2023 ICCAR

INTERNATIONAL CONFERENCE ON CONTEMPORARY ANTIMICROBIAL RESEARCH

BOOK OF ABSTRACTS

16 - 18 NOVEMBER 2023

Shonbeel:
The second largest seasonal wetland in Asia and the largest wetland in Assam is a famous tourist spot to visit.

ORGANISED BY
ADVANCED LEVEL INSTITUTIONAL BIOTECH HUB, ASSAM UNIVERSITY, SILCHAR

IN ASSOCIATION WITH
SOCIETY FOR ANTIMICROBIAL RESEARCH (SAR),
DEPARTMENT OF MICROBIOLOGY, SILCHAR MEDICAL COLLEGE AND
TRIPURA UNIVERSITY, AGARTALA

IN COLLABORATION WITH
VIJNANA BHARATI
6TH WORLD CONGRESS ON DISASTER MANAGEMENT

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01 Oct 2023

Dear Prof RM Pant
Vice Chancellor, Assam University
Silchar

I am very happy to learn that the Biotech Hub of Assam University is organising an International Conference on Contemporary Antimicrobial Research in mid-November 2023 at Silchar.

This initiative would be a significant stride in keeping with the sustainable goals of G-20 Declaration and GOI "Mission Antimicrobial Resistance".

There is a need for our young & talented researchers to focus on the vital issue of Antimicrobial Resistance for the well-being of entire humanity. I am certain that the Conference would be successful in highlighting not only the challenges but also scientific research required to confront them effectively.

I convey my appreciation to Assam University, Silchar for this endeavour and wish the event great success.

Yours sincerely

Raha

प्रोफेसर राजीव मोहन पंत
कुलपति
Prof. Rajive Mohan Pant
Vice-Chancellor

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सिलचर 788011 असम, भारत
ASSAM UNIVERSITY
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Silchar 788011, Assam, India

Date: 06-11-2023

MESSAGE

I am pleased to know that Assam University Biotech Hub is organizing 4th International Conference on Contemporary Antimicrobial Research from 16-18 November 2023 at Assam University. The conference is being organized in association with Society for Antimicrobial Research and in collaboration with Silchar Medical College and Vijnana Bharati.

I am delighted to mention here that Antimicrobial Resistance (AMR) is one of the focused areas of G20 and Govt of India has adopted MISSION AMR to combat the situation of infectious diseases arising out of Antimicrobial Resistance and initiatives of Assam University Biotech Hub is aligning to the National Mission of the country.

It is my firm belief that the conference will boost the minds of the researchers who are involved in the subject matter and will illuminate enough light for finding out suitable solution to this particular health hazard.

I welcome all National and International delegates who will be joining this conference from different parts of the world.

I congratulate the team Biotech Hub of Assam University for taking such an initiative which has been complementing the mission of Govt of India.

Vice Chancellor

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WELCOME ADDRESS

Distinguished Chief Guest of this Inaugural Session Prof. G.D Sharma , President , Association of Indian Universities, our all Guests of Honour, all distinguished invitees, all our international delegates, members of Society for Antimicrobial Research, Principal, Silchar Medical College-our collaborator Institute, Director, NIT, Silchar, Former Director, NIT Sri Nagar Prof. Rajat Gupta, Representatives from Industry and Investor Companies, Representatives and Guest of 6th World Congress on Disaster Management, Representatives from CDC India and ICMR President, North East Science Movement-the North East Initiative of Vijnana Bharati, All our invited speakers, all the young scientists, Hon'ble Vice Chancellor of Assam University, Prof. Rajive Mohan Pant -Chief Patron of this Conference, Registrar of Assam University-the Patron of tis conference, representatives of Teaching and Non-Teaching Association of Assam University, representatives from Assam University, Diphu Campus, Head of Different departments, Dean of different schools of Assam University, Principals of affiliated colleges, Media representatives, ladies and Gentleman, A very Hearty welcome to you all in this 4th International Conference on Contemporary Antimicrobial Research (ICCAR-2023).

I am delighted to inform you that Assam University Biotech Hub which is a DBT Govt of India funded Research Centre under the Hargovind Khorana School of Life Sciences is organizing this 4thInternational Conference on Contemporary Antimicrobial Research (ICCAR-2023) from 16-18 November 2023. This conference has been organized in association with Society for Antimicrobial Research. Department of Microbiology, Tripura University, Department of Microbiology Silchar Medical College, Vijnana Bharati and 6th World Congress on Disaster Management are our collaborators.

I may be allowed to let you know that Govt of India has prioritised Antimicrobial Resistance (AMR) in National Health Policy in 2017 and in the same year Mission AMR was launched by DBT, Govt. of India. In recent G20 New Delhi Leaders' declaration, tackling of AMR was identified as a priority and sustainable goal and as such our initiative for this conference is complementing the mission of Govt of India.

The initiative regarding organization of International Conference on Contemporary Antimicrobial Research (ICCAR) was taken by Assam University Biotech Hub in 2016 when first conference was held and a society in the name and style Society for Antimicrobial Research (SAR) was formed in first conference. It was decided that under the initiative of SAR every two years an International Conference on Contemporary Antimicrobial Research (ICCAR) will be organized in different parts of the country by different member institutes. Accordingly the 2ndInternational Conference on Contemporary Antimicrobial Research (ICCAR) was organized by IIT Kharagpur in 2018. The 3rd International Conference on Contemporary Antimicrobial Research (ICCAR) was organized by Acharia Institute at Bengaluru in 2021 and we are organizing the 4th one again in 2023.

Proposed 5th International Conference on Contemporary Antimicrobial Research (ICCAR) is likely to be held in NEHU, Shillong. Among other member institutes of SAR we have VIT,

Vellore, BHU, North Bengal University, Acharia Institute Bengaluru, Tripura University, Silchar Medical College and many others.

It's my pleasure to mention here that one year before announcement of Mission AMR by Govt of India, Assam University Biotech Hub initiated this Nation-wide movement involving a number of reputed institutes of the country to combat the situation of Antimicrobial Resistance (AMR).

It has been predicted that the next pandemic after COVID-19 will be from infectious diseases due to AMR. We need to be therefore all ready to face the situation with all our newer strategies and this conference will be able to extend significant help in that direction we believe.

We firmly believe that a little motivation from different corners of the society will help us to make this movement more intensive as tackling AMR is not the cup of tea of scientists alone. Social Scientists/ Social workers have to come forward, Media has to come forward to achieve the set goal. We accordingly have accommodated a good number of thought provoking talks from societal perspectives in the technical session of the conference. Also we have collaborated with World Congress on Disaster Management for making the society involved at a large scale in achieving our mission considering AMR as health disaster and as a silent pandemic and Pre Conference session of 6th World Congress on Disaster Management will be held here jointly with ICCAR- 2023 on 18th November where we will jointly discuss about how to disseminate the message of this conference to a greater perspectives intensifying our scientific and social movement against AMR.

Silchar, being a very small city has infrastructural limitation for arranging mega events like International conferences. Our humble request to all our guests to bear with us if there is any uncomfortable situation because of infrastructural issues.

In this conference we have invited speakers and oral/poster presenters from all the North Eastern States, from Delhi, West Bengal, Tamilnadu, Uttarakhand, Odissa and many other states. We have our International delegates mainly from Europe and Bangladesh. I extend a very hearty welcome to all of them.

Once again welcome to one and all present over here at this moment.

(Prof. M. Dutta Choudhury)
Organizing Chair
ICCAR-2023

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INVITED TALK

Antimicrobial Stewardship

Prof. Debadatta Dhar Chanda

Silchar Medical College and Hospital, Silchar

Antimicrobial resistance is a global public health threat. Although antibiotics have transformed the practice of medicine, making once lethal infections readily treatable and making other medical advances, like cancer chemotherapy and organ transplants, possible and prompt initiation of antibiotics to treat infections reduces morbidity and save lives, for example, The Centre for Disease Control (CDC) reports that at least 30% of prescribed antimicrobials in the outpatient setting are considered inappropriate. Inappropriate antimicrobial use and misuse is associated with the emergence of resistance and is considered as a most serious threat to public health The scale of the AMR threat is such that no country is free from its health and socioeconomic impacts: efforts to tackle the problem requires collaboration across national and continental boundaries. Antimicrobial resistance occurs when microbes become resistant to medicines to which they were initially susceptible. The development of drug-resistance occurs in many microbes causing a growing concern of wide variety of morbidities including common infections such as pneumonia, urinary tract infections, human immunodeficiency virus, tuberculosis and malaria. One major global driver for the development of AMR is the misuse or overuse of antimicrobials. A variety of factors can result in the misuse or overuse of antimicrobials in health care settings including: a lack of knowledge or up-to-date information on prescription of antimicrobials, lack
of treatment guidelines, lack of laboratory capacity to identify the organism and its antimicrobial susceptibility, unreliable or absent surveillance data on AMR and antimicrobial usage, unregulated over-the-counter use and poor antimicrobial stewardship (AMS). In addition, patient and public expectation and pressure to prescribe antibiotics, or situations that allow for financial benefit from the supply of medicines, can also drive inappropriate antimicrobial prescribing. Inadequate adherence to infection prevention and control (IPC) measures in health care facilities and poor hygiene and sanitation in communities exacerbate the spread of infections and increase the use of antimicrobial agents. This situation is made worse in many settings around the world by gaps that are known to still exist in knowledge and awareness of AMR, as well as the availability of quality teaching resources to address education in AMR.

Measures to tackle these challenges (including through collaboration of various stakeholders) are required to avert the growth of resistance, particularly in resource-constrained settings. If not appropriately addressed, common infections, minor injuries and routine elective surgery could be associated with life-threatening risk. The WHO Global Action Plan on Antimicrobial Resistance (GAP-AMR) sets out five main objectives to address the challenge of AMR. The domains of the WHO AMR competency framework are as follows:

A. Foundations that build knowledge and awareness of antimicrobial resistance
B. Appropriate use of antimicrobial agents
C. Infection prevention and control
D. Diagnostic stewardship and surveillance
E. Ethics, leadership, communication and governance.

The Global Strategy on Human Resources for Health: Workforce 2030 complements the GAP-AMR by offering policy guidance options on
broader policies and approaches to optimize health worker education and training. WHO plays a crucial role in collating and making available AMR education and training resources

to support educators, decision-makers and health policy planners to implement effective policies to control the emergence and spread of AMR.

To restrict the misuse or unnecessary antibiotic prescription, the Policy Statement on Antimicrobial Stewardship by Society for Healthcare Epidemiology of America (SHEA), the Infectious Diseases Society of America (IDSA), and the Paediatric Infectious Diseases Society (PIDS) strongly encourages healthcare institutions to develop stewardship programs

Antimicrobial stewardship is defined as a set of coherent actions aimed at promoting responsible antimicrobial use. It includes the following components:

a) Improving the diagnostic process (clinically, microbiologically or in other ways) as an inherent part of any AMS programme.
b) Prescribing appropriately according to treatment guidelines once there is a suspected or proven diagnosis.
c) Deploying strategies that cut across all levels (national, district, local) to promote responsible antimicrobial use.

Diagnostic stewardship is also integral to AMS as an overarching concept. Good diagnostic stewardship is essential for the generation of AMR data from the laboratory. These data, including patient meta-data and outcome data, contribute to accurate and reliable surveillance of AMR and provide valuable information on the burden of disease due to AMR, hence the association of diagnostic stewardship with surveillance. Noting the essentials of AMS, educators and instructors should aim to ensure, as a minimum, that the key principles are covered and emphasized in teaching pre-service and in-service students and that they are implemented in practice.

In India, there was no official body involved to supervise and standardise AMSP, and AMS teams are formed at the discretion of the hospital or medical institution. Nevertheless, we see a growing initiative taken by the Indian government in the form of the 2011 Jaipur Declaration, The 2013 Chennai Declaration and the NCDCs National Treatment Guidelines for Antimicrobial Use in Infectious Diseases.

The Indian Council of Medical Research (ICMR) New Delhi, India has developed AMSP guidelines where they have mentioned that ‘National Health Policy’ (2017), addresses antimicrobial resistance as one of the key issues and prioritizes development of guidelines. Unfortunately, most of hospitals in India lack structure and process of AMSP. Recognizing the importance to create AMSP structures in health care institutions in the country, ICMR has initiated activities by developing AMSP curriculum, conducting workshops and developing AMSP research projects.

In 2022, NCDC has initiated NAP-AMR involving medical colleges from different regions of India which is currently going on.

