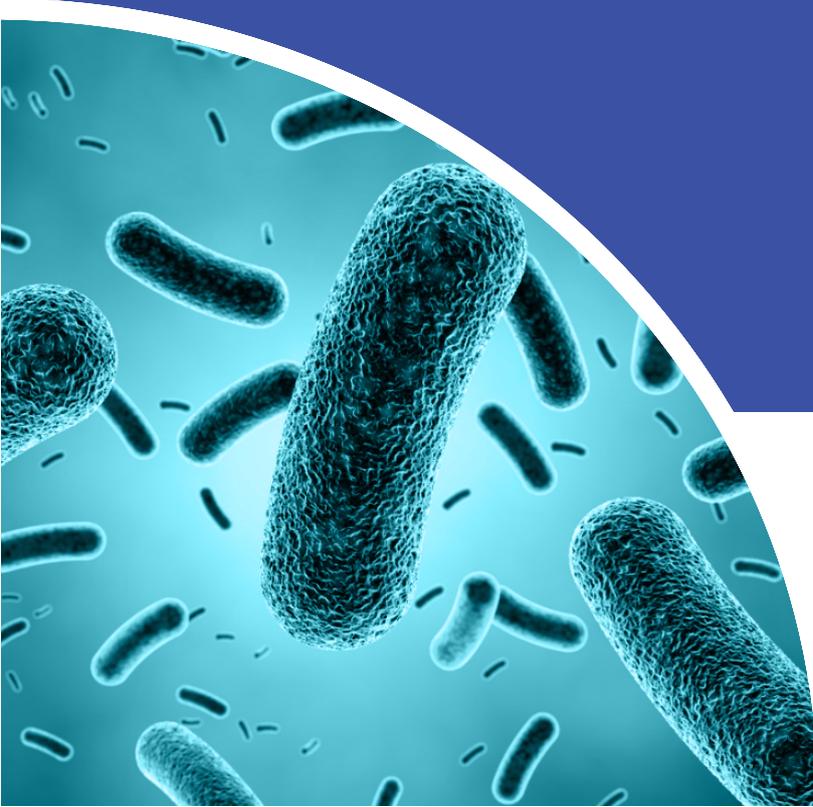




12th
International Conference
BIORADIANCE
2024

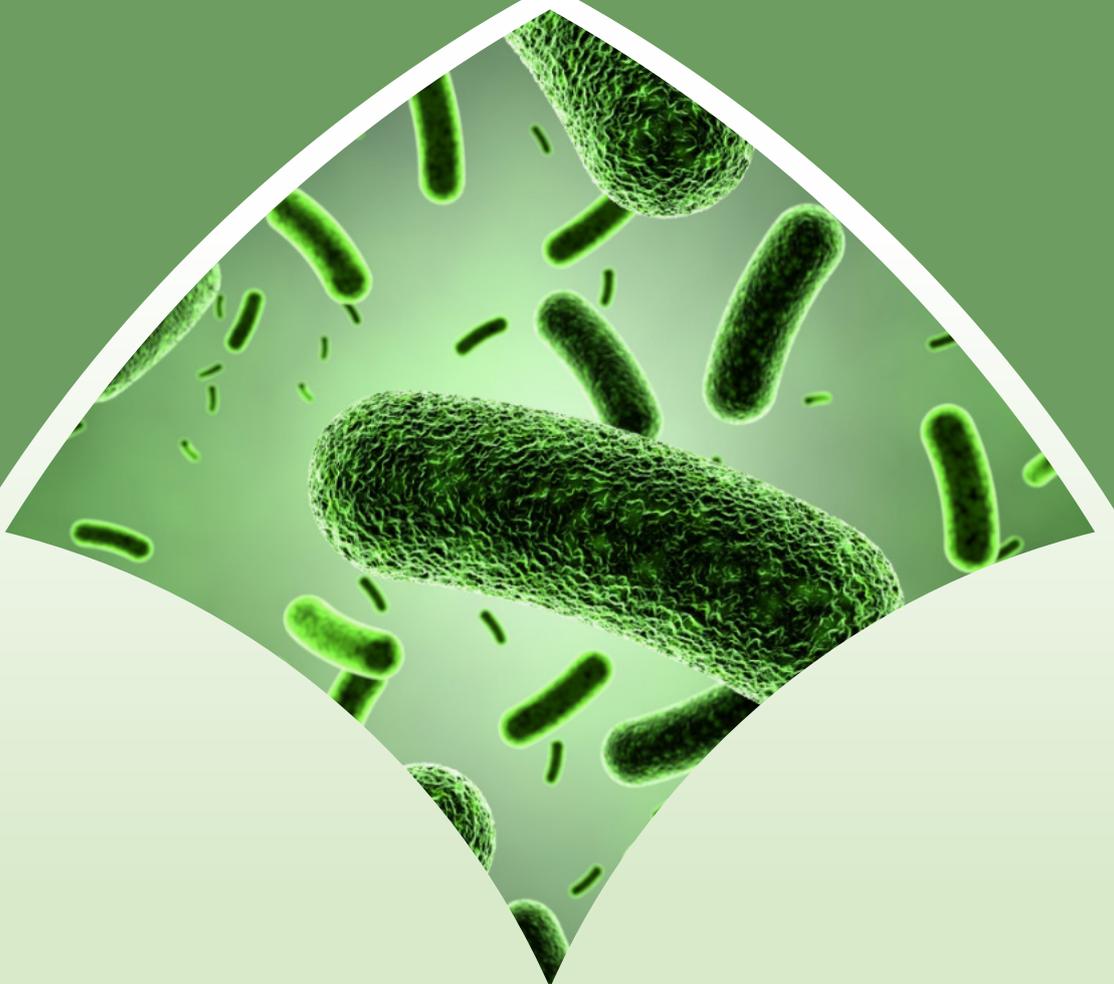




12th International Conference

BIORADIANCE - 2024

- Defeat superbugs, Preserve future -



BOOK OF ABSTRACTS
BIORADIANCE - 2024



12th
International Conference
BIORADIANCE
2024 Defeat Superbugs, Preserve Future

16th-18th MAY 2024
SENATE HALL, PUSHPAGIRI
INSTITUTE OF MEDICAL SCIENCES
AND RESEARCH CENTRE

Theme:
Frontiers In
Antimicrobial Sciences:
International Conference
On Global Advances &
Updates On Antimicrobial
Research And Resistance Strategies

ORGANISED BY
PUSHPAGIRI
RESEARCH CENTRE
(PRC)



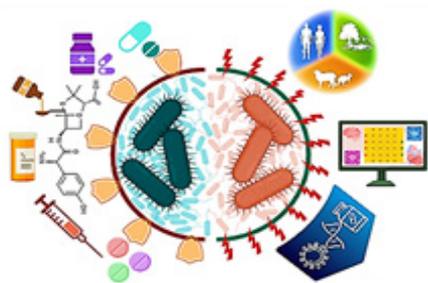
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12th International Conference

BIORADIANCE – 2024

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PROGRAMME SCHEDULE

DAY – 1 (16th May 2024)			
09:00 AM – 10:00 AM	REGISTRATION		
10:00 AM – 11:00 AM	PRAYER & INAUGURAL SESSION		
11:00 AM – 12.45 PM	TECHNICAL SESSION - I		
Chair Person: Dr. Maneesh Paul	11:00 AM 11:40 AM	Dr. Perumal Vivekanandan	Antimicrobial resistance in bacteria: looking beyond conventional mechanisms
	11:40 AM 12:10 PM	Dr. Anand Anbarasu	Understanding the emerging and re-emerging scenarios of antibiotic resistance patterns in clinically important bacterial pathogens through the bioinformatics lens
	12:10 AM 12:50 PM	Dr. Anand Manoharan	Surveillance of AMR- Academia- Pharmaceutical Industry Perspective
02:00 PM – 04:15 PM	LUNCH		
02:00 PM – 04:10 PM	TECHNICAL SESSION - II		
Chair Person: Dr. Paul Livingstone	02:00 PM 02:40 PM	Dr. Maneesh Paul	AMRACE – AMR Action Collaborative Engagement
	02:45 PM 03:25 PM	Dr. Mark Toleman	The importance of virulence and antibiotic resistance in Escherichia coli
	03:30 PM 04:10 PM	Dr. Anindya Sundar Ghosh	Non-active site amino acid residues as the potential targets for designing inhibitors against various classes of β -lactamases
04:15 PM – 04:45 PM	HIGH TEA		
04:50 PM – 06:30 PM	TECHNICAL SESSION - III		
Chair Person: Dr. Anindya S Ghosh	04:50 PM 05:30 PM	Dr. Amitabha Bhattacharjee	Secondary resistome: Potential reporter for AMR diagnostics
06:00 PM – 06:30 PM	Consultive Meeting and Discussion on Collaborative Action Plan to tackle AMR		
06:30 PM – 07:30 PM	CULTURAL PROGRAMMES		
07:30 Onwards	DINNER		

PROGRAMME SCHEDULE

DAY – 2 (17th May 2024)			
09:00 AM – 11:15 AM	TECHNICAL SESSION - IV		
Chair Person: Dr. Anand Anbarasu	09:00 AM 09:40 AM	Dr. Paul Livingstone	Exploring Antimicrobial Peptides from Myxobacteria – A new avenue to tackle AMR
	09:45 AM 10:25 AM	Dr. Murugan Sevanan	Molecular Characteristics, Antibiotic Susceptibility and Biofilm-Forming Ability of Clinical Methicillin Resistant Staphylococcus aureus isolates
	10:30 AM 11:10 AM	Dr. Donghyuk Kim	Blanket antimicrobial resistance gene database with structural information
11:15 AM – 11:45 AM	HIGH TEA		
11:50 AM – 12:30 AM	TECHNICAL SESSION - V		
Chair Person: Dr. Anand Manoharan	11:50 AM 12:30 AM	Dr. Muruganandam Nagarajan	The importance of surveillance for emerging and re-emerging respiratory viruses in the isolated islands of India
	12:35 AM 01:15 PM	Dr. Karthick Gunasekaran	Scrub typhus – A re-emerging infectious disease in South East Asia
12:30 PM – 02:00 PM	LUNCH		
02:15 PM – 04:00 PM	Discussion on Joint Collaborative Ventures to Disseminate Clinical Nosocomial Infections		
04:00 PM – 04:30 PM	HIGH TEA		

DAY – 3 (18th May 2024)	
09:00 AM – 12:30 PM	Oral and Poster Presentations
12:30 PM – 01:30 PM	LUNCH
01:30 PM – 02:30 PM	Prize Distribution, Vote of Thanks & Valedictory Session
02:30 PM – 05:00 PM	Lab Facility and Technical Visits

INAUGURATION SCHEDULE

Theme:

‘Frontiers in Antimicrobial Sciences: International Conference on Global Advances & Updates on Antimicrobial Research and Resistance Strategies’

Date & Venue:

16th May, 2024

Senate Hall, Pushpagiri Institute of Medical Sciences and Research Centre

Organised By:

Pushpagiri Research Centre (PRC)

Co-Sponsored By:

Department of Biotechnology (DBT), New Delhi

Kerala State Council for Science, Technology and Environment (KSCSTE)

In Association With:

Pushpagiri Institute of Medical Sciences

Pushpagiri College of Dental Sciences

Pushpagiri College of Nursing

Prayer Song	
Welcome Speech	Rev. Dr. Mathew Mazhavancheril (Director & Head, Pushpagiri Research Centre)
Presidential Address	Rev. Dr. Biju Varghese (Chief Executive Officer, Pushpagiri Group of Institutions)
Inaugural Address	Prof. Dr. Mohanan Kunnummal (Vice Chancellor, Kerala University of Health Sciences)
LAMP LIGHTING CEREMONY	
Keynote Address	Prof. Dr. Anand Anbarasu (Senior Professor, SBST, Vellore Institute of Technology, Vellore)
Guest of Honour	Prof. Dr. Nandakumar Kalarikkal (Senior Professor, MG University; Former Director, International and Interuniversity Centre for Nanoscience and Nanotechnology)
Felicitation	Rev. Fr. George Valiyaparambil (Academic Director, Pushpagiri Institute of Medical Sciences & Research Centre) Prof. Dr. Jacob Abraham (Vice Principal, PG Academics, Pushpagiri Institute of Medical Sciences & Research Centre) Prof. Dr. A. Devadathan (Dean, Faculty of Dental Sciences, Kerala University of Health Sciences)
Vote of Thanks	Dr. Aniket Naha (Scientist, Pushpagiri Research Centre & General Secretary, BIORADIANCE – 2024)
National Anthem	

INAUGURATION SCHEDULE

Theme:

**‘Frontiers in Antimicrobial Sciences: International Conference on
Global Advances & Updates on Antimicrobial Research and Resistance Strategies’**

Date & Venue:

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Senate Hall, Pushpagiri Institute of Medical Sciences and Research Centre

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In Association With:

Pushpagiri Institute of Medical Sciences

Pushpagiri College of Dental Sciences

Pushpagiri College of Nursing

Prayer Song	
Welcome Speech	Mr. George Varghese (Research Coordinator & Virology-in-charge, Pushpagiri Research Centre)
Presidential Address	Rev. Dr. Mathew Mazhavancheril (Director & Head, Pushpagiri Research Centre)
Keynote Address	Prof. Dr. Nebu George Thomas (Professor & Scientist, Pushpagiri College of Dental Sciences and Pushpagiri Research Centre, Co-Secretary, BIORADIANCE – 2024)
Prize Distribution	Dr. Aniket Naha (Scientist, Pushpagiri Research Centre, General Secretary, BIORADIANCE – 2024)
Feedback Speech	Dr. Paul Livingstone (Senior Lecturer, Cardiff Metropolitan University, UK)
Vote of Thanks	Dr. Yogesh Bharat Dalvi (Scientist, Pushpagiri Research Centre, Convenor, BIORADIANCE – 2024)
National Anthem	



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Department of
 BioTechnology,
 Government
 of India



Co-Sponsored By
DEPARTMENT OF BIOTECHNOLOGY (DBT), NEW DELHI
**KERALA STATE COUNCIL FOR SCIENCE,
 TECHNOLOGY AND ENVIRONMENT (KSCSTE)**

16th-18th MAY 2024

**SENATE HALL, PUSHPAGIRI INSTITUTE OF
 MEDICAL SCIENCES AND RESEARCH CENTRE**

In Association With
PUSHPAGIRI INSTITUTE OF MEDICAL SCIENCES
PUSHPAGIRI COLLEGE OF DENTAL SCIENCES
PUSHPAGIRI COLLEGE OF NURSING

» ABOUT PUSHPAGIRI RESEARCH CENTRE

Pushpagiri Research Centre (PRC) was established in 2010 and serves as the central research wing for various institutions under Pushpagiri Medical Society since its inception. PRC is an approved Ph.D. center by both Helsinki University, Finland and Kerala University of Health Sciences (KUHS), India. The Centre is also recognized as a Scientific and Industrial Research Organization (SIRO) by the Department of Scientific & Industrial Research (DSIR) under the Ministry of Science & Technology, Govt. of India. The center harbors variety of research laboratories including cell and molecular biology, tissue engineering, regenerative medicine, medical biotechnology, computational biology, biochemistry, clinical microbiology and CCSEA-approved animal house facility. PRC secures funding from various agencies of national and international repute like DST, DBT, ICMR, KSCSTE, Conferenza Episcopale Italiana and the Bill & Melinda Gates Foundation, besides actively hosting several international research collaborations. PRC's Institutional Animal Ethics Committee (IAEC) is registered with CCSEA while the Institution Review Board (IRB) are registered with Department of Health Research and CDSCO, facilitating animal experiments and Phase-I & II clinical trials. With active Memorandum of Understanding (MoUs) with national and international entities, both in governmental and private, PRC stands as a hub of interdisciplinary research excellence.



» ABOUT BIORADIANCE - 2024

Pushpagiri Research Centre is overwhelmed to announce the hosting of the 12th annual conference '**Bioradiance - 2024**' which serves as a beacon of research excellence for the center. The 12th edition signifies a remarkable milestone, expanding its spectrum from a national to an international level for the first time. This vibrant platform unites several undergraduate and postgraduate students, physicians, clinicians, faculties, scientists, research scholars and industrialists, providing them with the opportunity to showcase their work and engage with the experts

across diverse domains. The organizing team of 'Bioradiance - 2024' cordially invites one and all to the international conference bearing the theme "**Frontiers in Antimicrobial Sciences: International Conference on Global Advances & Updates on Antimicrobial Research and Resistance Strategies**" and foster to make this a grand success. This event aims to be a podium where global minds can converge to address the challenges and remedies to tackle the ardent catastrophe concerning antimicrobial resistance. Explore innovation's forefront from groundbreaking discoveries to collaborative efforts, and contribute to shaping a future where health triumphs over adversity.

» ORGANIZING COMMITTEE

Patrons

His Grace Most Rev. Dr. Thomas Mar Koorilos
Rev. Dr. Biju Varghese
Rev. Dr. Mathew Mazhavancheril
Rev. Fr. Aby Vadakumthala
Rev. Fr. George Valiyaparampil

Organizing Chairperson

Rev. Dr. Mathew Mazhavancheril
Dr. Anand Anbarasu
Dr. Reena Thomas
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Dr. Yogesh Bharat Dalvi

General Secretary

Dr. Aniket Naha

Additional Secretary

Dr. Nebu George Thomas

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Dr. Jacob Abraham
Dr. Sajit Varghese
Mr. George Varghese

Dr. Soumya RS
Dr. Betsy A Jose
Dr. Rosin George Varghese
Dr. Leya Elizabeth Babu

Dr. Serene Varghese
Dr. Purnima C
Dr. Sunil S
Dr. Benley George

Dr. Thomas George
Dr. Binoy T Thomas
Sr. Mary Jyothi OS
Mr. Renji George John

» PLENARY SPEAKERS: INTERNATIONAL



Dr. Mark Toleman
Cardiff, UK



Dr. Paul Livingstone
Cardiff, UK



Dr. Donghuk Kim
UNIST, S. Korea



Dr. Anand Manoharan
GSK, UK

» PLENARY SPEAKERS: NATIONAL



Dr. Anand Anbarasu
VIT, Vellore



Dr. Maneesh Paul
Microioma, Bangalore



Dr. Murugan Sevanan
KITS, Coimbatore



Dr. Manabendra D. Choudhury
Assam University, Silchar



Dr. Anindya S. Ghosh
IIT Kharagpur, W. Bengal



Dr. Amitabha Bhattacharjee
Assam University, Silchar



Dr. Perumal Vivekanandan
IIT Delhi, Delhi



Dr. Muruganandam Nagarajan
ICMR, Port Blair



Dr. Karthik Gunasekaran
CMC, Vellore

» FOCUS AREAS

- Scopes on Clinical, Food & Environmental Microbiology
- Advancement in Personalised Medicine
- Future Therapeutics: ML & AI Aided Drug Designing
- Research & Advances in Life Sciences
- Pharmaceutical & Industrial Biotechnology
- Recent Endeavours in Biosciences and Biochemistry
- Nanomaterials and Nanomedicine
- High Throughput Sustainable Drug Delivery Systems
- Diagnostics, Molecular Biology & Genetic Engineering
- Recent Advances in Tissue Engineering & Regenerative Medicine

REGISTRATION

CATEGORY	NATIONAL (INR ₹)	INTERNATIONAL (USD \$)
Students	1000	80
Research Scholars	1500	100
Faculty	2000	150
Industrialists	3000	200

For Online Registration:



<http://tinyurl.com/ykb52dvp>

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» ABSTRACT SUBMISSION AND GUIDELINES

Participants are encouraged to actively contribute in the International Conference by submitting abstracts for poster and oral presentations, aligning with the theme **"RESEARCH AND ADVANCEMENTS IN BIOLOGICAL AND MEDICAL SCIENCES."** Submitted abstracts will undergo a thorough review process and the acceptance of abstracts will be communicated through the registered email address.

» Language

English (within 250 words & 5 keywords)

» Font

Times New Roman; Title – Pt. 14, Bold, Centered;
Body – Pt 12, Justified

» Author Information

Include complete author names & current affiliations Clearly indicate the 'Presenting Author' and the 'Corresponding Author'

» Submission Deadline

Abstracts should be sent on or before May 13, 2024 to bioradiance2024@pimsrc.edu.in

» CONTACT DETAILS

For queries and concerns feel free to contact us at bioradiance2024@pimsrc.edu.in

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Dr. Nebu George Thomas

- +91 9447044726
- nebugeorgethomas@pushpagiri.in

PROCEEDINGS OF BIORADIANCE – 2024



From left to right:

Dr Aniket Naha (*Secretary & Scientist*), Dr Yogesh Bharat Dalvi (*Convenor & Scientist*), Prof. Anand Anbarasu (*Chairperson*), Rev. Dr. Mathew Mazhavancheril (*Patron, Director & Head*), Prof. Nandakumar Kalarikkal (*Guest of Honour*), Prof. Dr. Mohanan Kunnummal (*Chief Guest*), Rev. Dr. Biju Varghese (*CEO*), Rev. Fr. George Valiyaparambil (*Academic Director*), Dr. Jacob Abraham (*Vice Principal*), Prof. A. Devadathan (*Dean Dentistry, KUHS*) and Prof. Nebu George Thomas (*Additional Secretary*)

Pushpagiri Research Centre (PRC) has successfully organized and conducted the 12th annual conference, Bioradiance – 2024, spanned from 16th – 18th May, 2024. This year's conference, themed “Frontiers in Antimicrobial Sciences: International Conference on Global Advances & Updates on Antimicrobial Research and Resistance Strategies”, saw its expansion to an international platform, drawing over 250 delegates & participants from across the globe in hybrid mode amalgamating together to tackle the critical issue of antimicrobial resistance (AMR) in nosocomial pathogens. The conference was co-sponsored by the Department of Biotechnology (DBT), New Delhi and the Kerala State Council for Science, Technology and Environment (KSCSTE) implicating the importance of antibiotic stewardship and one-

health approach programmes in alignment to Nation's health plans schemes. The Kerala University of Health Sciences (KUHS) have wholeheartedly endorsed the programme and supported with us with medical and dental credit points.

