Male Wistar rats were administered aluminium chloride ($AlCl_3$) for 8 weeks to induce neurodegeneration. From week 5, they were divided into four groups which is $AlCl_3$ + Early Active Combined-exercise, $AlCl_3$ + Late Active Combined-exercise and $AlCl_3$ with sham exercise for both active phases. A combined aerobic-resistance exercise protocol was implemented for 4 weeks aligned with each group's active phase. Cognitive and behavioural performance was assessed using the Novel Object Recognition Test (NORT) and Open Field Test (OFT) at baseline, week 4 (pre-intervention), and after week 8 (post-intervention).

RESULTS: Exercise significantly improved exploratory behaviour in the Late Active Combined-exercise (LC) group ($p < 0.01$) as shown by increased centre zone entrance in the OFT indicating improved emotional resilience behaviour. Conversely, Early Active Combined-exercise (EC) groups showed significant improvements ($p < 0.01$) in recognition memory as evidenced by higher novel object preference in the NORT.

CONCLUSION: These findings suggest that the timing and combined exercise distinctly affect behavioural outcomes. Late-active phase exercise may favour emotional regulation, while early-active phase aerobic and combined exercise may better support memory function. Chrono combined exercise holds promise as a tailored, non-pharmacological intervention to mitigate cognitive decline in neurodegenerative conditions.

KEYWORDS: Chrono-exercise, Combined-Exercise, Circadian rhythm, Neurodegenerative, Behaviour, Cognitive

OP_016

IN SILICO SCREENING OF MICROBIAL METABOLITES REVEALS MOROMYCIN B AS A POTENTIAL PANCREATIC LIPASE INHIBITOR

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ABSTRACT

INTRODUCTION: Obesity is a chronic, multifactorial disease contributing to health burdens worldwide. An established therapeutic strategy involves inhibiting pancreatic lipase, the enzyme responsible for dietary fat breakdown in the digestive system. Inhibiting this enzyme prevents fat absorption and promotes excretion, which leads to weight loss. Currently, orlistat is the only FDA-approved pancreatic lipase inhibitor, but its gastrointestinal side effects call for safer alternatives, particularly from natural resources. Microbial metabolites, known for their structural diversity and bioactivity, offer promising potential. This study leverages *in silico* screening to discover novel microbial metabolites capable of inhibiting pancreatic lipase.

OBJECTIVE(S): To identify microbial metabolites that inhibit pancreatic lipase through *in silico* screening, and to evaluate their interactions with the enzyme's key catalytic residues, Ser152, His263, and Asp176.

MATERIALS & METHODS: The structure of human pancreatic lipase (PDB ID: 1LPB) was retrieved from the Protein Data Bank, and 36,454 microbial metabolites were sourced from Natural Product Atlas. Drug-likeness was filtered using Lipinski's Rule of Five. Molecular docking was conducted using AutoDock Vina, with orlistat as a reference. Top hits were analysed using the Protein-Ligand Interaction Profiler (PLIP) and visualised in PyMol.

RESULTS: Out of 36,454 metabolites screened, 27,297 passed Lipinski's filter. Among them, moromycin B, which is derived from Streptomyces, exhibited the highest binding affinity (-13.2 kcal/mol), surpassing that of orlistat (-6.7 kcal/mol). Moromycin B formed a hydrogen bond with the catalytic residue Ser152, suggesting favourable and potentially stable interactions within the enzyme's active site.

CONCLUSION: This *in silico* study identified moromycin B as a promising microbial inhibitor of pancreatic lipase. While previously recognised for its anticancer properties, its strong binding affinity and favourable interaction with a key catalytic residue in this study suggest a novel therapeutic application as an anti-obesity agent.

KEYWORDS: Moromycin B, Pancreatic Lipase, Molecular Docking, Microbial Metabolite, Anti-Obesity Agent

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