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INVITED TALK

Challenges in control of Carbapenem-resistant Enterobacterales (CRE) in Low-Middle-Income Countries (LMIC)

Dr Tuhina Banerjee, Professor, Department of Microbiology, Institute of Medical Sciences, Banaras Hindu University, Varanasi-221005

The increasing burden of antimicrobial resistance (AMR) has become an impending crisis, strengthened by the global dissemination of Carbapenem-resistant Enterobacterales (CRE) over the two decades. Unfortunately, AMR is higher in lower-middle-income countries (LMIC), superimposed with lack of basic amenities in these countries to tackle the problem. An estimated data of approximately 140000 healthcare associated infections (HAI) are reportedly caused by Enterobacterales annually as per reports from the developed nations, of which nearly 6.64% are due to CRE. Similar data from developing countries is not available, though there have been reports of their endemicity in the LMIC. Among the major barriers for AMR surveillance for CRE, inadequate laboratory facilities, shortage of trained manpower, lack of resources and data management systems are often implicated. At the same time, it should be realized that indiscriminate carbapenem use itself is the most important risk factor for CRE. Epidemiological studies have revealed a direct relation between antibiotic consumption, emergence and spread of AMR. With high burden of the ever-growing population in most of the LMIC, simultaneous burden of infectious diseases and increased demand for production of agricultural and industrial products also encourages overuse of carbapenems. Another unique challenge in this aspect is the variation in distribution of dominant types of carbapenemases based on geographical location. While metallo-beta-lactamases (MBLs) are the most common carbapenemases in Southeast Asia, serine carbapenemases are common in rest of the world. MBLs are present in minority in the US, where it accounts for less than 5% of the carbapenemase producers. In the same context, New Delhi metallo-beta-lactamase (NDM) enzymes were initially confined to Indian subcontinent until it became widespread. Similarly, OXA-48 represents one of the most common CRE enzyme. It is imperative to know the molecular epidemiology of CRE because the recently approved beta lactamase/ beta lactamase inhibitor combination like ceftazidime-avibactam, meropenem-vaborbactam, ceftolozane-tazobactam and imipenem-relebactam are not effective against MBLs. Additionally, a very pertinent issue is that most of the broad spectrum antibiotics are unavailable in LMIC. With severe limitation of resources and a bagful of challenges, no single solution can work for control of CRE in LMIC. However, prioritizing multimodal effective strategies based on local epidemiology could halt the emergence when implemented appropriately.

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INVITED TALK

NEWER ALTERNATIVES TO ANTIMICROBIALS

Dr. Ajanta Sharma MD, PhD
Professor and Head
Department of Microbiology
Gauhati Medical College & Hospital, Guwahati Assam

Antimicrobial resistance (AMR) is indeed a significant global health concern. Currently, antibiotic resistance (AMR) causes 700,000 patient deaths worldwide each year. By 2050, it is predicted that there would be 10 million deaths worldwide. The development of MDR, XDR, and PDR bacteria has put antibiotics' role in the success of medicine in jeopardy. We can evidence that hardly few newer antimicrobials being discovered following the golden age of antibiotics (1940s to 1960s). The ongoing battle against AMR necessitates the development of novel antimicrobials. When taken together, the data and facts highlight a crucial query: is the use of antibiotics coming to an end? Despite the fact that antibiotics have saved countless lives over the past 70 years or more, the rapid evolution of bacteria and AMR has made alternative solutions necessary.

The current WHO clinical antibacterial pipeline contains 43 antibiotics and combinations with a new therapeutic entity + 27 non-traditional antibacterial agents. WHO's Annual Antibacterial Pipeline Report of 2020 reveals a near static pipeline with only few antibiotics being approved by regulatory agencies. The report says, ***"overall, the clinical pipeline and recently approved antibiotics are insufficient to tackle the challenge of increasing emergence and spread of antimicrobial resistance"***.

Alternatives to Antibiotics are broadly defined as "any substance that can be substituted for therapeutic drugs that are increasingly becoming ineffective against pathogenic bacteria due to antimicrobial resistance" or "Non-compound (i.e. non-classic antibacterial compounds) approaches that target bacteria or approaches that target the host to treat bacterial infection".

Various novel approaches used as alternative to antimicrobials and hold promise includes a) Naturally occurring alternatives, b) Synthetically designed strategies and c) Biotechnology based alternatives and d) Nanotechnology based alternatives.

a) Naturally occurring alternatives:

- Bacteriophage therapy
- Antimicrobial peptides (AMPs)
- Bacteriocins
- Alteration of gut microbiota (Probiotics, Faecal Transplant Therapy)
- Predatory bacteria
- Antibodies

b) Synthetically designed strategies:

- Synthetic mimics of Antimicrobial Peptides (SMAMPs)
- Innate Defence Regulatory Peptides (IDRP)
- Antibacterial oligonucleotides
- Inhibitors of bacterial virulence

c) Biotechnology based alternatives:

- Genetically modified Bacteriophage therapy
- Lysins (Endolysins, Exolysins, Autolysins)
- CRISPR Cas 9
- Antibiotic inactivators

d) Nanotechnology based approaches:

- Inorganic nanoparticles (Titanium oxide, Silver, Copper oxide, Iron oxide, Magnesium oxide, Nitric oxide, Polyethylenimine and quaternary ammonium compounds etc)

- Organic nanoparticles ((Poly-ε-lysine, Quaternary Ammonium Compounds, Cationic Quaternary Polyelectrolytes, Benzoic Acid, Phenol, and p-Hydroxy Benzoate Esters, Peptides, Polymeric Nanosized Antimicrobials, Organometallic Polymers, Polycationic Nanoparticles etc).

Numerous alternatives have been developed; some are still at the experimental stage while others have advanced. For combating emerging resistant bacteria, the field in alternatives to antimicrobials is still emerging. Approval of bacteriophages as alternatives to antimicrobials for treatment and prophylaxis of infections exhibits potential for use. But it also has limitations as due to lack of rapid diagnostic platforms, a cocktail of multiple bacteriophages needs to be used. Also, bacteria can evolve to resist the phage. Despite receiving a lot of attention, AMPS has fallen short of expectations. Antibodies have been approved but their extensive use is limited by the cost and limited shelf life. Moreover, most of the alternative approaches are strain or species-specific, hence, multiple therapeutics would be needed for treatment of different infections. Hence, the subject is still in its infancy and needs further studies to produce anti-infectives of the next generation.

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INVITED TALK

Endophytes from the Tree of the 21st Century: A Potential Hidden Treasure for Antimicrobials

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Microorganisms living inside plants without causing harmful effects to the plant are called endophytes. The United Nation has declared *Azadirachta indica* (Neem) as the tree of the 21st century due to its many medicinal properties. Now it is the time to think whether these properties are of plant itself or its endophytes because endophytes produce the same or similar metabolites of the plant. Hundreds of endophytic fungi of more than 30 genera are reported from roots, fruits, leaves, stems and bulk of *A. indica*. They produce metabolites having antioxidant activities, and microbicidal, parasiticidal, nematicidal and insecticidal activities. Therefore, endophytes might be a hidden treasure for antimicrobial compounds. In our study, 17 endophytic fungal isolates (EFI) of 8 different genera from leaves, fruits and stems of *A. indica* were identified based on the complete sequences of the internal transcribed spacer 1 (ITS1), 5.8S ribosomal DNA (rDNA) and ITS2, and the partial sequences of large subunit of the fungal rDNA. The extracellular metabolites (EM) produced by axenic and co-culturing of the EFI at optimized temperature showed strong antimicrobial activity against multidrug-resistant bacterial and fungal superbugs, which were resistant to commercially available antibiotics. In addition, the EM from several EFI inhibited the growth of devastating phytopathogenic fungi *Fusarium* spp, *Phytopythium helicoids* and *Colletotrichum falcatum* isolated from diseased tomatoes, potatoes and sugarcane, respectively. Two EFI produced both peptide and non-peptide antimicrobial EM stabled at room temperature. The minimum inhibitory and microbicidal concentrations of the EM against clinical superbugs and phytopathogens were 0.125 to 1.0 µg/µL and 0.5 to 4.0 µg/µL, respectively. Whole genome sequencing and metabolic pathways analysis of one EFI identified as *Tricoderma* as well as the GC-MS analysis of its EM revealed the presence of novel antimicrobials biosynthesis. Therefore, the endophytes from *A. indica* are potential treasure for novel antimicrobials against clinical superbugs and phytopathogenic fungi.

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INVITED TALK

Antibiotic resistance in E. coli in different nations and the link in different locations between resistance and virulence

Dr. Mark Toleman
Cardiff University, UK

The last 30 years has seen enormous changes in our understanding of health and disease. This is especially due to the ease of genomic sequencing which has revealed a wealth of information regarding both antibiotic resistance and virulence in common human pathogens. Antibiotic resistance and virulence in *E. coli* is especially important because it is universally carried by all humans and is easily transmitted between individuals via the fecal-oral route. It is the cause of 80% of urinary tract infections and the main cause of bacteraemia's in many nations. The sequencing era has enabled us to easily separate individual strains of *E. coli* and compare common strains in different geographical locations. We now know that there are >10,000 different strains yet most people carry only a single strain. Interestingly, only a minority of these strains 6/10,000 are responsible for >60% of all serious (blood-stream) infections. Studies of *E. coli* strains in different nations have revealed interesting differences between strains carried in the western world compared to South Asia. The work has revealed that the western world has an epidemic of carriage of virulent *E. coli* strains causing *E. coli* sepsis rates to double over the last decade. However, carriage of virulent *E. coli* strains in the community is extremely low across South Asia. Conversely, South Asia has an epidemic of increasingly antibiotic-resistant *E. coli* strains which are not commonly carried in the western world. These observations are key to understanding the reasons behind the differences and will likely lead to intervention strategies to solve both of our problems.

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INVITED TALK

Microbial diversity dynamics of ice core samples of two Glaciers of Sikkim Himalayas—an evaluation of their Antibiotic-Resistance patterns and Xenobiotic potential

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Abstract

The massive ice masses worldwide consist of glaciers, ice shelves, ice sheets, and ice caps. Glaciers cover a substantial portion of the world and are home to biological populations that interact and feedback differently with their physical and chemical surroundings. Nearly ~15% of the Himalayas are covered by Glaciers and as located outside poles are regarded as the third pole on Earth. There are around 84 Glaciers in the Teesta basin (Sikkim Himalayas). However, in the recent century, climate change has accelerated and reached unprecedented levels and has affected the Himalayan Glaciers significantly. Concerning the effect of climate change, the studies on Glacier ecosystems have increased rapidly. However, very less is known about the Glaciers of the Sikkim Himalayas regarding their microbiological studies, Physicochemical parameters, and various hazards related to their retreat and industrial applications. Thus, the present study aimed to evaluate the above-mentioned aspects through High throughput sequencing technologies of two Glaciers of the Sikkim Himalayas viz Frey-Peak and Rathong Glacier. The microbial diversity analysis shows the prevalence of phyla Proteobacteria, Actinobacteria, Firmicutes, and Bacteroidetes. Elemental concentrations were less as compared to other ecosystems. There was a strong positive correlation between various elements and phyla as shown by Principle component analysis. The random forest model for variable importance also shows the significant contribution of various elements such as Na, Mg, K, Ca, and Zn towards the alpha diversity of the studied Glaciers. Among physical parameters pH was found to be contributing highest in shaping bacterial diversity. The other facet of this study was to evaluate the antibiotic-resistance patterns among these Glacier habitats. The present study shows the presence of various antibiotic-resistant genes corresponding to different classes of antibiotics such as Aminoglycoside, Tetracycline, Fluoroquinolone, Macrolide, and Elfamycin. Various pathogenic bacteria such as

Staphylococcus, Pseudomonas, Corynebacterium, Clostridium, Serratia, etc. were also found in this study. Statistical analysis shows a strong correlation between various antibiotic resistance classes, various elements, and different phyla. Network analysis shows that the antibiotic-resistant genes mainly interact with phyla Proteobacteria, Firmicutes, and Actinobacteria. Various studies have revealed the bioremediation potential among Psychrophilic microbes in Glacier ecosystems. Thus, we also evaluated the biodegradation potential in the studied Glaciers and it was found that many biodegrading genes and related pathways are present. The most abundant genes corresponding to different xenobiotic classes were Benzoate degradation, Chlorocyclohexane and chlorobenzene degradation, Aminobenzoate degradation, Nitrotoluene degradation, Atrazine degradation, Drug metabolism, Caprolactam degradation, Xylene degradation, etc. As this study was ice-core-based, the present findings highlighted many queries. The presence of mesophilic bacteria in the studied Glaciers may support the notion about the retreat of these Glaciers is due to climate change as suggested by other studies also. Antibiotic resistance may be occurred due to anthropogenic factors such as industrialization and urbanization in local geographical areas. This may also lead to the acquisition of local anthropogenic pollutants carried by the wind. Hence, the biodegradable potential of these habitats is prevalent. It is quite concerning that the Glaciers are being negatively impacted by the alarming global climate change. The melting of glaciers, which is the greatest effect of climate change, might release contaminants, antibiotic-resistant genes, and pathogenic bacteria into the water supply (perhaps endangering human health). Thus, a vigilant analysis of this subject is necessary and steps must be taken to confront this havoc.