The inaugural session witnessed esteemed dignitaries gracing the occasion and lighting the holy lamp. Significant personnel being Prof. Dr. Mohanan Kunnummal, Vice Chancellor of KUHS who has honored the event as the Chief Guest. Highlighting on the motto of the conference ‘Defeat Superbugs, Preserve Future’, Prof. Kunnummal highlighted the importance of such conferences and congratulated the organizing team for discussing such significant topics at a conference of such international

standard. He stated “Defeating superbugs is not just a regional effort; it requires a global commitment” and emphasized growth of research cultures in medical college setups. Motivating doctors and scientists, he highlighted that importance of translational research clubbed with machine learning and artificial intelligence. Prof. Dr. Nandakumar Kalarikkal, Senior Professor from Mahatma Gandhi University, was the Guest of Honour who too highlighted the emerging trends of multi-drug resistance and extensively drug resistance bacterial isolates in recent years. Rev. Dr. Mathew Mazhavancheril, Director & Head, PRC, delivered the Welcome Speech, followed by an inspiring Presidential Address by Rev. Dr. Biju Varghese, CEO of Pushpagiri Group of Institutions. Additionally, Rev. Fr. George Valiyaparambil, Dr. Jacob Abraham, Vice principal, PG Academics and Prof. Dr. A. Devadathan, Dean Dentistry, KUHS graced the event with their felicitation addresses. Dr. Aniket Naha, Scientist PRC and General Secretary of BIORADIANCE-2024 extended heartfelt thanks to all the delegates on and off the dais, plenary speakers, participants, organizing committee and all who have helped for the successful conduction of the conference.

A total of 12 national and international speakers, stalwarts in the field of antimicrobial drug discovery has delivered their plenary talks on topics such as Antibiotic Stewardship, One Health Approach, Sustainable Therapy, AMR Surveillance, Machine Learning, and Artificial Intelligence over a period of 2 days. The international and national delegates were Prof. Mark Toleman and Prof. Dr. Paul Livingstone from Cardiff Metropolitan University, UK; Prof. Donghyuk Kim (UNIST, South Korea), Dr. Anand Manoharan (GSK, UK); Prof. Anand Anbarasu (Vellore Institute of Technology, Vellore); Dr. Maneesh Paul (Microvioma, Bangalore); Prof. Murugan Sevanan (Karunya Institute of Technology and Sciences, Coimbatore); Prof. Dr. Anindya Sundar Ghosh (Indian Institute of Technology, Kharagpur), Prof. Perumal Vivekanandan (Indian Institute of Technology, Delhi); Prof. Dr. Amitabha Bhattacharjee (Assam University, Silchar); Dr. Karthik Gunasekaran (Christian Medical College & Hospital); Dr. Muruganandam Nagarajan (Regional Medical Research Centre, ICMR).

A consultive meeting and discussion on collaborative action plan to tackle AMR engaged delegates and faculties of PRC along with research scholars from different universities. The meeting was presided by Prof. Anand Anbarasu and active involvement of Dr. Maneesh, Dr. Anindya, Dr. Paul and Dr. Perumal.

The meeting displayed the research strengths and expertise of individual and planned for future joint collaborations, patents and big-grants proposal aids. The event concluded with a cultural flavour, with captivating dance performances showcasing Kerala’s rich heritage by the talented students of Pushpagiri Institute of Medical Sciences and Research Centre, Pushpagiri College of Dental Sciences, and Pushpagiri College of Nursing.

Over 64 abstracts for oral and poster presentations were received and scrutinized for under basic and medical research. Students, research scholars and faculty/scientists from Assam University, Silchar; Vellore Institute of Technology, Vellore; University of Calicut; Calicut Amrita Vishwa Vidyapeetham, Kollam; Believers Church Medical College Hospital, Tiruvalla; Jubilee Mission Medical College and Research Institute, Thrissur; Mar Athanasios College for Advanced Sciences, Tiruvalla; Jain (Deemed-to-be) University; NIMS University; St. Xavier’s College; Aluva, St. Berchman’s College, Changanassery; Lovely Professional University, Punjab; Fergusson College, Indian Institute of Technology Roorkee; Karunya Institute of Technology and Sciences; Tujaram Chaturchand College of Arts, Science and Commerce, Baramati; Mahatma Gandhi University of Medical Sciences and Technology, Jaipur, Himalayan Institute of Medical Sciences, Uttarkhand; St. Martha’s Hospital, Bangalore; MIMER Medical College, Pune; Sir H N Reliance Foundation Hospital and Research Centre, Mumbai; Pushpagiri Institute of Medical Sciences and Research Centre & Pushpagiri College of Dental Sciences, Tiruvalla actively participated and contributed to the success of the conference.

The three days conference ended with technical visits of delegates to the Research Centre Visit, visit to CCSEA and IAEC approved Animal House facilities by delegates and scholars. The valedictory session ended with prize distribution to the winners and runners-up students, research scholars and faculty/scientists for oral and poster presentations under medical and basic research category. Valedictory session concluded upon welcome speech by Mr. George Varghese, coordinator PRC, presidential address by Rev. Dr. Mathew Mazhavancheril, Director & Head, PRC, keynote address by Prof. Dr. Nebu George Thomas, additional secretary of BIORADIANCE, feedback address by Dr. Paul Livingstone and vote of thanks by Dr. Yogesh Bharat Dalvi, Scientist and Convenor – BIORADIANCE. The programme ended on a high note with National Anthem being sung by all attendees.



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financedirector@pushpagiri.in
🌐 www.pushpagiri.in

CEO's Message:

Distinguished Guests and Scholars,

I extend my sincerest greetings to each of you as we gather for the "International Conference on Frontiers in Antimicrobial Sciences: Bioradiance 2024," hosted by the esteemed Pushpagiri Research Centre in association with Pushpagiri Institute of Medical Sciences, Pushpagiri College of Dental Sciences and Pushpagiri College of Nursing.

As the CEO, I am deeply committed to foster academic excellence and research innovation and proud to support initiatives such as this conference, which serve as catalysts for interdisciplinary collaboration and knowledge exchange.

Since its inception in 2010, the Pushpagiri Research Center has been instrumental in advancing scientific inquiry, boasting state-of-the-art research facilities and earning recognition as a Scientific and Industrial Research Organization (SIRO) by the Department of Scientific & Industrial Research (DSIR) under the Ministry of Science & Technology, Govt. of India.

This conference represents a pivotal opportunity to explore the forefront of antimicrobial research and address the pressing challenges posed by antibiotic resistance. With the endorsement of prestigious institutions like the Kerala University of Health Sciences (KUHS), Trissur, and collaboration with esteemed entities such as the Department of Biotechnology (DBT) and The Kerala State Council for Science, Technology and Environment (KSCSTE), we are poised to make significant strides in advancing scientific knowledge.

I extend my heartfelt gratitude to the organizers, sponsors, and participants for their unwavering dedication to furthering scientific understanding and fostering innovation. Your contributions are invaluable in shaping the future of antimicrobial sciences and mitigating the threats posed by infectious diseases.

As we embark on this collaborative journey, I am confident that this conference will serve as a beacon of excellence, inspiring transformative research and forging enduring partnerships.

With warm regards,

Rev. Dr. Biju Varghese
CEO, Pushpagiri Institute of Medical Sciences



Fr. Dr. Biju Varghese
CEO
Pushpagiri Group of Institutions
Tiruvalla - 689 101

Institutions under Pushpagiri Medical Society

- Pushpagiri Institute of Medical Sciences and Research Centre
- Pushpagiri Medical College Hospital
- Pushpagiri Heart Institute
- Pushpagiri College of Dental Sciences
- Pushpagiri College of Pharmacy
- Pushpagiri College of Nursing
- Pushpagiri College of Allied Health Sciences
- Pushpagiri School of Nursing
- Pushpagiri Centre for CGFNS and IELTS Training
- Pushpagiri Research Centre

DIRECTOR'S MESSAGE



Rev. Dr. Mathew Mazhavancheril
Patron & Chairperson, BIORADIANCE - 2024
Director & Head, Pushpagiri Research Centre

On behalf of the management team at Pushpagiri Research Centre, it is my distinct pleasure to extend a warm welcome to each of you to the “International Conference on Frontiers in Antimicrobial Sciences: Bioradiance 2024”. Established in 2010, our research centre has been a cornerstone of pioneering research initiatives, fostering collaborations across various institutions under the Pushpagiri Medical Society. Recognized as a Scientific and Industrial Research Organization (SIRO) by the Ministry of Science & Technology, Govt. of India, we take great pride in our diverse array of cutting-edge research laboratories.

This conference represents a crucial platform for international discourse on the latest advancements and strategies in antibiotic research and resistance. Endorsed by esteemed institutions like the Kerala University of Health Sciences and co-organized with partners such as the Department of Biotechnology and The Kerala State Council for Science, Technology and Environment, alongside Elsevier as our academic partner, Bioradiance 2024 promises to facilitate an unparalleled exchange of ideas and knowledge dissemination.

The overwhelming response from contributors underscores the conference’s significance in addressing the challenges posed by antimicrobial resistance in the 21st century. Your invaluable contributions will undoubtedly enrich the proceedings and pave the way for future research endeavours. With a dedicated team and your active participation, we are confident that this conference will be a resounding success, driving forward the boundaries of antimicrobial sciences.

I eagerly anticipate engaging discussions, insightful presentations, and fruitful collaborations throughout the event. Together, let us advance towards a future where our collective efforts contribute to mitigating the global impact of antimicrobial resistance.

Warm regards,



Rev. Dr. Mathew Mazhavancheril

CHAIRPERSON'S MESSAGE



PROF. DR. ANAND ANBARASU
Chairperson, 'BIORADIANCE 2024'
Advisory Member, Pushpagiri Research Centre
Senior Professor, Vellore Institute of Technology, Vellore

It is with immense pride and a deep sense of responsibility that I welcome you to the abstract book of 'BIORADIANCE 2024', themed 'Frontiers in Antimicrobial Sciences: International Conference on Global Advances & Updates on Antimicrobial Research and Resistance Strategies'. As an advisory member of the Pushpagiri Research Centre (PRC) and Chairperson of this prestigious event, I am honoured to present the collective efforts of leading researchers, scientists, academicians, and industry professionals from around the globe. Antimicrobial resistance (AMR) stands as one of the most pressing global health challenges of our time. The relentless evolution of drug-resistant pathogens necessitates urgent and concerted efforts to manage and mitigate its impact. This conference seeks to address this urgency by fostering a platform for knowledge exchange, insightful discussions, and the forging of collaborations aimed at overcoming the barriers posed by AMR.

The abstracts compiled in this book represent cutting-edge research and innovative strategies that span the spectrum of AMR. They encompass the latest advancements and updates on antimicrobial research, resistance mechanisms, and novel therapeutic strategies. Moreover, this compilation underscores the importance of a One Health Approach, recognizing the interconnectedness of human, animal, and environmental health in combating AMR. Effective stewardship programs are critical in optimizing the use of antibiotics, thereby reducing the emergence and spread of resistant strains. Through strategic interventions, policy-making, and education, we aim to enhance the judicious use of antibiotics across all sectors.

The research findings presented here are a testament to the dedication and relentless efforts of the global scientific community. It is through such collaborative endeavours that we can hope to turn the tide against AMR. I extend my heartfelt gratitude to all contributors for their valuable research and insights. Let us together strive towards a future where antimicrobial resistance is effectively managed, ensuring the health and well-being of generations to come.

A handwritten signature in blue ink, appearing to read 'A Anbarasu', located below the main text.

Prof. Dr. Anand Anbarasu

CONVENOR'S MESSAGE



DR. YOGESH BHARAT DALVI, M.Sc., Ph.D.

Convener, BIORADIANCE – 2024
Pushpagiri Research Centre,
Pushpagiri Institute of Medical Sciences
Pushpagiri Research Center, Tiruvalla,
Kerala, India 689101

It is with great pleasure and anticipation that I extend a warm welcome to each of you to the “International Conference on Frontiers in Antimicrobial Sciences: Bioradiance 2024” on behalf of the Pushpagiri Research Centre, Pushpagiri Institute of Medical Sciences and Research Centre, Tiruvalla, Kerala, India 689101. Established in 2010, the Pushpagiri Research Center has been at the forefront of cutting-edge research, serving as the central hub for various institutions under the Pushpagiri Medical Society. Recognized as a Scientific and Industrial Research Organization (SIRO) by the Department of Scientific & Industrial Research (DSIR) under the Ministry of Science & Technology, Govt. of India, the centre boasts a diverse array of research laboratories.

This conference serves as a vital platform to explore the latest international advancements and strategies in antibiotic research and resistance. Our primary objective is to foster collaboration and partnership-building to advance microbial science research. With the endorsement of esteemed institutions such as the Kerala University of Health Sciences (KUHS), Thrissur, and co-organization by reputable entities like the Department of Biotechnology (DBT) and The Kerala State Council for Science, Technology and Environment (KSCSTE), alongside Elsevier as our academic partner, we are poised for a fruitful exchange of ideas and knowledge dissemination. The overwhelming response from contributors and educational communities underscores the significance of this conference in addressing the challenges posed by superbugs in the 21st century. I extend my heartfelt appreciation to all participants for their invaluable contributions, which undoubtedly enrich the conference proceedings and pave the way for future research endeavours.

I am confident that with the collective efforts of our dedicated team, this conference will be a resounding success, facilitating the exploration and application of the latest developments in antimicrobial sciences. I eagerly anticipate engaging discussions and fruitful collaborations throughout the event.

A handwritten signature in blue ink, appearing to read 'Y. Dalvi', enclosed within a circular flourish.

DR. YOGESH BHARAT DALVI

SECRETARY'S MESSAGE



DR. ANIKET NAHA, (M.Sc., Ph.D.)

Secretary, BIORADIANCE – 2024
Scientist & Student Coordinator,
Pushpagiri Research Centre
Tiruvalla, Kerala - 689101

It is with great pleasure and anticipation that I extend a warm welcome to you all to the 12th international conference, BIORADIANCE – 2024 organized by Pushpagiri Research Centre from 16 – 18th May, 2024. This milestone event marks the transition of our esteemed gathering from a national to an international platform, for the first time in our PRC's history.

“For I know the plans I have for you,” declares the Lord, “plans to prosper you and not to harm you, plans to give you hope and a future.” - Jeremiah 29:11

Since its inception, BIORADIANCE has been a catalyst for innovation and collaboration in the field of biomedical sciences. With each passing year, it has grown in stature and influence, attracting an ever-expanding community of students, physicians, clinicians, faculty, scientists, researchers and industrialists. The theme of this year's conference, “Frontiers in Antimicrobial Sciences: International Conference on Global Advances & Updates on Antimicrobial Research and Resistance Strategies”, reflects our commitment to fostering dialogue and collaboration on a global scale. We are happy to announce that our conference was wholeheartedly co-sponsored by the Department of Biotechnology (DBT), New Delhi and Kerala State Council for Science, Technology and Environment (KSCSTE).

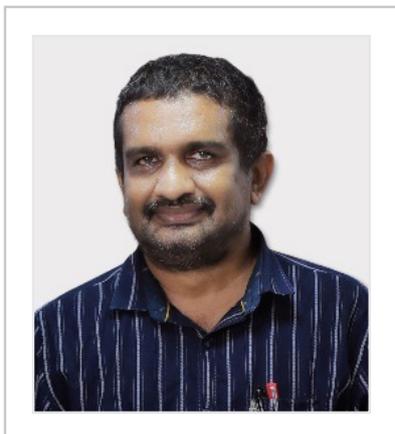
Bioradiance – 2024 serves as a dynamic platform for showcasing cutting-edge research, sharing insights, and engaging in meaningful discussions. As the threat of antimicrobial resistance looms larger than ever before, it is imperative that we come together to address this urgent global health crisis. BIORADIANCE – 2024 aims to be a catalyst for change, providing a forum where global minds can converge to develop innovative solutions and strategies to combat antimicrobial resistance and safeguard public health.

On behalf of the organizing team of BIORADIANCE – 2024, I extend a warm welcome to one and all to join us in this international conference and contribute to making it a grand success.

A handwritten signature in blue ink that reads "Aniket Naha". The signature is written in a cursive style and is positioned above a horizontal line.

Dr. Aniket Naha

ADDITIONAL SECRETARY'S MESSAGE



DR. NEBU GEORGE THOMAS (MDS, Ph.D.)
Additional Secretary, BIORADIANCE 2024
Professor, Pushpagiri College of Dental Sciences
Scientist, Tissue Engineering Lab, PRC

It is with great pleasure and anticipation that I extend a warm welcome to the esteemed gathering of researchers, scientists, and professionals at the 12th International Conference, Bioradiance 2024. This conference marks a significant milestone for us as we transition to an international stage, reflecting our commitment to advancing biomedical sciences globally.

Since its inception, Bioradiance has served as a beacon for innovation and collaboration in addressing critical issues such as antimicrobial resistance. This year, under the theme “Frontiers in Antimicrobial Sciences: International Conference on Global Advances & Updates on Antimicrobial Research and Resistance Strategies”, we are poised to explore groundbreaking research, share insights, and engage in meaningful discussions.

As scientists dedicated to combating antimicrobial resistance, we understand the urgency and complexity of this global health crisis. Bioradiance 2024 provides a unique platform to discuss and develop innovative solutions that can safeguard public health worldwide. Supported by co-sponsors like the Department of Biotechnology and the Kerala State Council for Science, Technology and Environment, our conference aims to catalyze impactful changes through collaborative efforts.

I invite each of you to join us in this pivotal event, contribute your expertise, and help us shape the future of antimicrobial sciences. Together, let's harness our collective knowledge and passion to address the challenges of antimicrobial resistance effectively.

Warm regards,

A handwritten signature in blue ink, appearing to read 'Nebu George Thomas'.

DR. NEBU GEORGE THOMAS



KERALA UNIVERSITY OF HEALTH SCIENCES

THRISSUR- 680596

Phone: 0487 2207646, 0487 2207738, Email: registrar@kuhs.ac.in

No: 13866/2024/AC1/Dent/A1/KUHS

Dated: 06-05-2024

To ,

Rev. Dr. Mathew Mazhavancheril
Director and Head, Pushpagiri Research Centre,
Pushpagiri Group of Institutions, Tiruvalla, Kerala, India – 689101

Dear Sir,

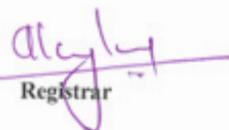
Sub : Endorsement of the 12th International Conference BIORADIANCE- 2024-reg:-

I am writing to express our full support and endorsement for the upcoming 12th Annual Conference, "BIORADIANCE-2024" organized by the Pushpagiri Research Centre (PRC). The event, scheduled from 16th to 18th May 2024, at the Senate Hall, PIMS & RC, Tiruvalla, Kerala, India, promises to be an exceptional gathering of minds in the field of biological and medical sciences. The theme of this year's conference, "**Frontiers in Antimicrobial Sciences: International Conference on Global Advances & Updates on Antimicrobial Research and Resistance Strategies**", reflects the pressing need for discussion concerning antimicrobial resistance, a critical issue facing the global community today.

Kerala University of Health Sciences, wholeheartedly endorse and support the smooth conduct of the conference.

Wishing every success to the venture,




Registrar



KERALA STATE MEDICAL COUNCIL OF MODERN MEDICINE
COMBINED COUNCIL BUILDING, RED CROSS ROAD, THIRUVANANTHAPURAM- 695 035, KERALA, INDIA.

No. C6/7284/2024/MC/CME

Date: 08/05/2024

To,

Dr. Rosin George Varghese
Assistant Professor
Dept. of Community Medicine
Pushpagiri Institute of Medical Services & Research Centre
Thiruvalla - 689101

Sir,

Sub:- Kerala State Medical Councils – Allotment of credit hours for CME programme on the subject **Bioradiance-2024** - reg
Ref:- Your application dated 19/03/2024.

With reference to the above, it is decided to allot by the CME committee of the Council of Modern Medicine **3 hours (Three hours)** credit time for the CME Programme on the subject **Bioradiance-2024** conducted by **Pushpagiri Institute of Medical Services & Research Centre** at **Senate Hall, PIMS&RC** on **16th to 18th May 2024**.

