ANTIMICROBIAL RESISTANCE CONFERENCE 2024 (AMRC 2024)

National Conference on

"Exploring the Bioresources of India to fight against Antimicrobial Resistance (AMR)"

www.amrconference2024.in

April 4-5, 2024

Organized by:

INSTITUTE OF BIORESOURCES AND SUSTAINABLE DEVELOPMENT (IBSD)
Takyelpat, Imphal, Manipur, India
www.ibsd.gov.in

ICMR-NATIONAL INSTITUTE OF CHOLERA AND ENTERIC DISEASES (ICMR-NICED)
P-33, C.I.T. Road, Beliaghata, Kolkata, India
www.niced.org.in

In Association with:

SOCIETY FOR ETHNOPHARMACOLOGY (SFE)
Shaktigarh, Jadavpur, Kolkata, India
www.ethnopharmacology.in

Venue: Science City, J.B.S. Haldane Avenue, Kolkata-700 046, India

AMR Conference 2024

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ANTIMICROBIAL RESISTANCE CONFERENCE (AMRC 2024)

Theme: "Exploring the Bioresources of India to fight against Antimicrobial Resistance (AMR)"

April 04-05, 2024

Organized by

INSTITUTE OF BIORESOURCES AND SUSTAINABLE DEVELOPMENT (IBSD)
Takyelpat, Imphal, Manipur, India
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In Association with

SOCIETY FOR ETHNOPHARMACOLOGY
Jadavpur, Kolkata, India
www.ethnopharmacology.in

Venue: Science City, Kolkata, India

PROGRAMSCHEDULE

REGISTRATION: 09:00 – 10:00 AM

Day 1: April 04, 2024
Venue: Science city auditorium, J.B.S. Haldane Avenue
Kolkata-700 046, India

INAUGURATION PROGRAM OF AMRC 2024: 10:00 – 11:20 AM

Prof. PadmanabhanBalaram, *Former Director, Indian Institute of Science (IISC) Bangalore, India*
Prof. Pulok K Mukherjee, *Chairman, AMRC 2024 & Director, Institute of Bioresources& Sustainable Development, Imphal, India*
Dr. Shanta Dutta, *Chairman, AMRC 2024 & Director, ICMR-National Institute of Cholera and Enteric Diseases, Kolkata, India*
Shri. Indraneel Das, *Vice President, Society for Ethnopharmacology, Kolkata, India*
Dr. Siddhartha Niyogi, *Director of Health Service, Ex Officio secretary, Department of Health & Family Welfare, Government of West Bengal.*
Dr. Subhra Chakraborty, *Director, National Institute of Plant Genome research, New Delhi, India*
Dr. S Indira Devi, *Organizing Secretary, AMRC 2024 & Scientist, Institute of Bioresources& Sustainable Development, Imphal, India*
Dr. Sushmita Bhattacharya, *Organizing Secretary, AMRC 2024 & Scientist, ICMR-National Institute of Cholera and Enteric Diseases, Kolkata, India*

Keynote address by:

Prof. PadmanabhanBalaram, *Former Director, Indian Institute of Science (IISC), Bangalore, India*

TEA BREAK : 11:20 – 11:30 AM

SCIENTIFIC SESSION I:
11:30 AM - 12:30 PM

"The crisis of AMR and Exploring Bioresources for the development of new generation antimicrobials"

Chairperson:

Dr. Arun Bandyopadhyay, *Director, Gujarat Biotechnological University, Gujarat, India*
Dr. Sagar Sengupta, *Director, National Institute of Biomedical Genomics, Kalyani, India*

Speaker	Title
Dr. Shanta Dutta Director ICMR-National Institute of Cholera and Enteric Diseases, Kolkata, India	Therapeutic intervention of *Shigella flexneri* by a herbal compound: anovel approach
Prof. Pulok Kumar Mukherjee Director Institute of Bioresources& Sustainable Development, Imphal, India	Medicinal Plants and other Bioresources of NER to combat AMR - New Generation Antimicrobials
Dr. Kh. Ranjana Head, Dept of Microbiology RIMS, Imphal	Infection Prevention and Control (IPC) in preventing Antimicrobial Resistance (AMR) in Healthcare facilities

SCIENTIFIC SESSION II:
12:30 - 01:30 PM

"Resistance, surveillance, transmission, epidemiology and therapeutic approaches for Gram positive and gram negative bacterial infection"

Chairperson:

Dr. Amit Ghosh, *JC Bose Chair Professor (NASI), ICMR-NICED*
Dr. V Ravichandiran, *Director, National Institute of Pharmaceutical Education & Research, Kolkata*

Speaker	Title
Dr. Tushar Kant Beuria Scientist DBT-ILS, Bhubaneswar	Targeting the bacterial efflux pump to combat antimicrobial resistance in Methicillin-resistant *Staphylococcus aureus*
Dr. Saugata Hazra Associate Professor IIT Roorkee, Uttrakhand	360 Degree AMR Management: Unveiling the Strategic Endeavors Employed by the Hazra Group in Mitigating Antibiotic Resistance (ABR), with a Focus on Beta-Lactamase as a Molecular Indicator
Prof. Sanjay Jachak Professor, NIPER, Mohali, Punjab	Natural products as a potential source of Bacterial pump efflux inhibitors: An Arsenal against AMR
Dr. Sulagna Basu Scientist ICMR-NICED, Kolkata	Towards understanding the exchange of genes in the gut: the *mcr* example

LUNCH : 01:30 – 02:00 PM

PANEL DISCUSSION I
i-Connect Program: Business Meet: 02:00 PM - 03:30 PM

"Bioresources to fight antimicrobial resistance (AMR) : Development of New Generation Antimicrobials"

Chairperson:

Prof. Pulok K Mukherjee, *Director, Institute of Bioresources& Sustainable Development,Imphal, India*
Dr. U.V Babu, *Director, Himalaya Wellness Company, Bengaluru, India*

PANELIST

Shri. Birendra K Sarkar President, Society for Ethnopharmacology, India & MD & CEO, Parker Robinson Pvt Ltd., Kolkata	**Anish Chakraborty** Chairman, Seacom Group &Seacom Skills University, Kolkata
Dr. Rajiv Rai Senior Vice President - Head R&D Emami Ltd., Kolkata, India	**Shri Indraneel Das** MD, Declibac Technologies Pvt. Ltd. Kolkata, India
Dr. V Ravichandiran Director, National Institute of Pharmaceutical Education & Research, Kolkata	**Dr. U.V Babu** Director, Himalaya Wellness Company, Bengaluru, India
Dr Anindya Dasgupta Scientific Manager, Himalaya Wellness Company, Bengaluru, India	**Prof. Sanjay Jachak** Professor, NIPER, Mohali Punjab, India
Dr. Gaurgopal Maiti Technical Advisor, Parker Robinson Pvt Ltd., Kolkata	**Dr. Sunil K. Dubey** General Manager Emami Ltd., Kolkata, India

SCIENTIFIC SESSION III:
03:30 - 04:45 PM

"Fighting AMR by intervening host pathogen interaction"

Chairperson:

Dr. Mamta Chawla Sarkar, *Scientist-F, ICMR-NICED, Kolkata*
Prof. Rajib Bandyopadhyay, *Professor, Dept. of Instrumentation and Electronics Engg, Jadavpur University, Kolkata*

Speaker	Title
Prof. Chittur V Srikanth Professor Regional Centre for Biotechnology, Faridabad	Salmonella mediated host epigenetic manipulation in immune evasion and chronic infections
Dr. S. Indira Devi Scientist, DBT-Institute of Bioresources and Sustainable Development (IBSD), Imphal	Antimicrobial peptides and bioactive metabolites from microbes and plant sources to combat against AMR
Dr. Mukesh Pasupuleti Principal Scientist CSIR-CDRI, Lucknow	Discovery and development of innovative novel next-generation biotherapeutics by Unveiling the Hidden Potential of the Innate Immune System:To tackle Emerging and Reemerging Pathogenic Infections
Dr. Anil Kumar Singh Scientist CSIR-NEIST, Jorhat, India	Resistome characterization of clinically relevant enteric bacteria for β-lactam antibiotic resistance

Panel Discussion Session II: ONE HEALTH
04:45 PM - 05:45 PM

Chairperson:

Dr. Subhra Chakraborty, *Director, National Institute of Plant Genome research, New Delhi, India*
Dr. Shanta Dutta, *Director, ICMR-National Institute of Cholera and Enteric Diseases, Kolkata, India*

PANELIST

Dr. Arun Bandyopadhyay Director, GBU, Gujarat, India	**Prof. Pallab Kanti Haldar** Director, SNPS, JU, Kolkata
Dr. Nanaocha Sharma Scientist, DBT-IBSD, Imphal	**Dr. Agniva Majumder,** Scientist, ICMR- NICED, Kolkata
Dr. Debjit Chakraborty Scientist, ICMR- NICED, Kolkata	**Dr. K Jeyaram** Scientist, DBT-IBSD, India
Dr. Falguni Debnath Scientist, ICMR- NICED, Kolkata	**Dr. Pardeep K. Bhardwaj** Scientist, DBT-IBSD, Imphal

POSTER SESSION I: 02:30 PM - 05:00 PM

Evaluators:

Dr. Pardeep K. Bhardwaj, Scientist, DBT-IBSD, Imphal
Prof. Sanjay Jachak, Professor, NIPER, Mohali, Punjab
Dr.SurajitBasak, Scientist, ICMR-NICED, Kolkata
Dr. Amrita Bhattacharjee, Scientist, ICMR-NICED, Kolkata
Dr.AnindyaSundar Ghosh, Professor, IIT, Kharagpur
Dr. Lokesh Deb, Scientist, DBT-IBSD, Imphal
Shri. Prabir Banerjee, EC Member, Society for Ethnopharmacology, India
Dr. Amit Kar, Project Scientist,DBT-IBSD, Imphal

Day 2: April 05, 2023

Venue: Science city auditorium, J.B.S. Haldane Avenue
Kolkata-700 046, India

HALL – 1: Scientific Session IV
10:00 AM - 11:00 AM

"Policy aspects of AMR and antibiotic stewardship"

Chairpersons:

Dr. Alok Deb, *Scientist G, ICMR-NICED, Kolkata*
Dr. Subhash C Mandal, *EC Member, Society for Ethnopharmacology, Kolkata, India*

Speaker	Title
Prof. Arun K. Singh Professor, Neonatology, AIIMS Jodhpur, Rajasthan	Strategies for Mitigating Antibiotic Resistance: A Comprehensive Policy Approach
Dr. Dipankar Majhi Deputy Director Public Health Dept. of Health & Family Welfare, Govt. West Bengal, Kolkata	
Prof. Suparna Chatterjee Professor, Dept. of Pharmacology, Institute of Postgraduate Medical Education & Research,Kolkata	

HALL – 1: Panel Discussion Session: III
11:00 – 12:00 PM

Lead Development and Combinational Approach To Mitigate AMR

Chairpersons:

Dr. Pardeep K Bhardwaj, *Scientist, DBT-IBSD, Kolkata*

Dr. SandipanGanguly, *Scientist F, ICMR-NICED, Kolkata*

PANELIST

Dr. Suman Kanungo Scientist-F, ICMR- NICED, Kolkata	**Dr. Pallavi Indwar,** Scientist-D, ICMR- NICED, Kolkata
Dr.Provash C. Sadhukhan Scientist-E, ICMR- NICED, Kolkata	**Dr.Agniva Majumder** Scientist-C, ICMR- NICED, Kolkata
Dr.Sandip Mukhopadhyay Scientist-E, ICMR-NICED, Kolkata	**Dr.Sushmita Ray** CARI ,Kolkata

HALL -2: Scientific Session V
11:00 AM - 12:00 PM

"Role of anti-microbial peptides, endophytes and microbiomes for prevention and control of AMR"

Chairperson:

Dr. Amit Pal, *Scientist G, ICMR-NICED, Kolkata*

Dr. K Jeyaram, *Scientist, DBT-IBSD, India*

Speaker	Title
Dr. Debprasad Chattopadhyay Former Director ICMR-NITM, Belagavi	Traditional Medicine: Can it be the Nature's Weapon against Drug-Resistance Microbes?
Dr. Sudipto Saha Associate Professor Bose Institute, Kolkata	Exploring microbial genes associated with antimicrobial resistance in the lung microbiome of respiratory disease patients
Dr. Rajlakshmi Viswanathan Scientist E ICMR-NIV, Pune	Antimicrobial resistance at animal human interface-A One Health Approach

HALL -1: Scientific Session VI
12:00 PM – 01:30 PM

"Reservoirs of antibiotic resistance genes, ecology and carriage"

Chairpersons:

Prof Asis Mazumdar, *Nodal Coordinator, RCFC (ER), Jadavpur University, Kolkata*

Dr. Kh. Ranjana, *Head, Dept of Microbiology, RIMS, Imphal*

Speaker	Title
Dr. Asish K Mukhopadhyay Scientist G ICMR-NICED, Kolkata	Carbapenem Resistance in clinical Vibrio cholerae O1 strains: A Challenge to Modern Medicine
Dr. Anindya Sundar Ghosh Professor, IIT Kharagpur, India	P-type ATPase zinc transporter Rv3270 of *Mycobacterium tuberculosis* enhances multi-drug efflux activity against structurally unrelated antibiotics
Dr. Vishwanath Bhagwath Himalaya Wellness Company Bangalore, India	Exploring Indian Medicinal Plants as Potential alternatives

HALL - 2: SCIENTIFIC SESSION VII
12:00 PM – 01:30 PM

"Mechanism of action of new compounds (natural and synthetic) and repurposed drugs"

Chairperson:
Dr. Lokesh Deb, *Scientist, DBT-IBSD, Imphal*
Shri. Amitavo Das, *Treasurer, Society for Ethnopharmacology, India*

Speaker	Title
Dr. Souvik Mukherjee Associate Professor, BRIC-National Institute of Biomedical Genomics (NIBMG), Kalyani, West Bengal	Deciphering the Host Microbiome Interactions that leads to the Development of Antimicrobial Resistance in Chronic Inflammatory Diseases in Humans
Dr. Alok Kr. Chakrabarti, Scientist, ICMR- NICED, Kolkata	Revitalizing Phage Therapy For Cholera: Isolation, Screening And Characterizationof Bacteriophages To Evaluate Therapeutic Potential
Dr. Sushmita Bhattacharya Scientist, ICMR-NICED, Kolkata	Unveiling the role of HMGB1 (High Mobility group Box1) inhibition in autophagy during *Helicobacter pylori* infection

LUNCH: 01:30 -02:00 PM

Hall 1 - ORAL PRESENTATION SESSION
2:00 PM - 03:30 PM

Dr. Kh. Ranjana, Head, Dept of Microbiology, RIMS, Imphal
Dr. W. Mohendro Singh, Administrative Officer, DBT-IBSD, Imphal, India
Dr. Alok Deb, Scientist G, ICMR-NICED, Kolkata
Dr.Mamta Chawla Sarkar, Scientist F, ICMR-NICED, Kolkata
Dr.Rajlakshmi Viswanathan, Scientist E, ICMR-NIV, Pune
Dr. Amit Kar, Project Scientist,DBT-IBSD, Imphal
Dr. Sujoy K Das, Scientist, CSIR-Indian Institute of Chemical Biology, Jadavpur, Kolkata

Valedictory Program: 03:30 PM - 04:30 PM
Distribution of Awards

Dr. Shanta Dutta, *Director, ICMR-National Institute of Cholera and Enteric Diseases, Kolkata, India*
Prof Asis Mazumdar, *Nodal Coordinator, Regional Cum Facilitation Centres, Jadavpur University, Kolkata*
Dr. Subhra Chakraborty, *Director, National Institute of Plant Genome Research, New Delhi, India*
Dr. SulagnaBasu, *Scientist, ICMR-National Institute of Cholera and Enteric Diseases, Kolkata, India*
Dr. S Indira Devi, *Organizing Secretary, AMRC 2024 & Scientist, Institute of Bioresources& Sustainable Development, Imphal, India*
Dr. Sushmita Bhattacharya, *Organizing Secretary, AMRC 2024 & Scientist, ICMR-National Institute of Cholera and Enteric Diseases, Kolkata, India*
Prof. Pulok K Mukherjee, *Director, Institute of Bioresources & Sustainable Development, Imphal, India*

AMR CONFERENCE 2024

Theme: "Exploring the Bioresources of India to fight against Antimicrobial Resistance (AMR)"

Dear participants,

Greetings from IBSD, Imphal and ICMR-NICED, Kolkata!

Welcome to the National Conference on "Exploring the Bioresources of India to fight against Antimicrobial Resistance (AMR)" (AMRC-2024) organized by the Institute of Bioresources and Sustainable Development (DBT-IBSD) and National Institute of Cholera and Enteric Diseases (ICMR-NICED) in association with Society of Ethnopharmacology (SFE), Kolkata at Science City Auditorium, J.B.S. Haldane Avenue, Kolkata during 4-5 April, 2024.

India's bioresources hold immense potential in the fight against antimicrobial resistance. By harnessing the rich biodiversity of the country and leveraging traditional knowledge with modern scientific approaches, India can contribute to the global effort to combat AMR and ensure a healthier future for generations to come. The collaborative efforts involving researchers, government agencies, pharmaceutical companies, and local communities are essential to harnessing the full potential of India's bioresources.

We extend my warmest greetings to all participants including distinguished guests, industry experts, and delegates from across the nation who have gathered to exchange ideas, share insights, and collaborate on the matter of global importance. I encourage all participants to actively engage in the sessions and explore the networking opportunities available throughout the conference. We have no doubt that the discussions and deliberations over the course of the conference will yield valuable insights and recommendations that will drive progress in AMR research. We would like to express my sincere gratitude to the sponsors and partners for their support in organizing this event. We gratefully acknowledge the dedication and hard work of the organizing committee in making this conference possible

Dr. S Indira Devi
Organizing Secretary, AMRC 2024 &
Scientist, IBSD, Imphal, India

Dr. Sushmita Bhattacharya
Organizing Secretary, AMRC 2024 &
Scientist, ICMR-NICED, Kolkata, India

सत्यमेव जयते

डॉ. राजीव बहल, एमडी, पीएचडी
DR. RAJIV BAHL, MD, PhD

सचिव, भारत सरकार
स्वास्थ्य अनुसंधान विभाग
स्वास्थ्य एवं परिवार कल्याण मंत्रालय एवं
महानिदेशक
भारतीय आयुर्विज्ञान अनुसंधान परिषद
Secretary, Government of India
Department of Health Research
Ministry of Health & Family Welfare &
Director-General
Indian Council of Medical Research

Message

Antimicrobial resistance (AMR) is one of the significant public health threats to the humanity. As the apex body for biomedical research in India, the Indian Council of Medical Research (ICMR) is committed to address the threat of antimicrobial resistance. For more than a decade, ICMR has been supporting evidence generation and research on AMR through the Antimicrobial Resistance Surveillance Network (AMRSN) in collaboration with collaborative efforts with healthcare providers and research institutions across the country, the aim is to strengthen the understanding of multifactorial drivers for developing AMR and to implement evidence-based interventions.

The development of new antimicrobial agents and alternative treatment strategies are crucial to combatting AMR effectively.India, with its rich biodiversity and natural wealth, is endowed with a treasure trove of bioresources that hold immense potential for scientific exploration against AMR. Research and innovation in this area are paramount, and the ICMR also supports and facilitates research initiatives aimed at discovering novel antimicrobial compounds and new therapeutic approaches.

It gives me great pleasure that ICMR-National Institute of Cholera and Enteric Diseases (NICED) and Institute of Bioresources and Sustainable Development (IBSD) are jointly organizing the National conference on "Exploring the Bioresources of India to fight against Antimicrobial Resistance" during 4 & 5 April, 2024 at Science city, Kolkata. This conference brings together experts on AMR and Indian bioresources and will enlighten the participants with interesting and innovative research ideas and outcomes which may add value in future implementation programme.

I convey my heartiest congratulations to the team and wish a grand success of the conference.

Rajiv Bahl

(Rajiv Bahl)

V. Ramalingaswamy Bhawan, Ansari Nagar, New Delhi-110029
Tel. : 011-26588204, Website : www.icmr.gov.in, E-mail : secy-dg@icmr.gov.in

Dr. Siddhartha Niyogi
Director of Health Services
Department of Health & Family Welfare
Government of West Bengal

Ref. No. ..... *Date* 02/04/2024

MESSAGE

It is my immense pleasure to note that the National conference on "Exploring the Bio-resources of India to fight against Antimicrobial Resistance" is being organized by ICMR-National Institute of Cholera and Enteric Diseases (NICED) and Institute of Bio-resources and Sustainable Development (IBSD), DURING 4th & 5th April, 2024 at Science city, Kolkata.

Antimicrobial Resistance (AMR) is a silent public health concern threatening the management of infectious diseases globally. We are aware that the pathogenic bacteria are increasingly becoming resistant to the commonly prescribed antibiotics resulting in no options for treating the infections. Developing adequate policies, programs and governance to tackle the problem is the need of the hour. The National Action Plan and State Action Plan emphasize strengthening the infrastructure at all tiers of public health delivery towards achieving diagnostic and antimicrobial stewardship and ensuring community participation along with other stakeholder from animal health and environment sectors to follow the one health approach.

I am happy to note that this conference is very timely with respect to the global research in favour of exploring and repurposing bio-resources in various health aspects including AMR. I expect that program officials, researchers, practitioners, pharmacologist and implement will benefit from the deliberations and get an insight towards developing novel, realistic and feasible solutions.

I heartily thank all scientists and staff of ICMR-NICED and IBSD for their untiring efforts and active engagements in organizing this conference successfully.

I am confident that this timely event will provide tangible outcomes, beneficial for the population at large. I extend my best wishes for the success of the conference.