Keywords: Glaciers, Psychrophiles, Antibiotic-Resistance, Xenobiotics, Metagenomics, Sikkim Himalayas

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INVITED TALK

A unique autochthonous *Shigella dysenteriae* strain isolated from the gut of a facultatively air-breathing fish, *Lepidocephalichthys guntea*, with all antibiotic resistance, heavy metal resistance, and a Type II secretion system, may operate as a barrier against infection by other enteropathogens.

Ranadhir Chakraborty#, Chandana Basak

#, Department of Biotechnology, University of North Bengal, P.O. NBU, Siliguri- 734013, West Bengal, India

Lepidocephalichthys guntea, a bottom-dwelling fish that thrives in stagnant, unclean water and is omnivorous, scavenger, detritus feeder, and a micropredator by habitat of feeding, is frequently exposed to levels of heavy metals and metalloids that exceed permissible limits, antibiotic residues, and a number of xenobiotic substances. It can survive in muddy, heated river water with little dissolved oxygen or at a dried-up water body due to alternate breathing through the intestine. The anterior and middle intestines of this fish are utilised for food digestion and assimilation, whereas the uncoiled gut is employed for air breathing. However, the posterior intestine has a radically different architectural layout, with blood capillaries punctured between columnar epithelial cells and a smaller absorptive surface than the rest of the gut. Due to these traits, we looked into the main bacteria that have colonised its gastrointestinal tract while keeping in mind that the natural environment is the main influencing factor. In both normoxic and hypoxic environments, *L. guntea*'s anterior and posterior guts were examined using high-throughput sequencing. According to correlation network research, normoxia led to the development of a more complex and interacting network, whereas hypoxia resulted in the involvement of fewer genera. Functional analysis showed that all other metabolic pathways were active in both situations, albeit with less hits in hypoxia, but only the fatty acid biosynthesis route was activated. Comparative investigations of the variety of gut bacteria revealed that, at different taxonomic levels, hypoxia caused more pronounced changes in the posterior gut bacteria than the anterior gut. As a consequence of hypoxia, several pathogen populations like *Aeromonas*, *Pseudomonas*, *Plesiomonas*, *Acinetobacter*, and *Enterobacter* were replaced by potential opportunistic pathogens like *Streptococcus*, *Escherichia-Shigella*, *Janthinobacterium*, and *Clostridia.* A surge in probiotic genera, including *Bifidobacterium, Lactobacillus*, *Blautia*, and *Cetobacterium,* was also seen along with the shift in the population of pathogenic bacteria. Side-by-side, we found that genes for antibiotic resistance and toxic metal/metalloid resistance are increasingly being found in freshwater environments. Hence, to corroborate

culture-independent data, we attempted to research the culturable core-intestinal bacteria in *L. guntea* because fish are both direct witnesses to and victims of the pollution that the host's extraordinarily mobile resistant microbiome causes. A novel *Shigella* strain may have evolved that outperformed the other environmental bacterial taxa in the intestinal environment, as evidenced by the higher percentage of *Shigella* in the fish intestines, which may have either been selected by the fish particularly from the habitat water. There has been a report of the first fully described Type II secretion system (T2SS) from a *Shigella* strain. This newly identified *Shigella* strain most likely acquired T2SS during the growth phase from an *Escherichia* strain. Numerous antibiotic resistance genes, heavy metal and metalloid resistance genes (ARGs), high pathogenicity islands, various insertion elements, transposons, and type I-E CRISPR-Cas systems have all helped this strain colonise the intestine of *L. guntea*.

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INVITED TALK

The role of Rapid Diagnostics in the Fight against Antimicrobial Resistance

Till T. Bachmann
On behalf of the DOSA Consortium[1]

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Antimicrobial Resistance (AMR) is a multi-faceted One Health problem spanning the human, animal, plant and environmental domains. Improved diagnostics are required to make better decisions affecting health and antibiotic use. The talk will provide insights in trends and drivers of diagnostics development, uptake and impact. As a successful example, we have taken a user driven approach in the DOSA Project to improved design and uptake of diagnostic solutions in the community which address challenges in the dairy sector, aquaculture and human health.

1 - https://dosa-diagnostics.org/

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INVITED TALK

Point of care diagnostics solutions for Human and Dairy settings

Ravikrishnan Elangovan, Professor,

Department of Biochemical Engineering and Biotechnology, IIT Delhi

Bacterial infections continue to be a major cause of deaths globally, particularly in resource-poor settings. The mortality and morbidity is mainly caused due to the empirical nature of treatment given to patients in the absence of early and low-cost diagnostic techniques. We are developing deployable diagnostics solutions based on microscopy. Tuberculosis (TB) is a major healthcare burden for developing countries. Microscopy-based tuberculosis (TB) diagnosis (Ziehl-Neelsen) screening still remains the primary diagnostic method in resource-limited countries. One of the major challenges with the present sputum smear microscopy is its low sensitivity (~60%) due to the requirement of a highly trained technician for manual cell identification and counting. To overcome this challenge, we have developed a novel, compact fluorescence microscopy device (iSeeTB) for automated cell counting of Mycobacterium tuberculosis (MTB) in sputum smear samples. The device aims to increase the sensitivity of MTB cell identification and to decrease the time for image processing in a sputum smear microscopy hence aiding in faster diagnosis. The iSeeTB consists of a fluorescent microscope integrated with the AI-based software to screen the sputum smear sample. It has a magnification of 40X, an optical resolution of 2058 X 2100 pixels, and can process more than 200 fields at a time. Along with this, I will be presenting a portable fluorescent reader for Mastitis diagnosis at the farm level.

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INVITED TALK

Prevalence of multidrug resistance in Enterobacteriaceae isolates and identification of plant-based efflux pump inhibitor of MDR *Shigella* spp.

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Abstract

Background: Increasing antimicrobial resistance in Enterobacteriaceae is one of the greatest threats to public health at present which needs integrated urgent action. This study aims to investigate the prevalence of multidrug-resistant (MDR) Enterobacteriaceae members in various clinical settings of Assam and to identify the plant-based remedies for efflux pump-mediated antibiotic resistance in *Shigella* spp.

Materials and Methods: In this, a total of 643 bacterial isolates were collected from different hospitals and primary health care centres of Assam during the period of 2016-2021 under a DBT, Govt. of India funded project (ethical clearance no. DU/Dib/ECBHR (Human)/2021-22/02). The isolates were identified through biochemical characterization and the antibiotic susceptibility pattern was evaluated. The MDR *Shigella* isolates were tested further for efflux pump over-expression using the Ethidium Bromide (EtBr) agar cartwheel method. To identify a potent efflux pump inhibitor against the efflux pump of *Shigella* spp., the antibacterial activity of some selected plant extracts was tested followed by confirmation through molecular docking and molecular dynamic simulation studies.

Result and Discussion: In our study, A total of 312 Enterobacteriaceae isolates were obtained from 208 clinical samples. The majority of the bacterial strains were recovered from urine (62%), followed by sputum (15%), 82 blood (7%), wound swab (6%), pus (3%), throat swab (2%), stool (2%) and other sources (3%). Among these 312 isolates, 43% were *E. coli*, 23% were *K. pneumoniae*, 12% *A. baumannii*, 8% *P. aeruginosa*, 4.5% *Shigella* spp. 2.7% *were Enterobacter* spp., 1.8% were *Salmonella* spp. and the rest were *Proteus* spp. Of the total isolates considered for the study, 67.6% (n=210) of the isolates were reported to be MDR. Among the MDR phenotypes prevalence was found to be higher within *E. coli* (n=114, 54.28%), followed by 64 *Klebsiella spp*. (30.47%). Resistance was highest against

94 amoxicillin/clavulanic acid (65.4%), followed by third-generation cephalosporins-ceftriaxone 95 (62.2%), ceftazidime (60.6%) and cefotaxime (51.6%). High percentage of resistance to co-trimoxazole (44.9%) and nitrofurantoin (45.5%) was also observed, challenging the use of sulfonamide and nitrofurantoin drugs. The antibiotic susceptibility profile showed that 80% of the isolated *Shigella* spp. were resistant to many antibiotics of fluoroquinolones, aminoglycosides and tetracycline class which are often mediated through efflux pump overexpression. Overexpression of the efflux pump in the isolates was observed from the Agar-cartwheel method which was confirmed further using CCCP based inhibition test. To find the most potent efflux pump inhibitor, extracts of some traditionally used plants were screened against the isolates using the Agar-well diffusion method. Ethyl acetate and methanol extracts of *Garcinia lanceifolia* showed the highest inhibitory activity against the tested isolates. The results of Multiple ligand simultaneous docking (MLSD) against AcrB revealed the highest inhibitory activity of Dihydrocapsaicin and GarcinexanthoneA. MD simulation of both the ligands revealed a more stable interaction of Garcinexanthone A than Dihydrocapsaicin which demonstrated its potential to act as an efflux pump inhibitor.

Conclusion: Our study concludes that the high prevalence of MDR *Shigella* spp. is one of the major health risks in North-East India and the country as a whole, establishing the shortage of effective therapeutic options for treatment and this situation needs strict urgent action.

Keywords: Antibiotic resistance, efflux pump, AcrB, Molecular docking, MD simulation, Garcinexanthone A

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INVITED TALK

Computational approaches to understand the mechanisms of antibiotic resistance and for designing potential inhibitors

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In recent decades, antimicrobial resistance has been augmented as a global concern to public health owing to the global spread of multidrug-resistant strains from different bacterial pathogens. This alarming trend and the lack of new antibiotics with novel modes of action in the pipeline necessitate the development of alternate methods to treat illnesses caused by these isolates. In modern biology, computational approaches have become crucial tools, particularly in one of the most challenging areas of multidrug resistance. The rapid advancements in bioinformatics have led to a plethora of computational approaches involving genomics, systems biology, and structural biology; and they are currently gaining momentum among Researchers since they can be useful and provide valuable information on the complex mechanisms of AMR research in clinically important bacterial pathogens. *In-silico* approaches would be helpful in elucidating the AMR mechanisms, identifying important hub genes/proteins, and their promising targets together with their interactions with important drug targets, which is a crucial step in new drug discovery.

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INVITED TALK

Rethinking Antimicrobial Resistance – A Systemic Design Approach

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This presentation is focused on how a systemic design approach can be applied to the challenge of anti-microbial resistance in Urinary Tract Infections (UTI) in a peri-urban and rural setting in Assam. Drawing on a UKRI, DBT and the Newton Bhabha funded research project, DOSA (Diagnostics for a One-Health user Driven Solution for AMR) we adopted a service design approach that is inherently user driven and systemic, to support the diagnostic development of a community-based test to tackle UTI. In addition, this transdisciplinary approach enabled the co-creation of knowledge across the disciplines within the team, and externally with stakeholders so that the community could be actively involved in sharing their healthcare knowledge and experiences.

By drawing on the local experiences of the ASHAs (Accredited Social Health Activists) and the community, our approach was to co-design a simple service solution around the test, so that knowledge could be built on symptoms and prevention whilst addressing the current barriers that lead to community members, particularly women, not seeking the correct treatment pathway for the condition. In addition, this systemic design approach, with multiple stakeholder input has co-designed a simple data capture system that has the potential to strengthen the healthcare system at an individual, community and district level, and ultimately the appropriate use of antibiotics.