This approval is based upon your adherence to the following instructions:-

1. A report on the programme shall be submitted to this office by the organizing Secretary with his Name, and KSMC Registration Number.
2. List of the participants with Kerala State Medical Councils Registration Number and copy of the certificate issued to the participants should be furnished to the Council within one month from the date of the programme.

3. Soft copy of the list of participants and their credit hours with Kerala State Medical Councils Registration number in Excel format is also to be forwarded to the Email ID of the Kerala State Medical Councils.
4. Attendance with Kerala State Medical Councils Registration Number should be marked for each day of the programme.
5. A representative of the Kerala State Medical Councils will visit the venue during the programme.
6. Provisional Registration with NMC is necessary for the participation of Foreign Faculties if any in the CME Programme.
7. Certificates should be distributed/awarded only at the closure of last session of the CME.
8. The application fee once remitted is non-refundable.
9. In case it is found that the certificate issued is false then the issuing Association/Organization will be debarred for future accreditation.



Yours faithfully,

REGISTRAR



KERALA DENTAL COUNCIL

www.dentalcouncil.kerala.gov.in

registrar.kdc@kerala.gov.in

No.CDE/5417/24/KDC

Date: 30/04/2024

To

The Principal
Pushpagiri College of Dental Sciences,
Pushpagiri Medicity, Perumthuruthy
MC Road, Thiruvalla

Sir,

Sub :- Kerala Dental Council – Pushpagiri College of Dental Sciences - Request for
CDE - Credit Points - Reg.

Ref :- Your application dated 17/04/2024 received in this office on 20/04/2024.

.....

With reference to the above, I am to inform that your request has been considered and decided to grant **6 (Six) Credit Points** for the CDE Programme on the Subject **"Bioradiance – 2024-Defeat Superbugs, Preserve Future"** scheduled at **Senate Hall, PIMS &RC** on **16th & 18th May 2024**. A report regarding the Programme conducted along with the list of participants with their Kerala Dental Council registration number and a specimen copy of the certificate issued to the participants should be furnished to the Council within one month from the date of the Programme. The report and the list of participants shall be counter signed by Kerala Dental Council observer.

KDC Observer : Dr. Jose Jacob

Yours Faithfully,

 Registrar

TC 27/741(3) AMBALATHUMUKKU, VANCHIYOOR P.O., THIRUVANANTHAPURAM, KERALA – 695 035
Phone:0471-2478757, 2478758, 2478759



Mark Toleman

Department of Medical Microbiology,
Division of Infection and Immunity,
Cardiff University,
Cardiff, United Kingdom
Presenting author:
tolemanma@cardiff.ac.uk

The Importance of Virulence and Antibiotic Resistance in *Escherichia coli*

ABSTRACT

Escherichia coli is a key human pathogen responsible for the majority of Urinary tract infections as well as the principal cause of serious bloodstream infection throughout the world. This is mostly because of its high carriage rate in the gut of humans (c. 100%) and infection is typically endogenous. Bloodstream infection with *E. coli* is not trivial and carries a near 20% mortality rate, this rate doubles to near 40% if the infecting strain is resistant to first line antibiotics. Controlling antibiotic resistance in *E. coli* is thus one of the most important challenges to modern medicine. The sequencing era has greatly increased our understanding of *E. coli* as a species and we now know that there are more than 13,000 individual strains classified by multi-locus sequencing. This sequence-based typing methodology has enabled us to understand the diseases caused by *E. coli* as well as to easily compare *E. coli* strains in different parts of the world. Our work with *E. coli* over the last two decades has uncovered the emergence of powerful antibiotic resistance mechanisms that originated within India including CTX-M-15 and NDM-1 and that have caused treatment failures throughout the world. The powerful combination of the CTX-M-15 resistance mechanism with the *E. coli* strain ST131 also originates from India with the earliest isolates being found in numerous tertiary care settings in India in 2,000. Interestingly, this combination is rarely found within India today yet is the main cause of treatment difficulties in the western world. More recently, we have studied pathogenic *E. coli* types in several different nations and found some striking results. In the western-world only 5-6 strains out of the known 13,000 *E. coli* strains are responsible for >60% of all serious blood-stream infection. Interestingly, these individual strains are carried at high rates in the western world and their carriage rates closely match regional *E. coli* sepsis rates within the UK. We have also recently made the same observations in the United States. However, we have also found that the human carriage of these strains is exceptionally low in South Asia. Thus, it appears that India has an epidemic of carriage of highly resistant *E. coli* strains which are typically of low pathogenicity. However, the western world is experiencing an epidemic of carriage of highly pathogenic strains which are generally of low resistance rates. We have evidence that bacteriophage abundance is at the route of these strain differences in the different nations and that only the study of antibiotic resistance in the context of pathogenicity and bacteriophage ecology is likely to solve our disparate problems.



Paul Livingstone†
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Exploring Antimicrobial Peptides from Myxobacteria – A New Avenue to Tackle AMR

ABSTRACT

Antimicrobial peptides (AMPs) are short peptides from a wide range of organisms, from animals and plants to bacteria and fungi. With the antimicrobial resistance increasing at a fast pace across the globe with significant health and economic implications, alternative therapeutic agents such as AMPs have gained prominence in recent times. We explored the genomes of Myxobacteria and found them to have some potential AMPs with promising antimicrobial activity. Cationic peptides of less than 50 amino acids based on their hydrophobicity, amphiphilicity and net charge were chosen to be synthesized. These synthetic AMPs derived from In Silico studies possess a wide range of bactericidal and biofilm eradication activities. A 41 amino acid peptide, Stig370a, with a net charge of 12.25 was found to have some promising antimicrobial features. We tested Stig370a against more than 150 clinical and type strains of a variety of gram-negative bacilli, and found to have very good activity (MICs between 4µg/ml and 32µg/ml) including multi resistant gram-negative bacilli such as ESBL, AmpC and carbapenemase producers. Looking at their toxicity, Stig370a was not cytotoxic in HaCat cells and non-hemolytic with sheep red cells (<256µg/ml). Besides, some AMPs such as RDP092CA_120, Coral_AMP411 and Myxo_mac104, although did not show significant bactericidal properties, they had good antibiofilm properties with a >70% reduction in the bacterial burden. Therefore, AMPs from Myxobacteria may be potential sources of antimicrobial agents to combat AMR.



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Blanket Antimicrobial Resistance Gene Database with Structural Information

ABSTRACT

Antimicrobial resistance (AMR) in pathogenic bacteria poses a significant threat to public health, yet there is still a need for development in the tools to deeply understand AMR genes based on genetic or structural information. In this study, we present an interactive web database named Blanket Overarching Antimicrobial-Resistance gene Database with Structural information (BOARDS, sbml.unist.ac.kr), a database that comprehensively includes 3,943 reported AMR gene information for 1,997 extended spectrum beta-lactamase (ESBL) and 1,946 other genes as well as a total of 27,395 predicted protein structures. These structures, which include both wild-type AMR genes and their mutants, were derived from 80,094 publicly available whole-genome sequences. In addition, we developed the rapid analysis and detection tool of antimicrobial-resistance (RADAR), a one-stop analysis pipeline to detect AMR genes across whole-genome sequencing (WGSs). By integrating BOARDS and RADAR, the AMR prevalence landscape for eight multi-drug resistant pathogens was reconstructed, leading to unexpected findings such as the pre-existence of the MCR genes before their official reports. Enzymatic structure prediction-based analysis revealed that the occurrence of mutations found in some ESBL genes was found to be closely related to the binding affinities with their antibiotic substrates. Overall, BOARDS can play a significant role in performing in-depth analysis on AMR.

Importance: While the increasing antibiotic resistance (AMR) in pathogen has been a burden on public health, effective tools for deep understanding of AMR based on genetic or structural information remain limited. In this study, a blanket overarching antimicrobial-resistance gene database with structure information (BOARDS)-a web-based database that comprehensively collected AMR gene data with predictive protein structural information was constructed. Additionally, we report the development of a RADAR pipeline that can analyze whole-genome sequences as well. BOARDS, which includes sequence and structural information, has shown the historical landscape and prevalence of the AMR genes and can provide insight into single-nucleotide polymorphism effects on antibiotic degrading enzymes within protein structures



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Surveillance of Antimicrobial Resistance (AMR)-Academic-Pharmaceutical Industry Perspective

ABSTRACT

Surveillance of Antimicrobial Resistance (AMR) from the perspective of academia and the pharmaceutical industry is crucial in combating the growing threat of antibiotic-resistant bacteria. Provided below is an overview of how each sector's role and needs fulfilment in containing AMR via surveillance. In my presentation, I will expand on each of the points below with my experience both from academia and industry.

1. Academia:

Research and Development: Academic institutions conduct extensive research to understand the mechanisms of antimicrobial resistance, identify emerging resistant strains, understand the epidemiology of resistance and develop new diagnostic tools therapies as well as novel bioinformatics-based systems.

Data Collection and Analysis: Academia often plays a pivotal role in collecting and analyzing data on antimicrobial resistance trends. This includes surveillance of resistance patterns in clinical settings, communities, and environmental reservoirs.

Collaboration, knowledge sharing via Networking: Academics collaborate with healthcare facilities, public health agencies, and other stakeholders to share data, expertise, and resources for effective surveillance and response to AMR. This collaborative approach helps to strengthen surveillance networks and improve the understanding of AMR dynamics.

2. Pharmaceutical Industry:

Drug Development and Innovation- Pharmaceutical companies invest in research and development to discover and develop new antibiotics and antimicrobial agents. Surveillance data on resistance patterns help inform the design of these drugs to target emerging resistant strains.

Monitoring Resistance Patterns: Pharmaceutical companies actively monitor resistance patterns to their products. This allows them to identify and respond to emerging resistance trends, update prescribing guidelines, and optimize treatment strategies

Post-Market Surveillance: After drugs are approved and in use, pharmaceutical companies conduct post-market surveillance to monitor for any signs of resistance development or unexpected adverse effects. This ongoing monitoring helps to ensure the continued efficacy and safety of antimicrobial agents.

Regulatory Compliance: The pharmaceutical industry must adhere to regulatory requirements for surveillance and reporting of antimicrobial resistance data. This includes providing data to regulatory agencies for drug approval and monitoring purposes.

Advocacy and Policy Engagement: The pharmaceutical industry advocates for policies and initiatives that promote antimicrobial stewardship via education and training health care providers in responsible antibiotic prescribing and use. By engaging with policymakers and healthcare stakeholders, pharmaceutical companies contribute to efforts to address the national-regional and global AMR crisis

Challenges and Opportunities:

Data Sharing: One of the key challenges in AMR surveillance is the need for improved data sharing and collaboration between academia, the pharmaceutical industry, healthcare providers, and public health agencies. Enhanced data sharing can lead to more comprehensive surveillance efforts and better-informed decision-making.

Rapid Diagnostic Technologies: Both academia and the pharmaceutical industry are working on developing rapid diagnostic technologies that can quickly identify resistant pathogens and guide appropriate treatment decisions. These technologies have the potential to revolutionize AMR surveillance and antimicrobial stewardship practices.

Global Coordination: AMR is a global problem that requires coordinated efforts across borders. Academia and the pharmaceutical industry can contribute to global surveillance networks and partnerships to monitor resistance trends on a global scale and facilitate the development and dissemination of effective interventions.

Overall, collaboration between academia and the pharmaceutical industry is essential for effective surveillance of antimicrobial resistance, which is crucial for preserving the efficacy of existing antibiotics, scope out new drug designs and develop other alternate strategies to



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Understanding the emerging and re-emerging scenarios of antibiotic resistance patterns in clinically important bacterial pathogens through the bioinformatics lens

ABSTRACT

Antimicrobial resistance creating healthcare concerns worldwide requires ardent exploration of alternative prophylactic strategies. The incidence of mutation-induced carbapenem-resistance, colistin-resistance, beta-lactamases' expression and dissolution of phenotypic markers is increasing globally among various nosocomial clones, which imposes major limitations by constricting empirical as well as last-resort measures. It is imperative to design the underlying molecular blueprint to explicitly understand the selection pattern of persistent drug resistant strains for sustainable therapeutic as well as diagnostics formulations. The present study delved deeper into the conventional targets in nosocomial multi-drug resistant pneumococci strains, beta-lactamases in nosocomial pathogens, colistin-resistance and virulence markers in hypervirulent *K. pneumoniae*. Mutations in nosocomial pathogens were identified from whole genome sequencing and prioritized based on their positions in the critical functional regions. The stability profile of the mutants were determined in the context of unfolding Gibbs free energy, vibrational entropy, atomic fluctuations, b-factors, solvent accessibilities, torsional energy and intra-molecular interaction patterns. Structural stability patterns in mutants were observed, predominantly governed by uncharged non-polar substitutions. The same correlated with the binding profile of the conventional antibiotics thereby elevating the clinical minimal inhibitory concentrations. Stable mutations in the functional domains also masked the phenotypic identification patterns in some clinical strains. The study therefore looked for alternative intervention strategies through computational drug-design pipeline. Non-steroidal antimicrobials, pyrrolidine derivatives, natural carbazole compounds, Food and Drug Administration Authority (FDA)-approved non-conventional drugs and a library of antimicrobial peptides were evaluated against mutant multi-drug resistant strains. The potential antimicrobial compounds with stable interaction dynamics, promising pharmacokinetics, chemical reactivity, and stereochemical integrity encourages future experimental evaluations.



Maneesh Paul

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AMRACE – AMR Action Collaborative Engagement

ABSTRACT

The AMRACE (Anti-Microbial Resistance Action Centre of Excellence) is an initiative of Microvioma nested at Bangalore Bio-innovation Centre (a Government of Karnataka undertaking).

We initiated the "Translational AMR Stewardship" program in March 2023, Pilot in June 2023, and launched it for Rotary Club of Bangalore on July 01, 2023.

- ✓ AMRACE is an attempt to catalyse the implementation of the AMS efforts of the Government through technology
- ✓ The major gaps were identified in the stewardship programs
- ✓ The key stakeholder (consumer / patient) is rarely engaged actively
- ✓ The outcome measured is not getting back to the source for measurable corrective activities
- ✓ Data that is selective rather than comprehensive which is impairing not only decision making but also contribute to the spread of AMR

The focus is on consumers/patients. AMRACE addresses this challenge by identifying the re-producible gaps, recommend solutions and further monitor its compliance.

The initiative is –

- ✓ To ensure that this is sustainable and practically implemented perpetually.
- ✓ To create public awareness about the “Silent Pandemic” of AMR
- ✓ To educate Doctors, Pharmacists and Patients about the proper use of antibiotics
- ✓ To bring in accountability in the various stakeholders
 - ◆ Creating Awareness, Communication, & Education for Stakeholders
 - ◆ Finding deviations between the Prescription – Dispensing – Compliance
 - ◆ Use Location based sewage analysis to study the presence of AMR at source and after treatment of the sewage
 - ◆ Recommending corrective measures in line with the National Antibiotic Policy



Amitabha Bhattacharjee[†]

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Secondary Resistome: Potential Reporter for AMR Diagnostics

ABSTRACT

Antimicrobial resistance (AMR) is a growing global threat with the emergence of new resistance mechanisms. One of the driving forces behind its expansion is the lack of suitable diagnostic intervention. The concept of a 'secondary resistance gene' or 'secondary resistome' refers to chromosomal or plasmidic nonessential genes that become essential in the presence of therapeutic concentrations of antimicrobials. Most of the routine diagnostic microbiology laboratories depend on the conventional Kirby-Bauer disk diffusion method for antimicrobial susceptibility testing. Recently, several automated antimicrobial susceptibility detection systems were introduced, which improved the interpretations. However, the time taken for the interpretation remains 16-24 hrs. Some rapid testing tools are commercially available that can effectively give results within 3 hrs, but are confined to a specific resistance mechanism, and sometimes have issues with their sensitivity. PCR-based detection of AMR was found to be rapid and reliable. However, the problem in research and diagnostic laboratories is that conventional PCR based detection has the limitation that only known genes are identified, and testing methods and target genes in laboratories are not uniform. The emergence of newer variants of resistance determinants further complicates this detection method. Therefore, an endogenous gene that is expressed during antibiotic stress could be a potential biomarker for AMR detection.



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* Corresponding author

Spatial Reorganization of Escherichia coli Chromosome During Stress: Implications on Hotspots for Mutations, Epigenetic and Transcriptome Changes

ABSTRACT

Changes in spatial organization of bacterial chromosomes under stress and its biological implications remain poorly understood. We mapped the structural landscape of wild-type and Δ dcm E. coli chromosomes under triclosan stress using Hi-C to identify triclosan-induced chromosomal interaction domains (CIDs). Two CIDs were common to the wild-type and Δ dcm E. coli, including a CID with a common boundary at *fabI* gene, which encodes the triclosan target. All mutations and structural variants under triclosan stress were observed within or in close proximity to triclosan-induced CIDs. Absence of Dcm methylation impacts short-range interactions in triclosan stress. Single-base resolution methylome maps reveal hypermethylation of adenines (in wild-type and Δ dcm) and cytosines (in wild-type) in the two common triclosan-induced CIDs. Furthermore, global gene expression profiling identified enrichment of highly expressed genes within the two common CIDs. Our findings suggest that triclosan stress-induced CIDs in E. coli are hotspots for genetic variations and are associated with enhanced transcriptional activity and hypermethylation of Dam/Dcm motifs.



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Molecular Characteristics, Antibiotic Susceptibility and Biofilm-Forming Ability of Clinical Methicillin Resistant *Staphylococcus aureus* isolates

ABSTRACT

Methicillin-resistant *Staphylococcus aureus* (MRSA) is a significant pathogen causing hospital and community-acquired infections. Biofilm formation by MRSA enhances its virulence and resistance to antibiotics, hindering treatment. This study investigated the prevalence, characteristics, and antibiotic susceptibility of biofilm-forming MRSA isolates obtained from tertiary care hospitals in and around Coimbatore, South India. Out of 259 isolates, 209 were reconfirmed as MRSA and underwent antibiotic susceptibility testing (disk diffusion/E-test), biofilm formation assessment through determination of minimum inhibitory/biofilm and inhibitory/eradication concentrations (MIC/MBIC/MBEC) for various antibiotics. Molecular typing (*agr*, *SCCmec*, *spa*, MLST) and biofilm visualization (SEM/CLSM) were also performed. The results revealed a high prevalence (80.7%) of strong biofilm formation in the reconfirmed isolates. All isolates were susceptible to linezolid, rifampicin, teicoplanin, and vancomycin, with daptomycin demonstrating the highest overall susceptibility (100%). Notably, 4.8% (10 isolates) were Vancomycin Intermediate *S. aureus* (VISA). Daptomycin and linezolid showed the strongest biofilm inhibition despite higher MBEC values. CLSM confirmed significant biofilm reduction with daptomycin treatment. Also, it was notable that, *agr* group I and *SCCmec* type III dominated biofilm-forming MRSA, with ST239 (hospital-acquired) and *spa* type t030 being most prevalent. All isolates harbored *icaA* and *icaD* genes, while other adhesion gene prevalence varies. The variable distribution of adhesion genes limits their use as biofilm formation markers. This study reveals a high prevalence of biofilm-forming MRSA, dominated by the hospital-acquired ST239 clone and suggests Daptomycin as potential alternative therapy as it showed promising activity against these biofilms.

Keywords: Methicillin Resistant *Staphylococcus aureus*, Biofilm, Molecular Typing, *icaA* and *icaD* genes



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Non-Active Site Amino Acid Residues as The Potential Targets for Designing Inhibitors Against Various Classes of Beta-Lactamases

ABSTRACT

Antibiotic resistance is an immense concern of the 21st century, and if not addressed in time, it might cause 10 million deaths per year by 2050. Bacteria deploy various mechanisms to acquire resistance to several antibiotics, including the most commonly used beta-lactam antibiotics, which currently share ~60% of the Global antimicrobial market. The main reason for beta-lactam resistance is the beta-lactamases, and the bacteria have developed several classes of beta-lactamases that can cleave penicillin, cephalosporins and the most robust class of beta-lactam, carbapenems. Beta-lactamase inhibitors, like clavulanic acid or sulbactams, had gained momentum in the chemotherapy. However, the effectiveness of the strategy seems short-lasting due to various reasons. Therefore, exploring an alternative route to prevent the function of such notorious enzymes is essential. To achieve that, our laboratory, for the last decade, has been involved in finding out the amino-acid residues present within the beta-lactamase molecules in places other than the active site, which can influence the activities of these beta-lactamases. One such non-active site area is the omega-loop of serine beta-lactamases, wherein a glutamic acid residue present supplies the water molecule to the active site at the time of hydrolysis of the beta-lactams. Accordingly, we have identified and validated several non-active site residues in various beta-lactamases that can influence their enzymatic performance, namely, E162 and E164 of SHV-14, E169 and N173 of CTX-M-15. Similarly, a few residues in the loop regions, which are in proximity to the active sites of New Delhi metallo beta-lactamases (NDMs), have been identified, namely, D192 and S217 of NDM-4, E152 of NDM-5 and S191 of NDM-7. Furthermore, we have identified a few non-active site residues in OXA-type carbapenemases influencing their functions, like W165 and L166 of OXA-23 and W169 and L170 of OXA-58. All these residues are now considered the soft targets within the respective beta-lactamase molecules, and we hypothesize that these residues might be utilized to design some peptide inhibitors against the beta-lactamases. Accordingly, peptide inhibitors are designed against the glutamic acid residue confined within the omega-loop of class-A serine beta-lactamases that generated an auspicious result against *E. coli* and *M. tuberculosis*. Finally, non-active site residues of beta-lactamases are considered valuable targets for generating peptide inhibitors against beta-lactamases, which might contribute to future antimicrobial chemotherapy.