02.04.24

(Dr. Siddhartha Niyogi)

Swasthya Bhavan, GN-29, Sector-V, Salt Lake City, Kolkata - 700 091
Phone : (033) 2357 7903 ; Fax : (033) 2357 7904 E-mail : dhswestbengal@gmail.com, dhs@wbhealth.gov.in

सत्यमेव जयते

डॉ. राजेश सु. गोखले
Dr. RAJESH S. GOKHALE

आज़ादी का अमृत महोत्सव

सचिव
भारत सरकार
विज्ञान और प्रौद्योगिकी मंत्रालय
जैव प्रौद्योगिकी विभाग
ब्लॉक-2, 7वां तल, सी.जी.ओ कॉम्पलेक्स
लोधी रोड़, नई दिल्ली-110003

SECRETARY
GOVERNMENT OF INDIA
MINISTRY OF SCIENCE & TECHNOLOGY
DEPARTMENT OF BIOTECHNOLOGY
Block-2, 7th Floor, CGO Complex
Lodhi Road, New Delhi-110003

Message

I am delighted to know that the Institute of Bioresources and Sustainable Development (DBT-IBSD) and National Institute of Cholera and Enteric Diseases (ICMR-NICED) in association with the Society of Ethnopharmacology (SFE), Kolkata is organizing a National Conference on the theme "Exploring the Bioresources of India to fight against Antimicrobial Resistance (AMR)" (AMRC-2024) from April 4-5, 2024, at Science City Auditorium, J.B.S. Haldane Avenue, Kolkata.

In recent years, antimicrobial resistance (AMR) has emerged as a global threat, posing challenges to healthcare systems worldwide. India's rich biodiversity houses a myriad of bioresources that in turn have a strong potential to combat AMR. It is imperative that we harness these unique bioresources to develop innovative solutions targeting AMR.

The Department of Biotechnology (DBT) has fostered an ecosystem of cutting edge-research innovation and entrepreneurship in the country. I am glad to know that the conference will serve as a platform for bringing together scientists, researchers, entrepreneurs, and other stakeholders to exchange ideas and identify actionable strategies for leveraging bioresources for meaningful advancements in the field of AMR.

I congratulate all the members of the organizing committee, dignitaries, faculties, clinicians, research scholars and all the delegates of the conference.

My best wishes for a grand success of AMRC-2024.

(Dr. Rajesh S. Gokhale)

Phone : 24362950/24362881, Fax : 011-24360747, E-mail : secy.dbt@nic.in

आई. सी. एम. आर. – राष्ट्रीय कॉलरा और आंत्र रोग संस्थान
ICMR - NATIONAL INSTITUTE OF CHOLERA AND ENTERIC DISEASES
स्वास्थ्य अनुसंधान विभाग, स्वास्थ्य और परिवार कल्याण मंत्रालय, भारत सरकार
Department of Health Research, Ministry of Health and Family Welfare, Govt. of India
WHO COLLABORATING CENTRE FOR RESEARCH AND TRAINING ON DIARRHOEAL DISEASES

Dr. Shanta Dutta, *MD, PhD, MAMS, FWAST. FNASc., FNAMS.*
Director & Scientist G

Message

It is my honour to welcome all dignitaries to the National conference on "Exploring the Bioresources of India to fight against Antimicrobial Resistance" jointly organized by ICMR-National Institute of Cholera and Enteric Diseases (NICED) and Institute of Bioresources and Sustainable Development (IBSD), during 4 & 5 April, 2024 at Science city, Kolkata.

Antimicrobial Resistance or AMR is global public health threat, and continues to threaten treatment of common infections. If unaddressed, AMR may cause up to 10 million global deaths annually by 2050. To arrest the spread of AMR, 178 countries, including India, have developed AMR national action plans aligned with the Global Action Plan (GAP) formulated at 2015 World Health Assembly. NICED has always been a strong ally in the fight against AMR with continuing research on mitigating AMR. A National Repository of drug-resistant bacteria has been initiated at ICMR-NICED. Drug-resistant isolates from diverse regions of India are archived at the repository to facilitate and accelerate basic and applied AMR research across India. Scientists from NICED have published one state of art document in 2022 on "Priorities for the environmental dimension of antimicrobial resistance in India" supported by the United Nations Environment Programme (UNEP) to explore environmental drivers that contribute to AMR risks and spread.

As part of our ongoing efforts to expand our understanding of AMR, it is our privilege to organize this conference that will highlight crucial and contemporary aspects of recent AMR trends, while exploring strategies for alternative therapeutics against AMR from the vast pool of bioresources available in our country. This conference will provide a unique platform to bring together researchers, practitioners, educationists with complementary expertise under one roof, where they can interact, discuss and present the recent updates of their research.
The conference will focus on AMR trends, potential phytochemicals and medicinal plants for developing new antibiotics, novel diagnostic assays, and discuss realistic challenges encountered in the implementation of the same and action plan adopted to overcome the challenges. We cordially invite you all to participate in this conference and explore the opportunities for new scientific horizons!

I gratefully acknowledge the cooperation of partner organizations and generous support from ICMR and other funding agencies. Without their contributions, holding the conference would not have been possible. I take this opportunity to thank all the NICED and IBSD scientists and staff for their active involvement, shouldering responsibilities and timely execution.

I am confident that this event will provide fruitful outcomes, beneficial for the entire population. I wish a grand success of the conference

S. Dutta

Dr. Shanta Dutta

पी-३३, सी.आई.टी. रोड, स्किम - १०एम, बेलियाघाटा, कोलकाता - ७०००१०, भारत
P-33, C.I.T. Road, Scheme - XM, Beliaghata, Kolkata - 700010, India
निदेशक/ Director : 91-33-2363 3373, 2370 1176, पि.बि.एक्स / PBX : 91-33-2353 7469 / 7470, 2370 5533 / 4478 / 0448
फैक्स / Fax : 91-33-2363 2398, 2370-5066, वेब / Website : www.niced.org.in

Institute of Bioresources and Sustainable Development (IBSD)

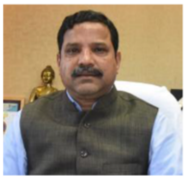
जैव संसाधनों एवं स्थायी विकास संस्थान

Takyelpat, Imphal 795001, Manipur, India

Prof. Pulok Kumar Mukherjee
Director

प्रोफ़ेसर पुलोक कुमार मुखर्जी
निदेशक

National Conference on "Exploring the Bioresources of India to fight against Antimicrobial Resistance (AMR)" (AMRC-2024)"



Welcome you all to the National Conference on "Exploring the Bioresources of India to fight against Antimicrobial Resistance (AMR)" (AMRC-2024), organized in collaboration with ICMR-NICED, DBT-IBSD, and the Society of Ethno-pharmacology (SFE), Kolkata, at Science city, Kolkata during April 04-05, 2024.

Our collective mission to address the pressing challenges posed by AMR demands collaborative efforts and innovative strategies. I am thrilled to witness the convergence of distinguished experts, researchers, and stakeholders in the field of antimicrobial resistance. Throughout the conference, we will delve into crucial and contemporary aspects of AMR research, emphasizing the exploration of bioresources to develop alternative therapeutics. Together, we will explore novel approaches, share insights, and chart pathways towards effective solutions. I encourage each of you to actively engage in discussions, share your expertise, and foster meaningful collaborations.

I extend my heartfelt thanks to all the participants, sponsors, and organizers from IBSD and ICMR-NICED for their unwavering support and dedication. Together, let us leverage the ancient heritage and bioresources of India to conquer AMR!

Hope you will have a wonderful stay and successful conference.

Prof. Pulok Kumar Mukherjee
FRSC, FAScT, FNAAS, FNASc
Director
Institute of Bioresources and Sustainable Development, India (IBSD), Imphal-Manipur//Gangtok-Sikkim// Shillong-Meghalaya//Aizwal-Mizoram

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SOCIETY FOR ETHNOPHARMACOLOGY, INDIA [SFE - INDIA]
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MESSAGE

Society for Ethnopharmacology, India (SFE – India), established in 2013 after the 1st international congress of Ethnopharmacology in India in February 2012 have been working on dissemination of knowledge and promotion and development of traditional resources of India to the global label. Presently the Society has 19 local Chapters with dynamic Coordinators for individual chapters and thousands members across the country. On this note we cordially invite you all to join this forum and encourage your colleagues and students to join and explore the opportunities.

On behalf of the Society for Ethnopharmacology, India, It is our great pleasure to welcome you all in the National Conference on Antimicrobial Resistance (AMR), 2024, with a focus on "Exploring the bioresources of India to fight against AMR", organized at the Science City Auditorium, Kolkata, during 04-05 April 2024. It is a great pleasure for us to be a part of the organizing committee of this AMR Conference 2024 along with the ICMR-National Institute of Cholera And Enteric Diseases (ICMR-NICED) and the Institute of Bioresources And Sustainable Development (IBSD).

The seminar will serve as a platform to delve into critical aspects of AMR research, focusing on recent trends and innovative strategies. We will explore avenues for the development of alternative therapeutics derived from bioresources, with a particular emphasis on the India's vast reservoir of medicinal plants and traditional knowledge. We cordially invite you to join us in this endeavor to combat AMR and explore collaborative opportunities to strengthen research initiatives. Your participation and contributions are integral to the success of this conference, as we strive to shape a healthier future for our communities and beyond.

We cordially invite you all to join SFE-India in our efforts of "Globalizing local knowledge; localizing global technologies".

Mr. Birendra Kumar Sarkar
President
Society for Ethnopharmacology,
Kolkata, India

Dr. Amit Kar
Secretary
Society for Ethnopharmacology,
Kolkata, India

AMR CONFERENCE 2024

Theme: "Exploring the Bioresources of India to fight against Antimicrobial Resistance (AMR)"

Venue: Science City Auditorium, Kolkata

Prof. Pulok Kumar Mukherjee
Coordinator / Director
IBSD, Imphal, India

Dr. S Indira Devi
Scientist
IBSD, Imphal, India

Dr. Nanaocha Sharma
Scientist
IBSD, Imphal, India

Dr. Pardeep K Bhardwaj
Scientist
IBSD, Imphal, India

Dr. Rajkumari Jobina
Project Scientist
IBSD, Imphal, India

Dr. Amit Kar
Project Scientist
IBSD, Imphal, India

Dr. Surajit Basak
Scientist
ICMR-NICED, Kolkata, India

Dr. Amrita Bhattacharjee
Scientist
ICMR-NICED, Kolkata, India

Dr. Shanta Dutta
Coordinator / Director
ICMR-NICED, Kolkata, India

Dr. Sulagna Basu
Scientist
ICMR-NICED, Kolkata, India

Dr. Sushmita Bhattacharya
Scientist
ICMR-NICED, Kolkata, India

Shri. Birendra Kumar Sarkar
President
SFE, Kolkata, India

Shri. Indraneel Das
Vice President
SFE, Kolkata, India

Shri. Amitava Das
Treasurer
SFE, Kolkata, India

Dr. Melissa Glenda Lewis
Scientist
ICMR-NICED, Kolkata, India

Dr. Monica Sharma
Scientist
ICMR-NICED, Kolkata, India

ICMR-National Institute of Cholera and
Enteric Diseases (ICMR-NICED)
आई सी एम आर - राष्ट्रीय कॉलरा और आंत्र रोग संस्थान
Department of Health Research, Ministry of Health and
Family Welfare, Government of India
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700010

Since time immemorial, eastern India, notably the Gangetic delta is considered as the "homeland" of cholera and a focal point of many of the epidemics and most of the pandemics. More than a century and a half have elapsed since Vibrio cholerae, the causative agent of cholera, was first described by Filippo Pacini and its water borne transmission was demonstrated by John Snow. In 1883, Robert Koch visualized the organism in Alexandria, Egypt and subsequently cultured it in Calcutta (now known as Kolkata). Nearly 70 years later, the toxin that caused cholera was discovered in India by S.N. De in Kolkata and by N.K. Dutta in Bombay (now known as Mumbai). The studies of De and Dutta, in effect, also proved Koch's postulate by replicating the disease in an animal model and revived the research interest in cholera. The Indian Council of Medical Research (ICMR) decided to establish "Cholera Research Centre" in Calcutta in 1962 to research on the prevention and control of cholera and other diarrhoeal diseases.

The Centre initiated a number of clinical trials for evaluation of newer therapeutic methods, two cholera vaccine field trials in collaboration with World Health Organization (WHO), Geneva, cholera carriers, serological and chemoprophylaxis studies. In 1968, the Centre was given the status of "International Reference Centre for Vibrio Phage Typing" by the WHO in 1968 following the outstanding studies of S. Mukherjee in Kolkata and later on, in 1978, it was designated as the "WHO Collaborative Centre for Reference and Research on Vibrios" in 1978. With the advancement in biotechnology, improved diagnostic procedures and discovery of a large number of pathogenic enteric micro-organisms during 1970s, this Centre also expanded its activities which motivated ICMR to elevate this Centre into a full-fledged research establishment with the status of a "National Institute" and renamed it as "National Institute of Cholera and Enteric Diseases" (NICED) in 1979. The WHO recognized this Institute as "WHO Collaborative Centre for Research and Training on Diarrhoeal Diseases" in 1980.

NICED conducts research on acute diarrhoeal diseases of diverse etiologies as well as on typhoid fever, infective hepatitis and HIV/AIDS related epidemiological research and screening. Aims of this Institute are to conduct research on these diseases in both basic and applied aspects. The Institute also trains health professionals for better management and prevention of diarrhoeal diseases and for rapid and correct diagnosis of the etiological agents. Epidemiological investigations of diarrhoeal diseases are carried out in different parts of India. Antisera against Vibrio cholerae are raised in this Institute and supplied to the national and international laboratories. Presently, specific monoclonal antiserum for detection of *Vibrio cholerae O139* strains have been developed and are supplied to WHO (SEARO), New Delhi for distribution to various national and international laboratories. As WHO Phage Reference Center, this Institute receives a large number of *Vibrio cholerae* strains from all over the world for Phage typing. NICED conducts research on antimicrobial resistance of enteric bacteria and it has been selected as AMR repository hub. The institute's is focussing on development of therapeutics, vaccines, and diagnostics. For details, please visit: www.niced.org.in

Institute of Bioresources and Sustainable Development (IBSD)

जैव संसाधनों एवं स्थायी विकास संस्थान

Dept. of Biotechnology, Ministry of Science and Technology, Govt. of India

Institute of Bioresources and Sustainable Development (IBSD), Imphal, an institute of the Department of Biotechnology, Ministry of Science & Technology, Govt. of India is working with the mission on "Bioresources development and their sustainable use through biotechnological interventions for the socio-economic growth of the North Eastern Region". Main goal of IBSD is "Scientific management of bioresources in the Indian region falling under Indo-Burma Biodiversity Hotspot". For the development of bioresources and other outreach activities, IBSD has established three other entities in NER including its Regional Centre at Gangtok in Sikkim and Research Nodes at Shillong in Meghalaya and at Aizawl in Mizoram.

For the development of integrated multi-disciplinary research and innovation programs, IBSD is working on different research verticals to identify the unique bio resources of NER and integrated study for their scientific validation, value addition to propel innovations, discoveries and inventions for catalyzing the growth of industry in the region for livelihood generation and boosting bioeconomy from bioresources

IBSD is synergizing all these research activities to boost the bioeconomy from the bio resources of NER with the development of processes/ products/ technologies. In this context, IBSD has initiated a programme on "Bioeconomy from Bioresources with special reference to NER" which was inaugurated by Hon'ble Shri M. Venkaiah Naidu, Former Vice President of India during 2021 and addressed by Dr. Jitendra Singh, Hon'ble Minister of State (Independent Charge) for Science and Technology and Earth Sciences during his visit to IBSD, Imphal.

IBSD has established the Phytopharmaceutical Mission to promote the documentation, scientific validation and evaluation of traditional healthcare practices. Under this mission, IBSD is working on documentation, evaluation and validation of traditional healthcare practices of NER to promote the drugs from our ancestors, drugs from nature and to explore the tradition to translation with innovation.

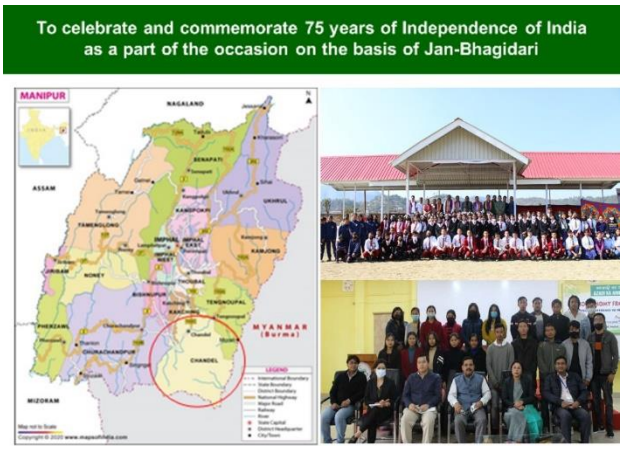
IBSD is promoting natural remedies as drugs through AYUSH, Phytopharmaceutical, Nutraceutical mode. In this context, a compendium has been developed for anti-viral plants of North East Region. The seventy plants compiled in this compendium are reported for their anti-viral activities and practiced as well as proven for its medicinal properties. IBSD has performed metabolomics analysis of numerous targeted as well as non-targeted metabolites in medicinal plants of NER using modern Omics approaches. IBSD is working on quality evaluation and therapeutic validation of Cucurbitaceae plants of NER. IBSD is exploring plant bioresources of NER for mass multiplication and production of quality planting material. Under flagship programme, IBSD is working on selected Orchids species for developing biobased entrepreneurship in North East India.

IBSD is working on the development of nutraceutical and dietary supplements from ethnic fermented foods and beverages of NER. In this context, IBSD has focused on microbiology, safety, development of starter culture consortium and development of fermentation processes and products. IBSD has explored the probiotic properties of selected starter culture consortium, chemical profiling and therapeutic values of selected fermented foods. Microbial repository centre of IBSD has huge collection of Bacteria, Actinomycetes, Yeast and Fungi from different unique ecological niches of NER viz., cave ecosystem, forest ecosystem, fermented food, endophytes, hot-spring, cold spring, lime stone deposits, high altitude ecosystems etc. IBSD is working on Anti-Microbial Resistance (AMR) for the evaluation of antimicrobial activity of the medicinal plants/microbial resources of NER. IBSD is also exploring wild mushroom from NER for nutraceutical and therapeutic potential.

For developing collaboration between industry and institute, IBSD has organized Industry-Connect (i-connect) Events in Manipur, Mizoram, Meghalaya and Sikkim. These events were attended by local entrepreneurs, traditional healers and experts from different industries/ institutes from different parts of India for the development of products/ processes/ technologies with value addition of bioresources and development bioeconomy from bioresources of NER.

IBSD has initiated working on Household Water Quality Management through Testing, Surveillance and Technological Interventions with water testing facility for drinking water, waste water etc to support the local people of NER. In this direction, IBSD has collected samples of drinking water from different localities of Manipur in association with State PHED Department for water quality monitoring, surveillance and developed a water testing kit (ERU Kit) for rapid monitoring of water quality. This year, IBSD has initiated many collaborative projects under 'Himalayan Bioresources Mission' to connect many research institutes from Eastern-Western Himalayas to explore rich bioresources and their sustainable utilization for livelihood generation and future socio-economic development. IBSD has signed several MoUs with national and international institutes for collaborative translational research on the development of bioresources.

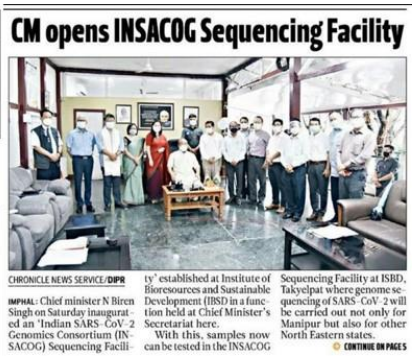
For the promotion of Start-ups in NER, IBSD has setup Bioincubators Nurturing Entrepreneurship for Scaling Technologies (BioNEST) incubator at IBSD, Node Meghalaya to develop women entrepreneurship through orchid floriculture in Meghalaya. Major focus of the programme is capacity building and training of women bio-entrepreneurs and farmers from different parts of Ri-Bhoi District of Meghalaya. In line with phytopharmaceutical mission, IBSD is working on documentation and validation of edible insects of NER for the development of therapeutics for health benefits.



IBSD has set up a 'Science Museum' in Chandel District of Manipur which is an Aspirational District of Manipur to develop scientific attitude and to inculcate awareness about the local bio resources among the students and common people of the region. During this period, IBSD has

organized many lab visits for the students of Dhanamanjuri University, Imphal, GP Women College, Imphal, Oriental College, Imphal to inculcate scientific temperament among students and scientific interventions for sustainable use of local bioresources.

Mobile Diagnostic Laboratory (I-LAB) for COVID Testing for the State of Mizoram



CM opens INSACOG Sequencing Facility

CHRONICLE NEWS SERVICE/DIPR

IMPHAL: Chief minister N Biren Singh on Saturday inaugurated an 'Indian SARS-CoV-2 Genomics Consortium (INSACOG) Sequencing Facility' established at Institute of Bioresources and Sustainable Development (IBSD in a function held at Chief Minister's Secretariat here.

With this, samples now can be tested in the INSACOG Sequencing Facility at ISBD, Takyelpat where genome sequencing of SARS-CoV-2 will be carried out not only for Manipur but also for other North Eastern states.

CONTINUE ON PAGE 5

IBSD has established the Indian SARS-CoV-2 Genomics Consortium (INSACOG) facility at IBSD, Imphal, which is the first time such an effort has been made in this part of the country. This sequencing platform/ laboratory within Manipur is a big leap in our collective fight and understanding of the novel coronavirus that has affected all aspects of our lives. Through this INSACOG network, the whole genome sequencing of SARS-CoV-2 virus across the nation, aiding the understanding of how the virus spreads and evolves. Till date, IBSD has sequenced more than 4000 COVID-19 positive samples from NER. In view of the increasing realization of disease spread, IBSD has launched Mobile Diagnostic Laboratory for COVID testing for the State of Mizoram on January 20, 2022. This Mobile I-Lab has facilitated large scale testing and detection of people in remote areas in the state of Mizoram and other states of NER.