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INVITED TALK

Antimicrobial Resistance: Patients' Perspectives

Mihir Kanti Choudhury*

Deputy Registrar, Metropolitan University, Sylhet, Bangladesh

The advent of antimicrobial resistance has raised concerns about the health of human beings, emphasizing the demand for effective and rational use of antimicrobial medications. Although antimicrobial drug effectiveness, safety, and resistance patterns have been thoroughly examined by medical experts, patients' viewpoints on these vital therapies have received less attention. This study intends to investigate patient attitudes toward antimicrobial medications and how they may affect treatment compliance and antimicrobial stewardship. A varied sample of patients from various healthcare settings participated in focus groups and in-depth interviews as part of the study's qualitative research methodology. The study aims at examining the conceptual levels including attitudes, beliefs, and experiences of patients with reference to antimicrobial medications through these interviews. The study will help clarify a number of important issues. First, it will throw focus on how well patients understand the validation for prescriptions for antimicrobial drugs and their awareness of antimicrobial resistance. Second, it will investigate how patients view the advantages and drawbacks of using antimicrobial medications. By offering important insights on patients' experiences, beliefs, and behaviors about antimicrobial treatments, this study seeks to close the knowledge gap that currently exists. The results of the study will provide guidance to medical practitioners and policymakers on ways to improve patient education, increase treatment adherence, and maximize antimicrobial stewardship measures to maintain the efficacy of these essential drugs.

Key words: Antimicrobial drugs, Antimicrobial resistance, patients' perspectives

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INVITED TALK

AMRACE- an interplay in One Health

Dr. Maneesh Paul. S, Ph. D., FRSPH

Abstract

The AMRACE (Anti-Microbial Resistance Action Centre of Excellence) is an initiative nested at Bangalore Bio-innovation Centre (a Government of Karnataka undertaking). We initiated the "Translational AMR Stewardship" program, Piloted in June 2023 at AIIMS Bhopal, and officially launched it through Rotary Club of Bangalore on July 01, 2023. This initiative is led by a Microbiologist, Clinical Pharmacologist, and a Technologist with Microvioma as a partner.

AMRACE is an attempt to catalyse the implementation of the AMRS efforts of the Government through technology (VaidyaRx - software tool).

The major gap identified in the stewardship programs is:

-The major stakeholder (consumer/patient) is rarely engaged actively

-The outcome measured is not getting back to the source for measurable corrective activities

-Data that is selective rather than comprehensive which is impairing not only decision making but also contribute to the spread of AMR The focus is on consumers/patients.

AMRACE addresses this challenge by identifying the re-producible gaps, recommend solutions and further monitor its compliance. For this we have developed an AI-driven tool VaidyaRx (a technology tool with SiCureMi) for the implementation of necessary corrective measures.

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OR 1

Noncanonical antimicrobial resistance mechanisms in bacteria

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Abstract

Background: The rise of antimicrobial resistance has enthralled the scientific community to understand the mechanism of resistance. Over the years of systematic investigations have led to the understanding of diverse ways of resistance including increased efflux pump activity, enzymatic degradation of the drug, modification of the target site and development of alternate physiological pathways to circumvent drug intervention. Owing to the clinical significance such studies took the centre stage. Nonetheless, over past two decades it has been realised that bacterial cells seem to have mastered the art of adaptation. In my talk I shall be focusing on these non-canonical antimicrobial resistance mechanisms in gram negative bacteria *Klebsiella* spp. belonging to Enterobacteriaceae family.

Methods and methodology: For these studies we have utilized various microbiological, molecular biology and biochemical studies. During the talk I shall be discussing about the experimental methodologies followed to during the investigation.

Results and Discussion: Our results indicated that the bacteria tweak their cellular metabolism and physiology such as growth rate, ATP production to survive the unfavorable condition. Such non- canonical responses are the result of stochastic variations at the population level leading to heterogenous response to an external stimulus.

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OR 2

Terminalia arjuna Extracts: Nature's Bounty for Antimicrobial Research

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Abstract:

This study explores the analysis of phytochemical components found in leaf and bark extracts of *Terminalia arjuna* and examines their possible contributions to antimicrobial properties. *Terminalia arjuna*, a commonly known medicinal plant in traditional medical practices, has previously exhibited noteworthy bioactive compounds in various investigations. In this research, a comprehensive analysis of the phytochemical composition of the leaf and bark extracts was conducted using advanced analytical techniques. The extracts were subjected to gas chromatography-mass spectrometry (GC-MS), to identify and quantify the phytochemical constituents. The phytochemical analysis revealed a diverse array of bioactive compounds present in the leaf and bark extracts of *Terminalia arjuna.* The agar diffusion assay method was employed as one of the methods for quantifying the ability of antibiotics to inhibit bacterial growth. The antimicrobial potential of these extracts was evaluated against a range of microbial strains. The findings offer valuable insights into the bioactive compounds present in the plant and their potential applications in combating microbial infections.

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OR 3

Story of a carbapenem-resistant bacterium, *Shigella sonnei* KRA01 that efficiently consumes antibiotics having beta-lactam ring is also capable of erasing beta-lactam's antibacterial properties

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Abstract

Multiple-antibiotic-resistant (MAR) bacteria are on the rise and spreading throughout the environment, posing an increasing threat to global health and challenging our ability to effectively fight infectious diseases. The development and spread of antibiotic resistance genes (ARGs) through antibiotic resistant bacteria (ARB) is significantly influenced by the presence of antibiotic residues in water and soil. Different sources of antibiotic residues, such as sewage from hospitals and industrial facilities, as well as wastewater treatment facilities, put strong selective pressure on native bacteria, forcing them to develop resistance to these pollutants and adapt to them as a resource for survival. This gives us a chance to use these bacteria as biodegraders of antibiotic residues distributed across the different layers of the environment. In the current study, the enteric bacterial strain KRA01 isolated from river water samples, resistant to carbapenem group of antibiotics, has demonstrated 10,000-fold growth using first and second generation beta-lactam antibiotics as the only carbon source at a concentration of 5 gm/L. We investigated it using a variety of biochemical techniques and discovered that it is a potent producer of metallo-beta-lactamase. To confirm KRA01's ability to lessen the antibacterial effects of leftover antibiotic residues in solution, we performed antibacterial assays. The genome sequence of this bacterium is also being analyzed using a variety of *in silico* techniques in an effort to determine its identity and mode of operation. With the help of this research, beta-lactam pollution of the environment can be cleaned up by using these bacteria to biodegrade antibiotic residues.

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OR 4

Mutations in metabolic genes induce anaerobiosis in *Escherichia coli* during adaptationto ciprofloxacin

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[*] corresponding author

Background:

Genomic basis of adaptive-evolution of antimicrobial resistance (AMR) is poorly understood. Although the interplay between core metabolism and AMR has recently been documented, thepresence of mutations in core metabolic genes and their biological role in adaptation to antibiotic stress remains elusive.

Methods:

E. coli K12 was exposed to increasing gradients of ciprofloxacin (from 0.5x to 8.0x MIC) over45-day period using the gradual habituation method along with transfer bottlenecking in between the cycles. Fitness costs in adapted subpopulations were estimated using maximum growth rate (μmax). To elucidate the underlying molecular basis of adaptive-evolution of ciprofloxacin resistance WGS (Whole genome sequencing) was performed using Oxford Nanopore sequencing from various selection levels. We identified novel mutations in non- canonical genes involved in metabolism during adaptation and investigated their biological role.

Results:

We observed gradual antibiotic adaptation via acquisition of high-fitness mutations in non-canonical targets. In total, we identified 5 mutations and 4 structural variations in adapted subpopulations including 3 non-canonical mutations in genes pivotal for arginine and carbohydrate metabolism. Functional assays indicate a role for the 3 metabolic gene mutations in modulation of total protein content, L-arginine levels, biofilm formation, facilitation of anaerobiosis and ATP production during ciprofloxacin stress.

Conclusion:

Our data suggests that bacteria may adopt a multifaceted genetic strategy to facilitate anaerobiosis and high biofilm and ATP production during adaptation to ciprofloxacin. In this work, we have identified mutations in metabolic genes as a central theme that enables physiological changes necessary for adaptation to ciprofloxacin stress.

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OR 5

Spatial reorganization of the *Escherichia coli* chromosome contextualizes triclosan stress-related genetic, epigenetic and transcriptome changes

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Abstract

Background: Changes in the spatial organization of bacterial chromosomes under stress conditions and its biological implications remain poorly understood.

Methods: We adapted wild-type and Δ*dcm E. coli* to triclosan, one of the most widely used non- antibiotic, anti-microbial (NAAM) biocide to understand triclosan-induced spatial reorganization using Hi-C. In addition, we also performed single-base resolution epigenetics and RNA sequencing analysis on triclosan-adapted wild-type and Δ*dcm E. coli*

Results: We mapped the structural landscape of wild-type and Δ*dcm E. coli* chromosomes under triclosan stress using Hi-C to identify triclosan-induced chromosomal interaction domains (CIDs). Two CIDs were common to the wild-type and Δ*dcm E. coli*, including a CID with a common boundary at *fabI* gene, which encodes the triclosan target. All mutations and structural variants under triclosan stress were observed within or in close proximity to triclosan-induced CIDs. Absence of Dcm methylation impacts both short- and long-range interactions in triclosan stress. Single-base resolution methylome maps reveal hypermethylation of adenines (in wild-type and Δ*dcm*) and cytosines (in wild-type) in the two common triclosan-induced CIDs. Furthermore, global gene expression profiling identified that *E. coli* genes upregulated in triclosan stress are enriched within CIDs associated with triclosan stress.

Conclusions: Our findings suggest that stress-induced CIDs in *E. coli* are hotspots for genetic variations and are associated with enhanced transcriptional activity and hypermethylation of Dam/Dcm motifs. Spatial reorganization of the bacterial chromosome may represent the forefront of the cascade of events that allow adaption to antimicrobial stress.

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OR 6

To Check the Synergistic Activity of *Centella asiatica* Extract Against Extended-Spectrum Beta-Lactamase-Producing Bacteria

Anupama Moirangthem and Birson Ingti

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Abstract

Background

Drug resistance has become one of the most significant barriers and setbacks in treating bacterial infections. The emergence of extended-spectrum beta-lactamase (ESBL) as well as metallo beta-lactamase (MBL) has created chaos in the treatment process and has become a matter of concern. There is a rapid increase in bacterial resistance to the existing drugs. Hence, there is an urgent need to search for new antimicrobial substances from other natural sources, such as plants. So, the present study aims to assess the synergistic effect of a medicinal plant extract, *Centella asiatica*, against a bacterial strain producing ESBL when it is combined with an antibiotic.

Method and Methodology

The crude extract of *Centella asiatica* was assessed for the presence of bioactive compounds by GC-MS analysis. It was followed by an *in-vitro* study using the disc diffusion method where the plant extract was combined with Ceftazidime, which was further validated by the *in silico* study. For the *in silico* study, the ESBL (protein) was downloaded from the Protein Data Bank. The structure of phytoconstituents (ligands) was downloaded from the PubChem database. The ligands were screened with a molecular docking study (Autodock) at targeted sites on the proteins.

Result and Discussion

The *in-vitro* study done against the ESBL-producing organism showed a synergistic effect. For further confirmation, an *in silico* study was carried out. Molecular docking revealed that castilliferol exhibited the best binding affinity against SHV-1 and OXA-10, with binding scores of -8.86 and -8.54, respectively. Castilliferol showed convenient interactions with SHV-1 forming hydrogen bonds with five of the active binding site amino acid residues, which include ALA237, ASP104, ASN132, SER70, and SER106. It also showed an interaction with the active sites of OXA-10, such as SER67 and PHE208.

Conclusion

The present study revealed that the phytoconstituents of *Centella asiatica* exhibit good synergistic activity against extended-spectrum beta-lactamases when combined with an antibiotic. Further research could lead to the generation of novel compounds with fewer side effects for the treatment of bacterial infections.