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The Importance of Surveillance for Emerging and Re-Emerging Respiratory Viruses in The Isolated Islands of India

ABSTRACT

Surveillance for respiratory viruses in the Nicobar Islands is incredibly important for several reasons, as outlined. The geographical proximity of the Nicobar Islands to Southeast Asian countries like Indonesia, Thailand, and Burma heightens the risk of cross-border transmission of respiratory viruses. Additionally, the unique vulnerabilities of remote communities, such as limited access to healthcare and cultural practices, necessitate targeted surveillance efforts.

This prospective study, which monitors acute respiratory infections (ARI) and severe acute respiratory infections (SARI) among the Nicobarese tribe and settler populations, fills a crucial gap in understanding the prevalence, seasonal patterns, and viral aetiologies of respiratory illnesses in the region. By employing molecular assays to detect respiratory viruses, the study was able to accurately identify the pathogens responsible for these infections.

The documentation of various viral aetiologies in the Nicobar Islands is invaluable for informing public health interventions and preparedness strategies. Collaborating with the Directorate of Health Services and the Andaman and Nicobar Administrations ensures coordinated efforts in implementing preventive and precautionary measures to mitigate the spread of respiratory viruses.

Continuing surveillance efforts across all human-inhabited islands in the Nicobar group is essential for maintaining vigilance against emerging and reemerging respiratory viruses, especially given their proximity to neighbouring Southeast Asian countries. By studying the sociodemographic factors associated with respiratory illnesses, this research can contribute to tailored interventions aimed at protecting vulnerable populations and promoting global health security.

Overall, your study not only enhances our understanding of respiratory virus epidemiology in remote regions but also underscores the importance of proactive surveillance and collaborative action in combating infectious disease threats.

ORAL PRESENTATION ABSTRACTS

BASIC RESEARCH

ORAL - Basic Research - (B.Sc./ B.Tech/ M.Sc./ M.Tech/ Ph.D./ Post-doc)				
ID	Title	Name	Position	Name of the Lab/Department & Institution
OB1	Ms.	Ankita Panigrahi	Student	Mazumdar Shaw medical foundation, Narayan ha
OB2	Ms.	Devika V Kumar	Student	M.Sc. Biotechnology, SB College
OB3	Ms.	Treesa Sani	Student	Biochemistry Laboratory, Pushpagiri Research Centre, PIMS&RC
OB4	Ms.	Elizabeth Annie George	Student	Medical Biotechnology and Computational Drug Designing Laboratory, Pushpagiri Institute of Medical Science and Research Center
OB5	Ms.	Kavyalekshmi G Prasad	Student	Medical Biotechnology and Computational drug designing, Pushpagiri Institute of Medical Science and Research Center
OB6	Ms.	Sandra Krishnan	Student	M.Sc. Biotechnology St Berchmans College, Changanassery
OB7	Ms.	Sneha R Unni	Student	Department of Biochemistry, Jain University
OB8	Ms.	Aditi Roy	Research Scholar	Medical and Biological Computing Laboratory, Vellore Institute of Technology
OB9	Ms.	Aswathy V U	Research Scholar	Division of Biotechnology, Karunya Institute of Technology and Sciences, Coimbatore
OB10	Ms.	Jabiya Eliza Varughese	Research Scholar	Central Research Laboratory
OB11	Mr.	Jinu Varghese	Research Scholar	NIMS University
OB12	Ms.	Kokelavani N B	Research Scholar	Division of biotechnology, Karunya Institute of Technology and Sciences
OB13	Dr.	Leena C.O	Research Scholar	Jubilee Centre for Medical Research,JMMC & RI, Thrissur,Kerala
OB14	Ms.	Mandeep Kaur Gill	Research Scholar	Clinical Microbiology & LPU Punjab
OB15	Mr.	Nageswar Sahu	Research Scholar	Division of Biotechnology, Karunya Institute of Technology and Sciences, Coimbatore
OB16	Ms.	Peali Banerjee	Research Scholar	Suresh Gyan vihar university
OB17	Mr.	Raushan Quraishi	Research Scholar	Karunya institute of technology and sciences
OB18	Mr.	Rhitam Biswas	Research Scholar	Medical And Biological Computing Laboratory, Vellore Institute Of Technology
OB19	Mr.	Sijo A	Research Scholar	School of Biosciences, MACFAST College, Tiruvalla
OB20	Ms.	Suvitha Anbarasu	Research Scholar	Medical and Biological Computing laboratory/Department of Biotechnology/VIT University
OB21	Dr.	Unnikrishnan B S	Research Scholar	Department of Biosciences and Bioengineering, IIT Roorkee
OB22	Ms.	Vanditha M	Research Scholar	Jubilee Centre for Medical Research,JMMC & RI, Thrissur ,Kerala
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OB1

Cu-Mofs Embedded Gellan/Zein Based Hydrogel For Wound Healing

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ABSTRACT

Recent efforts have been made to decrease bacterial resistance by the use of antibacterial mechanisms such lysozyme, photothermal treatment (PTT), and self-antibacterial materials. However, there are some limitations associated with these techniques. Here, using Gellan Gum a natural polysaccharide and Zein as building blocks, we create a polyphenol-loaded Cu-metal-organic framework (MOF) hydrogel that improves antibacterial activities and speeds the healing of infected wounds. SEM analysis showed interconnected pores which helps in proliferation of cells as well as increases the swelling capacity and water retention of our hydrogel that makes it ideal for regeneration of tissue. In addition to that Cu-MOFs slowly leaches into the wound, improving antibacterial effectiveness without medication resistance by disrupting the bacterial cell membrane and increasing the formation of reactive oxygen species (ROS). The produced hydrogel had a wide spectrum of activity against gram-positive and gram-negative bacteria, and it demonstrated biocompatibility in in-vivo system indicates its usefulness in treating infected wound.

Keywords: Cu-MOFs, tannic acid, Zein, wound healing

OB2

Microbiological Analysis Of Maize Starch

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ABSTRACT

Corn Starch or Maize Starch is the starch derived from the corn (maize) grain. The starch is obtained from the endosperm of the corn kernel. Starch being the renewable energy source is widely used in Food, and other industry. Maize starch was one of the earliest used excipients for pharmaceutical dosage forms. In the pharmaceutical industry, starch is also used as an excipient, as tablet disintegrant or as binder. Starch-based materials are biodegradable, offering a great advantage over traditional non-biodegradable synthetic polymers; hence it's become important to test this for any bacterial contamination before processing. Microbiological analysis is used to determine the microbial presence in any given substance. The microbiological analysis criterion; will stipulate that a type of microorganism, group of microorganisms, or toxin produced by a microorganism must either not be present at all, be present in only a limited number of samples, or be present as less than a specified number or amount in a given quantity of the substance. This paper reviews the Microbiological analysis of Maize Starch for different type of Enterobacteria with suitable selective growth medium and surface streaking techniques; and confirms the result by biochemical test. The analysis is to find the presence of Enterobacteria like *Escherichia coli*, *Salmonella* and *Shigella*.

Keywords: Maize Starch, Binder, Diluent, Enterobacteria, Biochemical test, Bacterial contamination, Microbiological analysis, pharmaceutical industry

OB3

In Vitro Antioxidant and Free Radical Scavenging Activity of Oldenlandia corymbosa

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ABSTRACT

Medicinal herbs endure popularity as an alternative medicine due to their affordability, efficacy, historical, cultural and religious preferences. Medicinal plants are considered a rich resource of components that can be utilized to improve pharmacopoeial, non- pharmacopoeial or engineered drugs. In this study, the preliminary phytochemical analysis and in vitro antioxidant activity of methanolic extract of Oldenlandia corymbosa leaf was checked. Phytochemical analysis showed the presence of phenolic compounds, tannins, alkaloids, glycosides, quinones, coumarins, steroids and saponins. The HPLC analysis revealed the presence of the phenolic compounds namely gallic acid, quercetin, caffeine, rutin and catechin. The total phenolic content of methanolic and hexane extract of O. corymbosa leaf was determined. The antioxidative potential of O. corymbosa leaf methanolic extract was analysed by DPPH, metal chelating activity, hydroxyl radical scavenging, reducing power, nitric oxide and superoxide scavenging activity and were compared with standard antioxidants like gallic acid, EDTA, catechin, quercetin, and ascorbic acid. The cytotoxicity effects of leaf extract were evaluated by MTT assay against L6 myoblast cell lines. The extract showed a dose dependent inhibitory effect on the growth of L6 cells. The results showed that the methanolic extract of O. corymbosa leaf is a valuable free radical scavenger in oxidative stress induced illness states and a possible of natural antioxidants.

Keywords: Oldenlandia corymbosa, antioxidative potential, medicinal plants, phytochemical analysis, DPPH

OB4

Designing Potential Anti-Bacterial Peptides Against Clinically Pertinent Extended Spectrum β -Lactamase Producing Escherichia coli: An in-silico Approach

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ABSTRACT

The advent of extended-spectrum β -lactamases (ES β Ls) in Escherichia coli posed a significant threat for clinicians in tertiary healthcare settings, rendering routine treatment ineffective with β -lactam- β -lactamase inhibitors (β L- β LI) combinations. This study aimed to develop potential inhibitors for β -lactamases, utilizing a library of antimicrobial peptide (AMP) mutants that were designed with enhanced antibacterial efficacy compared to their parent peptides. Five peptides, namely SAAP-148, HFIAP-1, Oxt 4a, PSCATH4, Camp 2006 and their mutants with favourable physicochemical profiles were identified through comprehensive

machine learning algorithms based on various pharmacokinetic properties such as cell penetrability and toxicity as well as immunogenic properties like allergenicity, antigenicity and haemolytic potential. Molecular docking analysis revealed HFIAP-1_M5 mutant as the most potent inhibitor, exhibiting the lowest binding energies against class-A (TEM, SHV1, SHV2, SHV8, SHV24), class-B (IMP4, NDM1, NDM5, NDM7, VIM1), class-C (AmpC) and class-D (OXA2, OXA7, OXA10, OXA30, OXA232) ESβL drug targets. Intermolecular interaction profiles demonstrated that AMPs formed hydrogen bonds and van der Waals hydrophobic interactions with the active amino acid residues of these drug targets. Molecular dynamics simulations (MDS) validated the stable backbone profile and minimal residue-level fluctuations of the protein-peptide complex throughout the simulation timeframe. This study proposed a novel approach, combining β-lactam with potential AMP (HFIAP-1_M5 mutant), which holds significant potential for inhibiting ESβLs and restoring β-lactam activity. Experimental validations of these in-silico findings could further pave the way for the designing promising therapeutic strategy against tackling ESβLs producing *Escherichia coli*.

Keywords: Antimicrobial peptides; Extended spectrum β-lactamases; Molecular docking; Molecular dynamics simulation; Pharmacokinetics

OB5

Enhancing The Efficacy of Susceptible Antibiotics In Combination With Phytocompound Against Nosocomial Pathogens

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ABSTRACT

Antimicrobial resistance (AMR) poses a significant global health threat because newer antimicrobials are proving ineffectiveness. Identifying the resistance mechanisms and reason behind this resistance is the need of the hour. This study investigates the antibacterial, antibiofilm potency of the methanolic and ethanolic extracts of *Terminalia chebula*, scrutinizing its synergistic effect in association with susceptible antibiotics. Urine and pus samples were collected from the hospital were subjected to morphological, cultural and biochemical characterization. Biochemical characterization and selective media confirmed that the selected strains as *Staphylococcus aureus* and *Klebsiella pneumoniae*. Antibiotic susceptibility test were performed showing *Staphylococcus aureus* and *Klebsiella pneumoniae* were MDR and XDR. Biofilm forming potential indicated *Staphylococcus aureus* and *Klebsiella pneumoniae* were highly biofilm producers. Solvent extraction were done to obtain crude extracts of *T. chebula*, followed by chromatographic techniques to decipher the unknown phytocompounds. Qualitative analysis of phytocompound determines the presence of phenols, tannins, flavonoids, aminoacids, saponins and glycosides. Antibacterial potency of the extracts were examined through Kirby-Bauer disk-diffusion method, the efficacy of phytocompound against bacteria were performed by both plant extract alone and in association with susceptible antibiotics, resulted in enhanced zone of inhibition when compared to antibiotic alone. Broth macrodilution were performed for estimating anti-bacterial potency and MIC₅₀ of plant extract, 8μg/ml for *S. aureus* and 12μg/ml for *K. pneumoniae*. Remarkably presence of phytocompounds found in plant extract provide therapeutic agents that can augment the antimicrobial activity of antibiotics and to develop a successful treatment strategy to overcome this multi-drug resistance.

Keywords: Antimicrobial resistance (AMR), Methicillin-resistant *Staphylococcus aureus*, Carbapenem resistant *Klebsiella pneumoniae*, *Terminalia chebula*, methanolic and ethanolic plant extract of *Terminalia chebula*, combination therapy

Micropropagation of *Bacopa monnieri* (L.) Pennell

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ABSTRACT

Bacopa monnieri, often called "Brahmi," is widely used in the traditional Indian Ayurvedic system of medicine. The present study was conducted to standardize the explant used for micropropagation as well as standardization of surface sterilant concentration and duration. Nodules and leaf segments of *Bacopa monnieri* were taken as explants for in vitro propagation. Effective micropropagation of any plant under in vitro conditions relies on the utilization of the right kind of plant growth regulator at the right concentration. Murashige and Skoog (MS) media were used as the basal medium, and it was supplemented with different combinations of auxins (NAA, 2,4-D), cytokinin's (BA), and BAP. Effective surface sterilization is essential for aseptic cultures; mercuric chloride was selected as the sterilizing agent. Concentration and duration analysis showed 0.05% HgCl₂ for 4 minutes and 0.1% for 2 minutes effectively reduced fungal contamination. Thus, the tissue culture technique can be further utilized for the genetic modification of the germ line followed by micropropagation to obtain a good number of new plants with the desired properties. Conclusively, the present study presents a fast, reliable, and most importantly, reproducible micropropagation protocol for the selected plants of *B. monnieri* that can be utilized for commercial-level production of quality planting material to ensure the reproducibility of developed plantlets with efficient medicinal properties.

Keywords: *Bacopa monnieri*, Micropropagation, MS medium, Explant, Surface sterilization

In-silico and in-vitro Studies Suggest Aerobactin As A More Reliable Marker For Identifying Hypervirulent Carbapenem-Resistant *Klebsiella pneumoniae* Due To The Instability Of RmpA2

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ABSTRACT

Background: The global rise in hypervirulent carbapenem-resistant *Klebsiella pneumoniae* (CR-hvKp) incidence is linked to various clones, causing nosocomial infections. Endemic high-risk clones acquire virulence plasmids carrying antimicrobial resistance genes, resulting in the emergence of CR-hvKp.

Methods and Methodology: Our study focused on Indian CR-hvKp, stemming from high-risk strains with virulence plasmids but lacking hypermucoviscosity. We identified 27 CRKp isolates with the *rmpA2* gene using whole-genome sequencing, assessing their resistance and virulence. We established *RmpA*, *RmpA2*, *IucA*, and *IutA* as robust markers for CR-hvKp clinical identification through protein modelling and stability analysis.

Results: These multidrug-resistant high-risk CR-hvKp clones (CG11, CG43, ST15, and ST231) primarily carried the carbapenemase OXA-232, followed by NDM. Altered *rmpA* and *rmpA2* genes on the virulence plasmid (IncHI1B replicon type) led to the absence of hypermucoviscous traits. Nonetheless, all high-risk clones expressed functional aerobactin. *In silico* analysis revealed that *IucA* and *IutA* had more stable domains than traditional *RmpA* and non-functional *RmpA2*, suggesting higher maintenance and expression costs, possibly leading to their loss over time in CR-hvKp as they express essential antimicrobial resistance and virulence components.

Conclusion: The global rise in antimicrobial resistance and virulence in *K. pneumoniae* highlights the necessity for dependable CR-hvKp markers. Non-functional *RmpA2* in high-risk clones underscores the significance of molecular identification. The limitations of the negative string test due to non-functional *RmpA2* challenge phenotypic screening. Nonetheless, aerobactin offers stability and swift detection of evolving CR-hvKp.

Keywords: Hypermucoviscosity, plasmid, whole-genome sequencing, nosocomial infection, virulence

Evaluation of the Antibacterial and Antibiofilm Efficacy of Parmotrema-Based Chitosan Nanoparticles against Gingivitis-Associated Oral Pathogens

OB9

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ABSTRACT

Gingivitis, a widespread inflammatory gum disease, is triggered by oral bacterial biofilms. Conventional chemical based medications like chlorhexidine and octenidine, face limitations due to antibiotic resistance and widespread side effects. Lichens, with their antimicrobial potential, present a promising alternative to resolve this issue. This study investigated the efficacy of *Parmotrema perlatum* (*P. perlatum*), a lichen traditionally used for oral ailments, against gingivitis-causing bacterial pathogens. *P. perlatum* extracts were fractionated, and their antimicrobial and antibiofilm activities were assessed against reference strains (*Acinetobacter baumannii* and Methicillin-Resistant *Staphylococcus aureus*) first; following which the most active fraction (Benzene:Chloroform) was characterized and employed for the biogenic synthesis of chitosan nanoparticles. Gingival swabs from suspected gingivitis patients were used to isolate and identify oral pathogens through 16S rRNA sequencing and the identified pathogens were used to assess the activity of synthesized *Parmotrema* based chitosan nanoparticles through antimicrobial and antibiofilm studies. The results of the study were positive and revealed the impact of *Parmotrema* as a good antimicrobial and antibiofilm agent. Also *P. perlatum* based chitosan nanoparticle can be further studied for its compatibility and toxicity in oral cell lines as it can be used as an effective therapeutic candidate for treating gingivitis.

Keywords: Gingivitis, Lichen, *Parmotrema perlatum*, 16S rRNA sequencing, Chitosan nanoparticles

Utility of saliva sample for detecting Influenza A virus in symptomatic cases using SYBR Green-based NAAT compared to probe based NAAT with nasopharyngeal swab

OB10

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ABSTRACT

Respiratory specimens such as swabs from the nasopharynx (NPS), throat and nostrils have been employed as the specimens for detecting Influenza A viruses by RT-qPCR and other molecular assays. However, collection of these specimens creates discomfort to patients and requires the assistance of a trained healthcare worker. The study has been aimed to validate saliva (easy and comfortable specimen) as an alternative sample for the detection influenza A viruses in symptomatic cases using SYBR-Green-based Nucleic Acid Amplification Test (NAAT) in comparison with nasopharyngeal swab by TaqMan chemistry. The study enrolled patients, both pediatric and adult, who presented with Influenza like illness. Nucleic acid extraction from saliva was carried out using kit-based and heat inactivation methods. We standardized a SYBR-Green based Polymerase Chain Reaction (PCR) test using primers specific for Influenza A viruses. The study involved comparison of the SYBR Green based tests results obtained with saliva (by both the methods of RNA extraction) with that of NPS based on probe based PCR. The sensitivity and specificity of saliva as sample using the developed SYBR-Green based test for influenza diagnosis were determined to be 90% and 98% respectively. Based on the high sensitivity and specificity along with the positive and negative predictive values, likelihood ratios, agreement percentage and the kappa statistics, we conclude that saliva can be used as an alternative sample for the detection of Influenza A viruses. We present the validation of a cost effective RT-qPCR method utilizing SYBR-Green chemistry with saliva as the sample for the diagnosis of respiratory illness caused by Influenza A viruses.

Keywords: Influenza A viruses, Saliva, SYBR Green, NAAT, Diagnosis

To assess the Occurrence and Distribution of Urinary Tract Infections Among Suspected Cases (Pyuria, With or Without Symptoms) During Pregnancy

OB11

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ABSTRACT

Aim and Objective: The purpose of this study is to address the gap in knowledge regarding the occurrence and distribution of urinary tract infections among suspected cases (pyuria, with or without symptoms) during pregnancy at Emirates Hospital, Dubai, UAE.

Background: Urinary tract infection is one of the most frequently seen medical complications in pregnancy.

Methods: Ethical approval was granted for this research. The study employed a time-bound prospective design, encompassing a total of 900 pregnant women.

Results: The statistical analysis for the data was done using SAS software (Version 9.4), Copyright © 2024. SAS Institute, Inc.

Suspected UTI cases during pregnancy were estimated at 30% (n=270), with an occurrence rate of UTI among suspected cases reported at 16.7% (n=45). The predominant organism responsible for urinary tract infections in these cases was *E. coli* (66.7%). Additionally, the study revealed that the second trimester had the highest infection rate, at 46.67%.