To commemorate the 75 years of Independence and to celebrate “Azadi Ka Amrit Mahotsav”, IBSD has organized more than 180 outreach activities including webinars, capacity building & training programmes, workshops, lab visits for researchers, scientists, school students, traditional healers, farmers, local entrepreneurs of NER. Since COVID-19 pandemic, IBSD has initiated International Webinar series on “Re-imagine ethnopharmacology” in association with Society for Ethnopharmacology, India (SFE-India) and International Society for Ethnopharmacology (ISE) and organized 75 webinars with deliberation of more than 85 eminent scientists from across the globe to grace the series. Many ideas have been discussed during the series for the development of local bioresources of the region. More than 12,000 participants have attended this international webinar series so far. IBSD has compiled all these outreach activities in the form of a book which may serve a reference material for the scientific awareness about local bioresources among the students, researchers, scientists, entrepreneurs, farmers of this region. For details please visit : www.ibsd.gov.in

SOCIETY FOR ETHNOPHARMACOLOGY

"Globalizing local knowledge and localizing global technologies"

23/3 Shaktigarh, Jadavpur, Kolkata 700032

(Affiliated to the International Society for Ethnopharmacology)

About Society:

The Society for Ethnopharmacology, India (SFE-India) is a registered society under the West Bengal Society Registration act and affiliated to the International Society for Ethnopharmacology (ISE), Switzerland. Society for Ethnopharmacology, India (SFE-India) was constituted in 2013 by the eminent academicians, researchers, industrialists and others with the vision of providing an environment for knowledge sharing among industrialists, researchers, students, healthcare practitioners, decision-makers and others interested in promotion of Ethnopharmacology and medicinal plant. The Society is extremely grateful to Late Dr. A.P.J. Abdul Kalam, former President of India, for his inspiration and support since its inception. The mission of the society is promotion and development of traditional medicine and medicinal plants through dissemination of knowledge and development of collaboration and cooperation with its vision on:

"***Globalizing local knowledge and localizing global technologies***"

The society organizes conferences, seminars, symposiums, workshops etc. in different parts of India and abroad for discussion and sharing knowledge on different issues for cultivation, production, quality evaluation, safety, clinical studies, biological screening and several other issues of natural product research. The Society helps in forming bridge between the academia and industry for developing cost effective natural remedies. Presently the Society has several local chapters with dynamic coordinators for individual local chapters and members across the country. Society of Ethnopharmacology, India (SFE-India) is dedicated for the dissemination of knowledge and information through different educational programs throughout India.

The major activities of the society are:

- Dissemination of knowledge for promotion and development of Ethnopharmacology and medicinal plants.
- To carry out the objectives of International Society for Ethnopharmacology.
- Organizing conferences, seminars, symposiums, workshops etc. in different parts of India.
- Promotion and development of Ethnopharmacology, Herbal Medicines, medicinal plants and other natural products in India.
- Promotion of the healthcare of the society.
- Sharing knowledge on various issues on cultivation, production and validation of traditional medicine, quality & safety evaluation, pre-

clinical screening & clinical studies and several other issues of natural products.

- Act as a resource at local level for individuals including students interested in
  Ethnopharmacology.
- Encourage career growth and Knowledge empowerment of its members.
- Publishing journals, newsletters, documents, books, etc. for promotion of knowledge in the field of natural product research.
- Conducting research in the area of Ethnopharmacology and traditional healthcare.

The society has established multiple local chapters to aid in the dissemination of knowledge. SFE local chapters are situated in different regions from India including Belgaum, Bhopal, Bhubaneswar, Delhi, Gujarat, Guwahati, Imphal, Jammu, Jorhat, Lucknow, Mangalore, Mumbai, Mohali, Mysuru, Nagpur, Pune and others with active leaderships of the local chapter coordinators.

Over the past few years, the number of active members in SFE India has witnessed a remarkable surge, signaling a growing and engaged community. This increase reflects the organization's success in fostering meaningful connections and providing valuable resources to its members. SFE India's commitment to promoting ethnopharmacology and knowledge-sharing about traditional medicine has attracted a diverse range of individuals, contributing to the expansion of its active membership base. The organization's emphasis on creating a supportive and collaborative environment has been a key factor in sustaining this positive trend. As more professionals recognize the benefits of being part of SFE India, the community continues to thrive, exemplifying a vibrant network that is well-connected and dedicated to advancing shared goals in the field.

To recognize the outstanding contribution in the area of medicinal plant research and Ethnopharmacology, the Society has instituted several awards, which are conferred during the International congress of the society every year.

The society has organized several seminars, webinars, conference etc. throughout the country since its inception. Some specific activities of the Society for Ethnopharmacology, India its different local chapters are as follows:

- 11th International Congress of Society for Ethnopharmacology, India organized by CSIR-IIIM, Jammu during February 16-18, 2024.
- 10th Convention of Society for Ethnopharmacology, India organized during November 28-30, 2023 at Jorhat India
- 22nd International Congress of the International Society for Ethnopharmacology (ISE) and the 10th International Congress of the Society for Ethnopharmacology India during February 24-26, 2023 at Imphal, Manipur, India

- National Conference & Workshop organized by Bhopal Local Chapter of SFE during January 18-19 January, 2024 at Bhopal, India
- National Seminar on “Role of medicinal plants to combat metabolic disorders and associated pathological complications” organized during June 30 and July 01, 2023 at Jadavpur University, Kolkata India
- One Day National “Symposium Health awareness” organized by Bhopal Local Chapter of SFE on May 11, & May 30, 2023 at Bhopal, India
- Traditional Healers Meet cum workshop organized by Eastern Himalaya Local Chapter of SFE on April 18, 2023 at Shillong, India

A Special issue on “Reimagine Ethnopharmacology: Globalization of Traditional Medicine” has been developed by the Society for Ethnopharmacology, India and published in Journal of Ethnopharmacology Elsevier Science, USA. This special issue has been made based on the scientific deliberations made in 22nd International Congress of the International Society for Ethnopharmacology (ISE) and the 10th International Congress of the Society for Ethnopharmacology, 2023 (ISE-SFEC 2023), Imphal, India. Prof. Pulok K Mukherjee, Dr. C K Katiyar, Dr. Pradeep Bharadwaj, Dr. S Indira Devi, Dr. Nanaocha Sharma and Dr. Amit Kar serving as the Editor of this special issue. https://www.sciencedirect.com/journal/journal-of-ethnopharmacology/about/call-for-papers#reimagine-ethnopharmacology-globalization-of-traditional-medicine

The society is publishing the Newsletter regularly in different aspects for development and promotion of medicinal plants and Ethnopharmacology involving the members of the society.

This year three more Local chapters including - Lucknow Local Chapter, Vellore Local Chapter and Gunter Local Chapter, joined with us which has strengthened the society for the promotion of Ethnopharmacology and Medicinal Plant Research.

We are very much excited by the keen interest of our members of SFE from a diverse number of institutes and industries throughout the country to share the knowledge in this regard. With our limited strength, esteemed efforts and keen interest of our members we have been working for the promotion and development of medicinal plants and ethnopharmacology in various ways.

We cordially invite you all to join SFE-India in our efforts of “Globalizing local knowledge: localizing global technologies” for a healthier tomorrow, capitalizing the very rich heritage and culture that is so ethnic, so ancient and yet so Indian. For details please visit: www.ethnopharmacology.in

Shri. Birendra Kumar Sarkar
President
Society for Ethnopharmacology
Shaktigarh, Kolkata, India

Dr. Amit Kar
Secretary
Society for Ethnopharmacology
Shaktigarh, Kolkata, India

CV & ABSTRACT OF SPEAKERS

National Conference on

"Exploring the Bioresources of India to fight against Antimicrobial Resistance (AMR)" (AMRC-2024)

April 04 – 05, 2024

Dr. Shanta Dutta

Director
ICMR-National Institute of Cholera and Enteric Diseases (ICMR-NICED), Kolkata, India

Dr. Shanta Dutta, MD, Ph.D., holds a distinguished position as Scientist G at the National Institute of Cholera and Enteric Diseases (NICED) in Kolkata. Her illustrious career as a clinical microbiologist and medical research scientist is marked by a rich tapestry of academic achievements and professional contributions. Dr. Dutta's academic journey began with her graduation in Medicine from Calcutta National Medical College in 1986. She pursued her postgraduation in Medical Microbiology from Kasturba Medical College, Manipal, where she honed her skills in microbiological sciences. In 1994, she embarked on her career at NICED, a premier institution under the Indian Council of Medical Research (ICMR), eventually ascending to the esteemed position of Scientist G (Director) in the Division of Bacteriology. Her pursuit of excellence led her to receive the prestigious RONPAKU fellowship from the Japanese Society for Promotion of Science (JSPS) during 2001-2005, culminating in a Ph.D. from Kyushu University, Japan. This enriching experience enabled her to delve into the realms of virulence, antimicrobial resistance, and molecular epidemiology of enteric bacterial pathogens. Throughout her career, Dr. Dutta has been actively involved in research, training, and teaching, focusing on the microbiological aspects of enteric diseases. Her interests span antimicrobial resistance, drug resistance mechanisms, and the antibacterial properties of bioactive compounds derived from herbal products. Dr. Dutta's contributions extend beyond the laboratory, as evidenced by her participation in vaccine trials, disease burden studies, and clinical trials evaluating the efficacy of probiotics. She has also played pivotal roles in projects aimed at ensuring drinking water quality and evaluating disinfection methods. Her scholarly endeavors are reflected in over 65 published research articles in prestigious national and international journals, along with numerous presentations at conferences worldwide. Additionally, Dr. Dutta serves as a peer reviewer for esteemed journals and holds editorial positions in various publishing agencies. Dr. Shanta Dutta stands as a beacon of excellence in the field of clinical microbiology, embodying a tireless dedication to advancing medical science and combating enteric diseases on a global scale.

Therapeutic intervention of *Shigella flexneri* by a herbal compound: a novel approach

Priyanka Basak, Sushmita Bhattacharya, Dr. Shanta Dutta
Division of Bacteriology ICMR-NICED, Kolkata
Division of Biochemistry, ICMR-NICED, Kolkata

Shigellosis, a gastrointestinal invasive infection caused by various species of Shigella, remains a public health concern, and contributes to the prevalence of acute and chronic diarrheal disease worldwide. Antibiotic resistance among Shigella spp. is a global crisis, recognized by the World Health Organization. The emergence of resistance demands the development of new and better antimicrobial drugs to address the challenge in treatment of such infection. Innovative solutions may be encouraged to combat the escalating problem which will preserve the efficacy of current treatments for this infection., This ongoing research aims to understand the mechanisms deployed by the pathogens to overcome host innate immune responses. Host Directed Therapy (HDT) is used to target pathogen-exploited pathways. Several host defence mechanisms like autophagy, inflammation etc. play major roles in protecting the host from pathogen invasion and its consequences. Natural compounds with antibacterial properties have become a subject of growing interest in pharmacological sciences. Several herbal compounds like resveratrol, quercetin, curcumin, ursolic acid, capsaicin etc. are known to have antimicrobial properties. Capsaicin and its derivatives are considered highly promising antimicrobial agents that could potentially serve as complementary or alternative treatment to antibiotics in combating the bacterial infections. But its effect on host directed therapeutic action was not well studied. The major focus of this study was to understand the effect of the herbal compound, Capsaicin in *S. flexneri* pathogenesis and decipher the underlying mechanism in the intervention on host pathogen interaction. We have investigated and observed that Capsaicin can outsmart the antimicrobial activity during *S flexneri* infection via autophagy and in doing so it may overcome pre-existing mechanisms of resistance. Capsaicin induced autophagy by targeting a transcription factor TFEB known for triggering autophagosomal genes. Enhancement of autophagy by overexpression of TFEB resulted in *S flexneri* death. Moreover, silencing TFEB, increased intracellular proliferation of *S flexneri* was found. This result on Capsaicin mediated autophagy induction and prevention of shigellosis by host directed therapeutic approach will help to fight against shigellosis caused by multidrug-resistant strains of *S. flexneri*.

Prof. Pulok Kumar Mukherjee
Director
Institute of Bioresources & Sustainable Development (IBSD), Imphal, India

Professor Pulok Kumar Mukherjee, the Director of the Institute of Bioresources and Sustainable Development (IBSD) under the Department of Biotechnology, Government of India, is a distinguished natural product chemist renowned for his work in drug discovery from natural resources, particularly in Chemical biology. His contributions span various domains of academic and research endeavors, focusing on developing the bio-economy from bioresources, with a special emphasis on traditional medicine-inspired drug discovery from Indian medicinal plants, ethnopharmacology, and evidence-based validation of medicinal herbs. Prof. Mukherjee's illustrious career is marked by numerous accolades and recognitions from prestigious institutions worldwide. He is a Fellow of esteemed bodies such as the Royal Society of Chemistry (FRSC), the National Academy of Sciences, India (FNASc), the National Academy of Agricultural Sciences, India (FNAAS), and the West Bengal Academy of Sciences (FAScT). His achievements include receiving the Commonwealth Academic Staff Fellowship from the Association of Commonwealth Universities (ACU), UK, the TATA Innovation Fellowship from the Department of Biotechnology, Government of India, and the Outstanding Service Award from the Drug Information Association (DIA), USA, among others. As the founder of the Society for Ethnopharmacology, India (SFE-India), and as the former President of the International Society for Ethnopharmacology (ISE), Switzerland, Prof. Mukherjee has played a pivotal role in advancing research in the field. His work on translational research in traditional medicine has been instrumental in developing bio-prospecting tools for drug discovery from natural sources. With numerous publications, patents, and a significant impact on the scientific community, Prof. Mukherjee's expertise extends to serving as a Consulting Editor, Associate Editor, and board member of several esteemed international journals. Additionally, his advisory roles in various governmental and non-governmental organizations underscore his commitment to advancing scientific research and its applications. For more information on Prof. Pulok Kumar Mukherjee's contributions and achievements, visit his website: www.pulokmukherjee.in.

Bioresources of NER to combat AMR - New Generation Antimicrobials

Pulok Kumar Mukherjee , S Indira Devi, K Jeyaram, Rajkumari Jobina, Amit Kar
Institute of Bioresources and Sustainable Development, Imphal, India

Antimicrobial resistance (AMR) poses both health and economic burden for patients and healthcare systems, globally. Antimicrobial resistance (AMR) is one of the top 10 public health threats the world is facing today. AMR does not discriminate, but the burden majorly falls on low-and-middle income group countries and AMR situation in India is alarming. The ongoing pandemic has led to the continuing high rate of antibiotic prescriptions, which may lead to even worse AMR situations post pandemic. The efficacy of several antibiotics is threatened by the emergence of resistant microorganisms. Bacteria differ in terms of the mechanisms by which they develop antibiotic resistance. Over the last couple of decades, novel mechanisms and dissemination of antibiotic resistance have been identified. The North East India is rich in biodiversity, and its traditional medicinal plants have been utilized for centuries by indigenous communities to combat various ailments and to enhance immunity. These traditional medicinal plants are often consumed in various forms such as decoctions, infusions, powders, or extracts, and their efficacy against AMR pathogens is supported by traditional knowledge, however there is a lack of scientific validation. These traditional medicinal plants and endophytes present therein a valuable source of bioactive compounds. While each plant may contain multiple bioactive compounds, some of them like Curcumin, Piperine, Allicin etc have demonstrated to synergistically enhance the efficacy of conventional antibiotics and combat antimicrobial resistance. Understanding the mechanism of action of these compounds, their synergistic interactions and optimizing their combination therapies can lead to the development of new drugs or therapeutic agents to combat AMR. Fermented foods and benficial microbes present therein serve as rich sources of antimicrobial compounds. Fermentation processes involving indigenous ingredients like bamboo shoots, soybeans, fish, and herbs lead to the production of bioactive metabolites such as organic acids, bacteriocins, and peptides with antimicrobial properties. These fermented foods have been traditionally used to preserve food and enhance flavour, while also exhibiting antimicrobial activity against pathogenic microorganisms. Incorporating NER fermented foods into diets not only promotes gut health but also offers potential antimicrobial benefits, contributing to overall well-being and disease prevention. Additionally, wild mushrooms indigenous to the Northeastern Region (NER) possess notable antimicrobial properties, making them valuable resources for therapeutic applications. These mushrooms produce bioactive compounds such as polysaccharides, terpenoids, and peptides that exhibit potent antimicrobial activity against a wide range of pathogens, including bacteria, fungi, and viruses. Traditional knowledge combined with modern scientific research has identified several NER wild mushroom species with promising antimicrobial potential. IBSD has more than 70,000 microbial isolates collection in its repository, which can be also a potential source to develop alternative antimicrobial therapeutics. Harnessing these natural resources could lead to the development of novel antimicrobial agents to combat infectious diseases and address the growing challenge of antibiotic resistance. Connecting the dots, the Institute of Bioresources and Sustainable Development has resources of microbes, plants and wild mushrooms derived antimicrobial peptides and bioactive phytomolecules, which can be an alternative efficacious antimicrobials to overcome the global threat of AMR.

Infection Prevention and Control (IPC) in preventing Antimicrobial Resistance (AMR) in healthcare facilities

Prof. Khuraijam Ranjana Devi
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The current scenario is an alarmingly increasing threat of AMR which is challenging a century of progress and advancements in the field of medicine. In the healthcare sector, it is becoming difficult to manage common minor diseases and undergoing life-saving major medical procedures has become riskier. The problem of AMR is worldwide irrespective of its economy. Healthcare facilities are high-risk environments because some of the deadliest resistant microbes reside and spread across the healthcare facilities. Patients can get infections from hospital sources such as devices, the environment, during or after procedures like surgery, or from the health care workers. Healthcare-associated infections (HAIs) with drug-resistant microbes thus contribute to poor patient outcomes. It not only leads to increased morbidity and mortality but also imposes a significant financial burden with longer hospital stays, and extra costs for medical care thus taking a toll on the health system of the hospital, community and public health system. Improving infection prevention and control (IPC) practices is the mainstay target to reduce HAIs and protect patients from getting infections with resistant organisms. To improve IPC practices, appropriate technical and behavior-modifying interventions need to be developed, strengthened and implemented in healthcare facilities. IPC measures reduce the opportunities for resistant pathogens to spread in healthcare facilities and contribute to the containment of antimicrobial resistance (AMR). The aim is to achieve quality care for all which is one of the five objectives in the AMR Global Action.

Dr. TUSHAR KANT BEURIA

Scientist F,
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Dr. Tushar Kant Beuria obtained his PhD degree from School of Biosciences and Bioengineering at IIT Bombay (https://www.iitb.ac.in/). After that he worked as a postdoctoral fellow at Department of Microbiology and Molecular Genetics, University of Texas, Health Science Centre at Houston, USA (https://med.uth.edu/mmg/). He has good expertise in the field of Microbiology, Molecular Biology and Biochemistry. Currently he is working as a Senior Scientist (Scientis-F) at Infectious Disease Biology Group, Institute of Life Sciences, Bhubaneswar, Odisha, India (www.ils.res.in). His group works to understand how the cell division machinery works in bacteria and the mechanism of antibacterial resistance. He was a Ramalingaswami Fellow Scientist at the Institute of Life Sciences from 2011 to 2016 and Dr. Beuria obtained his Ph.D. in Biochemistry and Cell Biology from the School of Biosciences and Bioengineering, IIT Bombay, in 2006, and his M.Sc. in Organic Chemistry from Ravenshaw College, Cuttack, in 1999. He holds a B.Sc. in Chemistry from Ravenshaw College, Cuttack, obtained in 1997. Dr. Beuria has received prestigious awards including the Ramalingaswami fellowship (2011-2016) and Senior Research Fellowship (SRF) and Junior Research Fellowship (JRF) sponsored by the Council of Scientific and Industrial Research (CSIR), India. He has also served as a visiting faculty at IISER, Berhampur, from 2019 to 2021.

Targeting the bacterial efflux pump to combat antimicrobial resistance in Methicillin-resistant *Staphylococcus aureus*

Dr. Tushar Kant Beuria
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Methicillin-resistant Staphylococcus aureus (MRSA) is a bacteria that is a significant threat to global health in healthcare facilities, and its antibiotic resistance complicates treatment regimens. In patients who have bacteremia, MRSA infection can lead to life-threatening sepsis, pneumonia, and heart failure. Furthermore, growing antibiotic resistance among bacteria exacerbates the worldwide health issue. MRSA employs a variety of tactics to avoid drugs' lethal effects. Enhancing efflux pump function is a technique for removing various antimicrobials from bacterial cells. Combining antibiotics with efflux pump inhibitors (EPIs) can improve the therapeutic efficacy of existing antimicrobials against Methicillin-resistant Staphylococcus aureus. Several EPIs have been discovered but have yet to achieve clinical approval due to concerns such as ineffectiveness, limited action range, incorrect pharmacokinetics, or significant toxicity. In our study, to discover novel efflux pump inhibitors, we developed a medium throughput assay to identify compounds with efflux pump activity. Using an FDA drug library, we identified several efflux pump inhibitory activities. The gene expression analysis revealed that the treatment with EPIs decreased the expression of the efflux genes and regulators in MRSA significantly. The EPIs were checked for cytotoxicity, and no cytotoxicity effect was observed towards mammalian cells. The synergy of EPIs with existing antibiotics was verified in an animal infection model. Compared to the antibiotics administered alone, antibiotics and EPIs significantly reduced the bacterial burden in a murine skin infection model.