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OR 7

Characterization of Extended Spectrum Beta-Lactamase Producing *Helicobacter pullorum* and *Escherichia coli* from Poultry Samples in Manipur, India

· **Blessa Sailo***[1], Chongtham Sonia[2], Lalhruaipuii[1], Lalmuankimi[3], and Sunil Doley[1]

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Abstract

A total of eighteen *Helicobacter pullorum* (n=18) and *Escherichia coli* (n=319) isolated between September, 2019 to April, 2023 from local market in Manipur, India were characterized for their *bla*$_{ESBL}$ genes, and other resistant genes respectively. The *H. pullorum* isolates (n=18) were tested for *bla*$_{ESBL}$ and other resistant genes, and revealed that *bla*$_{CTX-M-1}$ (n=2), *bla*$_{TEM}$ (n=15), *aac(6')-Ib* (n=4), *tet*A (n=6), and *tetB* (n=1) were positive. Out of the 319 *E. coli* isolates, thirty nine isolates (12.22%) were found to be *bla*$_{ESBL}$ positive isolates, with *bla*$_{CTX-M-1}$ (n=8), *bla*$_{CTX-M-2}$ (n=6), *bla*$_{CTX-M-3}$ (n=3), *bla*$_{TEM}$ (n=8), *bla*$_{CTX-M-1}$+*aac(3')IIa* (n=8), *bla*$_{CTX-M-1}$+*aac(3')IIa*+*tet*B (n=1), *bla*$_{CTX-M-3}$+*aac(3')IIa* (n=1), *bla*$_{TEM}$+*tet*B (n=2), and *bla*$_{TEM}$+*aac(3')IIa* (n=5) were the antibiotic drug resistant genes detected. Phylogrouping showed that the *E. coli* isolates belonged to group A (212/66.45%), B1 (43/13.47%), B2 (18/5.64%) and D (46/14.42%). Congo red binding test showed that 134 (42.00%) were positive. Antimicrobial susceptibility test was performed using twenty antibiotics, and it was found that penicillin-G has the highest resistant (307/96.23%), followed by vancomycin (298/93.41%), and ciprofloxacin (286/89.65%). Genotyping of the *bla*$_{ESBL}$ isolates using Repetitive Extragenic Palindromic-Polymerase Chain Reaction (Rep-PCR) of the *bla*$_{ESBL}$ isolates showed a distinct and similar clonality.

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OR 8

Antibiotic resistance pattern of *Staphylococcus aureus* in Backyard Pig production system in Mizoram, N.E. India.

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Abstract

Background and Purpose:

Staphylococcus aureus is an opportunistic human and animal pathogen causing food intoxication and a variety of infections ranging from skin and soft tissue infections to serious diseases including endocarditis, septicaemia, osteomyelitis, pneumonia and toxic shock syndrome. The drug resistance of *S. aureus* has gradually increased in the recent decades due to the misuse of antibiotics which resulted in bacterial evolution. In Mizoram limited study has been done so far in the antimicrobial resistance pattern of *Staphylococcus aureus* in Backyard Pig production.

Methodology:

A total of 156 skin scrappings were collected from pigs irrespective of age, sex, breed in an organized and unorganized farm in 3 districts (Champhai, Kolasib and Mamit) of Mizoram during July, 2022 to June, 2023 from clinical skin infection. Bacteria were isolated using selective media and identified using biochemical tests and polymerase chain reaction (PCR). Phenotypic resistance was determined using the disk diffusion method and selected resistances were investigated using PCR.

Result and discussion:

A total of 73 were identified as *Staphylococci* by 16S rRNA and twenty nine (29; 39.7%) were confirmed as *S. aureus* using PCR. A total of 6.8% (2/29) and 3.45% (1/29) were identified as methicillin resistant *S. aureus* (MRSA) through the *mec*A and *mec*C genes. The highest resistance was observed in gentamicin (61.3%) followed by oxacillin and penicillin (58.99%) and highest sensitivity was observed in piperacillin (91.39%).

Conclusion:

Presence of MRSA in backyard pig production system poses a public health concern in the region.

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OR 9

Identification of a mutation associated with adaptive evolution to salt tolerance in *Escherichia coli*

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Background:

Salt tolerance in bacteria is linked to enzymes that modify PG crosslinks in the cell wall. The interplay between antimicrobial resistance and salt tolerance remains poorly understood. Here, we sought to understand the mutation(s) associated with evolutionary rescue in *Escherichia coli* during adaption to salt stress and their role in the emergence of antimicrobial resistance.

Methods:

E. coli K12 strain was adapted to increasing gradients of salt concentrations (2% - 4% NaCl) by the gradual habituation method. Cells in each selection level were exposed to two cycles of higher salt exposure (four days with four passages) with an intermediate bottleneck, enriching adaptive-resistant subpopulation with beneficial mutations occurring at a low fitness cost. Oxford Nanopore sequencing was used for WGS (whole genome sequencing) to capture beneficial mutations driving adaptive salt-tolerance across selection levels.

Results:

Gradual habituation to increasing salt-gradients enriched *E. coli* with salt-tolerant subpopulations. While initial exposure of 2% and 4% NaCl killed about 65%-80% of the challenged-populations; the evolutionary rescue was more pronounced (over 2 to 4-fold higher) at the end of each selection level. Interestingly, in salt-tolerant subpopulation, we identified a mutation within the structural region of a DD-endopeptidase associated with the cleavage of PG crosslinks that led to ~3-fold increased MICs for meropenem.

Conclusion: Here, we identify a point mutation in a DD-endopeptidase associated with salt-tolerance in *E.coli* which also decreased susceptibility to meropenem. This work highlights a novel mechanism of salt tolerance that may have important implications on emergence of antimicrobial resistance in hypersaline habitats.

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OR 10

A feasible Planning for Bacterial-driven Ciprofloxacin removal from antibiotics-contaminated area

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Background and Purpose: Antibiotics are regarded as an emerging contaminant gaining global attention. Antibiotic resistance genes (ARGs) and antibiotic-resistant bacteria(ARB) spread more readily in the environment due to the persistence of antibiotic residues. Patients partially metabolise broad-spectrum fluoroquinolone ciprofloxacin (CIP), widely used against gram-positive and gram-negative bacteria, before it is released into the sewage system. The high adsorption coefficient (kd), causes CIP molecules to concentrate in the sludge as there are no suitable commercially accessible pre-treatment procedures. Therefore, the goal of the current study is to identify and evaluate the ability of microorganisms to break down CIP.

Methodology: An appropriate liquid enrichment medium was created to improve the recovery of CIP-degrading bacteria from sludge samples (said to contain a significant amount of CIP residues). The biochemical and molecular identification of the isolate was done. The antibiotic profiling, and growth kinetics using CIP as the sole source of carbon and its degradation were assessed. The best degradation parameters were optimized.

Results and Discussion: A dominating bacteria that could only grow on CIP (2g/L)was isolated after enrichment. The clonally pure strain, *Klebsiella pneumonia* SG01, being a multi-drug resistant strain was subjected to varied temperature, pH, and concentrations of CIP to ensure optimal degrading conditions. High-throughput ATR-FTIR and physiological evidence both support the strain's consumption of CIP. The degraded product's toxicity against bacteria revealed that it was less harmful than the parent molecule.

Conclusion: The isolated strain shows enough potential to be used as a biodegradation agent, capable of degrading CIP effectively.

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OR 11

Novel V8C Mutant of SAAP-148 as a Potent ESβL Inhibitor Restoring Sulbactam Activity against Nosocomial XDR *Acinetobacter baumannii*

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Abstract

Background:
The XDR strains of *Acinetobacter baumannii* causes several nosocomial outbreaks including ventilator-associated pneumonia, urinary tract infections, bloodstream and wound infections.

Method & Methodology:
Whole genome sequencing of pan-Indian isolates revealed 28 non-duplicate strains amongst which ~93% of the isolates expressed class-B (NDM1) and class-D (OXA23 and OXA58) carbapenemases. Phenotypic characterisation revealed high sulbactam MIC (256µg/ml) which is currently the drug-of-choice for treating *A. baumannii*. Extended spectrum β-lactamases (ESβLs) produced by these strains inactivate sulbactam, thus making the treatment procedure cumbersome. The potency of antimicrobial peptides (AMP) as β-lactamases inhibitors were screened upon constructing AMP mutant library through amino acid walking method which resulted in mutants with better antibacterial efficacy (~15-27% higher), physicochemical and immunogenic properties yet with intact structural descriptors.

Results & Discussion:
The study screened and explored the efficacy of novel mutant V8C of SAAP-148 as potent ESβL inhibitor inhibiting NDM1, OXA23 and OXA58 with the lowest binding energies of -1148.7, -1032.5 and -1148.7 kcal/mol respectively. Intermolecular interaction profile illustrated the interaction of SAAP-148-V8C with key active site residues of metallo β-lactamase [IPR001279] and penicillin binding transpeptidase [IPR001460] domains through hydrogen bonds and van der Waals hydrophobic interactions. The stability of the peptide-ESβL complex was further assessed through coarse-grained and molecular dynamics simulation analysis. The study hypothesised sulbactam restoration upon administration of SAAP-148-V8C as combination therapy thereby paving path towards designing successful therapeutic regimen to combat XDR traits of *A. baumannii*.

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OR 12

Review on Anti-Biofilm Effect of Silver Nanoparticles Against Different Microorganisms

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Abstract:

There has been a noticeable rise in infections caused by bacteria resistant to antibiotics during the past few years. Many of these diseases are predominantly caused by biofilms of multidrug resistant bacteria. Biofilms are made up of bacterial colonies that have adhered to a surface and are protected by their own extracellular polymeric matrix. Both Gram-negative and Gram-positive bacteria have the capacity to create biofilms on a variety of environmental surfaces as well as in many medical devices, tissues, tooth surfaces, artificial heart valves etc. Nanotechnology is one of the emerging approaches for combating the multiple drug resistant biofilm forming microorganisms. This review aims to evaluate the activity of AgNPs against various biofilm former microorganisms. The antimicrobial activity of AgNPs was tested within biofilms using a bioreactor under high fluid shears conditions and static conditions and recorded the log reduction in the number of CFU of different microorganisms on exposure to different concentrations of AgNPs. In conclusion, AgNPs are fatal to bacteria and can effectively stop or prevent the development of biofilms. Silver nanoparticles can be embedded into the matrices or materials used to make medical devices to prevent the growth of microbial biofilm on them. More research and development are required to turn this technology into therapeutic and preventive strategies.

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The ARG Conundrum in Geothermal Systems of Sikkim Himalayan Hot Springs

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Abstract

Given a dearth of information and study in antimicrobial resistance of geothermal systems, it is currently unknown how antibiotic resistance genes (ARGs) arise and are expressed in thermophilic bacteria. Functional metagenomic techniques have been used to do comparative profiling of ARGs and metal tolerance genes across thermophilic bacteria. Using the non-redundant resistance genes as a reference, shotgun metagenomic sequence data produced by high-throughput sequencing predicts the presence of putative ARGs and putative metal resistance genes (MRGs). Proteobacteria, Actinobacteria, Firmicutes, and Bacteroidetes were found to predominate the microbial flora in the Geothermal Systems of Sikkim Himalayan Hot Springs according to the culture-independent investigation. Shotgun gene sequencing results from ARG analysis of thermophilic bacteria were found to be negative. However, only a small number of genes were found, although they showed high similarity to mesophilic bacteria only. MRGs were also found in the hot spring isolates metagenome sequencing concurrently. The same message was likewise delivered by whole-genome sequencing analysis of the thermophilic *Geobacillus* reference genome sequence, which revealed the presence of MRGs and the absence of ARGs. Metagenomics research on ARGs and MRGs among culturable and nonculturable bacteria from Sikkim's hot springs revealed a preference for MRGs over ARGs. The co-selection of ARGs and MRGs in these contexts is likewise not supported by the lack of ARGs. It may have been required for survival in the geological craters, which have an abundance of various metals from earth deposits, that this evolutionary selection of metal resistance over antibiotic genes occurred.

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OR 14

Redefining the battle against antimicrobial resistance in *Pseudomonas aeruginosa* with Phage therapy

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Abstract

Background: *Pseudomonas aeruginosa* (PA) is a Gram-negative bacillus and one of the main opportunistic pathogens that have a leading role in nosocomial, acute and chronic infections. Escalating rise of antimicrobial resistance in *Pseudomonas aeruginosa*, has necessitated innovative approaches. Phage therapy, harnessing bacteriophages, offers a promising avenue due to its specificity, adaptability, and potential to mitigate resistance challenges. Recent studies (Smith et al., 2020; Brown and Wittebole, 2021) emphasize phage therapy's potential in combating *Pseudomonas* antimicrobial resistance.

Method and methodology:

1. Phage isolation, purification, and preparation
2. Transmission Electron Microscopy (TEM)
3. Antibiotic sensitivity assay and host range
4. Adsorption assay
5. Single-step growth curve
6. Temperature and pH stability assays
7. Antibiofilm assay

Results and discussions: We have isolated a native bacteriophage DT1 of family Podoviridae from waste water of Tezpur Town is showing impressive killing activity against PA. It has a latent period of 20 min and an average burst size of approx. 200 Phages per host cell. It is stable at a wide range of pH and stable upto 50^{o}C, can easily be stored in liquid and lyophilized form. It has a prominent biofilm clearing activity. This Phage can be used in Phage therapy against MDR PA.