Conclusion: Our study estimates the occurrence of urinary tract infections (UTIs) among suspected cases (pyuria, with or without symptoms) at 16.7%. The most prevalent strain causing UTIs in our study is *Escherichia coli* (66.7%). We recommend conducting routine urine culture tests periodically for all pregnant women to detect asymptomatic bacteriuria. This will facilitate the early detection of pregnant women at risk of UTIs who need appropriate antibiotic treatment to prevent potential obstetric complications during pregnancy. We recommend specific preventive measures for reducing the prevalence of uropathogens (*E. coli*), including improved sanitation practices, hygiene education, awareness about maintaining a healthy gestational life, and ensuring safe motherhood.

Keywords: Urinary tract infection in pregnancy, significant bacteriuria, symptomatic bacteriuria, asymptomatic bacteriuria, acute cystitis, pyelonephritis.

Extraction of Essential Oil from *Myristica fragrans* Houtt. And Qualitative and Quantitative Analysis for Bioactive Compounds

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OB11

ABSTRACT

Phytochemicals found in every day's foods have garnered attention for their potential anti-cancer properties, as they have the ability to target the molecular signaling alterations which controls the growth of cancer cells. *Myristica fragrans*, commonly known as nutmeg, has long been recognized for its medicinal properties. In this study, the extraction of essential oil (EO) from arils and seeds of nutmeg was done using hydro distillation process at different temperatures. The qualitative and quantitative analysis of phytochemicals for different temperatures was done using standard protocols. The HPTLC was performed with standards, Quercetin, and pyridine. The oil yield in dry arils was found to be higher than dry seed. The phytochemical screening shows the presence of flavonoids, terpenes, alkaloids and phenol compounds in EO. The quantitative estimation of phenol at varying temperatures for arils was found to be 46.4 mg GAE/g (60°C) and 157.6 mg GAE/g (100°C), and for seed, 31.89 mg GAE/g (60°C) and 36.75 mg GAE/g (100°C), respectively. The total flavonoid content at varying temperatures for arils was 17.68 mg QE/g (60°C) and 11.24 mg QE/g (100°C), and for seed, 26.281 mg QE/g (60°C) and 23.718 mg QE/g (100°C) respectively. The silica plates were visualized under UV at 254nm and 366nm. The Rf values were closely related to the standard Rf values, which confirms the presence of bioactive compounds such as flavonoids and alkaloids. Thus, the EOs of arils and seeds of *Myristica fragrans* exhibit promising anti-cancer potential due to the presence of various phytochemical compounds.

Keywords: Essential oil, Nutmeg arils, Nutmeg seeds, Phytochemicals, HPTLC.

Importance of Inflammatory Marker Ratio and Lipid Profile Ratio in Acute Ischemic Stroke

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OB13

ABSTRACT

Background: Acute Ischemic Stroke is a chronic inflammatory disease that is projected to be one of the leading causes of mortality affecting millions of people globally. It is essential to study the Platelet lymphocyte ratio (PLR), Neutrophil lymphocyte ratio (NLR) ratios and C reactive protein (CRP) in impacting the inflammatory status during stroke. It is also important that altered lipid metabolism could influence the inflammatory conditions associated with AIS. Hence analysing the relevance of lipid ratio and inflammatory ratio in the context of AIS is important to understand the pathophysiology of disease.

Methodology: The blood was collected from the participants for biochemical and hematological analysis such as lipid profile, CRP and Complete blood count for the quantitation of NLR and PLR.

Results: The groups involved in the study are AIS and healthy controls. The sample size for this study was n=151 in both AIS and control group. Inflammatory markers such as NLR, PLR, CRP and lipid profile ratio, TG/HDL-C and systolic & diastolic BPs where the parameters considered for comparison between control and AIS groups. The results revealed that there was significant differences in NLR, CRP, TG/HDL-C and BP between the study groups (p value<0.01). PLR value did not significantly altered between the groups (P=0.5).

Conclusion: The result showed that inflammatory markers, lipid profile and blood pressure play vital role in the occurrence of acute ischemic stroke.

Keywords: Inflammation, haematological, triglycerides, neutrophils, platelets.

Evaluation of antibiotic resistance and molecular characterization of bacterial strains causing prospective nosocomial infection

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OB14

ABSTRACT

Nosocomial Infections have been identified as a major cause of disability and death among patients. However, excessive usage of antibiotics has arisen another problematic issue that is antimicrobial resistance. The aim of this study is to describe the antibiotic resistance pattern of carbapenems class of beta lactam antibiotic of pathogens causing infections in hospitalized patients in a charitable hospital in Punjab, India. A cross-sectional study is conducted from August 2023. A total of 400 samples will be targeted with structure teaching programme. Till date 198 samples were collected from hospitalized patients who were stayed in hospital more than 24 hours. Depending on the symptoms and clinical history of the patients, samples were collected and subjected to antibiotic sensitivity testing. The culture and sensitivity pattern of clinical isolates from urine, tip, blood, endotracheal tube swabs, sputum, centerline insertion swabs were analyzed. A total of 105 and 93 specimens were obtained from males and females respectively. The most commonly isolated organisms were Gram negative non lactose fermenter. According to this study Escherichia coli, Acinetobacter baumannii and Klebsiella spp. were most common organism causing nosocomial infections. 15 organisms were found carbapenems resistant and 10 organisms were found partial resistant to carbapenems class. In most of the samples Acinetobacter baumannii and Klebsiella spp. Are resistant to carbapenem class of antibiotics. Carbapenem resistant bacterial infections leading to significant therapeutic challenges.

Keywords: nosocomial infections, antibiotic resistance, carbapenem, public health

Exploring the Influence of Different Carbon and Nitrogen Sources on Pullulan Yield by *Aureobasidium pullulan*

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ABSTRACT

Recent breakthroughs in polymer science highlight the potential of exopolysaccharides (EPS) as valuable bioactive macromolecules in various industrial applications. Pullulan, a high-molecular-weight polysaccharide derived from fungi, particularly *Aureobasidium pullulans*, stands out in this regard. This research focuses on the synergistic effects of carbon and nitrogen substrates on the growth of biomass and the production of pullulan. Key parameters considered during the screening of substrate included polymer recovery (PR), sucrose equivalent (SE), and protein impurities (PI). Experiments were conducted by using glucose, sucrose, and fructose in combination with three different nitrogen sources – $(\text{NH}_4)_2\text{SO}_4$, $\text{CH}_4\text{N}_2\text{O}$, and NaNO_3 . Results revealed that EPS yields reached 9.33 g/l under conditions of 40 g/l sucrose and 1.3 g/l NaNO_3 , with a SE of 0.40 mg/g and PI of 1.08 mg/g while under these circumstances, there hasn't been significant growth in biomass (2.57 g/l) observed. This study sets the stage for further optimization of pullulan bioproduction processes.

Keywords: Pullulan, *Aureobasidium pullulans*, Polymer recovery, Sucrose equivalent, Protein impurities, Optimization

Bioremediation of Lead Poisoning

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ABSTRACT

In 2019, 2020 world was fighting to survive through covid spread out. Normalisation has occurred and now the need has come to test the components of nature (water, air, soil) whether it has become toxic with the presence of heavy metals like lead, cadmium, mercury or not. Humans of today have lost their concentration power to a great extent. 100 students on being tested using memory test questionnaire produced a report which showed that around 70% of them with their own subject choice could not retain what they had learnt 1 day back. This can be one cause why suicide rates are increasing alarmingly after every competitive exam.

Can heavy metals toxicity of the environment be one cause for this low retention power (Mota et al., 2021)? If so what safe methods can be adopted to clean this environment and have proper nourished food?

Some work of this sort has been done in recent years:

Thakare et al., in 2021 (Thakare et al., 2021) found that bioremediation is possible for a large number of heavy metals. An extensive study has been done to show the effect of various microbes in abstraction of the heavy metals from nature.

Medfu Tarekn et al., in 2020 (Medfu Tarekn et al., 2020) made a study to conclude that microbes cause bioremediation of the environment safely and at a low cost.

Still it's yet to find out whether these microbes can safely be used with food products for bioremediation of toxic heavy metals.

Keywords: Lead toxicity, microbes, bioremediation, chemical removal of lead.

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Comparative Analysis of Pretreatment Methods for Improved Sugar Yield

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ABSTRACT

Nowadays, the pretreatment of lignocellulosic biomass is of great significance due to its substantial impact on the bioconversion process for biobased materials like bioplastics, green hydrogen, biofuel, and biogas. This research aimed to fractionate the intricate lignocellulosic biomass using various pretreatment methods. A comparative analysis was carried out on different pretreatment techniques, including deep eutectic solvent (DES), acid, alkali, and hot water treatment, to improve the enzymatic hydrolysis to produce reducing sugar from sugarcane bagasse. The findings of the study indicated that the alkali-pretreated biomass exhibited the highest amount of reducing sugar (22.73 g/L). Conversely, the acid and DES (choline chloride-acetic acid and choline chloride-formic acid) pretreated biomass yielded 15.32 g/L and 11.68 g/L of reducing sugar, respectively, which were relatively lower than the alkali treatment. Additionally, the hot water-pretreated biomass showed the least sugar production among the four pretreatment methods. Hence, the production of high levels of reducing sugar through pretreatment is crucial for enhancing the conversion of lignocellulosic biomass into value-added products or biobased materials.

Keywords- Pretreatment, Reducing sugar, Lignocellulosic biomass, Enzymatic hydrolysis Biobased materials.

OB18

Enhancing the treatment of pneumococcal meningitis by targeting penicillin-binding proteins using ketorolac and etodolac

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ABSTRACT

Background: *Streptococcus pneumoniae* is the primary cause of acute bacterial meningitis (ABM), with a high global mortality rate among children and the elderly. Conventional β -lactam antibiotics often fail to reach the central nervous system due to limited blood-brain barrier (BBB) penetration, leading to resistance in meningeal infections. This study aims to explore alternative therapies for Streptococcal meningitis.

Methods and Methodology: Virtual screening and pharmacokinetics/pharmacodynamics (PK/PD) assessments were employed to identify potential drugs. Molecular docking and structural dynamics simulations evaluated the drugs' binding affinity and interaction stability with Penicillin-binding protein (PBP) targets. The drugs were also assessed for interactions with other Streptococcal bacteria and relevant host targets.

Results: Non-steroidal anti-inflammatory drugs (NSAIDs) ketorolac and etodolac, with strong BBB permeation and antibacterial properties, were identified. These drugs showed consistent binding affinities to PBP1A, PBP2X, PBP2B, and PBP3, with low inhibition constants (<50 μM). Notably, ketorolac and etodolac exhibited higher binding affinities against PBP2B and PBP3 than penicillin and cefotaxime. Hydrogen bonds and non-canonical interactions with active site residues of PBPs drove these interactions. Structural dynamics simulations confirmed the stability of drug-bound complexes, with minimal average root-mean-square fluctuations (RMSFs) (<1.0 Å). The average binding affinities of ketorolac and etodolac with PBPs were comparable to their inflammatory targets.

Conclusion: Ketorolac and etodolac can potentially suppress the causes and effects of streptococcal meningitis. Further experimentation and validation are encouraged.

Keywords: Streptococcus pneumoniae, Beta-lactam antibiotics, Virtual screening, Pharmacokinetics, Pharmacodynamics

Prevalence and Antimicrobial Resistance Patterns of *Klebsiella pneumoniae* Isolated from Different Clinical Specimens

OB19

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ABSTRACT

Klebsiella pneumoniae is an important opportunistic pathogen responsible for various hospital-acquired infections, posing challenges in treatment, especially among vulnerable groups such as elderly, immunocompromised individuals, and infants with underdeveloped immune systems. The aim of this study is to investigate the prevalence and antimicrobial resistance patterns of *K. pneumoniae* isolated from various clinical specimens. This cross sectional study was conducted from January 2024 to March 2024 at a tertiary care hospital in Tiruvalla, Kerala. The study included patients of all ages and genders visiting both outpatient and inpatient departments of the hospital, excluding repeat isolates from the same patient. The identification and antimicrobial susceptibility testing were performed as per latest CLSI guidelines 2023. The detection of Extended Spectrum Beta-Lactamase (ESBL), AmpC Beta-Lactamase (AmpC) and Carbapenemase production was performed using different phenotypic methods. Out of 222 *K. pneumoniae* isolates across different clinical specimens, urine samples yielded the most with 115 (51.8%), followed by pus with 47 (21.17%), and the least from blood with 9 (4%) and other fluids. Males (55.40%) were more affected than females (44.59%). Notably, 63.5% were ESBL producers, 54.05% were AmpC β -lactamase producers, and 24.7% were Carbapenemase producers. The study highlights a concerning rise in ESBL-producing strains with no significant decline in antibiotic resistance, especially carbapenems. This poses a challenge for infection control. Continuous surveillance is crucial for guiding effective antibiotic therapy strategies.

Keywords: *Klebsiella pneumoniae*; Antimicrobial resistance; Hospital-acquired infections; ESBL; Carbapenem resistance

In-silico characterization of MUC5B in Lung Adenocarcinoma: A potential diagnostic Biomarker

OB20

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ABSTRACT

MUC5B, a gel-forming mucin, in lung adenocarcinoma (LUAD) is highly dis-regulated in LUAD. In this study, we explored the functional role of MUC5B through an integrated computational approach. Our analysis revealed a significant upregulation of MUC5B in LUAD (p-value = 0.01, log FC = 2.36). Network analysis of genes associated with MUC5B identified enrichment in two key pathways: immune suppression and O-linked glycosylation, particularly involving serine-threonine-rich tandem repeats. Further investigation demonstrated a positive correlation between mutant MUC5B and suppressive immune cells within the tumor microenvironment (TME), such as myeloid-derived suppressor cells and cancer-associated fibroblasts. Additionally, a positive correlation was observed between MUC5B and immune inhibitors, suggesting its potential role in promoting tumor proliferation and immune evasion. Structural analysis of the mutant MUC5B protein indicated a rigid N-H-backbone conformation (S2: 0.756), suggesting increased stability. Clinical data analysis revealed a correlation between MUC5B expression and advanced LUAD stages (lymph node N2, tumor T3). Patients with high MUC5B expression exhibited a lower median overall survival (<50 months) and a hazard ratio of 1.4. These findings collectively suggest that O-glycosylated and mutant MUC5B contribute to LUAD progression by promoting immune suppression and was further validated by clinical expression profile of MUC5. Thus, MUC5B could be a potential diagnostic biomarker for metastatic LUAD.

Keywords: Immune infiltration; mucins; network analysis; O-linked glycosylation; tumor microenvironment

Bioresorbable flexible biopolymeric hydrogel for effective wound management in Type1 Diabetes Mellitus

OB21

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ABSTRACT

According to the international diabetes federation, number of diabetic patients is expected to rise to 417.3 million by 2030 and to 486.1 million by 2045. The countries with the largest numbers of adults with diabetes aged 20–79 years in 2019 are China and India and are expected to remain so in 2030. A persistent illness known as diabetes mellitus is brought on by high blood glucose levels because an insufficient quantity of insulin is produced by the body. A shortage of insulin can harm numerous essential organs, resulting in potentially fatal and incapacitating conditions include heart attacks, neuropathy, kidney damage, and eye

disorders that can cause retinopathy or even blindness. We proposed a polymeric hydrogel technology in the present work to control diabetic wound healing. The substance for this biopolymer hydrogel wound dressing was created to be stretchy. The process involves adding stretchability and antibacterial activity to a PVA-Gelatin hydrogel system by use of silver nanowires. At room temperature, the different quantities of gelatin and polyvinyl alcohol were allowed to crosslink in the presence of a cross-linker. To create PGA, the hydrothermally produced silver nanowires were mixed with PVA-gelatin gel (PG). It was discovered that the finished gel was extremely elastic and self-healing. When PGA's in vitro antibacterial activity was evaluated on E. coli cells that expressed GFP, a notable amount of cell death was observed. Using cell lines, in vitro cytotoxic activity was examined; no discernible cytotoxicity was found. According to the results, better wound healing efficiency with antibacterial effects has been demonstrated in both in vitro and in vivo wound models.

Keywords: Diabetes, wound healing, hydrogel, silver, stretchable

Exploring Rheumatoid Arthritis Pathophysiology through plasma proteomics: Insights from Combined Mass Spectrometry and Bioinformatics Approach.

OB22

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ABSTRACT

This paper presents a comprehensive investigation into the pathophysiology of Rheumatoid arthritis (RA) employing a novel approach that combines mass spectrometry with bioinformatics. Rheumatoid arthritis (RA) stands as an autoimmune ailment marked by persistent synovial inflammation, characterized by cell hyperplasia, autoantibody production, systemic manifestations, and joint deformity. The global prevalence of RA approximates 1%, with a prevalence skewed towards women, encompassing two-thirds of cases. Despite extensive research, the underlying molecular mechanisms of rheumatoid arthritis pathophysiology remain incompletely understood. Rheumatoid arthritis blood samples were procured from a tertiary care hospital, adhering to ACR guidelines and under the guidance of a Rheumatologist. After immune depletion of highly abundant plasma proteins, low-abundance proteins were revealed through a high-throughput mass spectrometric analysis of these samples. Several differentially expressed low abundant plasma proteins were identified to be linked with Rheumatoid arthritis. Combining protein profiling with bioinformatics tools such as DAVID and STRING, highly enriched protein clusters within rheumatoid arthritis, pivotal in molecular cascades such as PRAR signalling, DNA repair, and the complement and coagulation cascade were identified culminating in chronic inflammatory responses. Notably, proteins like Fibulin, Vitamin D Binding protein, and Afamin appeared as differentially expressed, explicating joint inflammation. In the context of Rheumatoid arthritis, our study has found out some plasma proteins, differentially regulated and intertwined with inflammatory signalling pathways, thereby influencing Rheumatoid arthritis pathophysiology. The study could be a launching platform for understanding the molecular pathophysiology of RA helping in prognosis and diagnosis of RA.

Keywords: Rheumatoid arthritis, Proteomics, Auto immune, Mass spectrometry, Bio informatics

Screening of Chalcone Derivatives to Inhibit EGFR-TK for Cancer Treatment: A Machine Learning and Molecular Dynamics Approach

OB23

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ABSTRACT

The proliferation of more than 50% of cancer types is associated with upregulated activity of epidermal growth factor receptor tyrosine kinase (EGFR-TK). Targeting EGFR with small or medium molecules has emerged as an effective approach to cancer treatment. However, the emergence of resistance in patients at cancer stages requires the discovery of new inhibitors. This study uses in-silico techniques to screen new inhibitors of EGFR. A machine learning analysis, using the random forest algorithm on 2,640 chalcones, identified 412 candidates with potential activity and an excellent receiver operating characteristic (ROC) curve area of 0.99. These compounds were evaluated for drug-likeness, considering factors such as blood-brain barrier penetration and Lipinski's rule. Thirty compounds met all the criteria and underwent molecular docking; six demonstrated higher affinity and interaction with EGFR-TK compared to the reference compound, Erlotinib. Molecular Dynamics Simulations on four selected compounds (CID-375861, CID-375862, CID-23636403, and CID-259166) confirmed the stability of these interactions over 100 ns. MMPBSA binding free energy calculations showed strong affinities for EGFR-TK with binding free energies of -65.421 kJ/mol, -94.266 kJ/mol, -80.044 kJ/mol, and -79.734 kJ/mol, respectively. This study highlights Chalcone derivatives can be a promising lead for the development of cancer therapy.

Keywords: EGFR; Chalcone compounds; Machine learning; Molecular docking; MD simulation

In-silico repurposing of FDA approved drugs to Inhibit Dihydrofolate Reductase of *Salmonella enterica* serovar Typhi

OB24

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ABSTRACT

Salmonella enteric serovar Typhi (*S. Typhi*) is a serious threat to public health due to drug resistance. The solutions to this problem of drug resistance requires the advent of potent drugs with novel mechanisms of action. In order to combat drug resistance, repurposing the existing drugs with effectiveness is a suitable option. For screening, deep learning (DL) regression methods were implemented to screen

the FDA approved drug library containing 1930 drugs against dihydrofolate reductase (DHFR) of *S. Typhi*. A total of 500 compounds were screened through DL method, and then compounds were subjected to molecular docking. The top eight compounds were filtered through molecular docking, then compounds were subjected to molecular dynamics (MD) simulation. Analysis of MD simulations identified four potential drugs namely: Duvelisib, Amenamevir, Lifitegrast and Nilotinib, all of which showed effectiveness against the DHFR enzyme. These four drugs demonstrated good stability during the 100 ns trajectory period at 300 K in MD simulations. All the complexes demonstrated stability after a 40-ns trajectory period, we further calculated the RMSF, RG, SASA, and interaction energy for the last 60-ns trajectory period to gain more information about the stability of the complexes. Furthermore, the stability of the complexes was conferred by MM-PBSA analysis of the last 10 ns of the MD trajectory. These findings lead us to conclude that these drugs may be helpful in treating typhoid fever and may inhibit *S. Typhi* by interfering the function of DHFR enzyme.