360 Degree AMR Management: Unveiling the Strategic Endeavors Employed by the Hazra Group in Mitigating Antibiotic Resistance (ABR), with a Focus on Beta-Lactamase as a Molecular Indicator

Dr. Saugata Hazra
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Addressing the growing threat of microbial infections fueled by antibiotic resistance is a critical global challenge, particularly pronounced in developing nations where effective hygiene practices and medication adherence are essential yet often lacking. This abstract explores the pressing need for innovative strategies to combat drug-resistant strains of pathogens, focusing particularly on beta-lactam antibiotics like penicillin. These antibiotics inhibit bacterial cell wall synthesis by targeting transpeptidase enzymes, but bacterial pathogens counteract this mechanism by producing beta-lactamases, enzymes that degrade the antibiotic structure and confer resistance. The abstract highlights the complexity of bacterial resistance and emphasizes the importance of understanding beta-lactamase enzymes as molecular indicators to mitigate the risk of drug resistance. It introduces a multifaceted approach to studying beta-lactamases, including computational analysis to identify promising candidates, elucidating clinical mutations responsible for resistance, and developing novel diagnostics. The research presented by Hazra-lab adopts a comprehensive DTMS framework (Diagnostics, Therapeutics, Mapping, and Surveillance) to tackle drug-resistant pathogens. This framework encompasses diverse diagnostic methodologies, innovative therapeutics based on metal and nanomaterial-mediated reactive oxygen species (ROS) generation, and mapping and surveillance of antimicrobial resistance (AMR) across various environments, facilitated by the BL-tester series on-field diagnostics device. The abstract concludes by emphasizing the collective efforts towards an integrative one-health approach, which contributes significantly to the effective management of antimicrobial resistance. By combining advanced diagnostics, novel therapeutics, and comprehensive surveillance, this approach offers promising avenues for addressing the complex challenges posed by antibiotic resistance and safeguarding public health on a global scale.

Dr. SULAGNA BASU

Scientist F, Division of Bacteriology, ICMR- National Institute of Cholera and Enteric Diseases, Kolkata

Sulagna Basu is a Scientist at the National Institute of Cholera and Enteric Diseases, Kolkata. She joined the Institute in 2006. Her current research focuses on the colonization of the neonatal gut with Gram negative bacilli and bacterial resistance to antimicrobial agents in neonatal infections. Her laboratory has identified some of the currently widely disseminated antibiotic resistance determinants in bacteria causing neonatal infections. Sulagna Basu graduated from the University of Calcutta with B.Sc. in Chemistry. She earned her M.Sc. from the Department of Biochemistry, University of Calcutta. Dr. Basu received her Ph.D in 2003 from The Post Graduate Institute of Medical Education and Research, Chandigarh . During this period her research revolved around the purification and characterization of a lectin from Enteroaggregative *Escherichia coli* . She received the ACBICON 2003 award for the work on Enteroaggregative *E.coli*.

Towards understanding the exchange of genes in the gut: the mcr example

Dr. Sulagna Basu
Division of Bacteriology, ICMR- National Institute of Cholera and Enteric Diseases, Kolkata

Antimicrobial resistance genes can be exchanged via mobile genetic elements within the gut. Though this has been studied in case of different resistance genes such as blaCTM-15 or blaNDM-1, it has not been studied for the mobilised colistin resistance gene, mcr. mcr codes for phosphoethanolamine transferase which catalyzes the attachment of phospoethanolamineto lipid A which consequently leads to colistin resistance. This study investigates the presence and dynamics of mcr in rectal specimens of pregnant mothers and neonates. mcr-1.1 was identified in rectal samples from pregnant mothers but not in neonates. Interestingly, all mcr-positive mothers delivered healthy neonates, from whom rectal samples were not obtained, precluding the study of mcrtransmission between these pairs. mcr-1.1 was exclusively found in Escherichia coli (phylogroups A & B1), carrying a limited number of resistance and virulence genes. The isolates exhibited diverse sequence types, including two novel STs (ST12452, ST12455). mcr-1.1 was harboured on conjugative IncHI2 plasmids flanked by ISApl1 on Tn6630, with sequence similarities observed across study isolates. Phylogenetic analysis revealed relatedness between study isolates and mcr-positive isolates of animal origin from Southeast Asian countries. The dissemination of mcr-1.1 within this study population likely occurred through similar mcr-positive clones or plasmids bearing mcr. While direct evidence of mother-babytransmission was not established, the presence of such genes in maternal specimens may heighten the risk of transmission to neonates.

Dr. C.V. Srikanth

Professor, Regional Centre for Biotechnology
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Dr. C.V. Srikanth is a Professor located at the 3rd milestone of the Faridabad-Gurgaon expressway in Faridabad, India. With a diverse academic and research background, Dr. Srikanth has held positions as a Senior Postdoctoral Research Fellow at the University of Massachusetts Medical School and Massachusetts General Hospital, Harvard Medical School, among others. Currently serving as an Assistant and Associate Professor at RCB since 2011, he has been recognized with prestigious awards such as the Wellcome Trust DBT Intermediate Fellowship. His research interests primarily focus on microbial biology, particularly the molecular mechanisms underlying Salmonella infection and gastrointestinal disorders. Dr. Srikanth's significant contributions are reflected in his numerous publications in reputable journals and his involvement in various grants and extramural funding projects. He is also actively engaged in professional societies and has received accolades including membership in the American Society for Microbiology and grants from organizations like SERB and India Alliance DBT-Wellcome Trust.

Salmonella mediated host epigenetic manipulation in immune evasion and chronic infections

Prof. Chittur V Srikanth
Professor, Regional Centre for Biotechnology, Faridabad

Infections caused by Gram negative bacterial pathogen Salmonella typhimurium results in self-limiting gastroenteritis. In rare cases the disease manifests into chronic and more severe forms including systemic disease and blood stream disease. The cellular and molecular determinants of the switch, from a localized gastroenteritis to a systemic disease, largely remain unknown. Strategies employed by Salmonella to thrive in hostile host environments during chronic infections are complex and multifaceted. It is known that in chronic state, a coordinated action of bacterial effectors allows reprogramming of macrophages to M2 subtype and thereby creating a permissible replicative niche. However, the mechanistic details of these processes are not fully studied. In a recent work, we identified epigenetic modification of host to be modulated by Salmonella for establishing chronic infections. Interestingly, S. typhimurium infections activate host histone modifier, Kdm6B for immune evasion and establishment of chronic infections. Mechanistically, Kdm6B activation rewires host macrophages and thereby lead to activation of alternate metabolic pathways. This in turn render the macrophages into non-bactericidal reservoirs, enabling chronic infection. An inhibitor of Kdm6B was sufficient to significantly reduce the Salmonella burden in in vivo models. In line with this, Salmonella isolated from human patients from India show a high invasive index. These isolates harbour several polymorphisms which regulate immune invasion and pathogenesis in host. They also show unusual modes of manipulation of host systems including activation of the epigenetic modulator Kdm6b. The following presentation would cover these findings along with a twist about the outcome of these in the host. The presentation would also be an effort to review theprevailing knowledge emanating from a large volume of research focusing on various forms of non-typhoidal Salmonella infections including those that cause localized, systemic and persistent disease.

Dr. Sarangthem Indira Devi

Scientist E
Institute of Bioresources and Sustainable Development,
Imphal, Manipur, India

Dr. Sarangthem Indira Devi is a highly accomplished researcher affiliated with the Institute of Bioresources & Sustainable Development, Imphal. She earned her Ph.D. degree from C.C.S University, Meerut in 2004, where she was honored as a Gold Medallist in M.Sc Microbiology (1998). With over 20 years of research experience, Dr. Devi specializes in antimicrobial peptides and bioactive molecules sourced from microbial and medicinal plants for drug development against multidrug-resistant pathogens, addressing the urgent challenge of antimicrobial resistance (AMR). During her academic journey, Dr. Devi further honed her expertise through a post-doctoral fellowship at Washington State University, Pullman, USA, from 2013 to 2014. Dr. Devi's research contributions are evident through her numerous publications in esteemed peer-reviewed journals and book chapters, showcasing her dedication to advancing knowledge in her field. Her involvement in technology development has led to the acquisition of a patent, demonstrating her commitment to translating research into practical solutions. Recognized for her outstanding contributions, Dr. Devi has received several prestigious awards, including the Newton-Bhaba Fund Award for Female Leadership in Crop and Agricultural Sciences from Cambridge University, UK, in September 2016. Additionally, she was honored with the Rapid Grand Young Investigator Award from the Department of Biotechnology (DBT) in 2013 and a Visiting Scientist Fellowship Award from the University Grants Commission (UGC) in 2009, during her tenure at Madurai Kamraj University (MKU), Tamil Nadu. Dr. Sarangthem Indira Devi's comprehensive expertise, extensive research experience, and accolades underscore her dedication to combating antimicrobial resistance and advancing the field of microbiology and drug development.

Antimicrobial peptides and bioactive metabolites from microbes and plant sources to combat against AMR

Dr. Sarangthem Indira Devi
Institute of Bioresources and Sustainable Development, Imphal, Manipur, India

The World Health Organisation (WHO) reported resistant bacterial infection associated with nearly 4.95 million (M) deaths in 2019 and 1.27 M deaths are ascribed to antimicrobial resistance (AMR). Globally, it will result in an estimated 10 million deaths and an economic loss of 100 trillion GBP annually by 2050. To worsen the matter, the new addition of antimicrobial agents is diminishing because of rapid resistant development, prolonged research, and lack of profit from antibiotics research. In this current scenario, antimicrobial peptide (AMP) based therapeutics is an attractive candidate as alternative antibiotics since they have larger surface areas, greater chirality, and structural complexity. AMPs have shown antimicrobial, anticancer, immune-modulatory, and antibiofilm properties with reduced potential for resistance development. The Global Antimicrobial Peptides Market valued peptide drugs at 5 million US dollars in 2020, and it will reach 6 million by the end of 2027 at a compound annual growth rate (CAGR) of 5.4% between 2022 and 2027. From our study, we have isolated AMP, peoriaerin IBSD35 from the endophyte of *Millettia pachycarpa*. The LC/MS sequencing indicated the amino acids composition of the peptide is AAGIQAQAGFGLSDSIQGTGKQKCSFCK. It exhibited potential antimicrobial activity against *Staphylococcus aureus* ATCC 25923, *Escherichia coli* ATCC 25922, *Candida albicans* ATCC 10231, *Klebsiella pneumoniae* ATCC 4352, and *Salmonella typhimurium* ATCC 14028. There is also a growing interest in exploring plant-derived compounds as alternatives to conventional antibiotics. The crude extract of *T. citrine* inhibited the growth of *A. baumannii* isolates. The molecular docking displayed the interaction of outer membrane protein (OmpA) with the compounds generated via LCMS analysis. The compound 22-Deoxocucurbitacin D recorded the highest score of binding affinity. An altered the cellular morphology, shrinking of cells and inhibition of growth was observed in extract treated *A. baumannii*. The histopathological analysis showed that the extract treated mice did not show any adverse effects on major organs. From this perspective, we may be able to formulate the pharmacodynamics of the subfraction of *T. citrina*. Overall, it may be cited that phytocompounds offer a multifaceted approach in combating infections while minimizing the development of resistance.

Dr. MUKESH PASUPULETI

Principal Scientist, Division of Microbiology.
CSIR-Central Drug Research Institute, Lucknow

Dr. Mukesh Pasupuleti currently serves as the Principal Scientist and Associate Professor at the Central Drug Research Institute, a distinguished institution falling under the purview of CSIR (Council for Scientific and Industrial Research). Having earned his PhD in Clinical Medicine with a specialization in Immunology from Lund University, Sweden, in 2009, he also holds a master's degree in biotechnology from the University of Calicut, India. With an impressive track record, Dr. Mukesh has successfully completed seven research grants, and four ongoing projects highlight his commitment to advancing scientific knowledge. His extensive contributions are reflected in over 110 published papers across reputable journals, boasting a Total Impact Factor (I.F) of 270.16 and a Citation score exceeding 4200. As of the latest update, his H-index stands at 34, with an i-index of 66. Active in academic circles, Dr. Mukesh has been a prominent figure at more than 45 conferences, delivering over 15 invited lectures throughout India. He has supervised four PhD students and currently oversees the progress of eight others directly, with an additional 12 as Co-supervisor. Beyond doctoral mentoring, he has guided four Medical Doctors, four post-doctoral Fellows, and 12 master's students. His supervisory roles extend to institutions such as JNU (New Delhi), AcSIR (New Delhi), SRM University (Chennai), Manipal University (Manipal), and the University of Allahabad. Dr. Mukesh Pasupuleti serves as an Honorary Associate Editor for the Indian Journal of Medical Research and acts as a reviewer for esteemed international journals. He contributes to research as an Adjunct Faculty at Manipal University and serves on the Boards of Studies at IET Lucknow and Chaitanya Institute of Technology and Science, Hyderabad. His affiliations include life memberships in prestigious international organizations such as The British Society for Antimicrobial Chemotherapy and American Peptide Society, as well as national organizations like the Indian Immunology Society. Dr. Mukesh has received professional accolades including the "Senior Scientist Award-2016" by the Association of Biotechnology and Pharmacy.

Discovery and development of innovative novel next-generation biotherapeutics by Unveiling the Hidden Potential of the Innate Immune System: To tackle Emerging and Reemerging Pathogenic Infections

Dr. Mukesh Pasupuleti
Principal Scientist, Division of Microbiology, CSIR-CDRI, Lucknow

Infectious diseases continue to pose a significant threat to human health, with antimicrobial resistance presenting a formidable challenge to conventional treatment methods. While antibiotics have historically been effective in controlling infectious diseases, the escalating problem of antibiotic resistance renders many existing treatments ineffective against pathogenic bacteria. Antimicrobial resistance, particularly prevalent among WHO priority ESKAPE group pathogens, arises from various mechanisms including enzymatic inactivation, alteration of drug targets, and enhanced efflux mechanisms, rendering conventional antibiotics futile. Consequently, there is an urgent need for novel antimicrobial agents to combat these emerging and re-emerging pathogens. Amidst this crisis, the innate immune system emerges as a promising avenue for exploring new anti-infective agents. Evolutionarily conserved, the innate immune system serves as the first line of defense against pathogens, offering broad-spectrum effectiveness. Host defense peptides (HDPs), formerly known as antimicrobial peptides (AMPs), represent a key component of innate immunity. These short, amphipathic molecules exhibit both antimicrobial and immunomodulatory functions, making them attractive candidates for therapeutic development. HDPs act by disrupting bacterial membranes and modulating inflammatory responses, thereby effectively combating microbial infections while mitigating excessive inflammation. Their ability to selectively target pathogens without harming beneficial flora underscores their potential as alternatives to traditional antibiotics. However, the specificity of HDPs to different pathogens presents a challenge, necessitating the development of tailored approaches for individual pathogens. Despite this challenge, HDPs offer distinct advantages over antibiotics, including rapid action, modulation of host immunity, and target specificity. They are classified into three groups based on their synthesis: natural, synthetic, and cryptic HDPs, each offering unique advantages in therapeutic development. In conclusion, the exploration of host defense peptides represents a promising avenue in the quest for novel anti-infective agents amidst the escalating threat of antimicrobial resistance. While challenges remain, the multifaceted functions of HDPs offer hope for innovative therapeutic approaches in combating infectious diseases.

Dr. Anil Kumar Singh
Principal Scientist
Biological Sciences & Technology Division (BSTD)
CSIR-North East Institute of Science and Technology (NEIST), Jorhat, Assam, India

Anil Kumar Singh is a highly accomplished Principal Scientist with extensive expertise in bacterial drug resistance mechanisms, therapeutics, diagnostics, clinical and environmental microbiology, bacterial genetics, gene regulation, and bacterial genomics. He has a distinguished academic background, including a Ph.D. from Bose Institute, Kolkata, and postdoctoral fellowships at Necker Institute, Paris, France. Anil has held various research positions at CSIR-North East Institute of Science and Technology (NEIST), Assam, India, starting from Scientist Fellow to his current role as Principal Scientist. Anil's research focus spans several ongoing projects, including investigating the role of transcriptional regulators in biofilm formation and drug resistance in Mycobacterium abscessus, delineating the regulation of multi-drug resistant efflux pumps in clinical Mycobacteria, exploring potentially novel carbohydrases for waste management, and mitigating carbon emissions through eco-restoration. He has received prestigious fellowships and awards such as the Marie-Curie Fellow from the European Union, AXA Postdoctoral Research Fellow, and Indo-French Postdoctoral Fellowship. Anil has published prolifically in peer-reviewed journals and has contributed chapters to books, showcasing his expertise in various aspects of microbiology and molecular biology. Moreover, Anil is actively engaged in academic activities, including delivering lectures, conducting workshops, and participating in conferences globally. He has also been recognized as a potential reviewer for esteemed journals in his field. With a comprehensive skill set and a track record of impactful research, Anil Kumar Singh continues to be a leading figure in the field of microbiology, contributing significantly to our understanding of bacterial drug resistance and advancing novel strategies for combating infectious diseases.

Resistome characterization of clinically relevant enteric bacteria for β-lactam antibiotic resistance

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The emergence of β-lactam resistance is vying for clinical significance in Enterobacteriaceae, which the World Health Organization has classified as a global priority pathogen. The prevalence of numerous β-lactamase enzymes, mutational propensity, plasmid-adaptation pattern during horizontal gene transfer, and their fitness cost on the host remains a significant concern during resistance and virulence transmission in diarrhoeal infection. The current study highlights the first identified Escherichia fergusonii and Escherichia marmotae species from the northeastern part of India. For the first time, point mutations such as Arg32Ser, His92Tyr, and Leu147Phe were observed in the BlaSHV protein of two Klebsiella pneumoniae isolates, S-35 and S-46. Non-catalytic site H-bond interactions of Arg218, Ala223, Asn128, Ser126, Gln95, Asp100, Tyr101, Ser102, and Ala274 were found with a low binding affinity towards BlaSHV. This correlates with the high imipenem, ceftazidime, cefuroxime, ceftriaxone, and cefpodoxime resistance in the S-35 isolate with the additional influence of Arg32Ser and Leu147Phe mutations. The His92Tyr mutation was found to control the resistance in S-46. Moreover, In vitro conjugation and transformation showed the highest conjugation frequency (9.2×10-1) and transformation efficiency (1×103) in Escherichia species S-10. S-10 was detected with the highest plasmid carrying frequency (83.44%) and insignificant segregational loss rate (0.0004) until the 60th day with low plasmid cost on the host. Phage proteins, relaxosomal protein NikA, replication protein RepA,and plasmid maintenance proteins (ParA, RelE/ParE) aid stable plasmid maintenance in the S-10 genome. The first complete genome sequence of highly carbapenem and cephalosporin-resistant, β-lactamase OKP-A-11 producing K. quasipneumoniae S-2 from northeast India. The complete resistome of S-2 identified multidrug-resistant genes like blaOKP-A-11, blaTEM-116 ompK37, PBP, fosA, oqxA, etc. The presence of type II, III, IV, and VI secretion system proteins, type 1 and 3 fimbriae, ent siderophore, salmochelin, and sec-tet system, can mark this hypervirulent strain. Thirty-two genomic islands were identified with more transposase and phage proteins in the S-2 genome. Mobilization protein, replication protein, phage proteins, RelE/ParE, and ParB/Srx family partition system proteins also indicated a persistent plasmid population in the S-2 genome. The current study can be translated into further population studies on intra- and inter-genus plasmid-host adaptation with an in-depth genetic assessment of plasmid in resistance dissemination. These findings can also help better understand the drug-resistance burden of this increasingly important pathogen group in acute diarrheal infection**.**

Dr. DEBPRASAD CHATTOPADHYAY

Director, School of Life Sciences, Swami Vivekananda University at Barrackpore, Kolkata

Dr. Debprasad Chattopadhyay, a biomedical scientist of repute (Citations: 5874, h-index: 44; i-10 Index: 109), ranked among top 10 ICMR-Scientists and top 2% most-influential Global Scientists (Stanford University, and Elsevier lists). Dr Chattopadhyay has completed his Post-Graduation in Botany with Microbiology and PhD in Microbiology from Jadavpur University. He then moved to the Royal Hospital Medical College, London for post-doctoral training on the Clinical trial of Fosfomycin in UTI and at Staten Serum Institute, Copenhagen on Antibacterial non-antibiotics. On return Dr Chattopadhyay joined the CSIR-Indian Institute of Chemical Biology, Kolkata as CSIR-Senior Research Associate. He started his scientific journey at the ICMR-Regional Medical Research Center, Port Blair in December 1993, and transferred to ICMR-Virus Unit Kolkata in 1997. In 2016 Dr Chattopadhyay was selected as the first Director of RMRC-Belgaum; which was upgraded to ICMR-National Institute of Traditional Medicine under his leadership in Feb 2017, where he served as the Founder-Director until September 2021. Presently he is associated as the Director, School of Life Sciences, Swami Vivekananda University at Barrackpore, Kolkata after serving at School of Health Sciences, NSHM Knowledge Campus, Kolkata and Durgapur as Research Advisor. Dr. Chattopadhyay's research spans over 28 years, demonstrating the bioactivities of 17 traditional formulations and identifying molecules with various medicinal properties. Notable achievements include establishing the antibacterial activity of methdilazine, conducting clinical trials on Fosfomycin, and validating healthcare practices among tribal communities. He holds patents, authored books, and published extensively. Dr. Chattopadhyay supervised numerous theses and dissertations, contributing significantly to
Scientific advancement.

Traditional Medicine: Can it be the Nature's Weapon against Drug-Resistance Microbes?

Dr. Debprasad Chattopadhyay
Director, School of Life Sciences, Swami Vivekananda University at Barrackpore, Kolkata

Integration of scientifically validated traditional medicine(s) with modern therapeutics is now considered as a major area in the management of drug-resistant chronic and infectious diseases. Scientific validation of traditionally used therapies of diverse culture, especially plant-based medicines of Indian system of medicines (ISM), can be a unique source of nature's principals to combat difficult-to-treat diseases with narrow therapeutic window, including drug-resistant microbial infections. Today, almost all classical antibiotics, some antivirals and anticancer therapeutics are ineffective against serious diseases; while most emerging and re-emerging diseases lack effective drug(s). To face this global threat scientists and industry are looking for repurposing of known agents or in search of alternative agents from nature. Decades of global studies revealed that diverse secondary metabolites of plants, produced for plant-defense, are found to be beneficial to combat human diseases, including microbial infections by targeting the life cycle of invading pathogen(s) or the communicating system of the host including modulation of host immune response or signaling. This presentation will portray some selected multitargeted phytos to alter, break or reverse drug-resistance by damaging or altering surface structure, inactivating or denatured enzymes/proteins or interfering with replication of microbial pathogens in preclinical studies and a few human trials.