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Emerging Trends in Antimicrobial Resistance and Virulence in *Salmonella* Typhi and *Salmonella* Paratyphi A Pediatric Isolates: A Genomic Exploration

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Abstract

Background: In this study, we examined the antimicrobial resistance (AMR) landscape and virulence factors in *Salmonella* Typhi (*S. Typhi*) and *Salmonella* Paratyphi A (*S.* Paratyphi A) isolates from a pediatric settings. Our aim was to assess the current AMR situation in these geographic regions compared to globally circulating AMR strains.

Method and Methodology: The raw genome sequences from twenty clinical isolates of *S.* Typhi and *S.* Paratyphi A was obtained from the National Center for Biotechnology Information - Sequence Read Archive database. These isolates underwent comprehensive screening for prevalent Antimicrobial Resistance Genes (ARGs) and Virulent Factors (VFs). The comparison study performed with resistance profiles against reference strains of *S.* Typhi and *S.* Paratyphi A.

Results and Discussion: AMR analysis revealed the presence of common ARGs, including *sul1*, *sul2*, *dfrA7*, *tem-1*, *AH(6)-Id*, and *APH(3")-Ib*, as reported by CARD, NCBI-AMR, ARG-ANNOT databases. Whole-genome analysis provided insights into the genetic characteristics of AMR and VFs. Notably, azithromycin-resistant *S.* Typhi isolates exhibited the highest prevalence of AMR genes. In comparison of global isolates, we observed a trend of concurrent resistance to macrolides, β-lactams, fluoroquinolones, tetracyclines, ansamycins, and aminoglycosides. Interestingly, there was relatively low observed sulphonamide resistance, which may warrant attention as a potential future threat. As a result, we suggest the development of new antibiotic regimens for treating azithromycin-resistant *S.* Typhi, while taking precautions to avoid exacerbating sulphonamide resistance. Identifying ARGs and virulence factors in pediatric clinical isolates aids future research in designing antibacterial compounds against *S.* Typhi and *S.* Paratyphi A.

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Analysis of Potential Antivirulence Targets Against Hypervirulent *Klebsiella Pneumoniae*: An *In Silico* Gene Network Anlaysis Approach

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ABSTRACT

Background: Hypervirulent *Klebsiella pneumoniae* (HvKp) is a virulent pathotype, critically associated with several nosocomial as well as community acquired infections like pyogenic liver abscess. Although susceptible to antibiotics, the emergence of MDR-HvKp strain has raised the health concern globally. Due to continuous selection of novel anti-microbial resistance (AMR) mechanism, alternatives such as antivirulence strategy can be an effective approach for the treatment of this evolving superbug.

Method & Methodology: In this study, a large number of *K. pneumoniae* virulence genes were collected from VFDB and NCBI database. With the use of bioinformatics tools like STRING, Cytoscape and its plug-ins and DAVID, a network of virulence genes with their associated functional partners were constructed as well as clustering, topological and functional properties of the virulence gene network were investigated.

Results & Discussion: Using STRING and Cytoscape, a network of 379 genes associated with 3827 functional partners were constructed. Subsequently, 146 clusters were obtained by clustering analysis with MCODE plug-in of Cytoscape. The network topological analysis with Network Analyzer plug-in filtered out the genes which were then subjected to functional enrichment analysis using DAVID database. The DAVID analysis revealed the functional properties of all the clustered genes that have important roles in virulence of the organism.

Conclusion: Further analysis of these important genes and targeted strategies can be opted for designing novel antivirulence drugs as an alternative therapy against evolving HvKp pathotype.

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OR 17

Potential use of Enterococcus isolated from the gut of Eri silkworm (*Samia ricini*) as probiotic

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Abstract

A total of six pentose bacteria were isolated from acid the midgut of healthy mature Eri silkworm. Further analysis of 16S rRNA gene sequences revealed the highest prevalence of up to Enterococci isolates. The Eri silkworm is reared for its silk and the knowledge of its gut bacteria with the ability to produce lipases lies in the significance as far as boosting production of this insect via development of probiotics to enhance commercial Eri rearing. Silkworm needs higher protein & probiotic in their diet to help its body repair cell & to make fiber. Nutrition of silkworm is sole factor which at most individually quality and quantity of silk. Hence in the present investigation an attempt is made to study the impact fortification of castor leaf with probiotic microorganism Enterococci isolated from the gut of Eri silkworm on larval weight and larval length. The data was collected and subjected to the statical analysis. The results indicated that there is a better larval weight and larval length when fed with the probiotic Enterococci was used. Silkworm were fed five different doses of Enterococci along with castor and one control. These finding presented the perspective of non-mulberry silkworm that could also be used as the model for further applying to new trends of the sericulture industry.

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OR 18

Whole Genome characterization of methicillin-resistant *Staphylococcus* spp. isolates from aquaculture-cultivated shrimps

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Abstract

Aquaculture is one of the fastest-growing agricultural sectors serving as an invaluable animal protein source. The increasing use of antimicrobials in these facilities has significantly contributed to the selection of antimicrobial resistance (AMR) among existing microbial populations. Presence of pathogenic microbes and antimicrobial resistance is a major concern in aquaculture and because of which they are now considered as hotspot for AMR. India being one of the top five shrimp producers, accounting for 11.4% of global production in 2018 (Miao, 2020) underscores the need to investigate antimicrobial resistance within the microbial communities of shrimp farms, including understanding the genetic origins of these AMR-harboring pathogens. Hence, in our study, we undertook the task of characterizing the genomes of 12 *Staphylococcus* spp. isolates, using whole genome sequencing, from Indian shrimp farms to better understand the genetic makeup of the aquaculture isolates and their relatedness to human pathogens. Comparative genomic analysis of these isolates revealed that they are very closely related to human isolates/pathogens, indicating their human-origin. Among all twelve isolates, *S. aureus* isolates (n=4) exhibited quite an extensive resistome and virulome, comparable to that of human pathogens. Overall, the findings indicates that these isolates from aquaculture have high pathogenic potential and could pose a significant risk to human health. Therefore, the study call attention to monitoring the proper implementation of the biosecurity measures in aquacultures farms in order to avoid entry and enrichment of such isolates.

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OR 19

Multidrug-Resistant *Acinetobacter baumannii*: A Retrospective Study in a Tertiary Hospital

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Abstract

Background:

Multidrug resistance in *Acinetobacter baumannii* is constantly on the rise. During the last years, this pathogen displayed multidrug resistance (MDR), mainly due to extensive antibiotic abuse and poor stewardship. There has also been an increase in the morbidity and mortality of patients with infection by the same pathogen. This study aimed to assess the patterns of antibiotic resistance exhibited by *Acinetobacter baumannii* in CSF samples, examine the risk factors associated and the clinical outcomes.

Study Design:

Retrospective cross-sectional study.

Materials and Methods:

Reports of 60 isolates of *Acinetobacter baumannii* obtained from patients admitted in a tertiary hospital were used for the study. Identification and determination of antibiotic resistance patterns were done using Vitek2. The presence of probable risk factors was noted. The pattern of clinical outcomes of the patients was analysed. Data analysis was done using descriptive statistics.

Results:

More than 70% of isolates showed resistance independently to imipenem and meropenem. Higher rates of susceptibility were observed with Tigecycline and Colistin. Isolates obtained from patients in the intensive care unit (ICU) showed resistance to a greater number of antibiotics than those in the wards. 78% of the patients were discharged, 20% expired, and 1% were shifted. A positive correlation was found between the duration of hospital stay and number of antibiotics to which the isolate was resistant.

Conclusion:

In this study, a large number of isolates exhibited resistance to carbapenems and the use of other antibiotics such as Tigecycline and Colistin, to which higher susceptibility was observed.

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OR 20

Microbiological Profile of Catheter Associated Urinary Tract Infection In Adult Intensive Care Unit Patients At Civil Hospital In South Assam

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Abstract

Background:
Catheter-associated urinary tract infection is the commonest hospital-acquired infection (HAI). Urethral Catheter is the most prevalent cause of nosocomial infection and gram negative bacteremia.

Objective:
1. To determine the prevalence and the etiological agents of Catheter-associated UTI in ICU
2. To evaluate the antimicrobial susceptibility pattern of the isolated organisms

Materials and Methods:
The patients admitted in Intensive Care Unit (ICU) of SMDEB Civil Hospital, Silchar who were on Urinary Catheter insertion for more than 48 hours, who developed signs and symptoms of UTI were included in the study. The duration of study was of 3 months from 1st of July 2023 to 30th of September 2023. Under aseptic conditions, fresh urine samples were collected from clinically suspected cases of Catheter Associated UTI. The samples were processed in District Public Health Laboratory, SMDEB Civil Hospital as per standard protocols. Uropathogens were isolated, identified and subjected to Antimicrobial sensitivity testing.

Results:
216 Patients admitted in ICUs were on indwelling catheter, with catheter days ranging from 3-6 on an average. Out of 216 patients, 52 patients developed clinical signs and symptoms of Urinary tract Infection. Of the 52 urine samples processed, 36(69.2%) yielded growth of single organism [*Escherichia coli*(16), *Klebsiella species*(9), *Proteus species*(2), *Pseudomonas species*(4) and *Staphylococcus aureus*(5)] and 16 showed no evident growth of organism. All Gram Negative Bacilli were sensitive to 3rd and 4th generation of cephalosporins, aminoglycosides and Carbapenems. Few organisms were resistance to broad spectrum quinolones.

Discussion:
Identifying the cases and analysis of microbiological profile of Catheter Associated UTI will guide us towards rational use of antibiotics as well as following of proper measures to avoid such Hospital acquired infections.

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The Antimicrobial activity of mucolytic bacterial species isolated from healthy human faeces

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Abstract

Background: The human gut harbours a diverse and complex bacterial community and significant section of microbiota (~0.9%) comprises a subset of mucolytic bacteria that play a significant role in host health and diseases. The knowledge of the mucolytic bacterial population with antibacterial activities against serval pathogenic bacteria is still in infancy.

Method & Methodology: Human faecal samples were used to isolate mucin degrading bacteria and evaluated for mucin degradation attribute. Quantitative and qualitative mucin degradation ability was determined. Agar well assay was used to ascertain antimicrobial activity

Results & Discussion Three mucin degraders i.e. *Priestia flexa* KS1, *Enterococcus gallinarum KS4 and Enterococcus durans G322S* identified via meta-genomic technique. The amido black assay implies a halo around the colonies manifesting release of mucolytic enzyme. The findings demonstrated decrease in carbohydrate concentration (56-75%) and protein content (5-31%) in mucin spent medium further confirmed mucin degradation. All three strains exhibited antagonistic activity against enteric pathogens including *Escherichia coli* NCDC249, *Staphylococcus lentus* (ON035499), *Klebsiella pneumoniae* MTCC530 and *Pseudomonas aeruginosa* MTCC1035. Further, antibiotic susceptibility data manifested variation in antibiotic resistance profile. Antimicrobial activity is a multifactorial event involving different inhibition mechanisms such as the production of various organic acids, acetoin, bacteriocins, hydrogen peroxide, and other metabolites. Future study is required to unearth the mechanism behind the antimicrobial activity of the isolates.

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OR 22

Diagnostic electrochemical biosensor platform for rapid antimicrobial resistance testing at point-of-care

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Abstract

Antibiotic resistance is one of the biggest threats to public health and modern health care [1]. Especially, the growing resistance rates of Gram-negative bacteria causes increasing concerns. The occurrence of the easily transferable, plasmid-encoded *mcr-1* colistin resistance gene further enhanced the risk of the occurrence of highly difficult to treat bacterial infections. Therefore, there is a strong case for new rapid molecular diagnostic tests for the detection of *mcr-1* gene associated colistin resistance besides other resistance genes.

Electrochemical impedance spectroscopy (EIS) is a well-suited method for rapid antimicrobial resistance detection as it enables rapid, label-free target detection in a cost-efficient manner [2, 3]. Here, we describe the development of an EIS-based *mcr-1* gene detection test, including the design of *mcr-1* specific peptide nucleic acid probes and assay specificity optimisation through temperature-controlled real-time kinetic EIS measurements [4]. A new flow cell measurement set-up enabled for the first time detailed real-time, kinetic temperature-controlled hybridisation and de-hybridisation studies of EIS-based nucleic acid biosensors. The temperature-controlled EIS set-up allowed single nucleotide polymorphism (SNP) discrimination.