Keywords: Salmonella enteric serovar Typhi; Dihydrofolate reductase; Drug repurposing; FDA approved drug; Deep learning

Identification and prioritization of sample-based clear cell renal cell carcinoma biomarkers through integrated in-silico systems biology approach

OB25

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Abstract

Genomic alterations complicate the comprehensive understanding of the molecular mechanisms underlying clear cell renal cell carcinoma (ccRCC). Their functional role in ccRCC heterogeneity promotes tumour progression as well as diagnostic escape. Hence, more reliable biomarkers are imperative for sustainable diagnosis. The present study utilized *in silico* tools for a rapid, economic and time-saving identification of diagnostics biomarkers from high throughput ccRCC expression data. The user-convenient integrated protocol comprises of expression analysis, interaction network analysis and statistically validated interpretations. From 140 samples and 3657 differentially expressed gene-set, a network of 1867 up-regulated genes were constructed and thoroughly analysed using clustering, centrality parameters and topological matrices. Besides clinically validated marker *VEGFA*, other associated markers like *FN1*, *EGFR*, *MYC*, *IL6*, *CD4*, *PTPRC*, and *TLR4* were identified. Identification of the clinically validated biomarker further confirmed the accuracy of the proposed methodology. The specific pathways of ccRCC identified using functional enrichment analysis of the hub-gene clusters indicated the role of the identified hub genes in the enriched pathways further validating the functional significance of the hub-genes. To further substantiate the translational benefits of the identified hub-genes, we validated the hub-genes with expression-based parameters [based on median transcript per million (TPM) with ANOVA p-value ≤ 0.05] from clinically curated ccRCC dataset. We also designated the priority of biomarkers that were sufficiently correlated with network outputs for different sample categories such as histological grades, tumour, metastatic and pathological stages. Our results confirm how quality diagnostic biomarkers can be designed for medicine using the proposed reiterated validating protocol.

Keywords: Biomarkers; Gene interaction networks; Renal cell carcinoma; Systems biology; Theranostics

ORAL PRESENTATION ABSTRACTS MEDICAL RESEARCH

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Management Of Maxillary Incisors Having Internal Resorption and Open Apex by MTA Apexification And Bleaching- A Case Report

OM1

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ABSTRACT

Introduction: Resorption is defined as a condition associated with either a physiologic or a pathologic process resulting in loss of dentin, cementum or bone.

MTA apexification is very predictable and easy approach for the management of open apex cases

Discussion: Bioactive materials provide successful results in the treatment of the areas where the pulp tissue is covered or associated with periodontal and bone tissue

MTA is one of the most preferred materials among these materials

MTA apexification and intracoronal bleaching can provide a predictable outcome in cases with open apex and discolored tooth

Conclusion: MTA apexification is a very predictable and easy approach for the management of open apex cases and healing of lesions

Eventhough tooth resorption is a unfavourable side effect of non vital tooth bleaching, careful performance of the procedure will help to manage the discoloration caused by internal resorption

References: Manisha vijayaran, Seema choudary: MTA apexification a novel approach for traumatised young permanent teeth

Esthetic Management Of Midline Diastema Using Ceramic Veneers: A Case Report

OM2

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ABSTRACT

Midline diastema, also known as diastema, refers to the clinical term for anterior midline spacing exists between teeth. The space can occur either as a transient malocclusion or created by developmental, pathological or iatrogenic factors. Although various treatment options have been documented for addressing midline diastemas, achieving a satisfactory and durable esthetic outcome relies on a thorough diagnosis and meticulous treatment planning. The presence of diastema is an esthetically challenging clinical situation that could be managed by surgery, orthodontic treatment, restorative and fixed prosthodontic approaches, or a combination of the aforesaid. The restorative closure of diastema can be achieved by using direct composite veneers, indirect composite veneers, porcelain laminate veneers, all ceramic crowns etc. Veneers are considered a reliable restorative procedure due to their color stability, strength, biocompatibility, most conservative, excellent clinical performance, and high esthetic outcome. The idea of providing minimally invasive treatment and understanding the options for the preservation of teeth are some of the important aspects of prognosis. Minimal-thickness laminate veneers provide a satisfactory outcome while preserving the dental structure as a whole. Thus, this clinical report describes a conservative and esthetic approach of closing of midline spacing utilizing ceramic veneers.

Keywords: Midline diastema, Teeth, Veneers, Esthetics, Restorations, Lithium disilicate

Presenting author:

Comparative Evaluation Of Fluoride Release And Recharge Of Conventional Glass Ionomer Cement, Resin Modified Glass Ionomer Cement And Cention N.

OM3

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ABSTRACT

Aim & Objective: To quantitatively assess and compare the fluoride release and recharge of Conventional Glass ionomer cement, Resin modified Glass ionomer cement and Cention N.

Materials and methods: 10-disc shaped pellets having dimension 5 x 3 mm were made in Conventional Glass ionomer (Shofu), Resin modified glass ionomer (Hybond Resiglass, Shofu) and Cention N (Ivoclar Vivadent). Each pellets were individually dipped in 15 ml deionized water in centrifuge tubes for 24 hrs. After 24 hrs specimens were removed and elutes were collected. The solution was replenished daily and quantity of fluoride ions released in the solution was analyzed after 24 hours, 7th day and 15th day. After 15 days, all samples from each group were recharged with Fluoride containing dentifrice for 4 minutes and were reimmersed in 15 ml of fresh deionized water. Fluoride analysis was carried out on 16th day, 22nd day and 30th day by a digital ion analyzer having a specific fluoride ion electrode and the results are statistically analyzed and evaluated.

Keywords : Fluoride, Glass Ionomer Cements, Release and recharge.

Resuscitation Of Avulsed Permanent Tooth With Inflammatory Root Resorption Via MTA - A Case Report

OM4

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ABSTRACT

Introduction: A putty mixture of MTA inserted in the root canal can eliminate bacterial biofilm, inactivate endotoxins, improve resistance to biological degradation (resorption), and promote bone regeneration. The MTA will provide structure and strength to the tooth by replacing the resorbed tooth structure. This case is a documentation to highlight the healing of teeth with extensive inflammatory root resorption (IRR) following avulsion using a nonsurgical root canal therapy using MTA,

Methods: A 17-year-old girl reported to the Department of Conservative and Endodontics after an accidental fall, causing the avulsion of her maxillary anterior teeth. The intraoral examination revealed that the maxillary permanent central incisor (tooth 21) was avulsed with lacerations of soft tissue of gingiva. The avulsed teeth had been wrapped in tissue paper from the moment of trauma until emergency visit 45 minutes later. The crown of the avulsed teeth was intact, and the roots had closed apices. The tooth was splinted back in position and root canal treatment was initiated. The tooth was obturated with MTA

Results: At 6 months of follow-up, the clinical, 2-dimensional (intraoral periapical radiographs) and 3-dimensional (cone-beam computed tomography) images showed arrest of inflammatory root resorption (IRR). On clinical examination absence of clinical symptoms, teeth mobility were noticed.

Conclusions: Although tooth avulsion is one of the most complicated types of teeth traumas. The 2 month follow up reports of this case shows promising results. We plan to maintain a 5-year follow-up of the replanted teeth to assess redevelopment of root resorption or ankylosis. A regular clinical and radiographic examination follow-up every 6 months is fundamental.

Keywords: MTA, avulsion, root resorption, computed tomography

Effect of Blood Contamination and Decontamination on the Micro tensile Bond Strength of 5th And 6th Generation Adhesives: An In vitro Study

OM5

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ABSTRACT

The effectiveness of dentin bonding systems after suitable application protocols is required to ensure the longevity of restorations. Even though contemporary dentin adhesive systems are easier and less technique sensitive, blood, saliva and GCF contamination may compromise the bond strength and marginal seal. The aim of this study is to compare and evaluate the effect of blood contamination on the micro tensile bond strength and to evaluate the effect of contaminant removing treatments on the recovery of bond strength for 5th and 6th generation adhesive system.

35 extracted human maxillary premolars were wet ground occlusally to create flat exposed dentin surfaces. They were randomly divided into 2 groups for Etch and Rinse adhesive and self-etch primer (FL BOND II, SHOFU) and subjected to contamination with blood at various steps. A comparative evaluation of micro tensile bond strength was done in each case using a Universal Tensile machine (INSTRON). Recorded data was then subjected to statistical analysis.

Results obtained showed that Self Etch Adhesives exhibited better bond strength than Etch and Rinse Adhesives in blood contaminated samples. In non-contaminated cases, Etch and Rinse portrayed a better bond strength than Self Etch Adhesives

Candida auris: Prevalence & Antifungal Susceptibility Patterns

OM7

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ABSTRACT

Candida auris is a novel emerging pathogenic *Candida* species first reported in Japan in 2009, now reported from 5 continents. There are separate clonal strains displaying distinct mechanisms of antifungal resistance. It is notorious in causing multidrug resistant nosocomial infections associated with high case mortality. It can persist in hospital environments and cause outbreaks in hospitals especially the intensive care units (ICU's). Genetic analysis suggests, simultaneous emergence of separate distinct clades of this organism from different geographical location

Issues with the identification of *C. auris* using both phenotypic and molecular techniques have raised concerns about detecting the true scale of the problem. *C. auris* isolates have been misidentified as a range of other *Candida* species most commonly, as *C. haemulonii* followed by *C. catenulate*, *C. lusitaniae*, *C. guilliermondii*, or *C. parapsilosis* by both phenotypic and biochemical methods and commercial identification systems like API 20C, Vitek 2 (bioMérieux), Phoenix (BD), and MicroScan (Beckman Coulter, Pasadena, CA).

Recent reports of isolates from India and United Kingdom reported susceptibility of *C. auris* isolates to 5-flucytosine and raised MICs of multiple classes of antifungal agents, raising the possibility of pandrug resistance. Reports suggest that most of these invasive isolates are resistant to fluconazole which is the preferred drug of choice in empirical therapy and management of fungal infections

In this study we aim to determine the prevalence of *Candida auris* isolated in blood cultures from patients attending our hospital and retrospectively analyse antifungal susceptibility patterns of these isolates.

Leveraging Photogrammetry in Prosthodontics: Enhancing Precision and Efficiency

ABSTRACT

Photogrammetry, an innovative technique utilizing photography to measure distances and reconstruct three-dimensional (3D) structures, has emerged as a transformative tool in prosthodontics. By leveraging the principles of photogrammetry, clinicians can capture detailed digital representations of dental structures, revolutionizing traditional prosthodontic practices.

The integration of photogrammetry into prosthodontics offers numerous advantages, primarily centered around precision, efficiency, and patient comfort. Unlike conventional methods relying on physical impressions, photogrammetry enables the non-invasive acquisition of high-resolution images, minimizing patient discomfort and enhancing workflow efficiency. Additionally, the digital nature of photogrammetric data facilitates seamless integration with computer-aided design (CAD) software, streamlining the fabrication process of dental prostheses with unparalleled accuracy.

Moreover, photogrammetry enhances treatment planning by providing clinicians with comprehensive digital models of patients' oral anatomy. From designing fixed or removable prostheses to assessing occlusal relationships and soft tissue contours, photogrammetry empowers clinicians to make informed decisions and deliver tailored treatment plans that meet individual patient needs.

The technological advancements driving the evolution of photogrammetry further amplify its impact on prosthodontics. The integration of intraoral scanners and three-dimensional (3D) printing technologies expands the capabilities of photogrammetry, enabling clinicians to achieve even greater precision and efficiency in prosthodontic procedures. With these advancements, clinicians can seamlessly transition from digital impressions to the fabrication of patient-specific dental prostheses, reducing turnaround times and enhancing overall treatment outcomes.

The adoption of photogrammetry in prosthodontics marks a paradigm shift in the field, offering unprecedented levels of precision, efficiency, and patient satisfaction. By harnessing the power of photography and digital imaging, clinicians can elevate the standard of care, paving the way for a future where precision-driven, patient-centric prosthodontic practice becomes the norm.

Osseoperception With Biohybrid Implants- A Substitute For Natural Teeth In Future

OM9

Merin Basil, Riya Sabu

ABSTRACT

Although dental implants are considered an available treatment in the paradigm shift from traditional dental therapies, such as fixed dental bridges and removable dentures, the fundamental problems must be overcome prior to their clinical use in young patients who are still undergoing jawbone growth. Here, we show a novel bioengineering method for a functional bio-hybrid implant that is combined with adult-derived periodontal tissue and attached with bone tissue as a substitute for cementum. "Osseoperception" described as the capability of osseointegrated titanium implants to transmit certain sensibility. The absence of periodontal ligaments and Ruffini-like endings around implants is responsible for the decrease in osseoperception of dental implants. Autologous dental progenitor cells (DPCs) have the ability to form organized periodontal tissues on titanium implants and can lead to significant improvement in current implant therapies.

This bio-hybrid implant restored physiological functions, including bone remodelling, regeneration of severe bone-defect and responsiveness to noxious stimuli, through regeneration with periodontal tissues, such as periodontal ligament and cementum

Predictive Modeling in Clinical Microbiology: Leveraging Machine Learning to Anticipate and Treat Recurrent Urinary Tract Infections

OM11

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ABSTRACT

Introduction: Recurrent urinary tract infections (rUTIs) pose a significant global health and day to day clinical challenge. This study utilizes data mining to analyse a five-year dataset of 2678 rUTIs cases, exploring risk factors like medical history, demographics, and microbial isolates. The goal is to develop predictive models for identifying high-risk individuals, facilitating targeted interventions and personalized treatment strategies.

Methodology: Anonymized medical records from 2678 patients with recurrent UTIs were analysed over five years using Orange, a data mining software. The process involved cleaning and normalizing data, selecting relevant features, identifying risk factors and microbial isolates, constructing predictive models using algorithms like logistic regression (LR), decision trees (DT), and random forests (RF), and evaluating model performance using metrics such as area under the receiver operating characteristic curve (AUC) and confusion matrices with tenfold cross-validation.

Results: The study's models show promise in identifying rUTIs risk, highlighting factors like diabetes, chronic renal disease, immunosuppressive drugs, and urinary catheterization, along with pathogens *E. coli*, *K. pneumoniae*, and *S. aureus*. Random forests (RF) excel over logistic regression (LR) and decision trees (DT). LR: AUC 0.75 (train), 0.72 (test). DT: AUC 0.82 (train), 0.79 (test). RF: AUC 0.88 (train), 0.86 (test), with TP=420, TN=400. This boosts sensitivity (89.36%) and overall accuracy (88.33%) compared to DT.

Conclusion: Data-driven predictive modeling helps to understand the complexities of rUTIs, guiding targeted interventions by identifying high-risk individuals. Further validation and exploration of additional predictors are imperative for enhanced accuracy, fostering collaboration among clinical microbiologists, physicians, and data scientists.

Keywords: recurrent urinary tract infections, machine learning, predictive modeling, artificial intelligence, data analytics

Evaluation Of Surface Morphology Of Gutta Percha Following Various Cutting Methods-A Sem Study

OM

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ABSTRACT

Aim: to investigate the surface morphology of tip of standardized gutta-percha cone after cutting with different methods.

Materials and methods: The apical 2 millimeters of thirty standardized gutta-percha cones size 40 were cut off using NMD Gutta percha gauge adjuster cutter; BP blade and Scissors. 10 samples in each group were then examined under scanning electron microscopy (SEM) for topographic deformity.

Results: Scores obtained were statistically analyzed using Kruskal Wallis H test and Post Hoc_ Dunnett's test and it was found that there was statistically significant difference(p value <0.05) between BP blade group with other two groups.

Conclusion: Samples cut using BP blade against flat surface of glass slab produced regular cutting surfaces with least deformation when compared to samples cut using NMD gutta percha cutter and scissors.

Clinico-microbiological profile of bloodstream infections due to *Acinetobacter baumannii*

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OM12

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ABSTRACT

Introduction: Bloodstream infections (BSI) when not treated with a susceptible antibiotic before the cascade of sepsis begins can be life threatening. The mortality further increases when the causative organism is multidrug resistant. Infections caused by *Acinetobacter baumannii* are difficult to treat as the antimicrobial resistance is very high among them. Hence, early and aggressive use of appropriate antimicrobials is essential in improving the clinical outcome of these patients.

Aim: The aim of this study was to analyse the carbapenem susceptibility of *Acinetobacter baumannii* and clinical outcome of patients with BSI.

Materials and Methods: Blood cultures were processed from patients who presented with BSI. Analysis for carbapenem susceptibility and clinical outcome of patients were done for those samples which grew *Acinetobacter baumannii*.

Results: In 2023, *Acinetobacter baumannii* was isolated from blood of 60 patients. Of these 37 (61.7%) isolates were resistant to carbapenems. Carbapenem resistance among these isolates were found to be a significant factor which contributed in these patients to require critical care (73%). Mortality rates were also significantly high in those patients with blood stream infections caused by carbapenem resistant isolates when compared to those infected with carbapenem sensitive isolates (59.5% vs 8.7%).

Conclusion: BSI with Carbapenem resistant is associated with high mortality and higher rates of ICU admission

Keywords: Bloodstream infections (BSI), Carbapenem resistant *Acinetobacter baumannii* (CRAB)

Anagement Of Maxillary Central Incisor With Open Apex - A Case Report

OM14

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ABSTRACT

Introduction: Interference in the development by trauma or infection can lead to interruption and arrest of root development which presents with thin and fragile dentinal wall and an absence of natural apical constriction that can create challenging clinical situations. Incomplete root development can be caused by trauma, caries and other pulpal pathosis absence of natural constriction at the end of the root canal presents challenge and makes the three dimensional filling of the root canals become difficult apexification provides a apical barrier against which obturating material can be compacted

Discussion: Apexification is defined as ‘a method to induce a calcified barrier in a root with an open apex or the continued apical development of an incomplete root in teeth with necrotic pulp’. As always, success is related to accurate diagnosis and a full understanding of the biological processes to be facilitated by treatment. Mta is a material which has less leakage, better antibacterial properties, high marginal adaptation, ph of 12.5 and is more biocompatible. Scaffolding is provided for hard tissue formation by mta. It stimulates the production of interleukins and cytokines release. Hence, it is capable of promoting hard tissue formation. When looking for an alternative options apexification with calcium hydroxide has been standard treatment for decades

POSTER PRESENTATION ABSTRACTS BASIC RESEARCH

POSTER - Basic Research - (B.Sc./ B.Tech/ M.Sc./ M.Tech/ Ph.D./ Post-doc)				
ID	Title	Name	Position	Name of the Lab/Department & Institution
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PB2	Ms.	Hanna Sherin N K	Student	Medical Biotechnology And Computational Laboratory, PRC
PB3	Ms.	Meghana U	Student	Jain (Deemed-To-Be University), School Of Sciences
PB4	Ms.	Avani Panickar	Research Scholar	Medical And Biological Computing Laboratory, Vit, Vellore
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Enhanced Antibacterial Efficacy against Multi-Drug Resistant *Escherichia Coli* through the Combined Use of Piper betle and Susceptible Antibiotics

PB1

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ABSTRACT

Escherichia coli is a normal commensal found in the human gut and an important model organism for research microbiology. Multi drug resistant *E. coli* has become a major concern for public health leading to serious health problems due to its resistance against antibiotics such as ceftriaxone, aztreonam, cefepime, cefotaxime, ofloxacin and ciprofloxacin. This resistivity is due to its ability to acquire resistant genes thereby causing a series of infectious diseases. This study aims to discern the synergistic effect of the plant *Piper betle* in combination with susceptible gentamicin. *Piper betle* is found to have antibacterial properties that can kill the growth of many Gram-positive and Gram-negative bacteria and is an effective approach in the treatment against MDR *E. coli*. Isolation onto selective media and biochemical characterization confirmed the isolates as MDR *E. coli*. Furthermore, tests such as qualitative tests for biofilm were done that includes tube test and congo red assay test where E1, E2, E3 formed strong biofilm, E4, E5, E6 formed intermediate biofilm and E7, E8, E9 formed less biofilm. Phenotypic characterization were done consisting of antibiotic Susceptibility test, where the zones were interpreted as resistant, towards the antibiotics confirming that the isolates were MDR. Zone of inhibition were manifested where the strains E1, E2, E3, E4, E6, E9 were identified as MDR. Methanolic extraction was done by rotary evaporator from the plant *Piper betle* with a yield of 7.8µg/ml followed by thin layer chromatography producing multiple bands based on polarity. Presence of flavonoids, tannins, phenols, carbohydrates and total flavonoid content were done under qualitative and quantitative tests respectively. Through column chromatography, separation of polar and non polar fractions were performed and the zone of inhibition through disc diffusion method was done. Non polar fractions alone showed ZOI and the combination with the antibiotic (Gentamycin) showed increased ZOI, showing an effective synergistic activity of the compounds from the plant *Piper betle*. The use of phytochemicals with the combination of antibiotics is a useful approach, however, the dosage and conditions are to be properly maintained.