Dr. SUDIPTO SAHA

Associate Professor, Department of Biological Sciences, Bose Institute, Salt Lake, Unified Academic Campus, Kolkata, India

Dr. Sudipto Saha did his Ph.D. (Bioinformatics) in 2007 from Jawaharlal Nehru University (work done at CSIR-IMTECH, Chandigarh), followed by two Postdoctoral research work, one at Indiana University, School of Informatics, Indianapolis, USA from 2007-2008 and the other at Case Western Reserve University, School of Medicine, Cleveland, USA from 2008-20012. He joined Bose Institute as a DBT- Ramalingaswami Re-entry Fellow in 2012 and is now working as an Associate Professor in the Department of Biological Sciences, at Bose Institute. His research interests focus on understanding lung diseases like asthma/COPD and tuberculosis using bioinformatics and systems biology approaches. He has published 80 peer-reviewed journals, and several book chapters and authored a book on "Pulmonomics: Omics Approaches for Understanding Pulmonary Diseases"

Exploring microbial genes associated with antimicrobial resistance in the lung microbiome of respiratory disease patients

Dr. Sudipto Saha
Associate Professor, Department of Biological Sciences, Bose Institute

The identifications of clinical isolates of antibiotic-resistant pathogenic bacteria causing respiratory diseases like tuberculosis (TB) are well cataloged, however, the role of the drug -resistant genes (DRG) within the lung microbiome is not very well explored and is not completely defined. A manually curated repository of mutation data of drug resistance-associated genes (DRAGs) across ESKAPE and other bacteria with a special focus on Mycobacterium tuberculosis (MTB) was developed by our group (named DRAGdb). Our analyses of mutations in drug-resistant genes listed in DRAGdb revealed homoplasy and pleiotropy phenomena to be associated with resistance. We also studied whole metagenome shotgun sequencing (WMSS) runs coming from the sputum of five airway diseases: asthma, bronchiectasis, chronic obstructive pulmonary diseases (COPD), cystic fibrosis (CF), and tuberculosis (TB). We observed several gene families specific to the drug-resistant associated genes from opportunistic pathogens in the sputum microbiome of all five diseases. In summary, the role of DRGs in the lung microbiome needs to be explored for the development of new therapeutic strategies in respiratory diseases.

Carbapenem Resistance in clinical Vibrio cholerae O1 strains: A Challenge to Modern Medicine

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Carbapenem-resistant enteric pathogens are spreading rapidly and are causing an escalating global concern as this group of antibiotics is considered the last line of defense for treating life threatening infections caused by multidrug-resistant (MDR) Gram-negative pathogens. However, this resistance phenotype has rarely been seen in the case of cholera enteric pathogen Vibrio cholerae O1. Due to distinct genetic makeup and extraordinary plasticity, V. cholerae strains are becoming resistant to many commonly used antibiotics and even carbapenem by acquiring exogenous DNA. Therefore, the present study aimed to decipher the mechanisms of resistance of recently emerging El Tor variant carbapenem-resistant V. cholerae O1 strains isolated from clinical samples in Gujarat, India in 2019. A total of 50 strains were screened for major virulence associated genetic alleles of the genes along with the determination of antibiotic resistance profile. All of the strains were found to contain hypervirulent Haitian alleles of virulence genes and exhibited resistance patterns similar to the multidrug-resistant El Tor vibrios. However, interestingly 12% (6/50) of them showed resistance against carbapenem antibiotics along with other β-lactams, and aminoglycosides and hence further characterized by whole genome sequencing (WGS). The WGS analysis revealed the presence of a 142-kb mega-sized plasmid belonging to IncA/C1 which harbours three NotI restriction sites and genes conferring resistance against different antibiotics. The plasmid was also conjugally transferred into other enteric pathogens and depicted similar resistance patterns which may pose a high risk in the management of enteric diseases. Overall, the present study shed light on the mechanism underlying carbapenem resistance through conjugative plasmid which possesses a high risk of dissemination of resistance genes to other sensitive bacteria that could have serious disease outcomes in the future.

P-type ATPase zinc transporter Rv3270 of Mycobacterium tuberculosis enhances multi-drug efflux activity against structurally unrelated antibiotics

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Metal homeostasis is maintained by the uptake, storage and efflux of metal ions that are necessary for the survival of the bacterium. Homeostasis is mostly regulated by a group of transporters categorized as ABC transporters and P-type ATPases. Interestingly, efflux pumps often play a linkage in drug-metal cross-resistance. Apart from extruding antibiotics, toxins, quorum-sensing molecules, and adhesins, efflux pumps are involved in various fundamental metabolic, physiological and biochemical pathways for the survival and virulence of the bacterium. Here, we report the ability of a P-type ATPase, Rv3270, known for its role in combating Zn2+ metal ion toxicity in Mycobacterium tuberculosis, in influencing the extrusion of multiple structurally unrelated drugs and enhancing the biofilm formation of E. coli and Mycobacterium smegmatis. Overexpression of Rv3270 increases the tolerance of host cells towards multiple flouroquinolones, aminoglycosides and anti-tubercular drugs. Significantly lower accumulations of norfloxacin, EtBr, Bocillin FL, and levofloxacin are observed in the cells harboring Rv3270 than that of the host cells indicating its role in enhancing efflux activity. Although over-expression of Rv3270 does not alter the susceptibility to levofloxacin, rifampicin and apramycin, a low-level tolerance towards these drugs are observed in the presence of a sub–inhibitory concentration of Zn2+. It is also noted that the expression of Rv3270 enhances the biofilm-forming ability of the host cells that strengthens its contribution to anti-microbial resistance. Therefore, the study indicates that the over-expression of rv3270 enhances the drug efflux activity of the microorganism where zinc might facilitate the drug-metal cross-resistance for some antibiotics.

Dr. RAJLAKSHMI VISWANATHAN

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Dr Rajlakshmi Viswanathan is a medical microbiologist with more than two decades of experience. After completing her MD in Microbiology form Madras Medical College, Chennai, she began her research career with a woman scientist fellowship from the Department of Science and Technology, GoI, for working on neonatal sepsis in a remote rural sick new born care unit in West Bengal. She has contributed significantly to the development of microbiology services for early detection of neonatal sepsis. Dr Rajlakshmi subsequently joined the ICMR-National Institute of Virology, Pune in 2013, where she has led the establishment and successful running of a bacteriology laboratory. She holds an intermediate career fellowship in clinical and public health from the DBT Wellcome India Alliance. Her areas of interest are infections of mother and child, including vaccine preventable diseases like pertussis and congenital rubella syndrome, antimicrobial resistance in the context of One Health, and the role of the gut microbiome in disease evolution. Dr Rajlakshmi has successfully worked for establishment of laboratory networks across the country for congenital rubella syndrome and pertussis. She has documented the occurrence of cholera in Maharashtra, confirming five such outbreaks. She has been also been part of outbreak investigations for cholera, Zika virus and KFDV and provided support to the public health system after natural disasters. Dr Rajlakshmi has more than 50 publications in national and international journals and leads several funded projects. She has a passion for ethics in biomedical research and health communication and contributes actively on these fronts as member secretary of NIV's ethics committee and as one of the nodal communication officers.

Antimicrobial resistance at animal human interface - A one health approach

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Antimicrobial resistance (AMR) is one of the major threats to global health. With the emergence of the concept of One Health which links humans, animals and the environment, comparative studies on AMR in indicator organisms common to human and livestock species are of importance. AMR is recognized as a One Health challenge because of the rapid emergence and dissemination of resistant bacteria and genes among humans, animals and the environment on a global scale. The emergence of AMR from antibiotic overuse in the animal sector is an unmeasured burden in India. To explore the antimicrobial resistance trends in the bacterial indicator organisms common to humans and animals. An observational community-based collaborative study was undertaken at Karnawadi village, Khandala Taluka of Pune district, Maharashtra. Participants included farm workers and farm animals. Food of animal origin food was also screened. Indicator organisms (Escherichia coli, Staphylococcus aureus, Enterococcus spp., and Salmonella spp.) were isolated from appropriate samples, and screened for antimicrobial resistance. From farm workers, 180 nasal swabs and 97 fecal samples were collected. S. aureus was isolated from nasal swabs of 22 (12.2%) participants. E. coli (80/97) was the predominant isolate in fecal samples (82.5%) followed by K. pneumoniae (36/97, 37.1%), and Enterococcus spp 23 (23.7%). The mecA gene was detected in 5/22 (22.7%) of S. aureus, and VanA in one Enterococcus isolate. blaTEM was the most common AMR determinant, detected in 27% of E.coli and blaSHV (25/31, 80.64%) in K. pneumoniae isolates. Three K. pneumoniae and 11 E.coli isolates resistant to ciprofloxacin tested positive for the gyrA gene. 579 samples from farm animals and environment and 480 food samples were collected. A total of 187 E. coli (32.29%); 61 S. aureus (10.53%); 104 Enterococcus spp, and 36 Salmonella spp. (6.21%) were isolated from animal and poultry samples. The bacterial occurrence was comparatively high in raw foods of animal origin. E. coli showed maximum resistance to ampicillin, tetracycline, cefazolin, and ceftriaxone. Detection of AMR genes in bacterial isolates revealed the widespread prevalence of the blaTEM gene and TetA gene in all four bacterial species irrespective of their source. mecA-positive S. aureus was isolated from bovine raw milk samples. This pilot collaborative study explored the prevalence of AMR in bacterial indicator organisms common to humans and animals. The occurrence of AMR at this interface is worrisome and indicates the possibility for widespread transmission of AMR across the three pillars of One Health.

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Dr. Souvik Mukherjee did his M.Sc. (Biochemistry) and Ph.D. (Biotechnology) from University of Calcutta. During his Ph.D. he carried out research on Population Genetics and Molecular Evolution of Innate Immunity Genes in Humans. For this he undertook large scale DNA sequencing of pre and post agricultural populations from different parts of India. He carried out his post-doctoral research in an Indo-Spanish Collaborative Project working jointly in NIBMG, India and Universitat Pompeu Fabra, Barcelona, Spain. For a brief period of time, he also participated in the next generation sequencing of cancer patients in the International Cancer Genome Consortium-India Project on Oral Cancer. In 2014, he joined as an Assistant Professor in BioMedical Genomics Centre, Kolkata where he started working on the role of human microbiome in health and disease. In 2016, he joined National Institute of Biomedical Genomics where he is studying host-metagenome interactions in chronic human diseases. He also serves as the Academic Co-coordinator of the regular Ph.D. program of NIBMG. He has published in high impact peer-reviewed journals like PNAS, Nature Communications, Scientific Reports, Microbiology Spectrum, Frontiers in Cellular and Infection Microbiology and Genome Biology and Evolution. He is a life member of Indian Society of Human Genetics (Life Member) and Calcutta Consortium on Human Genetics (Life Member). He has also served in committees of ICMR and CSIR on diarrheal diseases and microbiome research respectively. He has served as a guest editor in Frontiers in Microbiology journal. He has presented his work in more than 40 national and international conferences and has authored a couple of book chapters on the role of human skin and gut microbiome in human health. He is the recipient of International Travel Award from ICMR in 2016 and DST-SERB in 2013, SERB Young Scientist Grant in 2015, SciGenom Research Grant in 2016, India-EMBO Symposium Grant in 2019 and SERB Core Research Grant in 2024. He is the nodal officer of INSACOG sewage surveillance for the state of West Bengal for detection of COVID virus in the wastewater from different regions of West Bengal, Sikkim, Mizoram and Assam.

Deciphering the Host Microbiome Interactions that leads to the Development of Antimicrobial Resistance in Chronic Inflammatory Diseases in Humans

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The human microbiome consists of about 50% cells in our human body and is termed as the "forgotten organ" that had not been given much attention with respect to the development of chronic inflammatory diseases in humans. The technological advancements in the form of massively parallel sequencing have made it possible to identify both the culturable as well as the viable but non-culturable (VBNC) microorganisms from biospecimens collected from different human samples like stool samples, skin swabs, wound biopsies and oral plaques. Besides the taxonomic identification, metagenomic studies have also unleashed the detection of microbial gene families and pathways that performs essential functions in the maintenance of homeostasis by interacting with the host. Any perturbations in the host-microbiome interactions lead to the development of chronic inflammatory diseases in humans. The indiscriminate use of antibiotics has ushered in an era of antimicrobial resistance and growing evidence suggests that the dysbiotic human microbiota shows higher carriage of potential AMR species. The skin is the largest organ of the human body that acts as the first line of host defence and harbours a considerable number of microbial species termed as the skin microbiome. We have characterized the first healthy human skin microbiome in any Asian/Indian population and have also identified the differences from the European skin microbiome profile. Currently, we are involved in understanding the host-microbiome interactions in (a) chronic inflammatory skin diseases and antibiotic resistant wounds and (b) maternal and child health. In another study, we have shown distinct differences in the upper respiratory tract (URT) microbiome composition and diversity between individuals infected by different subtypes (omicron, delta) of COVID virus. During my presentation, I will provide a broad overview of our research on host microbiome interactions aimed at understanding the development of chronic dry skin disorders like Atopic Dermatitis as well as how the higher AMR carriage leads to the impairment of wound healing in Diabetic patients. The importance of probiotic approach and phage therapy in the management of such conditions will also be discussed as an alternative to the usage of antibiotics.

Revitalizing Phage Therapy for Cholera: Isolation, Screening and Characterization of Bacteriophages to Evaluate Therapeutic Potential

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The discovery of antibiotics marked the golden days of modern medicine, saving countless lives by controlling the major infectious diseases. However, their widespread use has led to multidrug (MDR) and antimicrobial resistant (AMR) bacterial strains, prompting the scientific community to explore alternatives to save the world from moving towards pre-antibiotic era. Bacteriophages, the natural killer of bacterial strains are the bacterial viruses hosted by bacteria. The use of phage to treat bacterial infection or thephage therapy, a century-old, almost obsolete concept, is regaining importance as a promising alternative to antibiotics for treating MDR/AMR bacterial infections. We are creating a phage repository and exploring the possible application of bacteriophages in the management of diarrheal infections, primarily those caused by *Vibrio cholerae*. Bacteriophages were isolated from sewage water samples using *V. cholerae* O1 biotype ElTor strain MAK757. Plaque morphology was used for initial screening, and host range was determined. Phage nucleic acid was purified, analyzed, and whole genome sequencing performed. Stability of phagesdetermined at different pH and temperature ranges. Purified phages were used to conduct in vitro experiments and preliminary mouse studies. This study identified bacteriophages specifically active against *V. Cholera* O1 biotype ElT or strains, classified as Caudovirales and belonging to Podoviridae and Siphoviridae families. DNA was identified as phage genetic material, and next-generation sequencing revealed a close relationship with the proposed therapeutic phage ICP1. The analysis of other physicochemical parameters revealed distinct variations among the isolated phage.Phage JPW, a potent phage with genebank accession number OR039881.1, was identified as a potential therapeutic candidate.The preliminary animal challenge experiments demonstrated that cholera phage and phage cocktail effectively prevent *V.cholerae* infection in experimental mice. The current situation necessitates an urgent evaluation of the effectiveness, benefits, and drawbacks of bacteriophages in treating and managing bacterial AMR/MDR infections. This study suggests that cholera bacteriophages can be used for antibacterial therapy and prophylaxis, but there's a need for newer, accessible phagesto enrich the phage repository.

Unveiling the role of HMGB1 (High Mobility group Box1) inhibition in autophagy during *Helicobacter pylori* infection

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Infection with *Helicobacter pylori* is one of the key factors responsible for causing gastric disorders and a major risk factor for progression to gastritis and gastric cancer. Once infected, clearance of *H pylori* is difficult by the immune system. Moreover, antibiotic resistance makes it complicated for effective eradication. For clearance, host cells induce different pathways like autophagy. But *H. pylori*subverts the autophagy mechanism to survive in the gastric niche. High Mobility Group Box 1 (HMGB1) a host proteinserves as a key regulator of autophagy and exhibits increased expression levels in severaldiseases and various types of cancer including gastric cancer. However, the role of HMGB1in autophagy during *H. pylori* infection has not been explored till date. The purpose of this study is to investigate the role of glycyrrhizin, a known HMGB1 inhibitor, in autophagy during *H. pylori* infection. *H. pylori* infection was established in human gastric cancer (AGS) cells followed byglycyrrhizin treatment. To investigate the expression of autophagy proteins, western blot was performed. Using fluorescence assays, autophagy and lysosomal activities were determined. HMGB1 knockdown was carried out to confirm the effect of glycyrrhizin. An *in vivo*mice model of *H. pylori* infection was developed, and the impact of glycyrrhizin treatment was further investigated. *H pylori* infection inhibits the autophagy mechanism by inducing lysosomal membrane permeabilization (LMP) which is reversed by inhibition of HMGB1 due to glycyrrhizin treatment in gastric cancer cells. Hence, glycyrrhizin treatment restored the lysosomal membrane integrity. The restored lysosomal function inhibits intracellular *H. pylori* growth and inflammation.

ORAL PRESENTATION

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Candida tropicalis Xta1874 could be a better choice for Cd(II) Bioremediation: An alternative approach of waste water treatment

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Cd(II) is a potentially toxic heavy metal having carcinogenic activity. It is becoming widespread in the soil and groundwater by various natural and anthropological activities. This is inviting its immediate removal. The present study is aimed at developing a Cd(II) resistant strain isolated from contaminated water body and testing its potency in biological remediation of Cd(II) from aqueous environment. The developed resistant strain was characterized by SEM, FESEM, TEM, EDAX, FT-IR, Raman Spectral, XRD and XPS analysis. The results depict considerable morphological changes had taken place on the cell surface and interaction of Cd(II) with the surface exposed functional groups along with intracellular accumulation. Molecular contribution of critical cell wall component has been evaluated. The developed resistant strain had undergone Cd(II) biosorption study by employing adsorption isotherms and kinetic modeling. Langmuir model best fitted the Cd(II) biosorption data compared to the Freundlich one ($R^2_{27°C Langmuir}$ 0.978 > $R^2_{27°C Freundlich}$ 0.973). Cd(II) biosorption by the strain followed a pseudo second order kinetics. The results depict remarkable removal capacity (75.682 ± 0.002%) of Cd(II) by the developed resistant strain from contaminated aqueous medium using 500 ppm of Cd(II). Quantitatively, biosorption for Cd(II) by the newly developed resistant strain has been increased significantly ($p<0.0001$) from 4.36ppm (non-resistant strain) to 378.41ppm (resistant strain). It has also shown quite effective desorption capacity (87.527 ± 0.023%) at the first desorption cycle and can be reused effectively as a successful Cd(II) desorbent up to five cycles. The results suggest that the strain has considerable withstanding capacity of Cd(II) stress and can be employed effectively in the Cd(II) bioremediation from wastewater.

AMRC/2024/A-04

Assessment the bioactivity of *Terminalia citrina* against sepsis causing multidrug resistant *Acinetobacter baumannii*

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Antimicrobial resistance presents a significant global challenge at present. The escalation of multidrug-resistant bacteria has resulted in a notable increase in morbidity and mortality associated with sepsis. Researchers are vigorously pursuing the discovery of new antibiotics, with many exploring plant-based traditional medicine as a potential solution. Manipur as a part of North east India is one of the rich diversities and possesses distinctive traditional medicinal systems, characterized by the extensive utilization of various plants. The present study is to evaluate the antimicrobial potential of aqueous extract of *Terminalia citrina* against multi-drug resistant clinical strain *Acinetobacter baumannii*. Aqueous extraction of *T. citrina* by infusion method for carrying out antimicrobial activities against A. baumannii followed by Minimum inhibitory Concentrations (MICs). The methodology also involves Scanning Electron Microscopy (SEM) to examine cellular structures, Liquid Chromatography-Mass Spectrometry (LCMS) profiling for preliminary identification of potential compounds in *T. citrina*, and the evaluation of cell cytotoxicity through the 3-[4,5-dimethylthiazol-2-yl]-2,5 diphenyl tetrazolium bromide (MTT) assay. The results shows that the aqueous extract of *T. citrina* possess an antimicrobial activity against A. baumannii. The aqueous extract shows bacteriostatic against clinical strain *A. baumannii* with MICs range from 2000µg/ml-3.96µg/ml and Scanning Electron microscopy of the plant extract against *A. baumannii* shows cells deformity. LCMS interpretation data shows a promising bioactive compound present in *T. citrina*. Further in-vitro studies were caried out which shows no cytotoxicity effect on CaCo2 cell lines. This finding reveals that *T. citrina* has potentials antimicrobials properties, which could lead to overcome the current scenario of Antimicrobial resistance. Further experiment like mode of action and structure elucidation is underway.

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Comparative study on the renoprotective effect of linagliptin and dapagliflozin in diabetic rats

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Diabetic kidney disease (DKD) is most important cause of end stage kidney disease. The major approach in DKD management is blockade of renin angiotensin-aldosterone system associated with the risk of significant adverse events. Therefore, new molecules are needed for prevention of DKD which can increase compliance, decrease side effects and are also cost effective. To compare the renoprotective effect of linagliptin and dapagliflozin in diabetic rats. Twenty-four healthy male rats (150-200g) were screened; out of which 6 rats selected as group 1, then hyperglycemia was induced in remaining rats. After 1 week hyperglycemia was confirmed and rats divided in 3 groups (group2, 3 and 4). Group 1 (normal control group) and group 2 (hyperglycemic control group) were treated with vehicle. Group 3 and group 4 received linagliptin at the dose of 0.45mg/kg/day and dapagliflozin at the dose of 0.9mg/kg/day respectively till 3 weeks. On 28th day, significant reduction in serum urea and creatinine levels in linagliptin group [gr 3] ($p< 0.001$), ($p< 0.05$) respectively and dapagliflozin group [gr 4] ($p< 0.001$) when compared with gr 2. Significant higher serum urea ($p< 0.001$) and serum creatinine ($p<0.05$) when gr 3 compared to gr 1. Significant increase in creatinine clearance (CrCl) of gr 3 ($p< 0.05$) and gr 4 ($p <0.001$) groups as compared to gr 2 group. Gr 3 when compared to gr 1 had significant lower levels of CrCl ($p<0.001$). No significant difference ($p> 0.05$) when gr 4 was compared to gr 1. Dapagliflozin was more effective in improving the renal function parameters. Thus, dapagliflozin was more renoprotective when compared to linagliptin.