This newly developed AMR gene detection test enabled the direct, specific label and amplification-free detection of *mcr-1* and bla_{NDM} gene harbouring plasmids from *Escherichia coli.* This is an important step towards the development of an EIS-based rapid, point-of-care molecular diagnostic test for AMR diagnosis to optimise patient treatment and reduce the mis-use of antibiotics.

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OR 23

Rapid Detection of Urinary Tract Infection with Quantitative Antibiotic Susceptibility Testing

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Abstract

Background: The improper use of antibiotics significantly contributes to the development of antimicrobial resistance. To address this pressing issue, a novel technology has been developed to swiftly identify bacteriuria and provide quantitative assessments of uropathogen susceptibility to antimicrobials in clinical urine samples, all within an hour. This innovative approach utilizes a bioluminescence assay, where the presence of bacterial adenosine triphosphate binds to luciferin-luciferase, enabling rapid and efficient analysis. Additionally, a point-of-care device is being developed to automate the assay workflow in a load-and-go fashion, further enhancing its accessibility and usability for healthcare professionals.

Materials and Methods: An external validation study was conducted using data from two medical centres. It included 249 urine samples from patients with UTI symptoms, which were analysed using the rapid method and compared to reference laboratory results. In Test 1, a 10 µL urine sample was mixed with Reagent 1, incubated for 10 minutes at 37°C, combined with Reagent 2, and had its signal output measured at 560nm. Test 2 divided 70 µL of urine into seven 10 µL samples, each added to 1.4 mL of Reagent 1, which included one control and six samples with different antibiotics. After a 5-minute pre-incubation at 37°C, the mixtures were combined and incubated for 30 minutes at 37°C. Each chamber was subsequently mixed with 160 µL of Reagent 2, and the signal output at 560nm was measured.

Results and Discussion: The results confirmed the effectiveness of the rapid method, with Test 1 achieving 97.1% sensitivity and 92.0% specificity, and Test 2 showing an overall sensitivity of 94.1% and an overall specificity of 90.5%. Importantly, the method significantly improved UTI treatment success from 68.3% to 92.7%, highlighting its effectiveness in mitigating antimicrobial resistance.

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Endophytic fungi associated with leaf of *Solanum pimpinellifolium* L. and their antagonistic activity against *Alternaria alternata* causing leaf spot disease in tomato

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Abstract

Background:

The use of pesticides to control various pests and disease carriers in our agricultural fields have degraded the water quality and soil health which leading to environmental pollution. Wild relatives of the crop plants have wide genetic resources which make them tolerant to different diseases. There are numerous reports where these endophytes isolated from wild relatives of crop plants were introduced as bio-inoculants in their close cultivars to suppress the growth of plant pathogens. Therefore, endophytic fungi can be an alternative environment friendly option for suppressing the diseases in crops.

Method & Methodology:

The leaves of *Solanum pimpinellifolium* which is a wild relative of cultivated tomato were collected from two remote villages of Assam and endophytic fungi were isolated. The pathogen causing leaf spot disease in tomato was isolated and identified as *Alternaria alternata*. Secondary metabolites were extracted from the endophytes and were evaluated for their antagonistic activity against the selected pathogen. SEM imaging was also done to observe the destruction of mycelial growth in dual culture plates.

Results & Discussion:

A total of 205 endophytes were isolated from the study sites. The endophytic fungal extracts from *Colletotrichum* sp. and *Penicillium* sp. were able to inhibit the growth of *A.alternata*. Severe rupturing in the mycelial walls of the pathogens were observed in SEM imaging when treated with the potential endophytes. Therefore, exploring the endophytes can lead to the development of novel compounds to control diseases giving a sustainable agricultural approach.

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P - 2

Studies on Shotgun Metagenomic Analysis of Traditionally Fermented Rice-based beverages from Ethnic Tribes in Southern Assam

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Abstract

Background:

Traditional fermented foods have long been recognized for their numerous health benefits along with their potentiality to aid in the treatment of gastrointestinal disorders. These fermented foods have been shown to promote gut health and contribute to a longer, healthier life.

Methodology:

In this study, the high-throughput sequencing V3-V4 region on the Illumina MiSeq platform was employed to investigate the microbiome communities of rice-based fermented beverages consumed by ethnic tribes in Southern Assam, namely Zeme Naga, Hmar, Karbi, Dimasa Kachari, and Tea tribe.

Results:

The fermented rice-based beverages were highly predominated by *Firmicutes, Bacteroides, Proteobacteria,* and *Actinobacteria* exhibiting the highest relative abundance across all tribes. At genus level, significant abundance of *Pediococcus, Lactobacillus, Bacillus, Leuconostoc, Acetobacter, Staphylococcus, Delftia, Erwinia, Klebsiella* and *Chrysebacterium* were found amongst these ethnic tribes.

Conclusion:

Understanding the fermented food microbiome will help to know the relationships between microbial communities and their effect on health of humans amongst the tribes. Furthermore, the use of these fermented products could provide enhanced health benefits to Southern Assam region.

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P - 3

Prevalence and distribution pattern of *AmpC* β-lactamases in ESBL producing clinical isolates of *Klebsiella* spp.

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Abstract

Background: The production of extended-spectrum β-lactamases (ESBLs) and AmpC β-lactamases is the most common explanation of multidrug resistance in clinical isolates of *Klebsiella* spp. The present study was conducted to investigate the prevalence and distribution pattern of AmpC β lactamases genes *bla* $_{CIT}$, *bla* $_{DHA}$, and *bla* $_{FOX}$ in ESBL co-producing clinical isolates of *Klebsiella* spp. in the upper Assam part of Northeast India.

Materials & Methods: For the present study, a total of 160 isolates of *Klebsiella* spp. were procured from the DBT-NER project with ethical clearance no. BT/PR24808/NER/95/858/2017. These were earlier collected from various health settings of upper Assam and identified as drug-resistant. The isolates were screened for antibiotic susceptibility and phenotypic tests were performed on multidrug resistant isolates to confirm ESBL and AmpC β-lactamases production. The distribution pattern of ESBL and AmpC β-lactamase genotype was investigated by polymerase chain reaction (PCR).

Results & Discussion: Results showed that among 107 MDR isolates of *Klebsiella* spp., 67.28 % of isolates were ESBL producers and 56.07 % were potential AmpC producers. 42.99 % of isolates exhibited the coexistence of both ESBL and AmpC phenotype. The PCR results revealed that *bla* $_{CTX-M}$ was the most prevalent ESBL genotype. Among the ESBL producers, 11.11 % of isolates showed co-occurrence with plasmid-mediated AmpC β lactamases genotype which indicated the high prevalence of ESBL and AmpC co-producers in *K. pneumoniae* and *K. oxytoca*, suggesting the possibility of serious public health concerns. Therefore, it is crucial to regularly monitor the spread of multidrug resistance among clinical isolates.

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Evaluation of Antibacterial Potential of Marine Macroalgal Endophytic Bacteria

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Abstract

Background:

Over the last few decades, many antimicrobial compounds were extracted for marine organisms, most of there were secreted by associated microbes. Macroalgae are the ecosystem engineer species in the rocky intertidal marine environment. They evolved with endophytic microbes, who are residing inside of the cell and have a significant mutualistic association with their host, for example, exchange of nutrients, host cell wound repair, stress tolerance, and defense mechanisms. Previous studies shown that, macroalgae associated fungal endophytes can secrete various antimicrobials; however, the potential of their bacterial endophytes was so far overlooked. Main objective of the present study was to evaluate the antimicrobial potential of the marine macroalgal endophytic bacteria.

Method and Methodology:

The macroalgal samples were collected across Visakhapatnam seacoast. The macroalgal fronds were washed, surface sterilized and homogenized to isolate endophytic bacteria using Zobell marine agar plates. Pure cultures were obtained by repeated by streaking on agar plates. The antibacterial activities were tested using cross-streaking and agar overlaying methods against 10 potential human pathogens.

Results and Discussion:

A total of 64 endophytic bacterial isolates were obtained from 24 different macroalgal hosts. Out of 64, 20 isolates exhibited the antibacterial activity against at least one of the potential human pathogens used in this study. Further characterization of those positive isolates and their compounds are ongoing. Our preliminary results suggested that marine macroalgal endophytes could be the potential source for novel antimicrobial compounds.

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P - 5

Isolation and Screening of Potent Cellulose Degrading Microbes (CDMs) and Evaluation of their Antagonism against Significant Tea Pathogen

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Abstract

Antimicrobial resistance is an emerging and alarming problem faced by clinicians while prescribing treatment to patients. Some causative factors behind the increasing rate of AMR are inappropriate dosage of drugs, incomplete drug treatment, prolonged and continuous pathogenic exposure, etc. It is to mention that not only humans but other animals and plants also suffer from AMR. Economically important plants especially the consumable ones are screened and treated well before human use. One of the major objectives of this experiment was the screening of potential Cellulose Degrading Microbes (CDMs) and evaluating their antagonism against significant tea pathogens. In this study, the sample was collected from Tocklai Tea Garden, Jorhat, Assam as it has a broad supplier chain. The physical properties and microbial content of the samples were evaluated. Among all the isolated strains two strains (CDM1 and CDM2) had shown promising antifungal properties against *Pestalotia theae* after performing the poison food technique. The results affirmed the presence of potential antifungal agents in the soil sample which might have provided the tea plants health benefits from the most common disease in the tea estate area of the region, the Grey blight of tea. Due to the presence of multiple types of pathogenic strains, and their antagonistic activity among each other, formation of AMR is a common event. These two strains on the other hand have shown great antifungal properties against the soil microbes overcoming the AMR.

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P - 6

Study of Antibiotic Resistance and Efflux Activity in multidrug-resistant *Serratia marcescens*, isolated from the mid-gut of *Antheraea assamensis* Helfer.

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Abstract

Background:

The multi-drug resistance is a major issue that represents a complicated phenotype characterized by resistance to a variety of structurally unrelated cytotoxic chemicals, and may also be related to antimicrobial treatments. *Serratia marcescens* being predominant in *Antheraea assamensis* Helfer (silkworm) gut, exhibits a high genetic flexibility enabling it to sustain ubiquitously. It has a high level of multi-drug resistance, resulting from the interaction of innate and adaptive resistance components. Aside from their significant nutritional content, silkworms also have various pharmacological qualities that make them advantageous to humans. It aids in lowering blood pressure, thwarts cancer, halts tumor growth, secures the liver, strengthens the immune system, controls blood sugar and lipid levels, and prevents apoptosis. Being a foremost diet in North-East and South-East Asia and its gut harbors drug-resistant *Serratia*, it raises potential health issues. Therefore, the current investigation aims to study the antibiotic resistance pattern and efflux pump activity in *S. marcescens* isolates.

Materials and Methods:

The silkworms were collected from the Dhemaji district of Assam. The silkworm midgut was eviscerated and incubated in Peptone water for 24 hours, to allow bacterial growth. Pure colonies were grown on culture media and identified by biochemical test. Kirby-Bauer's disk diffusion method was used to find out the resistance pattern to different classes of antibiotics. The standard Ethidium Bromide-agar Cartwheel method was used to examine the Efflux pump activity.

Result and Discussion:

The biochemical tests revealed that *Serratia* was prominent in the midgut of *A. assamensis*. The isolates were found to be resistant to penicillin, cephalosporin, carbapenem, tetracycline, fluoroquinolones, and macrolides and through the cartwheel method, it was found that there was an overexpression of efflux pump among the isolates.

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P - 7

An *in-silico* approach to study and characterization of the antimicrobial compounds produced by yeast isolates of traditional rice beer of Tripura

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Abstract

North-east India is full of cultural diversity in traditional believes, rituals as well as in food habit aspects. Each of the seven sister states of north east India has their own variety of fermented food and beverages made in specific manner. Tripura has many tribal communities who prepare their own rice beer with specific delicacies as introduces by the ancestral practices. In this work, rice beer prepared from Chuwak or Zu by tribal communities of Tripura has been collected for screening of yeast associated with them. From these samples two strains- NN/BKS/J1 and NN/BKS/K1 were selected for mass culture. After completion of 15 day mass culture, crud compound has been isolated and purified after purification. These bioactive compounds were subjected for antimicrobial evaluation using standard technique. After obtaining positive antimicrobial analysis, the bioactive compounds were subjected to structural and component evaluation using TLC, UV-VIS spectroscopic analysis, FTIR, NMR and LC-MS study. In the initial phase of component analysis, presence of two compounds was affirmed via TLC. Presence of Carbonyl and Nitroso compounds was confirmed via UV-VIS spectroscopy. FTIR analysis confirmed the presence of several functional groups. LC-MS results confirmed presence of non-volatile compounds as well. The result clearly signifies these bioactive compounds derived via mass culture of NN/BKS/J1 and NN/BKS/K1 as a novel potential antibiotic.