Keywords: Antibacterial efficacy; Multi drug resistant; Piper betle; Synergistic effect; Zone of inhibition

Exploring The Antibacterial And Antibiofilm Potency Of *Terminalia bellirica* In Synergism With Susceptible Antibiotics Against Nosocomial *Pseudomonas aeruginosa* And *Acinetobacter baumannii*

PB2

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ABSTRACT

Antimicrobial resistance (AMR) acquired by bacteria is a serious threat to public health due to the lack of sufficient treatments and high rate of infection, spreading among people. The study was aimed to explore the antibacterial and antibiofilm potency of *T. bellirica* in synergism with susceptible antibiotics against nosocomial *P.aeruginosa* and *A.baumannii*. The methanolic extract of *Terminalia bellirica* was prepared

by using soxhlet extraction process and rotary evaporation. Crude extract with concentration 20 µg/ml was obtained. This was subjected to column chromatography and fractions obtained based on polarity. The crude extract and fractions underwent analysis using the TLC resulting in the formation of distinct bands. Presence of flavonoids, glycosides, reducing sugar, terpenoids, steroids, and carbohydrates were detected under qualitative analysis. Isolation, morphological characterization, biochemical test and cultural characteristic were done and identified as *Pseudomonas* (P1, P2, P3) and *Acinetobacter* (A1, A2, A3). Biofilm test tube assay was conducted and *Pseudomonas* (P3) was recognized as a strong biofilm producer. Antibiotic susceptibility test were performed and the strains P1, P2, P3, were confirmed as sensitive, whereas, A1, A2, did not show any zones and hence were confirmed as PDR. A3 was found to be sensitive to all antibiotics. Zone of inhibition of phytochemicals were analyzed. Crude extract was found to be more effective against all strains of *Pseudomonas* and *Acinetobacter* giving increased ZOI. The ultimate goal of this study was to find out an effective and efficient way to treat multi drug resistant *P. aeruginosa* and *A. baumannii* in combination with *T. bellirica* and antibiotics. Microtitre assay was used to determine inhibition of biofilm. This work manifests a method where the antimicrobial activity of antibiotics can be enhanced and optimized through synergism with *T. bellirica* fruit extract.

Keywords: Terminalia bellirica; Zone of inhibition; Synergism; Antibiotic susceptibility test; Pan drug Resistant

Assessment of Wound Healing Properties in Water Extracts from Endemic Plants

PB3

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ABSTRACT

Wound healing is a complex process that can be aided by natural products. This study investigates the wound healing potential of extracts from two endemic plant species. We prepared water extract from the leaves of both plants and evaluated their activity in an in vitro HEK293 cells. Human Embryonic Kidney cells (HEK293) were cultured in DMEM/F12 with 10% FBS and 1% Penstrep followed by 24hrs incubation in complete medium before they were exposed to the test compound at different concentrations for 24hrs. After 24hrs the complete medium was replaced with fresh medium and MTT. The test sample induced cell death in 24hrs. Whereas, media control also did not induce any cell death even after 24hrs. The cell toxicity of each test category was determined after 24hrs exposure by measuring OD, using ELISA plate reader (Bio-base) at 570nm.

The wound closure rate and cell migration will be assessed to compare the efficacy of the extracts. Additionally, we will investigate the presence of known wound healing compounds, such as flavonoids, terpenoids. Migration ability was determined by the migration rate of migrating cells up to 48hr. The area that the cells had migrated (toward the initially scratched midline, from the borderline) was measured. This study aims to identify promising endemic plant species for the development of novel wound healing therapies.

Keywords: endemic species, HEK293, migration rate, MTT, Wound healing

Biomedical Application of Polyherbal Extract Infused Chitosan Hydrogel

PB5

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ABSTRACT

In recent years, biopolymers have garnered substantial interest in tissue engineering owing to their commendable biocompatibility and biodegradability. Chitosan, with its attributes of easy administration, low toxicity, and excellent water retention, aligns with the requisites of an ideal medication delivery system. Given the susceptibility of medicinal plants to degradation, an efficient delivery system becomes imperative to preserve their antioxidant and anti-microbial properties. Consequently, the incorporation of polyherbal extracts into chitosan not only ensures the retention of medicinal properties but also facilitates sustained delivery. This study focuses on the development of cross-linking chitosan hydrogel loaded with polyherbal extracts, evaluating its physicochemical characteristics, drug loading, and drug release properties. The efficacy of polyherbal extract-infused chitosan hydrogels for drug delivery is further examined in vitro through cytocompatibility and hemocompatibility testing. Scanning electron microscopy (SEM) analysis unveils a highly porous hydrogel structure. The MTT assay demonstrates a remarkable fibroblast cell survival rate exceeding 90% at 72 hours. Additionally, the hydrogels exhibit no blood cell aggregation and less than 1% hemolysis. The combined attributes of sustained drug release and biocompatibility position chitosan hydrogels as promising candidates in the realm of tissue engineering.

Early identification of common bacterial pathogens and antibiotic resistant genes from blood culture broth using PCR

PB6

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ABSTRACT

Sepsis is a leading cause of hospital deaths worldwide, and its incidence is increasing. Blood-culture, the standard method for detecting pathogens, has limitations such as being time-consuming and unable to identify certain microbes. This method is also challenging for patients who have taken antibiotics. Film array assays are expensive cannot be employed for routine testing. Automated blood-culture diagnosis can be enhanced by incorporating rapid Polymerase Chain Reaction (PCR) technique to detect the DNA of the pathogens as well as the presence of antibiotic resistant genes within 12 hours, enabling prompt treatment. The present study standardized an in house procedure with less turnaround time for extraction of DNA from blood culture broth positive for Gram positive and Gram negative bacteria. Further we

standardized a conventional PCR protocol for the identification of common blood stream pathogens (*Staphylococcus aureus*, *Klebsiella pneumoniae*, *Escherichia coli*, *Pseudomonas aeruginosa*, *Acinetobacter baumannii*) as well as genes coding for Carbapenem (NDM-1, OXA-48) and Methicillin resistance (*mec-A*). Out of the 77 blood culture broth (Bact/Alert) which indicated positive with Gram negative bacilli, 45 were identified as *Klebsiella pneumoniae*, 19 as *Acinetobacter baumannii*, four as *Pseudomonas aeruginosa* and seven as *Escherichia coli* by the standardized PCR protocol. Among these, carbapenem resistance by NDM-1 was detected in 39 samples, OXA-48 in eight and one showed detection of both NDM-1 and OXA-48. Among the 14 Gram positive cocci broth cultures 4 were identified as *Staphylococcus aureus* with *mec A* gene (MRSA). We expect to contribute towards antimicrobial stewardship by further validating the standardized methods for early identification of blood pathogens.

Keywords: Blood pathogens, Carbapenem resistance, Blood culture broth, Antibiotic resistant genes, Polymerase Chain Reaction (PCR)

Limosilactobacillus mucosae from human breast milk - A novel probiotic with antibacterial potential

PB7

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ABSTRACT

Research on probiotics continues to expand our comprehension of the complex relationships between microbes and their hosts, offering hopeful avenues for enhancing human health outcomes. Moreover, probiotics present a promising avenue for alternative or supplementary antibacterial treatments. Probiotic strains of human origin has been linked with safety and functionality for human use and therefore the present study evaluated the *in vitro* probiotic capabilities of bacterial strains isolated from human breast milk and infant feces based on the ICMR-DBT guidelines. Among the 12 isolated bacterial strains the Lactic Acid Bacterial (LAB) strain which satisfied all the required probiotic properties including anti-bacterial activity against Multi Drug Resistant Bacteria was chosen for further investigations. The strain was identified as *Limosilactobacillus mucosae* by 16S rRNA sequencing. Evaluation of the antibacterial property showed that the cell free supernatant of the strain inhibited pathogenic bacteria at low pH as well as at neutral pH suggesting production of a compound/metabolite other than organic acid. *L. mucosae* is a LAB and carries the gene coding for mucus-binding protein enabling efficient intestinal colonization. Previous studies have isolated the species from animal sources and human feces and demonstrated its probiotic and anti-bacterial properties. Here, we report the isolation of *L. mucosae* from human breast milk for the first time. Our study highlights its probiotic and anti-bacterial potential, making it a promising candidate for use in dairy products and as an alternative antibacterial agent. Further investigations will be based on examination of *in vivo* probiotic properties and characterization of the antibacterial property of the strain.

Keywords: *Limosilactobacillus mucosae*. Human Breast Milk, Probiotic, Infant feces, Anti-bacterial property

Presence of *bla*_{IMP} metallo beta-lactamase producing *Escherichia coli* of multidrug resistant phenotype within a tertiary referral hospital in Northeast India

PB8

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ABSTRACT

Background: A significant issue facing the world today is antibiotic resistance, especially beta-lactam resistance. Multidrug resistant organisms, particularly pathogens that harbour beta-lactamases, pose a significant threat to global public health, leading to increased rates of morbidity and mortality as well as increased financial expenses. Imipenemase, also known as IMP-type metallo-β-lactamase (MBL), was first identified in Japan in the 1990s and since then has gained increased recognition, particularly in Asia. The current study characterizes the presence of *bla*_{IMP} producing *Escherichia coli* of multidrug resistant phenotype within a single centre in Northeast India.

Methodology: A total of 70 clinical isolates of *Escherichia coli* were obtained from a tertiary referral hospital of northeast India. Susceptibility testing against different antibiotics like imipenem, meropenem, ceftazidime, cefotaxime, aztreonam, cefepime, ciprofloxacin, amikacin, gentamicin and co-trimoxazole was done and results were interpreted as per CLSI, 2023 guidelines. Molecular characterization of the confirmed *E. coli* isolates was performed by PCR targeting *bla*_{IMP} gene.

Results & Discussion: Antibiotic susceptibility testing showed that majority of the study isolates were resistant to ciprofloxacin (100%) and cefotaxime (100%) followed by imipenem (90.9%), amikacin (90.9%) and the other antibiotics and the lowest resistance was observed for aztreonam (63.6%). Eleven isolates, out of the seventy isolates, were found to be harbouring *bla*_{IMP} gene on genotypic characterization. The study highlighted an increased occurrence *bla*_{IMP} producing *Escherichia coli* within a single study centre and warrants further investigation on their dissemination.

Keywords: Antibiotics, Antimicrobial resistance, Multidrug resistant organism, Metallo-β-lactamase, *Escherichia coli*

Multi-drug resistant *Escherichia coli* carrying *bla*_{TEM} with extended spectrum cephalosporinase activity in a tertiary referral hospital of North-East India

PB9

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ABSTRACT

Background: Recent spread of multi-drug resistant (MDR) bacteria reports a significant problem for treatment due to the outbreak of extended-spectrum β-lactamases (ESBLs) producing bacteria. The possible reason for this may be that the β-lactam antibiotics, which includes penicillin derivatives, cephalosporins, monobactams, etc. are one of the most commonly used antibacterial agents in

clinics. Extraintestinal pathogenic *E. coli* have the ability to cause diverse and serious diseases. Thus, the escalating MDR isolates of *E. coli* from the health care settings is a major concern for public health. The current study aims to study the antibiotic resistance profile and genetic background of *E. coli* isolates obtained from a hospital in North-East India.

Methodology: 106 *E. coli* isolates of clinical origin were subjected to Kirby-Bauer disc diffusion method using antibiotics, namely, Imipenem, Meropenem, Cefotaxime, Ceftazidime, Aztreonam, Cefepime, Ciprofloxacin, Amikacin, Gentamicin and Co-trimoxazole. Two sets of multiplex PCR was performed to identify the presence of ESBL genes.

Result & Discussion: A total of 98 isolates were identified to be resistant to multiple drugs under study. 47.96% of these isolates were found to be carrying one or more genes responsible for producing ESBLs, which included CTX-M, TEM, SHV, OXA-10 and OXA-2. 49% of ESBL-producing *E. coli* were found to be carrying *bla*_{TEM}.

Conclusion: This study highlights that *bla*_{TEM} has a contributing role in extended spectrum cephalosporinase activity in multi-drug resistant phenotype of *E. coli*.

Keywords: Multi-drug resistant, extended-spectrum β -lactamases (ESBLs), β -lactam antibiotics, antibiotic resistance, cephalosporinase

Histidine Kinase EvgS: A Potential Therapeutic Target at the Convergence of Antimicrobial Resistance and Virulence in Multi-Drug Resistant *Shigella flexneri* 2a str. 301

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PB10

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ABSTRACT

Multi-drug resistant *Shigella flexneri* 2a (MDR-Sf2a) poses a significant challenge due to its role in diarrhoeal mortality and its ability to evade treatment. This study employed gene interaction network analysis (GIN) to identify potential therapeutic targets by elucidating interactions between antimicrobial resistance (AMR) and virulence genes at the cellular and molecular level. The analysis incorporated statistically significant differential gene expression (DGE), protein structural features, and dynamic properties to pinpoint biomarkers for developing sustainable treatment regimens against MDR-Sf2a. Functional enrichment and network topology revealed *evgS*, *ybjZ*, *tolC*, *gyrA*, *parC*, and their interacting partners as putative contributors to diverse AMR mechanisms. Histidine kinase EvgS emerged as a central hub protein due to its high prevalence (71.6%) within the AMR cluster and its role in interconnecting virulence-associated genes (45.8%), suggesting a potential link between the two processes. DGE profiles of a Δ PhoPQ mutant strain (lacking PhoP and PhoQ) confirmed the upregulation of the EvgS a two-component system (TCS), further supporting EvgS as a promising therapeutic target. To assess EvgS's druggability, the study evaluated its thermal stability, backbone rigidity, and coarse-grained dynamics. Structure-function relationships were established, identifying the C-terminal extracellular domain as a potential drug-binding site, which was validated through molecular dynamics simulations. Elucidation of the identified biomarker's structure, along with secondary and tertiary structural validation, holds promise for future therapeutic interventions that can simultaneously combat both AMR and virulence in MDR-Sf2a.

Keywords: Antimicrobial resistance, Functional enrichment, druggability, Biomarker, Molecular Dynamics Simulation

Dissecting PmrB Mutations in Colistin-Resistant *Klebsiella pneumoniae*: Unveiling Structural insights as Targets for Novel Therapies

PB11

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ABSTRACT

Carbapenem-resistant *Klebsiella pneumoniae* (CRKP) poses a significant global threat due to its limited treatment options, with colistin remaining a last-line therapeutic agent. However, the emergence of colistin-resistant *K. pneumoniae* (COLR-Kp) underscores the urgent need for novel therapeutic targets. This study delves into the structural impact of prevalent PmrB mutations associated with colistin resistance in *K. pneumoniae*. Clinical isolates exhibited heterogeneous colistin susceptibility profiles despite harbouring mutations like T157P, G207D, and T246A. In silico modelling of mutant PmrB proteins derived from sequenced genomes facilitated a comprehensive analysis of their structural alterations. Molecular dynamics simulations, free-energy landscapes, and protein flexibility profiles were employed to elucidate the functional consequences of these mutations. The results suggest that altered protein backbone flexibility may be a critical factor in the selection of COLR-Kp mutants, providing valuable insights for the development of future intervention strategies. Therefore, PmrB, identified as a highly druggable target, was subjected to virtual screening against a library of 1396 FDA-approved drugs. Among the top candidates, amphotericin B demonstrated exceptional binding affinity (binding energy < -8 kcal/mol) and stable interactions (RMSF < 0.7 Å) with PmrB druggable pockets, irrespective of the mutations present. This finding warrants further investigation of amphotericin B as a potential therapeutic agent, potentially in combination regimens, to combat the emergence of COLR-Kp.

Keywords: Carbapenem resistant, Mutations, Therapeutic target, Virtual screening, Molecular dynamics simulations

Early identification of common bacterial pathogens and antibiotic resistant genes from blood culture broth using PCR

PB12

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ABSTRACT

Sepsis is a leading cause of hospital deaths worldwide, and its incidence is increasing. Blood-culture, the standard method for detecting pathogens, has limitations such as being time-consuming and unable to identify certain microbes. This method is also challenging for patients who have taken antibiotics. Film array assays are expensive cannot be employed for routine testing. Automated blood-culture diagnosis can be enhanced by incorporating rapid Polymerase Chain Reaction (PCR) technique to detect the DNA of the pathogens as well as the presence of antibiotic resistant genes within 12 hours, enabling prompt treatment. The present study standardized an in house procedure with less turnaround time for extraction

of DNA from blood culture broth positive for Gram positive and Gram negative bacteria. Further we standardized a conventional PCR protocol for the identification of common blood stream pathogens (*Staphylococcus aureus*, *Klebsiella pneumoniae*, *Escherichia coli*, *Pseudomonas aeruginosa*, *Acinetobacter baumannii*) as well as genes coding for Carbapenem (NDM-1, OXA-48) and Methicillin resistance (*mec-A*). Out of the 77 blood culture broth (Bact/Alert) which indicated positive with Gram negative bacilli, 45 were identified as *Klebsiella pneumoniae*, 19 as *Acinetobacter baumannii*, four as *Pseudomonas aeruginosa* and seven as *Escherichia coli* by the standardized PCR protocol. Among these, carbapenem resistance by NDM-1 was detected in 39 samples, OXA-48 in eight and one showed detection of both NDM-1 and OXA-48. Among the 14 Gram positive cocci broth cultures 4 were identified as *Staphylococcus aureus* with *mec A* gene (MRSA). We expect to contribute towards antimicrobial stewardship by further validating the standardized methods for early identification of blood pathogens.

Keywords: Blood pathogens, Carbapenem resistance, Blood culture broth, Antibiotic resistant genes, Polymerase Chain Reaction (PCR)

PB13

Assessment of Wound Healing Properties in Water Extracts from Endemic Plants

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ABSTRACT

Wound healing is a complex process that can be aided by natural products. This study investigates the wound healing potential of extracts from two endemic plant species. We prepared water extract from the leaves of both plants and evaluated their activity in an in vitro HEK293 cells. Human Embryonic Kidney cells (HEK293) were cultured in DMEM/F12 with 10% FBS and 1% Penstrep followed by 24hrs incubation in complete medium before they were exposed to the test compound at different concentrations for 24hrs. After 24hrs the complete medium was replaced with fresh medium and MTT. The test sample induced cell death in 24hrs. Whereas, media control also did not induce any cell death even after 24hrs. The cell toxicity of each test category was determined after 24hrs exposure by measuring OD, using ELISA plate reader (Bio-base) at 570nm.

The wound closure rate and cell migration will be assessed to compare the efficacy of the extracts. Additionally, we will investigate the presence of known wound healing compounds, such as flavonoids, terpenoids. Migration ability was determined by the migration rate of migrating cells up to 48hr. The area that the cells had migrated (toward the initially scratched midline, from the borderline) was measured. This study aims to identify promising endemic plant species for the development of novel wound healing therapies.

Keywords: endemic species, HEK293, migration rate, MTT, Wound healing

Unveiling Nature's Potential: *Phellinus Caryophylli*, a therapeutic fungal biofactory

PB14

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Presenter: Dr. Ruby Varghese

ABSTRACT

Since the pre-historic era mushrooms have been favored as gourmet food and as a single medicine/single ingredient (ottamooli in Malayalam) against various diseases in the traditional medicinal system due to their multi-target effectiveness. Higher basidiomycetes are a great source of bioactive secondary metabolites with abundant therapeutic properties.

Mushrooms belonging to the Hymenochaetaeaceae family have been extensively studied due to their historical importance and usage in folk medicine for ages. Though various studies are carried out on the species like *Phellinus linteus*, *Phellinus ignarius*, and *Phellinus baumii* only scanty works are available on *Phellinus caryophylli*. The present study evaluated the anticancer and anti-diabetic activity of *Phellinus caryophylli* in murine models by alleviating aberrations caused by cancer and elevated blood glucose levels at cellular, biochemical, and molecular levels

Keywords: Alloxan, Angiogenesis, Antioxidant, Tumor, Apoptosis, Dalton Lymphoma Ascites, Inflammation

Identification of High-Affinity Antimicrobial Peptides against Clinically Relevant β -Lactamases of Gram- Negative ESKAPE Pathogens: A Computational Biology Approach

PB4

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ABSTRACT:

The global rise of Anti-Microbial Resistance (AMR) necessitates the urgent development of novel therapeutic strategies. While Antimicrobial Peptides (AMPs) have demonstrated broad-spectrum efficacy, recent evidence suggests an increase in resistance among ESKAPE pathogens, particularly against membrane-targeting AMPs. This study addresses this challenge by utilizing in-silico methods to design a library of 60 AMPs. Following a comprehensive evaluation of their physicochemical properties, each AMP was subjected to virtual docking simulations against four key β -lactamase enzymes prevalent in Gram-negative ESKAPE pathogens. Among the most potent mutants identified, a Lactoferricin B variant (M4) exhibited exceptional binding affinity towards SHV-1, OXA-48, NDM-1, and AmpC β -lactamases, with respective docking energies of -842.0 kcal/mol, -774.8 kcal/mol, -1103.3 kcal/mol, and -858.8 kcal/mol. Coarse-grained clustering and flexibility analyses revealed stable residue-level conformations within the high-affinity protein-peptide complexes. Notably, Lactoferricin B_M4 displayed the strongest interaction with NDM-1, facilitated by a network of hydrogen bonds, salt bridges, and hydrophobic interactions with the metallo- β -lactamase domain, particularly involving the critical active-site residue Asp124. To further validate these findings, molecular dynamics simulations confirmed the remarkable stability of the Lactoferricin B_M4-NDM1 complex, characterized by minimal residue-level root-mean-square deviations (RMSD), low atomic fluctuations, and a compact radius of gyration (Rg). This in-silico study lays the groundwork for future experimental validation and underscores the potential of computational approaches for identifying promising AMPs to combat drug-resistant pathogens.