AMRC/2024/A-15

Understanding the transmission of NDM-harboring plasmids in the gut of pregnant mothers

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The gut serves as a hub of antibiotic-resistant genes. The microbial diversity and nutritionally-rich environment of the gut facilitates horizontal gene transmission of antibiotic-resistant determinants across the species. This study highlights the transmission of NDM+ve plasmids between multiple bacterial isolates from single rectal specimens of pregnant mothers. As a part of BARNARDS study, rectal swabs collected from pregnant mothers right before delivery were processed further to isolate carbapenem-resistant Gram-negative bacteria. The isolates were characterized in terms of antibiotic susceptibility, determination of blaNDM variants, transfer of blaNDM via conjugation and whole genome sequencing to assess ST types, plasmid types, blaNDM genetic contexts. The carriage of β-lactamases (CTX-M-15, NDM and OXA-48 like) were found in 48%, 8% and 2% of maternal specimens respectively. Among the NDM+ve rectal specimens, seven were colonized with more than one NDM-possessing species which included *Escherichia coli*, *Klebsiella pneumoniae*, *Acinetobacter baumanni* in different combinations. To understand blaNDM transmission within these multiple isolates, they were analyzed further. The isolates were resistant to other antibiotics apart from β-lactams and susceptible to tigecycline, fosfomycin. Several NDM variants (NDM-1/4/5/7) were detected. NDM-1 was predominant followed by NDM-5, NDM-7 and NDM-4. NDM-5 was prevalent in *E. coli*, NDM-1 in *K. pneumoniae*, *A. baumannii* whereas NDM-7 only in *K. pneumoniae*. The NDM-possessing isolates belonged to diverse ST types. Enterobacteriaceae isolates harbored varied plasmid scaffolds carrying NDM which were conjugally transferred via several replicons such as IncFII, IncFIIk, IncFIB etc. and possessed complete/truncated ISAba125 (upstream) and bleMBL (downstream) of NDM. The multiple species from individual patients mostly harbored differed NDM-variants and plasmid types although showed similarities in genetic contexts might indicate transposition of NDM. The carriage of different NDM-variants in gut of mothers at different time points suggest independent acquisition of NDM. Further plasmid characterization will depict the transmission events of NDM. However, colonization of such carbapenem-resistant bacteria in gut of mothers if transmitted to neonates can cause neonatal sepsis.

AMRC/2024/A-18

Phylogeny, resistome and mobile genetic elements of emerging oxacillinase-48-like carbapenemases: Snapshot from a neonatal unit

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Oxacillinase (OXA)-48 is a Class D serine carbapenemase, providing resistance towards carbapenem. Variants of OXA-48 endemic to India are OXA-181 and OXA-232 (collectively called OXA-48-like). They are major cause of nosocomial outbreaks in Indian subcontinent. Dissemination of OXA-48-like is either due to specific clone or through mobile genetic elements (MGEs) (plasmids, transposons, insertion sequences-IS, etc.). MGEs picked up OXA-48 (which was initially chromosomal) and disseminated it to the bacterial community leading to the establishment of multidrug resistance (MDR). Hence, assessing role of MGEs in spread of this carbapenemase is imperative. To study association of OXA-48-like with different MGEs and evaluate their role in escalation of carbapenem resistance in a neonatal unit. OXA-48-like-harboring Enterobacteriaceae collected during 2008-2016 from blood of septicemic neonates admitted in a neonatal unit of a tertiary care hospital at Kolkata were analyzed in terms of resistome, transmissibility, MGEs associated with carbapenem-resistant plasmids and compared them with global strains. Emergence of $bla_{OXA-48-like}$ (n=11) in this neonatal unit was noted from 2013 and in *Klebsiella pneumoniae* only. Two variants of $bla_{OXA-48-like}$ identified are $bla_{OXA-181}$ (n=7) and $bla_{OXA-232}$ (n=4). Four $bla_{OXA-181}$ co-harbored bla_{NDM-5} (Class B metallo-β-lactamase). Strains belonged to high-risk international clones (sequence type14/15/23/231). $bla_{OXA-181,232}$ was found on a non-conjugative ColKP3 plasmid restricting its spread compared to blaNDM-5 present on a conjugative IncFII. Conjugal transfer of $bla_{OXA-181}$ was successful in strains co-harboring bla_{NDM-5}. Both $bla_{OXA-181,232}$ and blaNDM-5 exhibited a conserved genetic background i.e. ΔISEcp1-$bla_{OXA-181,232}$-ΔlysR-ΔereA within ΔTn2013 and ΔISAba125-bla_{NDM-5}-ble_{MBL}-trpF within ΔTn125 respectively. One $bla_{OXA-181}$ which showed conjugal transfer was present on a IncFII plasmid and exhibited a novel genetic background consisting of metabolic pathway genes, transposases, toxin-antitoxin system, transfer cassette, etc. Comparison with global strains showed relatedness with strains from other parts of world including neonatal outbreak strains from Tanzania and Ghana. This study is the first to describe occurrence of dual carbapenemases in *K. pneumoniae* from neonatal settings. $bla_{OXA-181,232}$-harboring strain from a single neonatal unit exhibited remarkably diverse genomes, ruling out clonal spread and emphasizing role of MGEs in the transmission of carbapenem resistance.

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Searching Antimicrobial Activity in 2-Phenoxyacetamide Analogues

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Antimicrobial resistance is one of the top global public health issues. It is making infections harder to treat and also resulting in sharp increase in life threatening risks in medical procedures, like, surgery, caesarean sections, chemotherapy, etc. This is also creating serious economic burden worldwide. This study searched the antimicrobial potential of some novel scaffold to meet the ever-increasing global demand of new antibacterial agents to fight against these upcoming infections worldwide. Some novel 2-phenoxyacetamide analogues have been synthesized in laboratory with moderate to high yields (57-96%). These have been subjected to assay of inhibitory potential against *Escherichia coli*, *Salmonella typhi*, *Staphylococcus aureus* and *Bacillus megaterium* by using disc diffusion method. Then the compounds were tested for the inhibitory potency against two fungi, like, *Aspergillus flavus* and *Aspergillus niger*. Subsequently, the compounds have been observed for the in vitro antiinflammatory potency by the denaturation of albumin assay and RBC membrane stabilization assay. Finally the compounds have been tested for analgesic properties by using the acetic acid induced writhing inhibition assay. The phenoxyacetamides gave no zone of inhibition in tests antimicrobial property. But these showed promising antiinflammatory protential in this study. While observing the inhibition of writhing in mice, the compounds showed IC_{50} values ranging from 1.6 mg/kg to 20.7 mg/kg. In preventing denaturation of egg albumin, they had IC_{50} values from 103 μg/mL to 294 μg/mL, where diclofenac showed had IC_{50} as 170 μg/mL. In stabilizing human red blood cells, they had IC_{50} values of 5.3 μg/mL to 266 μg/mL, The biological study was followed by docking studies for predicting possible interactions in the binding site of Cyclooxygenase enzyme. The phenoxyacetamide derivatives represents a scaffold not having any antimicrobial property. But this represents a promising scaffold that can be further explored for searcing new antiinflammatory pharmacophore for future researches.

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Inhibition of methicillin resistant *Staphylococcus aureus* biofilm by cell free supernatant lactobacillus. Spp isolated from fermented beverages

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Methicillin-resistant *Staphylococcus aureus* (MRSA) has been listed by the World Health Organization (WHO) as a high-priority category pathogen. Its ability to form biofilms contributes substantially to global health challenges related to antibiotic resistance in hospital and community-associated infection. The current study aims to evaluate the antibacterial and antibiofilm potential of Lactobacillus. spp isolated from fermented beverages from Manipur against Methicillin-resistant *Staphylococcus aureus* (MRSA). Cell-free supernatant of Lactobacillus. spp isolated from fermented fruit beverages were assessed for their antibacterial activity using agar well diffusion and spot lawn assay methods. The minimum inhibitory concentration and the minimum bactericidal concentration were determined through a 96-well microplate assay, along with confocal imaging for bactericidal and bacteriostatic effects of Lactobacillus. spp against MRSA ATCC 33519. Furthermore, the crystal violet staining method and microscopy imaging were employed to evaluate the anti-biofilm activity of Lactobacillus. sp for inhibition and eradication of MRSA biofilm. Lactobacillus. spp isolated from fermented fruit beverages exhibited antibacterial activity through the zone of inhibition (diameter). The MIC determination was shown at 4-fold dilution while MBC at 3-fold dilution. Furthermore, it notably inhibits 35% of biofilm formation and contributes to biofilm eradication. The microscopy imaging demonstrated a reduction in MRSA biofilm cell formation. Hence the potential antibacterial and antibiofilm properties of Lactobacillus. spp from fermented fruit beverages against MRSA could be a promising lead for exploring alternative antibiotics in addressing the ongoing issue of antimicrobial resistance.

AMRC/2024/A-23

The antityphoid efficacy of 2-Benzoxazolinone (BOA) identified from active fractions of root extract of *Scoparia dulcis*

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Scoparia dulcis is a well-known herb traditionally used for its anti-inflammatory, antioxidant, antimicrobial, anti-diabetic, and wound-healing properties. But there are very few works have been done to evaluate the antibacterial activity of *Scoparia dulcis* root extract especially against *Salmonella typhi*. In our research work, we identified the presence of the active compound 2-Benzoxazolinone (BOA) in active fractions of root extract of *Scoparia dulcis*. BOA is a phytochemical that acts as a defense mechanism in plants against pathogens and herbivores. The objective of our study was to evaluate the antibacterial activity of BOA against *Salmonella typhi*. The physicochemical properties were computationally screened to detect drug-likeness and to predict possible toxicity. We performed microbroth dilution to detect MIC and MBC, time-kill assay, and antibiofilm assay against *Salmonella typhi* strains. The computational docking was performed with two of the Salmonella proteins murA and folA. The in vitro enzyme assay was performed to test the inhibition of folA activity in presence of BOA. The therapeutic activity was studied on BALB/c mice which were challenged with a clinical isolate of *Salmonella typhimurium*. The computational screen of physicochemical properties showed that BOA had zero violation in Lipinski's rule of five in Drug likeness and its fall under acute toxicity class IV with predicted LD_{50} of 890 mg/kg (in mice). MIC and MBC of BOA ranged from < 1.87 mg/ml to > 0.46 mg/ml and < 3.75 mg/ml to > 0.93 mg/ml respectively. The Salmonella Typhi strains showed a decrease in growth rate in the presence of BOA and had mild antibiofilm activity. In docking, BOA showed more affinity towards folA protein with a docking score of -6.01. The enzyme assay showed the inhibition of the activity of folA in the presence of BOA. In In vivo, test groups treated with BOA showed 100 percent survival and less colonization of *Salmonella typhimurium* in the liver and intestine compared to the untreated group with 33 percent survival. BOA a naturally occurring active compound which was identified from fractions of *Scoparia dulcis* root extracts in our research work, has antibacterial activity against *Salmonella typhi* and has the potential to be used as therapeutics to treat typhoid.

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Capsaicin reduces inflammation and gastric tissue damages during *Helicobacter pylori* infection

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The present study investigates the potential of capsaicin as a therapeutic agent for intervening *Helicobacter pylori* (*H. pylori*) infection which is a major risk factor for gastric disorders and cancer. Another major problem with *H. pylori* is antibiotic resistance. *H. pylori* triggers host inflammatory pathways, including the NF-kB pathway, leading to inflammation and gastric complications. Targeting NF-kB is crucial to mitigate *H. pylori* pathogenesis, and its associated gastric complications. Capsaicin, a known NF-kB inhibitor, was studied for its effects on inflammation and gastric tissue damages in both in vivo and in vitro models of *H. pylori* infection. Our investigation encompassed both in vivo mouse models and in vitro infection models and downstream experiments of ELISA, western blotting, real time PCR etc, focusing on deciphering the influence of capsaicin on the NF-kB-miRNA promoter binding network. The results showed that capsaicin reduced the upregulation of pro-inflammatory cytokines at protein and gene level, along with a decrease in NF-kB activation. Interestingly, capsaicin also affected the NF-kB–miRNA network, specifically reducing the expression of miRNAs mir21 and mir22. This downregulation had downstream effects on Akt, a protein associated with inflammation and carcinogenesis, and e-cadherin, a protein linked to epithelial-mesenchymal transition (EMT). The findings suggest that capsaicin treatment can inhibit inflammation and improve gastric tissue damages during *H. pylori* infection. This alternative approach could offer a new direction for *H. pylori* treatment, potentially reducing the risk of gastric problems and combating anti-microbial resistance as an alternative therapeutic. Further research is needed to fully understand the mechanisms involved and to explore the clinical implications of capsaicin in managing *H. pylori*-related gastric disorders.

AMRC/2024/A-31

Exploring the antimicrobial efficacy of biomaterial derived from pumpkin seed protein and its application on raw meat preservation

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Exploring bioresources for food preservative materials is crucial for sustainable and effective solutions in food preservation, ensuring safety and extending shelf life while minimizing environmental impact. The aim of this study was to develop a composite film with antimicrobial and biodegradable activity based on pumpkin seed protein and Curcumin. Pumpkin seed protein concentrates were prepared using aqueous protein extraction techniques (alkali extraction-isoelectric precipitation). Protein concentration was determined using biuret and nanodrop method. SDS-PAGE was utilized to determine the molecular weight distribution of proteins. The Meat preservative biomaterial from the isolated pumpkin protein film was developed with incorporation of curcumin as cross-polymerizing agent. The percentage yield of the isolated protein is about 28.7% and the SDS-PAGE Migration pattern indicates that the pumpkin seed protein have polypeptide chain ranges from 35 KDa to 245 KDa. Experimental results on the application in chilled fresh chicken meat sample showed that the developed biomaterial could play an antimicrobial role on food borne pathogens when incorporated with curcumin, indicating their great potential for meat packaging.

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Nano-molecular formulation of propolis: a new dimension in traditional anti-inflammatory therapies

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Propolis, a bee-hive derivative, presents therapeutic potential for ulcer treatment due to its nano-molecular formulation. Its anti-inflammatory, anticancer, and antimicrobial properties make it an effective remedy or nano-carrier. To assess the efficacy of propolis nano-formulations in treating inflammation. An extract rich in cinnamic acid derivatives, gallic acid, ellagic acid, caffeic acid, and other phytochemicals was synthesized. Safety was confirmed via acute toxicity study. Efficacy was evaluated in three groups: control (saline), low-dose (200 mg/kg), and high-dose (400 mg/kg) propolis. Healing progress was monitored at intervals on the 15 days. Propolis demonstrated significant therapeutic effects, with accelerated wound healing observed in treated groups compared to controls. Propolis nano-formulations show promise for ulcer management, potentially attributed to their phyto-constituents and nanomolecular structure. Further research is warranted to explore their full therapeutic potential.

AMRC/2024/A-03

Antibiofilm and antiquorum-sensing activity of *Macrolepiota detersa* against clinical strain methicillin-resistant staphylococcus aureus and *Pseudomonas aeruginosa*

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Macrolepiota detersa belonging to family Agaricaceae is highly appreciated for its pleasant taste and nutritional value and considered functional foods with diverse biological activities. With the advent of the antibiotic era, the overuse and inappropriate consumption of antibiotics have driven the rapid emergence of multidrug-resistant pathogens. The problematic increase in multidrug-resistant bacteria translates into the urgent need to discover novel and effective antimicrobial substances. Herein, mushrooms could be a promising alternative of natural source of new antimicrobial agents. Evaluation of Phenolic and organic acid content. Antibiofilm and antibacterial activities of *M. detersa* against Methicillin-resistant Staphylococcus aureus clinical strain and Pseudomonas aeruginosa ATCC 15442. The crude extract of *M. detersa* was used for phenolic compounds and organic acids quantification by semi-preparative HPLC and antibacterial assays. Minimum Inhibition concentration (MIC) determination and antibiofilm activity were performed against MRSA clinical strain and P. aeruginosa ATCC 15442. Anti-quorum sensing activity and inhibition of violacein pigment against *Chromabacterium violaceum* MTCC 2655 were also performed. The methanolic extract of *M. detersa* exhibits antibacterial activity against both pathogens with MIC value of 25µg/ml each. It also exhibits 78.98% inhibition of violacein pigment formation by *Chromabacterium violaceum* MTCC 2655 and inhibits biofilm formation in MRSA clinical strain and P. aeruginosa ATCC 15442 at a concentration of 1 mg/ml concentration. Better inhibition was observed against P. aeruginosa ATCC 15442. *M. detersa* has rich bioactive compounds which possess antibacterial and antibiofilm properties against drug-resistant pathogens.

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Profiling of antioxidant mineral zinc among ten edible flowers of West Bengal using atomic absorption spectroscopy

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Flowers are important part of a plant that contain a great variety of natural antioxidants and many other bioactive and nutraceutical compounds. Zinc is required for the structure of proteins and cell membranes, it also regulates gene expression, cell signalling, helps in hormone release and transmission of nerve impulses in human body. The antioxidant potential of zinc involves neutralizing free radicals, and stabilizing cell membranes thereby protecting cells from oxidative damage. The objective of the present research work was profiling of antioxidant mineral zinc among ten edible flowers viz. *Musa acuminata*, *Carica papaya*, *Nyctanthes arbor-tristis*, *Ocimum sanctum*, *Clitoria ternatea*, *Sesbania bispinosa*, *Nymphaea stellata*, *Azadirachta indica*, *Hibiscus rosa-sinensis*, and *Tagetes erecta*, commonly consumed by the people of West Bengal. The concentration of zinc was determined by an Atomic Absorption Spectrophotometer. The sample was prepared for the estimation of micronutrients are wet oxidation method. In this method, the sample was first digested with nitric acid and again digested with perchloric acid and then diluted. The current study established the zinc content of the ten edible flowers where it was found that *Clitoria ternatea* flowers contain the highest amount of zinc content followed by *Carica papaya* and *Sesbania bispinosa*. The present findings conclude the edible flowers as rich source of zinc, and can provide good antioxidant support for human health. Therefore, future study can be extended for preparation of herbal formulations with these edible flowers serving as the potent nutritional and antioxidant source of zinc.

AMRC/2024/A-07

Synergistic antibacterial activity by asiatic acid and traditional antibiotics against multidrug resistant *Shigella flexneri*

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Bacillary dysentery or Shigellosis caused by Shigella spp. accounts for 5 to 15% of global diarrheal burden, affecting mostly low socioeconomic countries and killing 1.1 million annually. Lack of vaccine and treatment failure due the emergence of resistance, particularly multidrug resistance (MDR) has created global health concern. Therefore, novel approaches effective in curing drug resistant infections and preventing its spread should be explored. These approaches include using herbal/ small molecule compound or combining antibiotic therapy with herbal/ small molecule compounds. Asiatic acid, derived from *Centella asiatica* possess broad antimicrobial properties. Therefore, the aim of this study is to investigate the interaction between Asiatic acid (Aa) and Antibiotics (Ab) and to evaluate the potential use of Asiatic acid as an adjuvant in antibiotic treatment against MDR *Shigella flexneri*. The interactions between Asiatic acid and antibiotics (Ampicillin, Chloramphenicol, Ciprofloxacin and Nalidixic acid) against standard and drug-resistant strains were determined by fractional inhibitory concentration index (FICI). Cell co-culture assay and murine model of shigellosis was used to check drug interactions in-vitro and in-vivo respectively. Finally, cytokine analysis, biofilm viability, membrane leakage, and surface morphology were checked to understand the mechanism of action of the synergistic drug pair. Asiatic acid showed substantial anti-shigella activity against all test strains. Surprisingly, all Aa- Ab combinations showed promising synergistic or additive effect based on FICI. However, only Aa-Cip and Aa-Nal combination synergistically prevented intracellular bacterial growth both in-vitro and in-vivo conditions. Further studies showed increase in membrane damage, nuclear leakage and reduction in biofilm formation as probable causes for enhanced killing of *S. flexneri* by Aa-Cip combination compared to monotherapy. Asiatic acid, a potent antibacterial compound synergistically enhanced the activity of Ciprofloxacin and Nalidixic acid and may appear as a promising adjuvant to antibiotic therapy for eradicating MDR *S. flexneri* infection.

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Metabolite profiling of elite *Cinnamomum tamala* sample and its therapeutic potential as anti-microbials for drug discovery

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Cinnamomum tamala or 'tejpatta' is a plant that belongs to the Lauraceae family. Although *C. tamala* leaves are mainly used as spices, the plant has many medicinal properties. It is reported to be hypoglycaemic, stimulant, carminative and also used in cough, diarrhoea, gonorrhoea, rheumatism, boils, conjunctivitis and itching. To compare the phytochemical potential of *Cinnamomum tamala* (Buch.-Ham.) T. Nees and metabolite profiling of the elite sample revealing its therapeutic potential as anti-microbials for drug discovery. Crude extracts were obtained from *C. tamala* samples collected from different sites of NE India using cold maceration method. TPC, TFC and Antioxidant Scavenging activities were evaluated to identify the elite sample. The phyto-constituents were studied by using GC-MS with Quadrapole detector using Thermo Scientific having TG-5MS column and LC-MS with Agilent LC-QTOF 6546 system with C18 column. Mass Hunter vB.0.8.00 software was used for the analysis of MS data for compound identification. Anti-microbial activity was also determined using 96-well Broth Micro Dilution method. The elite sample showed 181.02 mg GAE/gram (TPC), 18.28mg QE/gram (TFC), IC_{50}-16.703 µg/ml (DPPH), IC_{50}-47.94 µg/ml (ABTS). GC-MS analysis showed the presence of Eugenol (60.98%) followed by β-Thujene (17.48%). LC-MS analysis identified 413 compounds out of which 20 compounds are antimicrobial potential compounds (score ≥90%). *C. tamala* showed anti-microbial activity against *S. aureus, B. cereus, E. coli, P. aeruginosa, S. typhi* and Shigella with MIC values 7.0, 6.0, 8.5, 9.5, 2.5 1.25 mg/ml respectively. The results suggested that *C. tamala* from NE India have high medicinal value and can be used for developing ethnopharmacological products.

AMRC/2024/A-10

Elsholtzia griffithii: identification of essential oil by GC-MS and its antimicrobial and antioxidant activities

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Elsholtzia griffithii plant belongs to Lamiaceae family and has been used as domestic folk medicine, food, spices, cosmetics, and aromatherapies. Pharmacological studies reveal its potential for various health benefits, including antibacterial, anti-inflammatory, antioxidant, and myocardial ischemia protection. To determine the composition of the essential oil of *Elsholtzia griffithii* by GC-MS and its antimicrobial and antioxidant activities. Methanolic extraction and hydro-distillation method were used to extract essential oils and crude extract from the sample, which is collected from various districts of Manipur. CG-MS was used to determine volatile compound present in the essential oils of the *E. griffithii* leaves. Antioxidant activity was evaluated by ABTS and DPPH assay. Antimicrobial activity were determined by well diffusion method. Phytochemical screening of *E. griffithii* extract revealed the presence of bioactive compounds like phenol, flavonoid, etc. GC-MS analysis showed the presence of various compounds such as α-Citral (46.45%), Photocitral B (39.47%), Geraniol (3.17%), etc. as the major compounds in the essential oils of the *E. griffithii* leaves. Crude methanolic extract exhibited excellent % free radical scavenging activity (27.03±0.23 and 139.44±0.41 in ABTS and DPPH, respectively). Inhibition zones against all tested strains were consistently observed in all sample, with MIC values range from 4.1 to 7.4 mg/mL. The present study demonstrates that the presence of bioactive compounds with great therapeutic potential in *Elsholtzia griffithii* leaves can be used as natural alternatives to synthetic drugs against several pathogens without any side effects.

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Presence of CRISPR-Cas systems in *Klebsiella pneumoniae* and its association with multidrug resistance (MDR)

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Antimicrobial resistance is one of the top ten global public health problems and is facilitated by horizontal gene transfer (HGT) of different antimicrobial resistance genes (ARGs) primarily harboured on plasmids. This menace requires urgent attention, particularly in nosocomial pathogens such as *Klebsiella pneumoniae*. Bacteria have evolved an "adaptive immune system" called CRISPR-Cas system, which targets exogenous DNA in a sequence-specific manner. Chief components of this system are cas1 (for adaptation), cas3 (for excision) and spacers (sequences targeting exogenous DNA). CRISPR-Cas systems can be used to control HGT by targeting plasmids harbouring ARGs. However, a correlation paradox exists between presence of CRISPR-Cas systems with multidrug resistance (MDR) in bacteria which needs to be resolved. This study aims to detect presence of ARGs in MDR septicaemic *K. pneumoniae* as well as to analyse presence of different CRISPR-Cas systems among these MDR and non-MDR strains. *K. pneumoniae* were characterised by antimicrobial susceptibility tests and assessed for the presence of different ARGs and cas genes. Whole genome sequencing (WGS) of MDR and non-MDR strains possessing cas genes were performed and analysed. Chi-square analysis was performed to find association between CRISPR-Cas systems and MDR. Among the studied strains, 78% were MDR with presence of different ARGs. Twenty-eight percent strains possessed complete Type I-E* CRISPR-Cas systems (commonly found in *K. pneumoniae*) bearing both cas1 and cas3 genes. Numerous spacers were found targeting different plasmid and phage sequences. Among MDR and non-MDR strains, 54% and 23% spacer sequences were unique respectively. Some spacers targeted specific sequences within ARG-bearing plasmids, but not ARG sequences. No significant association was noted between presence of complete CRISPR-Cas system with MDR. Type I-E* CRISPR-Cas system was found in clinical *K. pneumoniae*. No significant association between MDR and CRISPR-Cas system was noted. Though ARGs were not targeted by spacers, targeting of ARG-bearing plasmids indicated putative CRISPR-Cas-mediated activity.

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Effects of curcumin against planktonic bacteria and biofilm formation of multi drug resistant shigella

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Shigella, the leading cause of bacterial diarrhea worldwide, with around 74,000-600,000 deaths annually. Besides, Antibiotic resistivity, biofilm forming capability of drug resistant Shigella impedes conventional preventive and control strategies, which lead towards the urgency to develop new antibiotics. Undesirable side-effects of certain antibiotics with emerging antimicrobial resistance create hindrance in the way of present treatment regime which in turn opens a hunting scope for alternative therapies including prospective phyto-chemicals like Curcumin. Curcumin is well documented for its high efficacy against a wide array of microbial pathogens. However, its antimicrobial properties require further detailed investigations into clinical MDR isolates of Shigella for both planktonic form as well as biofilm. 108 MDR isolates of Shigella spp. obtained from the Infectious Diseases Hospital, Kolkata, India were tested to determine the minimum inhibitory concentration (MIC) of Curcumin. Effect of Curcumin on Shigella Biofilm formation and dispersion were detected by CFU method followed by CLSM and SEM. The mRNA expressions of efflux pump genes were analyzed by real-time PCR. Molecular docking studies were performed to support its inhibitory role as EPI. The MIC of Curcumin against planktonic Shigella ranged from 100-600µg/ml. The results demonstrated that the cell membrane in the planktonic growth mode exhibited irreversible destruction after curcumin exposure. Curcumin was shown to have a significant inhibitory effect on biofilm formation and also the viable bacterial count with concentration from 50-100µg/ml. Probably, curcumin acting like an EPI and Inactivating Efflux Pumps abolishes bacterial biofilm formation. Curcumin showed significant down regulation of Shigella efflux pump genes like acrA, acrB and tolC. The molecular docking studies of curcumin along with efflux pumps identified plausible binding mode and site for this natural product. These data provide novel insights into Shigella behavioural responses to curcumin exposure and suggest its potency to effectively constrain Shigella and its biofilm formation. These initial findings can have immense future prospect in usage of curcumin in current Shigellosis treatment.

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Characterization of *Klebsiella pneumoniae* isolates collected from septicemic neonates

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Klebsiella pneumoniae (Kp) is an opportunistic, Gram-negative, encapsulated pathogen found in both environment and healthcare settings. It is responsible for causing systemic infections by the acquisition of virulence genes such as capsular polysaccharide synthesis (cps) (rmpA/A2), siderophore production (iroB, iucA, entB), type-I (fimH) and type-III (mrkD) fimbriae genes etc. The treatment procedure is getting increasingly intricate due to enhanced potential of acquired resistance genes including blaCTX-M, and carbapenemases like blaNDM, blaKPC, blaOXA-48, etc. Hence, in this era of antibiotic resistance, it is important to assess resistance and virulence markers among Kp found in vulnerable population like neonates. This study characterises Kp in terms of virulence and resistance determinants isolated from septicemic neonates. During 2023, 29 isolates were collected from blood of septicemic neonates admitted in a tertiary care hospital in Kolkata. Identification and antimicrobial susceptibility testing (AST) of isolates were performed using VITEK®2 Compact system. PCR was performed to identify resistance and species-specific virulence determinants. Serotypes were identified based on previously reported multiplex PCR of virulence associated serotypes (K1, K2, K5, K20, K54 and K57). Kp was identified as prevalent (n=25) followed by *Escherichia coli* (n=3) and Enterobacter cloacae(n=1). Hence, further analysis were done on Kp due to its prevalence. AST profile revealed, majority of the Kp isolates were resistant to different antibiotics such as Meropenem, Ciprofloxacin, Piperacillin-tazobactam, Cefoperazone and ceftriaxone. However, isolates were moderately susceptible to Tigecycline and Gentamicin. blaNDM was the major carbapenemase present followed by blaOXA-48 and blaKPC genes conferring resistance to carbapenems. Among the studied virulence determinants, enterobactin (entB), type-I-fimbriae (fimH), and type-III-fimbriae (mrkD) were the most prevalent. The cps genes, rmpA2 (n=5) and rmpA (n=4) were present. K2 (n=6) followed by K54 (n=1) were the most prevalent serotypes identified among the tested capsular serotypes. Notably all K2 isolates were carbapenemase positive and harboured blaNDM. The increased presence of virulence factors along with resistance markers may contributing to increased burden of Kp in neonates.

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Emerging ST985, K39 carbapenem-resistant hypervirulent klebsiella pneumoniae (CRhvKp): a deviation from conventional hvKp

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Klebsiella pneumoniae (Kp) is evolving from an opportunistic classical pathotype (cKp) to a more pathogenic hypervirulent pathotype (hvKp) which causes a diverse range of community-acquired infections. Hypermucoviscosity within K1/K2 serotypes and siderophore synthesis are identified causes of heightening infectivity of hvKp. However, the presence of all these determinants is not always associated with increased pathogenicity. Lack of consensus makes the identification of hvKp more cumbersome. Surprisingly, previously reported antibiotic-susceptible hvKps are now emerging as Carbapene-resistant hvKp (CR-hvKp), resulting in treatment failure and mortality. New sequence types (STs) and serotypes gradually evolve as CR-hvKp by harbouring virulent and resistant plasmids. This study attempts to address the lacunae by characterizing a CRhvKp (ST985/K39) isolated from septicemic neonate diverging from conventional hvKps. To address the question of low pathogenicity of the isolate despite harbouring all virulence determinants. Identification, susceptibility testing, genotypic characterization and transmissibility of virulence and resistance plasmids were analysed. STs, serotypes and plasmid replicon types were determined through whole-genome sequencing. To assess virulence pathotype string test, biofilm, serum resistance and mice mortality assays were executed. The identified Kp, Kp80 belonged to ST985 and K39 serotype harboured all the virulence determinants (rmpADC, rmpA2, iucABCDiutA, iroBCDN) in a pLVPK-like plasmid with repB/IncHI1B(pNDM-MAR) replicon types and blaNDM-1 bearing IncFIB(pQIL)/IncFII(K) plasmid. Conjugation resulted in the movement of IncFII(K) plasmid carrying blaNDM-1. It was capable of producing biofilm and showed resistance to human serum. However, it showed negative results in string test with no mortality in mice after intraperitoneal injection of 105 CFU/ml isolate. This low pathogenesis and non-hypermucoid phenotype might be the consequence of frameshift mutation of RmpD. The emergence of CRhvKp within different lineages is worrisome. The study shows that harbouring virulence plasmid is not always associated with lethality which was evident in Kp80 where mutated rmpD resulted in non-hypermucoid phenotype with low pathogenicity. In-depth molecular characterization is needed to resolve the ambiguity in diagnosing hvKp.

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Novel sequence type of carbapenem- and colistin-resistant *Acinetobacter baumannii* ST2339

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Carbapenem-resistant *Acinetobacter baumannii* is now recognized as a clinically significant pathogen associated with life-threatening nosocomial infections. Colistin is the last therapeutic option for carbapenem-resistant *A. baumannii* associated infections. Colistin, a polycationic peptide, interacts electrostatically with the negatively charged lipopolysaccharide (LPS) of Gram-negative bacilli outer membrane, leading to disruption and permeabilization. But as a result of increasing use of colistin, a number of colistin resistance mechanisms in *A. baumannii* have been identified, including complete loss of LPS by inactivation of the biosynthetic pathway (lpxACD) or modification of LPS by phosphoethanolamine (pmrCAB). The continual occurrence of mutations in different colistin resistant determinants have led to the emergence of pan-drug resistant superbugs, leaving no treatment option. The study explored different mechanisms of colistin and carbapenem resistance of *A. baumannii* belonging to novel sequencing type. A carbapenem and colistin-resistant *A. baumannii* strain AB1 was identified at Delhi Safdarjung Hospital. The strain was characterized in terms of antimicrobial susceptibility testing, whole genome sequencing, multilocus sequence typing, presence of different antibiotic resistant genes at NICED. AB1 belonged to a novel sequence type 2339 (ST 2339) and had high minimum inhibitory concentrations for all carbapenems (>16 mg/L) and colistin (64 mg/L). PCR and genome data revealed that the isolate harboured carbapenem resistance genes blaOXA-23 and blaOXA-144. Other resistance genes including blaPER-7, blaADC-25, armA, ant(2")Ia, msr(E), sul1, sul2, dfrA1, mph(E), tet(B), qacE, aadA1, aph(6)-Id were also detected. The isolate carried single nucleotide polymorphisms (SNPs) in LPS modifying gene lpxD (4Q→4K) and pmrB (227A→227V, 169P→169T) which probably played important role in colistin resistance. Transmission electron microscopic images also revealed loss of LPS. Different efflux pumps (adeABC), evaluated in this study, did not play any role in increased colistin resistance. This study identified a novel *A. baumannii* isolate ST2339 which is resistant to last-line antibiotics carbapenem and colistin and explored different mechanisms of resistant. Outbreak of such superbugs are worrisome.

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QSAR and Molecular Docking studies on PBP2A inhibitors for Antimicrobial activity against

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Methicillin resistant Staphylococcus aureus (MRSA), the main culprit causing bacterial infections in humans, is emerging with a high morbidity rate and high incidence of resistance, annually across the globe. The resistance is developed by producing drug-insensitive penicillin-binding proteins (mainly PBP2A) and hydrolyzing β-lactam medicines to prevent them from acting on their target. To develop a prediction model for virtual screening of antimicrobial active phytochemicals based on Quantitative Structure-Activity Relationship (QSAR) approach and exploration of binding mode of action on target protein PBP2A of MRSA through molecular docking studies. MLR based QSAR model was developed and ADMET and Lipinski's Ro5 analysis was done to predict the druggability and bioavailability of phytochemicals. Molecular docking studies were performed to assess the binding affinity against PBP2A. The developed QSAR model showed the regression coefficient (R^2) of 0.97 for the training dataset, 0.93 for the test set, adjusted R^2 of 0.96 and R^2_{LOOCV} of 0.94. The chemical descriptors namely, Hmin (Electrotopological), ATSC4c, AATS7s (auto-correlated) and SpMax6_Bhs (Burden Modified Eigenvalues) regulating the activity. A total of 2,721 phytochemicals were virtually screened using derived QSAR model. Out of which only 13 were predicted to be active based on derived applicability domain, having good binding affinity to PBP2A. The developed QSAR model resulted in four conserved physicochemical properties, significantly correlated with the antimicrobial activity against PBP2A. Phytochemicals namely, 1-O-sinapoyl-beta-D-glucose, 7-methylxanthosine, and alpha peltatin were predicted as possible lead compounds with significant binding affinity at both active and allosteric sites of PBP2A.

AMRC/2024/A-22

Multidrug-resistant gram-negative organisms archived at the national repository of antimicrobial resistant bacteria (NRAMRB): the first national antimicrobial resistance hub of India

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To address antimicrobial resistance across the country, the first National Antimicrobial Resistance Hub (National Repository of Antimicrobial Resistant Bacteria, NRAMRB) in India was established at ICMR-NICED, Kolkata in 2019 to create a facility enabling AMR research at pan India platform. Bacterial isolates from nodal centres of ICMR's Antimicrobial Resistance Surveillance and Research Network are preserved at NRAMRB to generate evidence by analyzing the data and to provide authentic AMR strains to researchers across the country. Identification of the strains was confirmed using biochemical tests and VITEK-2-system. Susceptibility of the isolates was done by broth micro-dilution method and VITEK-2-system. Detection of antimicrobial resistance genes, MLST, virulence genes was carried out by PCR and whole genome sequencing. At NRAMRB, 475 Gram-negative organisms including *Escherichia coli*, *Klebsiella pneumoniae*, Salmonella spp, Shigella spp, Non Typhoidal Salmonellae, *Pseudomonas aeruginosa*, and *Acinetobacter baumannii* are currently available. Gram-negative strains showed high resistance against different antibiotics including carbapenem although colistin resistance was low. SHV and CTX-M-Group-1 were predominant ESBLs whereas ArmA was predominant 16S rRNA methylase. qnrB, qnrS and aac(6')-Ib-cr were detected as plasmid-mediated fluoroquinolone resistance genes and oqxA, oqxB & qepA were detected as efflux-mediated fluoroquinolone resistance genes. Among the AmpC β-lactamases, CIT and DHA were predominant. NDM-1 was the predominant carbapenemase followed by KPC and OXA-48. The strains were diverse as detected by REP PCR and WGS. Carbapenem-resistant isolates mostly belonged to the plasmid groups IncFIB, IncFIB-M, IncFIA, IncA/C, IncFIIK and IncFIB-KN. The most common virulence genes detected among *K. pneumoniae* were wabG, entB, uge, markD and fimH. However, 15% K. pneumoniae were hypervirulent. *E. coli* possessed virulence genes mostly fimH, cnf, iutA and traT. NRAMRB facility will preserve highly characterized AMR strains from different geographical regions of India and thus provide a useful platform to cater several advantages over time in connection with controlling AMR.

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Genetic exchanges in shigella phages shapes the dissemination of antibiotic resistant genes in environment

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The ability of bacteriophages to exchange genetic material are important factors in the evolution and pathogenicity of their hosts because they take up genes from other phage genomes and contribute genes to bacterial genomes as well. The primary aim was to identify the genetic exchanges occurring in the Shigella phage and associate them with the infecting host species and functions. We identified genetic exchanges between phages that are not related to one another through weighted gene repertoire relatedness (wGRR) calculation and link these transfers to the host species and lifestyles of the phages through the Louvain community clustering algorithm. Functional annotation of recent transferred genes and presence of AMR genes among transferred genes were detected through freely available software. Our results demonstrate that homologous phage pairs not only infect single host strain but also two different host species. Phage pairs with a single lifestyle were found to have a higher wGRR value than phage pairs with two distinct lifestyles. The genetic similarity network formed homogenous clusters with respect to their lifestyle but phages infecting different host strain were found to be dispersed between clusters. We found 441 recently transferred genes homologous genes between distant phages (wGRR<0.5) with high similarity (>80% identity) and 5535 ancestral genes with a minimal level of similarity (<35% identity). Those genes with extreme GC composition were found majorly to be recent horizontally transferred genes. We found that among the horizontally transferred genes, Shigella phage SfII and Sf6 contains PmrC gene which is responsible for multi-drug resistance in Shigella sp. and few other enteric pathogens. Genetic exchanges in Shigella bacteriophages is a contributing factor to the host expansion of bacteriophages along with the dissemination of antibiotic resistance genes in Shigella and other enteric bacteria.

AMRC/2024/A-25

New Delhi metallo-β-lactamase (NDM)-harbouring epidemic clone ST410 of *Escherichia coli* causing neonatal sepsis: antibiotic resistance and virulence over a decade

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Extraintestinal pathogenic *Escherichia coli* (ExPEC) is a major cause of neonatal sepsis. Presence of carbapenemases, particularly New Delhi metallo-β-lactamase (NDM) in ExPEC is a matter of concern as it confers resistance against all β-lactam antibiotics. Acquisition of virulence and resistance determinants promoted the emergence of specific *E. coli* lineages such as sequence type (ST)101, ST131, ST167 that have disseminated worldwide and are designated as epidemic clone. ST410 is also one such emerging epidemic clone, which is associated with high burden of antimicrobial resistance. In this study prevalence of ST410 in ExPEC causing neonatal sepsis were assessed for a period of ten years and their resistome and virulome were analysed. Bacterial isolates were collected from neonatal blood and identified as *E. coli*. Antibiotic susceptibility tests were carried out by disk diffusion and different resistance and virulence determinants were detected by PCR. Phylogroups and multi-locus sequence types (MLST) were determined. bla_{NDM}-possessing ST410 were further subjected to whole genome sequencing for comparative genome analysis. Seventy isolates were identified as *E. coli* collected from blood of septicaemic neonates during 2009-2020. Most of them were multidrug-resistant and distributed in different phylogroups such as, B2 (38%), A (21%), D (13%), B1 (13%), C (11%) and F (4%). MLST data revealed that 8.6% isolates belonged to ST410 (phylogroup C) and possessed a repertoire of virulence determinants (traT, fyuA, fimH, iucC, papACG, usp, iha $iron_{E.c}$, and afa). 4/6 ST410 isolates were resistant to meropenem and possessed blaNDM (bla_{NDM-1}, bla_{NDM-5}) along with other resistance determinants present in IncFIB, FII type plasmids. The genetic environment of blaNDM-1 and blaNDM-5 were similar i.e., intact/ truncated ISAba125 upstream and ble_{MBL} downstream. $blaNDM^{+ve}$ ST410 study isolates were close according to genome-based phylogeny but distant from globally reported ST410 isolates. The emerging ST410 in neonatal unit warrant stringent surveillance. In depth understanding of virulence and resistance in such epidemic clone is an effective means to rational treatment.