Keywords: Antimicrobial Peptide, Antimicrobial Resistance, ESKAPE, β -Lactamases, Molecular Docking

POSTER PRESENTATION ABSTRACTS MEDICAL RESEARCH

POSTER - Medical Research - (B.Sc./ B.Tech/ M.Sc./ M.Tech/ Ph.D./ Post-doc)				
ID	Title	Name	Position	Name of the Lab/Department & Institution
PM1	Dr.	Shemeera Saidalavi V P	Student	Pathology Department, PIMS & RC Thiruvalla
PM2	Dr.	Jo Ann Philip	Student	Pathology Department, PIMS & RC Thiruvalla
PM3	Dr.	Anju Maria Biju	Student	Pathology Department, PIMS & RC Thiruvalla
PM4	Dr.	Aparna K	Student	Department Of Periodontics, Pushpagiri college Of Dental Sciences, Thiruvalla
PM5	Dr.	Rajasree.A.R	Student	Department Of Periodontics, Pushpagiri college Of Dental Sciences, Thiruvalla
PM6	Dr.	Kavya .S	Student	Pushpagiri College Of Dental Sciences, Thiruvalla
PM7	Dr.	Firoz Khan	Student	Department Of Prosthodontics and Crown and Bridge Pushpagiri College of Dental Sciences
PM8	Dr.	Hamna Hussain	Student	Pedodontics And Preventive Dentistry
PM9	Dr.	Adithya R Pillai	Faculty / Scientist	Central Research Laboratory, BCMCH

Sarcina Ventriculi Infection: A Rare Cause of Gastric Outlet Obstruction

PM1

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ABSTRACT

Introduction: *Sarcina ventriculi* (now known as *Clostridium ventriculi*) is a gram positive bacterium, able to survive in extreme low pH environment. Its 1st description dates from 1842 by John Goodsir after the microscopic analysis of the gastric content of a patient with daily vomiting.

Materials and methods: 56/M presented with c/o intermittent dyspepsia, fullness of stomach and nausea. Upper GI endoscopy shows Pyloric stenosis & scope could not be negotiated beyond pylorus. Food residues were present in stomach. Biopsy from pylorus was sent for histopathological evaluation.

Result: Microscopic Sections showed fragments of gastric mucosa with intact foveolar epithelium. Lumen and mucosal surface showed organisms arranged in tetrads and octads-consistent with *Sarcina ventriculi*. Hence diagnosed as mild gastritis with *Sarcina ventriculi*

Discussion: The natural habitat of the *Sarcina ventriculi* bacteria is the soil and is also found in water and air, in the form of spores. The infection of human or other animals is caused by contamination of food. Because *Sarcina* organisms are difficult to grow on cultures and molecular methods of confirmation are not available in many parts of the world, histopathologic examination for the classic morphologic features remains a key to the diagnosis until specific microbiologic diagnostic methods become available.

Tinea Corporis- The Ring Worm

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PM2

ABSTRACT

Introduction: Dermatophytes are a group of related filamentous fungi that have ability to invade and colonize the keratinized tissues of human and animals. Infections caused by these fungi accounts for 3% to 4% of dermatological consultations and are known as dermatophytosis (ringworm, tinea). Tinea corporis is a dermatophytosis of glabrous skin.

Materials and methods: 68/F presented with skin lesion over back of left elbow. Underwent punch biopsy of skin lesion for histopathological evaluation.

Result: Microscopic sections from the punch biopsy skin showed epidermis with compact hyperkeratosis, focal parakeratosis and epidermal hyperplasia. Clear spaces were noted in stratum corneum. Superficial dermis showed moderate lymphoplasmacytic infiltrate. Special stains such as PAS &GMS showed fungal pseudohyphae and spores in the parakeratotic layer. Diagnosed as Tinea corporis.

Discussion: Tinea corporis is a superficial fungal skin infection of the body caused by dermatophytes. Biopsy from dermatophyte infection shows 3 characteristic changes which are:

- a. presence of neutrophils within the spongiotic vesicle
- b. hyphae within the orthokeratotic layer and
- c. sandwich sign – presence of hyphae “sandwiched” in between an upper but normal basket weave stratum corneum and a lower layer of recently produced stratum corneum that is abnormal in being compact orthokeratotic or parakeratotic in type. The diagnosis is supported by special stain like GMS& PAS.

Advancements In The Management Of Anxiety In Pediatric Dental Practice

Aparna K

PM4

ABSTRACT

Dental anxiety is a heightened fear of dental procedures ranging from restlessness to full-blown tantrums. Prevalence estimates of dental anxiety in youth ranges from 5 to 20%. Children who have low or moderate levels of fear or anxiety can be effectively managed by establishing proper behavior guidance strategies whereas, highly anxious/fearful or phobic children may necessitate targeted pharmacological support in addition to the utilization of behavior guidance strategies. Research indicates that modern parents are less tolerant of physical behavior management techniques than previous generations, and may be more inclined to accept or request conscious sedation or general anesthesia for their child's dental treatment. As a result, pharmacological behavior guidance is now commonly employed in pediatric dentistry.

The different routes of sedative drug administration in pediatric dental practice include oral, intranasal, inhalational, intravenous and newer techniques for sedation delivery like Target-controlled infusions (TCI). Medications like nitrous oxide, midazolam, Ketamine, Dexmedetomidine, Fentanyl, Propofol, Etomidate, Chloral hydrate, Pentobarbital, Hydroxyzine, Sevoflurane and Melatonin are used alone or in combinations.

Nitrous oxide at concentrations of $\leq 50\%$, blended with oxygen, and without any concurrent administration of other sedatives, opioids, or depressant medications is one of the top choices for mild sedation during dental procedures.

Keywords: Anxiety, Behavior guidance, pharmacological behavior guidance, pediatric dentistry.

Efficacy Of Diffuse Reflectance Spectroscopy Based Probe In Evaluation Of Periodontal Inflammation In Gingivitis And Periodontitis

PM5

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Dr. Nebu George Thomas,

ABSTRACT

Introduction: Traditional diagnostic procedures for the detection of periodontitis have certain limitations which may lead to inaccuracies in diagnosis as well as prognosis of periodontal diseases. This study assesses the efficacy of a low-cost handheld probe that utilizes diffuse reflectance (dr) spectroscopy to measure the state of periodontal health.

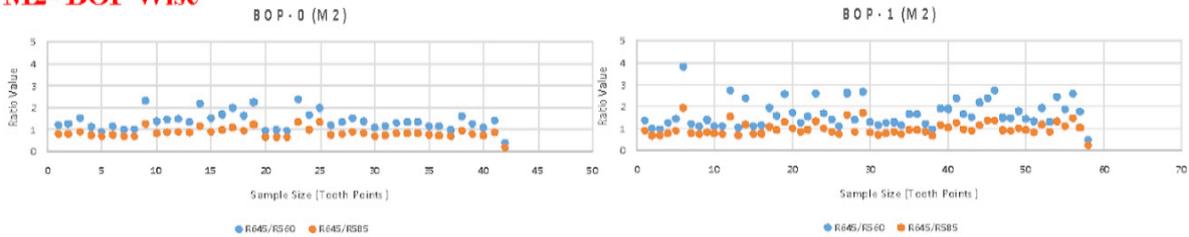
Aims & objectives: The aim of the study is to evaluate the efficacy of diffuse reflectance spectroscopy-based probe in detecting periodontal inflammation in comparison to gold standard of diagnostic techniques. Objectives of the study are to check the clinical validity of diffuse reflectance spectroscopy-based probe for the detection of periodontal inflammation & to correlate diffuse reflectance (dr) measurement data with the conventionally determined parameters.

Materials & methods: Through this project we intend to conduct clinical tests to check the diagnostic accuracies of diffuse reflectance spectroscopy-based probe, developed for the detection of periodontal-inflammation. An android software application installed on the smartphone controls the device the data thus obtained would be analyzed using appropriate statistical model and interpreted based on the correlation with conventionally determined parameters.the device would be validated if it exhibits sensitivity and specificity greater than 80%.

Results & observations:

Clinical Trial Data Analysis Sample Size - 4 Subjects (6 tooth)

M2- BOP Wise



Measurement with 'M2' probe				
	BOP - 0		BOP - 1	
	R645/R560	R645/R585	R645/R560	R645/R585
Mean	1.414	0.873	1.748	1.031
STDEV	0.397	0.185	0.508	0.248
% Variation	28.085	21.167	29.082	24.020

Sample Size - 4 Subjects(6 tooth from each)



Preclinical Analysis Of 3D Printed Scaffolds For Craniofacial Regeneration

PM6

Kavya.S , Lekshmi.M

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ABSTRACT

Tissue engineering, is an emerging multidisciplinary field involving biology, medicine, and engineering that is likely to evolutionize the way we improve the health and quality of life. Oral and craniofacial tissue engineering has been achieved with limited success by the utilization of a variety of approaches such as cell-occlusive barrier membranes, bone substitutes and autogenous block grafting techniques. Historically, the gold standard for such applications has been autologous bone. Yet, challenges like donor site morbidity and the scarcity of scaffolding have constrained its employment.

Three-dimensional (3D) printing, an additive manufacturing method, offers a promising solution. This modality not only facilitates the creation of intricate 3D geometries but also extends meticulous control over the macro and micro-architectures of tissue scaffolds, mirroring the intricacies of the extracellular matrix . Conventional bone scaffolds designed for reconstructing alveolar bone defects have presented a range of challenges, including brittleness, high cost, unordered pores, and insufficient porosity. These limitations have hampered their ability to effectively mimic the Extracellular Matrix for robust cell interaction. With advancements in manufacturing technology, 3D-printing has emerged as a game-changer. It offers the capability to produce scaffolds with precisely ordered pores and customized constructs. 45S5-bioglass (45S5-BG) and hydroxyapatite are superior in osteoconductive and osteoinductive abilities, has been at the forefront of tissue engineering. This research underscores the development of a scaffolds that is both biocompatible and economically feasible for bone tissue engineering.

Keywords: Tissue engineering,3D printing Scaffolds,45S5 Bioglass, Hydroxyapatite, Regeneration

BIONIC EAR

PM7

Riya Ann Joseph , Firoz Khan N

ABSTRACT

The development of the bionic ear marks a significant milestone in the field of auditory prosthetics, offering novel solutions for individuals with hearing impairments. This poster presentation delves into the evolution of the bionic ear, tracing its technological advancements, clinical applications, and the impact on auditory perception.

Beginning with an overview of the anatomy and function of the human ear, the poster elucidates the mechanisms underlying hearing loss and the challenges it poses to communication and quality of life. It then transitions to the inception of cochlear implants, highlighting the pioneering work of researchers and engineers in bridging the gap between sound and perception.

Central to the discussion are the technological innovations driving the evolution of the bionic ear. From early models characterized by rudimentary electrode arrays to contemporary systems featuring sophisticated signal processing algorithms and neural interfaces, each iteration has contributed to improved auditory outcomes and user experience. Moreover, advancements in miniaturization and biocompatibility have rendered these devices more accessible and less intrusive, catering to diverse patient populations.

The clinical efficacy of cochlear implants is examined through empirical evidence and patient testimonials, showcasing their ability to restore speech intelligibility, enhance music appreciation, and facilitate social integration. Furthermore, the poster explores ongoing research endeavors aimed at expanding the capabilities of bionic ears, such as incorporating wireless connectivity, optimizing electrode design, and exploring alternative stimulation modalities.

In conclusion, this poster underscores the transformative impact of the bionic ear on the lives of individuals with hearing impairments, reaffirming its status as a cornerstone of modern auditory rehabilitation. By elucidating its technological underpinnings and clinical outcomes, it seeks to foster awareness, appreciation, and continued innovation in the realm of auditory prosthetics.

RECENT ADVANCES OF PAIN MANAGEMENT IN PEDIATRIC DENTISTRY

PM8

Hamna Hussain

ABSTRACT

Pain is defined as “ An unpleasant sensory and emotional experience associated with, or resembling that associated with, actual or potential tissue damage.” Pain has an emotional or affective component. It is also associated with reflex withdrawal response and autonomic changes mediated via autonomic nervous system such as sweating changes in blood pressure, heart rate and respiration.

A child's pain is very different from that which is experienced in adults. Different emotional and psychological factors can affect the child's pain comprehension and stimulate his/her response. It is known that children can feel pain and that it has long-term effects that last through childhood into adulthood.

Pain control is particularly an important component of pediatric dentistry. Effective pain control ensures a safe and quality dental care in pediatric dental patients. An ideal anesthetic technique includes a painless procedure, either during the delivery of the local anesthesia or during the operative procedure. It is often paradoxical that the agent used to eliminate pain can itself be a source of pain. Dental phobia among children is due to the fear of the conventional syringe used to deliver local anesthetic agent. Adequate pain control can instill in positive oral health attitudes in children. Thus newer approaches such as intranasal spray, centbucridine, jet injectors, buzzy devices, and acupressure have been developed provide near-painless injections while reducing dental anxiety.

Keywords: pain control, local anesthesia, children, adult

EVALUATION OF MICRONUCLEI FREQUENCY IN RECURRENT PREGNANCY LOSS FEMALES: A SIGN OF GENOMIC INSTABILITY

PM9

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ABSTRACT

Micronucleus assay is one of the techniques used to measure DNA changes. A micronucleus is a tiny nuclear object containing whole chromosomes or chromosomal fragments. Such small nuclei might originate from the acentric fragments (chromosomal fragments lacking a centromere) or the chromosomes that cannot migrate with other chromosomes during cell division anaphase. The advantages of this technique compared to the other techniques evaluating the DNA damage are its simplicity, non-invasiveness, and low cost. 12% to 15% of all pregnancies spontaneously terminate through an early miscarriage, and the incidence is markedly influenced by the woman's age. The frequency with which miscarriages occur has been extraordinarily stable over time. In past decades, pregnancies conceived both spontaneously and through assisted reproductive technology had a similar incidence of miscarriage. Our aim is to investigate the genetic damage in the whole blood cells obtained from recurrent pregnancy loss females and control subjects, using the micronucleus assay. A hospital-based cross-sectional study was conducted in the Department of Reproductive Medicine, Believers Church Medical College Hospital, Thiruvalla. The study was carried out during a period of 5 months with effect from January 2024 to May 2024. A total of 60 women with history of recurrent pregnancy loss were included in the study. The mean age among participants was 30.28 ± 5.48 years. The average number of abortions was 2.53 ± 1.02 . About 85.34% had micronuclei and nearly equal proportion of (48.27% and 46.56%) of the participants had Nuclear bridge and nuclear bud. Most common complication were thyroid disorder (50.06%) and epilepsy (12.06%). Women with history of recurrent pregnancy loss encountered increased micronuclei, nuclear bridge and nuclear bud when compared to that of general population, which indicates genotoxicity. The definition, diagnosis and treatment of patients with a history of RPL remains difficult. Increased antenatal surveillance to reduce the risk of pregnancy complications with better screening of the family history and the necessary investigations to identify a treatable cause associated with previous miscarriages can lead to early prophylactic interventions for a better outcome.

ABOUT PUSHPAGIRI RESEARCH CENTRE

ABOUT PUSHPAGIRI RESEARCH CENTRE (PRC)

Pushpagiri Research Centre (PRC) is a unit of Pushpagiri Medical Society, which has been the pioneering force in providing super specialty health care in Central Travancore region of Kerala State. Established in 2010, PRC has grown to become one of the best research centers in the state, in private sector. Pushpagiri Research Centre features open-plan, multifunctional research laboratories, which have all the facilities for conducting interdisciplinary biomedical research.

Pushpagiri Research Centre is a Scientific and Industrial Research Organization (SIRO) recognized by Department of Scientific & Industrial research (DSIR); Govt. of India. Kerala University of Health Sciences (KUHS) has also approved PRC for its Ph.D. programmes. The centre has received funding from prestigious agencies like DST, DBT, ICMR, KSCSTE and Bill & Melinda Gates foundation and has been part of many international research collaborations. PRC is unique among all the research centres of Kerala as it has active Memorandum of Understandings (MoUs) with an array of institutions from government and private sectors.



OUR VISION

We aim is to create breakthroughs in medical field, by taking research outcome from bench to bedside, with high ethical standards, and to develop transformative technologies, to meet growing challenges in the area of human health and illness, with an innovative approach. It provides a platform, to develop strategies of therapeutic intervention to improve the quality of life, and to alleviate human sufferings. Our state-of-the-art infrastructure, and domain of expertise, catalyzes the translation of laboratory research of academia and industry to hospital bed.

OUR HISTORY

Pushpagiri Group of Institutions is located in the heart of Tiruvalla, a scenic town in Central Travancore in Kerala. This land is blessed with the visit of Saint Thomas, the disciple of Jesus. It harbours Sri Vallabha Temple, Saint John's Cathedral, Parumala Church to enrich the rich spiritual heritage of Tiruvalla. This place is richly ornamented with the lush green paddy fields and coconut grooves. The branches of Pushpagiri Medical Society comprise of Pushpagiri Institute of Medical Sciences, Pushpagiri College of Dental Sciences, Pushpagiri College of Pharmacy, Pushpagiri College of Nursing, & Pushpagiri College of Allied Health Sciences.

Pushpagiri Research Centre better known by the acronym PRC is a Scientific and Industrial Research Organization (SIRO) recognized by the Department of Scientific and Industrial Research (DSIR), Ministry of Science & Technology, Government of India. It was initiated in the year 2009 and functions in Pushpagiri Medical College Campus as a Central Research Facility. PRC features open-plan, multifunctional research laboratory and it conducts, promotes research in interdisciplinary areas of sciences such as Tissue Engineering and Regenerative Medicine, Medical Biochemistry, Bioinformatics and Drug Designing, Medicinal and Phytochemical Research, Molecular Biology, Cell Culture, Microbial Technology, Cancer Research and Epidemiology studies.

PRC offers a unique, pluralistic and open research culture that is supported by high-end infrastructure and instrument facilities. Various research schemes are funded by State & Central Government agencies like DST, DBT, ICMR, BRNS and International agencies like Bill and Melinda Gates Foundation, CEI, etc. PRC mainly focuses on translating the ideas from laboratory to commercial market. The Research Centre is currently carrying out various researches in wound healing, tissue regeneration, antimicrobial resistance and usage of novel phytocompounds, in-silico research and computational drug designing, molecular biology, virology, infectious disease, clinical epidemiological studies and clinical trials, which is in collaboration with various institutions. PRC is having MoU with various government institutes like CIFT-Kochi, MG University-Kottayam HLL, Trivandrum and private institutes like MACFAST Tiruvalla, Bishop Moore College Mavelikara, CUSAT (Cochin University of Science Technology), SJRI (St. John Research Institute, Bangalore, Stockholm University, Vellore Institute of Technology (VIT), Vellore.

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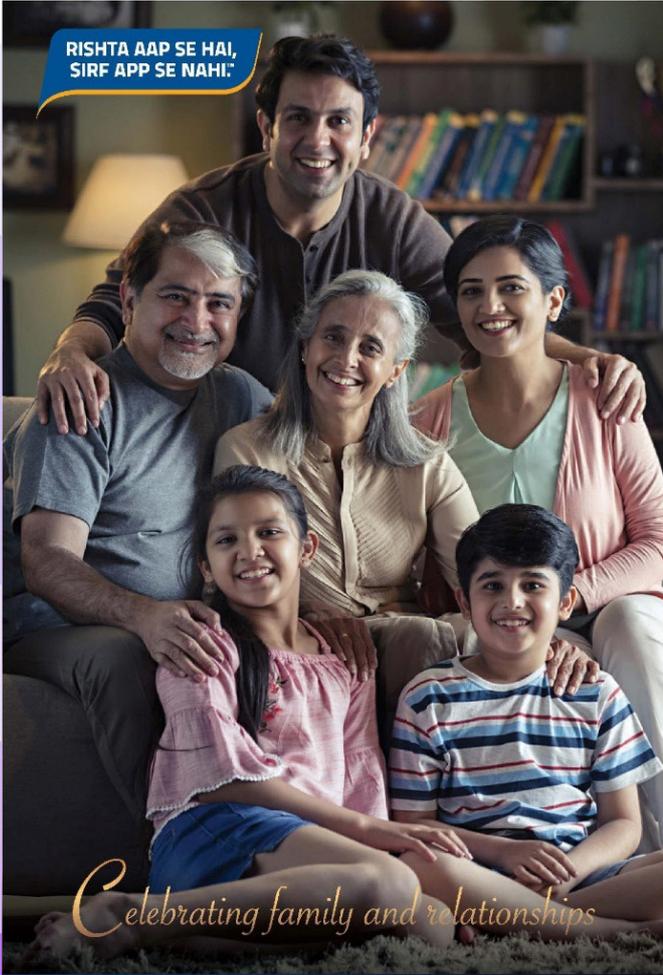
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