AMRC/2024/A-27

Potential use of small molecule sodium butyrate (SB) as an anti-virulence agent against *Vibrio cholerae*

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Vibrio cholerae, a comma-shaped, Gram-negative, facultative anaerobic bacterium causes severe food and waterborne diarrhoeal disease known as cholera. Current therapies for cholera involve oral rehydration therapy combined with the use of antibiotics to shorten the duration of the disease. However, overuse of antibiotics has led to the emergence of MDR bacterial strains resulting in prolonged hospitalizations and greater risk of death. Therefore, to overcome the increased global burden of antimicrobial resistance in enteric pathogens, using small bioactive compounds can be a new alternative approach. In this study, we investigated the potential effects of Sodium Butyrate on the virulence potential of *V. cholera*. Elucidation of possible mode of action of sodium butyrate in in-vitro conditions. Assessing the therapeutic potential of sodium butyrate in in-vivo conditions. The antibacterial effect of Sodium butyrate was determined by broth dilution method. Detection of Cholera toxin was done by GM1-CT ELISA. The fold change in RNA levels of virulence genes were checked by qRT-PCR followed by the western blot analysis. Promoter binding assays were performed to check ToxT binding to virulent factors. The production of cholera toxin was significantly repressed in a dose dependent manner in presence of Sodium butyrate as assessed by GM1-CT ELISA. The expression of *tcpA* and *ctxAB* were considerably attenuated in presence of 20 mM of sodium butyrate. Western blot analysis revealed significant decrease in TcpA levels. These findings indicate that SB possesses inhibitory activity against *V. cholerae* pathogenesis. Our experiments revealed that Sodium Butyrate acts as an inhibitor of cholera toxin production and thereby reduce pathogenesis. SB also reduce the expression of toxin related virulence genes. No substantial membrane damage of HT-29 cells was observed upon treatment with SB indicating that the compound is non-toxic in in vitro cellular conditions. Moreover, it acts as an anti-virulent therapeutic agent during infection in in vivo conditions.

AMRC/2024/A-28

Evaluating the efficacy of plant extracts from North-East India against multi-drug resistant sepsis-causing bacteria

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Sepsis, a potentially fatal disease, is caused by an unbalanced host response to infection. Because of its rising prevalence and significant pathophysiology, molecular, genetic, and clinical complexity, sepsis poses a significant burden to global healthcare system. In this context, the recent emergence of antimicrobial resistance further complicates the management of infections, leading to treatment failures and increased mortality rates. The current study is undertaken to investigate the potential inhibitory effects of herbal extracts against a panel of multi-drug resistant bacteria commonly responsible for causing sepsis. Extracts from various medicinal and aromatic plants (MAPs) belonging to the rich biodiversity of North-east India were meticulously collected and processed. A total of 16 plant extracts where systematically screened for their antibacterial activity by using standard Microtiter Broth Dilution method. Initial screening revealed 6 plant extracts exhibiting the most promising antibacterial activity against the test pathogens (namely *E. coli*, *Klebsiella pneumoniae*, *Acinetobacter baumannii*). Survival kinetics and live/dead assay were performed to check the antibacterial activities of a few potential plant extracts. These extracts were further subjected to LC-MS analysis to identify the bioactive molecules responsible for their inhibitory effects, providing valuable insights into the chemical composition of these natural compounds. To further understand the therapeutic potentials of the identified biomolecules, a bioinformatics analysis was conducted to explore their interactions with host proteins, specifically, drug-protein interaction networks were constructed to elucidate their underlying molecular mechanisms. The findings of the study contribute to our overall understanding of the antimicrobial properties of plant-derived compounds obtained from North-east India. The insights gained from this study have significant implications for the development of novel therapeutic strategies against sepsis-causing bacterium, addressing the global health threat posed by antibiotic resistance.

AMRC/2024/A-29

Emergence of SXT susceptible pattern among the southern region *Vibrio cholerae* strains and studying the virulence attributes of the recently circulating strains in India

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Vibrio cholerae is the causative agent of acute dehydrating diarrhoeal disease cholera. This study aimed to document an analysis of differential hypervirulent features of *Vibrio cholerae* O1 strains isolated during the period from 2022 to 2023 from the cholera endemic region in India. A total of 458 V. cholerae O1 clinical strains from different regions in India (West Bengal, Gujarat, Maharashtra, Karnataka and Kerela) were analysed. Biotypic and genotypic features was screened, biofilm-forming capability were also analysed, the Vibrio seventh pandemic island II (VSP II) genomic region was also screened and the AMR profile was done by disc diffusion method. All the strains belong to the Ogawa serotype, polymyxin B-sensitive, hemolytic and carried Haitian genetic alleles of ctxB, tcpA and rtxA. A differential pattern of susceptibility was observed among the southern region strains. The outcomes of this study led to a better understanding of the pathogenicity of recently circulating Vibrio cholerae strains. Routine surveillance is also needed for the AMR profile because our data suggests that the strains from the southern region have a susceptible pattern towards sxt and streptomycin but not the strains from the western and eastern regions. This event increases optimism that using old antibiotics will be effective if antibiotic use is controlled and simultaneous reconsideration of switching to old conventional therapy may be recommended in the future.

AMRC/2024/A-30

Molecular characterization of carbapenem and colistin resistant Enterobacter Cloacae Complex (ECC) isolated from blood of sepsis patients admitted in intensive care unit of Kolkata from 2017-2023

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In developing nations, Blood stream infections (BSI) can cause life-threatening bacterial sepsis. The majority of sepsis cases are caused by Multi-drug Resistant Gram-Negative Bacilli (GNB) and Enterobacter cloacae complex (ECC) is one of the notable pathogens. Sepsis treatment currently involves carbapenems and Colistin, however, the emerging resistance towards them is a burden to public health. The present study investigated the prevalence, antimicrobial resistance (AMR) profiles, and molecular subtypes of ECC blood-borne strains resistant to carbapenems and/or colistin. A total of 96 carbapenem-resistant ECC (CR-ECC) isolates from blood of from sepsis patients admitted to ICU of eight different tertiary care hospitals in Kolkata from January 2017 to December 2023 were included. Antimicrobial susceptibility to carbapenems (Meropenem, Imipenem, Doripenem, Ertapenem) was assessed by disc diffusion, while colistin and carbapenem MICs were determined by broth-microdilution. The AMR genes were validated by PCR and sanger sequencing. MLST was performed to determine the Sequence Type. PFGE was used to determine bacterial clonal relatedness. AMR gene transferability and plasmid profiles were determined using liquid mating experiment. WGS analysis was done on Illumina Novaseq 6000 and Oxford Nanopore Minion platforms. Among the 96 CR-ECC study isolates, 84 (87.5%) were pan-resistant to 19 different antibiotics tested and additionally 31 (32.29%) were resistant to colistin. The most predominating carbapenem and colistin resistance genes in CR-ECC were blaNDM (n=75; 78.12%) and mcr-9 (n=5; 5.20%). Besides, the ESBL blaCTX-M-15 was found in 33.33%) isolates. Strikingly, two carbapenamase (blaNDM-5 and blaoxa-181) were co-transmissible via single IncC (117 kb) conjugative plasmid. The MLST analysis classified 96 isolates into 42 different ST, with seven (ST2011, ST2018, ST2055, ST2721, ST2722, ST2869, and ST 2951) being typed as novel. The dendrogram of CR-ECC (n=96) using PFGE showed vast diversity (30.4% similarity) among the circulating isolates. The high prevalence of carbapenemase (blaNDM), ESBL (blaCTX-M-15) and mcr-9 producing CR-ECC in Kolkata highlights the importance of antibiotic stewardship and hospital screening policies to curb antibiotic resistance.

AMRC/2024/A-32

Accelerated clarithromycin resistance profiling from *Helicobacter pylori* infected biopsies through two-step nested PCR validation

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The eradication of *Helicobacter pylori* stands as the most effective strategy for treating gastroduodenal diseases associated with *H. pylori* infection. Among the antibiotics employed for this purpose, Clarithromycin, a member of the macrolide family, remains pivotal. However, the increasing prevalence of clarithromycin-resistant *H. pylori* strains, primarily due to point mutations in the V region of the 23S rRNA, poses a significant challenge to effective treatment. Addressing this urgent concern, our study focuses on validating a newly developed two-step nested PCR approach to accelerated clarithromycin resistance profiling in *H. pylori* biopsies by conventional methods such as agar dilution method, transformation assay and Sanger-sequencing. Using template DNA from 50 *H. pylori* positive biopsy specimens by boiling template method, we evaluated the performance of our developed PCR. Then, the observations were compared to the "Gold standard" approach of phenotypic identification of the susceptible and resistant strains by agar dilution method in order to evaluate the sensitivity and specificity of this unique protocol. In addition to this, the 23S rRNA of 5 randomly chosen representative strains was sequenced to confirm the PCR-based identification. Finally, transformation assay was employed to further support our sequencing outcomes. Our developed PCR assay using DNA isolated from biopsy specimens detected point mutation in 23S rRNA gene in 9 (18%) of 50 biopsy tested. The agar dilution method showed that all these 9 strains were resistant to clarithromycin having MIC value > 0.5 µg/ml indicating the perfect match of the PCR based results along with 100% sensitivity and specificity. Additionally, the sequencing study also identified the A to G mutation at 2143 position in 23S rRNA gene of the resistant strains only. Transformation decodes this point mutation can be transferable to the next generation and supports the sequencing results. Validation of the two-step nested PCR using conventional methods accelerates the detection of A2143G point mutation conferring the clarithromycin resistance which in turn aids in avoiding blindly prescribing empirical treatment and in the selection of rightly effective antimicrobial agents which reduces the probability of treatment failure and cost of treatment.

AMRC/2024/A-33

Genomic analysis of Salmonella Kentucky ST198 resistant to ciprofloxacin and cefotaxime causing acute gastroenteritis among children in Kolkata, India

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Emergence of multi-drug resistant (MDR) non-typhoidal Salmonellae (NTS) poses significant burden in healthcare system, mostly affecting the developing countries. *S. kentucky* has been reported earlier from European, North American, African and Asian countries from agricultural products, foods and various animal species (livestock, pets and wildlife), but is rarely documented from clinical samples. In this study, we have focused on genomic analysis of MDR *S. kentucky* isolates from stool samples of children with acute gastroenteritis. Rectal swabs from children ≤ 5 years of age with acute gastroenteritis attending the OPD of Dr. B.C Roy Post Graduate Institute of Paediatric Sciences from 2017 to 2023 were collected and processed following standard microbiological protocols for NTS identification. The isolates were tested for antimicrobial susceptibility, AMR genes, plasmid profiles, and multi-locus sequence typing (MLST). Whole genome sequencing (WGS) (Illumina Novaseq 6000) was performed for four MDR *S. kentucky* isolates from India. A total of 76 (1.12 %) NTS isolates were recovered by screening 6732 rectal swabs from children with acute gastroenteritis. A total of 15 serovars were identified of which *S. typhimurium* was predominant (n = 22; 28.94 %) followed by *S. kentucky* (n = 11; 14.47 %). Resistance to ≥ 1 antimicrobials was found in 54% of NTS isolates, of which 28% were MDR. Among the serovars, MDR was predominantly observed in *S. kentucky* (n=10/11; 91%) with a high rate of resistance towards Ampicillin, Nalidixic acid, Ciprofloxacin (100% each), Tetracycline (91%), Streptomycin (45%), Cefotaxime, Ceftazidime, Ceftriaxone and aztreonam (36% each). Less resistance was seen in Gentamicin, azithromycin and cotrimoxazole (< 30%). WGS analysis of MDR *S. kentucky* revealed the presence of following AMR genes blaCTX-M-15, blaTEM-1, blaOXA-9, tetA, aadA1 and aadA2. Double mutation in gyrA (D87Y, S83F) and single mutation in parC (S80I) was responsible for ciprofloxacin resistance in this MDR isolates. A single plasmid of IncC type and sequence type 198 was found in all the isolates. Increasing AMR was observed against cephalosporins and fluoroquinolones which are the current drug of choice for infection control. The results indicate continuous monitoring of the AMR profiles of the resistant organisms to prevent further spread of AMR gene in other organisms.

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Challenges and catalysts to combat antimicrobial resistance by one health approach-A review

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Antimicrobial resistance is a priority problem, leading to 1.27 million and 4.95 million deaths directly and indirectly, respectively (WHO). There are several challenges and catalysts to combat the antimicrobial resistance problem. In this study we implement the One Health approach to find out the challenges and catalysts to fight antimicrobial resistance in human, animals and environment. The objective of the study is to implement the One Health approach to find out the challenges and catalysts to fight antimicrobial resistance in human, animals and environment. In this literature review, all the articles regarding barriers and facilitators of antimicrobial resistance in humans, animals and environment were included from two databases, Pubmed and Google Scholar. For hospital-based studies, the challenges in the developed countries are lack of key personnel, problematic data and information systems, inadequate financial resource etc. whereas insufficient human resources, lack of microbiology laboratory support and limited government support are the barriers observed in Low- and Middle-Income Countries (LMIC)s. The facilitators in the developed countries are adequate personnel and technology support, audit and feedback, use of real time alert and authorization before use of antimicrobial whereas availability of antibiotic guidelines, antibiotic stewardship program protocol and multidisciplinary committee, and prompt laboratory support are the catalytic factors observed in LMICs. In animal antibiotic resistance, education, proper diagnostics and collaborative attitude between farmers and veterinarians are supportive factors whereas lack of alternative treatments, long delays in diagnostic tests, and fear of economic consequences are the challenges observed. In environmental antimicrobial resistance, conventional water treatment was noted as a barrier, whereas nanotechnology-based antibiotic adsorption and degradation, microalgae-based technologies act as facilitators. The findings of this study will help to evaluate the challenges and catalysts to combat antimicrobial resistance.

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Panchavalkala marvel: tapping into the potential against resistant microbes: A comprehensive review

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In an era where the threat of drug-resistant pathogens looms large, the day-to-day evolution of drug-resistant pathogens represents a formidable challenge rendering many conventional antibiotics ineffective against a wide range of pathogens. This alarming trend jeopardizes our ability to treat common infections and possess a severe threat to public health worldwide. This aggravating problem coupled with the decline in the number of antibiotics being developed from the pharmaceutical industry has stimulated the search for alternative antibacterial agents. Also, WHO has drafted a strategy for the integration of TCMs into national healthcare systems, to provide a wider range of promotive, preventive, curative, and rehabilitative healthcare options that are safe, effective, and affordable to the population. Medicinal plants, with their long history of therapeutic use, offer a promising avenue in the quest for combating drug-resistant pathogens. Within this realm, Panchavalkala has emerged as a potential powerhouse, holding immense potential for the development of novel antibiotic. Panchavalkala, an Ayurvedic formulation which is composed of five plant barks, possesses a wide spectrum of bioactive compounds capable of combating pathogens in a manner distinct from conventional antibiotics. To elucidate the phytochemical composition of Panchavalkala and its therapeutic potential against AMR. A comprehensive review of the published scientific literature indexed in electronic databases such as PubMed, Scopus, and Web of Science was conducted to gather evidence supporting these mechanisms. Results: Studies have shown that its phytochemicals exhibit a broad spectrum of antimicrobial activity against both Gram-positive and Gram-negative bacteria. The scientific evidence supports the efficacy of Panchavalkala in inhibiting the growth of bacteria such as *Escherichia coli*, *Klebsiella pneumoniae*, and *Enterococcus faecalis* which are increasingly becoming resistant to multiple antibiotics. By targeting key virulence factors and metabolic pathways essential for bacterial survival, Panchavalkala's phytochemicals offer a promising therapeutic approach for managing and combating antimicrobial resistance.

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Bioremediation of fluoride: Current status & possible future in sustainable water treatment

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Fluoride anion naturally found in soil and water is highly harmful even in small amounts. It is one of the crucial issues that has to be addressed. Fluoride ion hurts living organisms by disrupting their natural chemical balance and important metabolic activities. Up to 1.5 mg/L amount of fluoride in drinking water is the permissible limit recommended by the World Health Organization. This study has explored the potential application of modern technology in fluoride bioremediation as a cost-effective and sustainable methodology. This review has been done based on facts and figures available from 152 research articles. Skeletal and dental fluorosis occur due to chronic consumption of fluoride-contaminated drinking water in which the concentration of fluoride exceeds 2.0 mg/L. Traditional methods of removing fluoride from the contaminated water are a slow, difficult and highly expensive method which makes it highly difficult to implement in the long run. We require an affordable solution. Bioremediation is one of the cost-effective and sustainable alternative solutions that can be applied for fluoride removal from contaminated water bodies. This process involved the use of bacteria, fungi, and algae to remove fluoride ions from water bodies and recover them. This review article has highlighted the present status and possible future of the application of fluoride bioremediation strategy for water treatment. Further research on the molecular mechanism of fluoride bioremediation will be beneficial to develop more effective strains for expected outcomes in dynamic environment settings.

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Capsaicin inhibits *Helicobacter pylori* infection by inducing autophagy

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Helicobacter pylori infection increases the risk of developing gastrointestinal disorders such as gastritis, gastric ulcers, and gastric cancer. Autophagy inhibition is a key strategy employed by the bacterium that destroys cellular homeostasis and promotes disease progression. Triple therapy, comprising amoxicillin, clarithromycin, and a proton pump inhibitor, represents the primary treatment regimen for *H. pylori* infection. However, the rising prevalence of antibiotic resistance in *H. pylori* poses a global concern. Herein, this study aims to explore the role of capsaicin in autophagy during *H. pylori* infection. A drug-protein interaction network was constructed using a bioinformatics approach to assess potential interactions between capsaicin and human autophagy-related proteins, which were mapped from the protein-protein interaction network. AGS cells (human gastric adenocarcinoma) were subjected to infection with the *H. pylori* 26695 strain, followed by treatment with capsaicin, alongside an uninfected control group. Western blot analysis was performed to check the expression of autophagy proteins. Immunofluorescence microscopy was studied to investigate the localization of LC3B and LAMP1 in AGS cells. Real-time PCR analysis quantified the expression of autophagy-related genes. Additionally, a CFU assay determined the intracellular bacterial load in both infected and capsaicin-treated infected cells. Among the 225 proteins associated with H. pylori infection, JUN, CEBP-β, and DAPK1—were linked with autophagy. Although no direct interaction occurred between capsaicin and autophagy proteins, secondary interactions via MAPK1/3 and TP53 were observed. Previous studies have shown *H. pylori* suppresses autophagy in the maturation stage via MAPK-ERK pathway activation and regulating its intracellular proliferation. This study reveals that capsaicin increases autophagic flux by promoting autolysosome formation while inhibiting Erk activation, thereby reducing intracellular *H. pylori* growth. Altogether, our results indicate that capsaicin enhances intracellular clearance of *H. pylori* by reducing phosphorylation of Erk 1/2 and increasing autophagic flux. Activation of autophagy by capsaicin will be a novel approach to reduce *H. pylori* burden and might address the problem of AMR in the near future.

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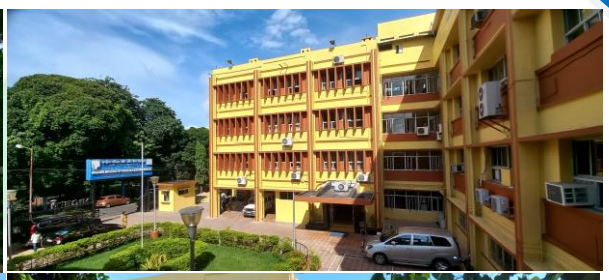
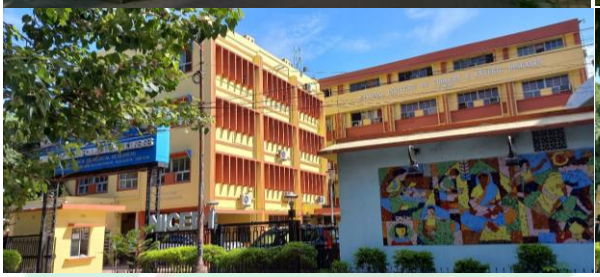


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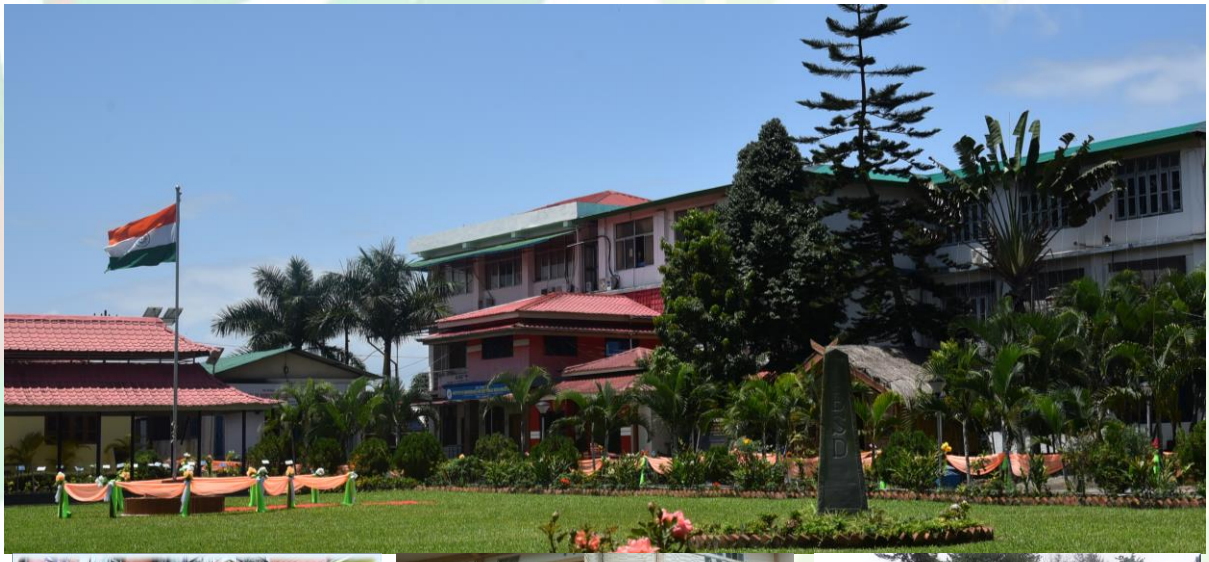


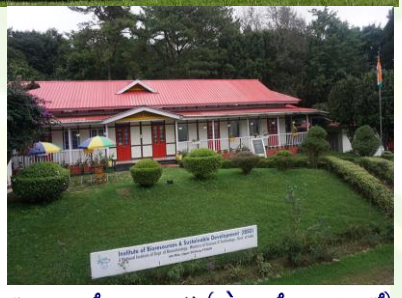

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