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Molecular Characterization of Carbapenemase mediated Antibiotic Resistance Pattern in *Acinetobacter baumannii* strains isolated from North East India

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Abstract

Background:

The rising antibiotic resistance in *Acinetobacter baumannii* is an extremely serious global crisis. In the last few years, reports of carbapenem-resistant *A. baumannii* have increased due to the extensive use of antibiotics that cause life-threatening hospital-acquired infections and frequent outbreaks.

Materials and Methods:

In this cross-sectional study, *A. baumannii* strains were collected from various sources from different hospitals and primary health care centers of Assam during the period of 2016-2021 (DBT-NER Twinning project ID- BT/PR16669/NER/95/239/2015 dated 18/10/2016, ethical clearance no. DU/Dib/ECBHR (Human)/2021-22/02). The isolates were identified through morphological and biochemical characterization. Antibiotic susceptibility profiling was done by following the Kirby-Bauer disk diffusion method and the results were interpreted as per the CLSI guideline, 2022. Phenotypic characterization of the carbapenemase production (ESBL, MBL, and AmpC) was done by performing different phenotypic tests. PCR amplification of carbapenemase genes was performed for confirmation at the molecular level.

Result and Discussion:

In our study, we isolated 86 *A. baumannii* isolates from different hospitals in Assam and their antibiotic susceptibility profile was prepared. More than 80% of the isolates are resistant to cephalosporins and 50% are resistant at least to one carbapenem drug. Only 13% were sensitive to Cefazolin, 5.1% to Amoxyclave, and 28% were susceptible to tetracycline. On the other hand, 10.32 % of the isolates are found to be resistant to all antibiotics including colistin. Dominance of Bla-TEM, Bla-CTX-M, Bla-SHV, Bla-IMP, Bla-VIM, Bla-OXA-23, and Bla-OXA-58 have been observed in most of the strains.

Conclusion:

Our study concludes that the high prevalence of Multidrug-resistant *Acinetobacter baumannii* is one of the major health risks in North-East India and the country as a whole, establishing the shortage of effective therapeutic options for treatment and this situation needs strict urgent action.

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Novel curcumin derivative can inhibit MurC ligase to obstruct peptidoglycan biosynthesis in multi-drug resistant *Salmonella* Typhi: Evidence from Molecular Docking and Dynamics Simulations

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Abstract

Background:
The emergence of multi-drug resistance in recent *Salmonella* Typhi isolates, causative agent of enteric Typhoid fever, have compelled us to evaluate for alternative therapeutic strategies. The World Health Organization reported 11-20 million cases with 128,000–161,000 deaths per year due to typhoid fever globally. Higher incidence of typhoid fever is seen in children (2-5 years), which is aggravated by elevating antimicrobial resistance in *Salmonella* strains towards first-line antibiotics.

Method & Methodology:
The current study amalgamated ligand-based virtual screening, ADMET screening and antibacterial activity prediction to screen out potent lead molecules whose binding affinities (BAs) were recorded against major druggable *S.* Typhi protein targets, and were compared with that of standard anti-Typhi drugs. The top-docked complexes possessing superior intermolecular affinities were checked for residual-fluctuations through course-grained dynamics simulations.

Results & Discussion:
BA assessment revealed deoxy-tetradeutero- curcumin derivative to be a novel bioactive compound having low binding energy (BE) towards UDP-N-acetylmuramate–L-alanine ligase (MurC) protein, one of the major enzymes contributing towards peptidoglycan biosynthesis. From docking and dynamics simulations, it was interpreted that the curcumin derivative (BE with MurC= -8.00±0.02kcal/mol) can be a potent competitive inhibitor of ATP (BE= -7.65±0.19kcal/mol) for MurC-catalytic domain (contributed by Hydrogen bonds and non-canonical interactions) having low relative RMSF (0.59Å) to inhibit MurC-induced peptidoglycan biosynthesis. The lead molecule additionally showed better binding and inhibition profile against MurC than other commercial antibiotics against their corresponding protein targets. The present findings can pave new paths for designing potential therapeutic strategies against *S.* Typhi.

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A gene interaction network analysis study to understand the mechanism of multi-drug resistance of *Enterococcus faecalis* V583

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Abstract

Background:
Multi-drug-resistant (MDR) pathogenic bacterial strains have caused significant antibiotic resistance worldwide. This challenge requires a thorough understanding of antimicrobial resistance (AMR) genes and mechanisms. The opportunistic and nosocomial bacterial strain *Enterococcus faecalis* V583 has acquired exogenous genes that confer resistance to Chloramphenicol, Tetracycline, Vancomycin, Linezolid, Ampicillin, and other antibiotics.

Method & Methodology:
The current study investigated an gene interaction network analysis of 8 antimicrobial resistance genes and 40 functional partners. ARDB and STRING database provides the information on antibiotic resistance genes and predict protein-protein interactions. Cytoscape is used for constructing of network, modelling and visualising the interaction.

Result & Discussion:
The application of clustering analysis resulted in 4 highly interconnected clusters (C1-C4) that were found to be linked to 3 AMR mechanisms. These mechanisms represent alterations in drug target sites (pbps, mur, and van genes), complete replacement or bypass of target sites (van genes), and the involvement of ATP Binding Cassette (ABC) transporter efflux pump mechanisms (msrA, EF_1680, EF_1682, and pbps). Our study indicate that certain genes, such as pbp1A, 1C, 2A, 2B for β-lactam resistance, ddl, vanBHBRBSBWXYB for glycopeptide resistance, and msrA, EF_1680, EF_1682 for Erythromycin, Macrolides, Lincosamide and Streptogramin-B (MLSB) resistance, as well as murABBCDEFG genes, are significantly involved in the mechanisms of MDR. The application of network analysis has revealed that the genes mraY, pbpC, murE, murG, and murD exhibit 26, 24, 23, 22, and 22 interactions, respectively. The greater number of direct interactions suggests that these genes possess characteristics of hub genes, making them a viable option for targeted drug development in the field of novel drug discovery.

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P - 11

Unravelling the mechanism of multidrug resistance in *Salmonella enterica* serovar Typhi CT18 through gene interaction network studies identifies promising drug targets

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Abstract:

Background:

Salmonella enterica subsp. enterica serovar Typhi (S. Typhi), the causative agent of typhoid fever in humans, has developed resistance to numerous antibiotics over time. Therefore, it is important to focus on comprehending the mechanism of multidrug resistance (MDR) and identifying the potential drug targets for future drug development against *S. enterica* serovar Typhi CT18.

Methods & Methodology:

This study employed gene interaction network analysis, focusing on 44 genes with 275 interactions. Through this, three highly interconnected clusters (C1-C3) were produced by clustering study. The result of functional enrichment analysis revealed drug target modification and the presence of three distinct multi-drug efflux pumps, which were responsible for antibiotic resistance. Notably, seven genes (arnA, B, C, D, E, F, and T) were found to confer resistance to cationic Anti-Microbial Polypeptide (CAMP) molecules by using membrane lipopolysaccharide (LPS) modification. Additionally, we observed that macB played a key regulating hub of the network crucial for the MacAB-TolC efflux pump. Furthermore, we identified five genes (mdtH, mdtM, mdtG, emrD, and mdfA) involved in the Major Facilitator Superfamily (MFS) efflux system, with acrAB contributing to the tolC gene.

Results & discussion:

The five genes, tolC, macB, arcA, acrB, and mdfA, which were associated with a number of resistance pathways, may serve as potential pharmaceutical targets for ineffective therapeutic approaches. Therefore, our study provides profound insights into the multi-drug resistance mechanism in S. Typhi CT18, offering potential drug targets for effective treatment strategies. These findings will prove valuable for experimental biologists in their pursuit of new approaches to combat *Salmonella enterica*.

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P - 12

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

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Abstract

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

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

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

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

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In silico and *in vitro* evidence indicates that aerobactin is a more promising marker than unstable rmpa2 for the detection of hypervirulent carbapenem-resistant *Klebsiella pneumoniae*

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Abstract

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

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

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

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

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P - 14

Antibacterial Activity and Plasmid Curing Analysis of *Phlogacanthus thrsiformis* against CTX-M-Producing Bacteria

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Abstract

Background

The most prevalent extended-spectrum β-lactamases in these past few years in nosocomial as well as community settings are CTX-M enzymes. Due to this, a significant clinical concern arisesas the treatment options of the patients admitted to the hospitals are limited to only carbapenems such as imipenem, meropenem, and ertapenem and fewer inhibitors, which are tagged along with afew β-lactams. So, in order to combat this fast-spreading resistance, there is an urgent need to find alternative antimicrobial substances that also have fewer side effects and less toxicity. So, the present study aims to assess the antibacterial and curing properties of a medicinal plant, *Phlogacanthus thyrsiformis,* against CTX-M-producing bacteria.

Method and methodology

The plant was collected and identified by obtaining accession no. from Guwahati university. The crude extract of *Phlogacanthus thyrsiformis* was assessed for antibacterial activity against CTX-M producing *E. coli* through agar diffusion method. Further, the presence of bioactive compounds was analyze using GC-MS followed by a plasmid elimination assay. An *in silico* study was also performed to analyse the binding affinity between the CTX-M (protein) and phytoconstituents (ligands) using the AutoDock function of MGL tools. The protein was downloaded from the Protein Data Bank, and the structure of phytoconstituents (ligands) was downloaded from the PubChem database.

Result and Discussion

The extract from *Phlogacanthus thyrsiformis* showed antibacterial activity against the CTX-M-producing *E.coli* strain, showing a zone of inhibition. Further, in the plasmid elimination assay, it was observed that the plasmid was successfully eliminated after the 5th treatment (120 hrs). Molecular docking also revealed that most of the ligands identified from *Phlogacanthus thyrsiformis* showed good interactions with the active sites of the selected CTX-M proteins. Among them, beta-sitosterol showed the highest binding score of -7.88, forming two hydrogen bonds with THR216 and ARG276; it is followed by betulin with a binding score of -7.30, forming a hydrogen bond with SER70, SER237, and ASP240.

Conclusion

The findings revealed that the phytoconstituents of *Phlogacanthus thyrsiformis* have good antibacterial properties against CTX-M-producing bacteria and has a good binding affinity against the protein. So, this medicinal plant may be further assessed to check its antibacterial activity against other MDR strains.

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Expression of transcriptional regulator *mgr*B is enhanced in colistin-resistant *Klebsiella pneumoniae*: A report from India

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Abstract

Background: Colistin is considered the last treatment option for multidrug-resistant Gram-negative bacteria. Colistin resistance in *Klebsiella pneumoniae* is mainly due to the lipopolysaccharide modification mediated by PhoPQ and PmrAB as well as the inactivation of the *mgr*B gene. Cases of colistin resistance have been reported in *Klebsiella pneumoniae*, still, studies related to the underlying molecular mechanisms of this resistance are lacking.

Methodology: Eight colistin-resistant clinical *Klebsiella pneumoniae* were selected. Screening of the isolates for colistin resistance was done by Broth microdilution and Rapid polymyxin NP test. PCR was performed for different types of *mcr* genes. *Mgr*B was amplified and sequenced. Quantitative real-time PCR was carried out for *mgr*B, *Pmr*A, *Pmr*B, *Pho*P and *Pho*Q genes. Clonal analysis of the isolates was done by ERIC PCR.

Results and Discussion: 4µg/ml colistin MIC was shown by the isolates. No *mcr* gene was detected. Positive amplification for the *mgr*B gene was found in all the isolates. No mutation was found within *mgr*B gene however, higher expression in the intrinsic resistance genes could be observed when the isolates were exposed in colistin and Mg^{2+} pressure. Clonal analysis exhibited seven different haplotypes of *Klebsiella pneumoniae*. This study provides firsthand knowledge about molecular mechanisms of colistin resistance in *Klebsiella pneumoniae* isolates in this region. Enhancement in the expression of *mgr*B in the presence of colistin and Mg^{2+} pressure regardless of any mutation poses a striking impact in the scenario of resistance mechanisms to colistin in clinical *Klebsiella pneumoniae.*

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P - 16

Antibiogram pattern of virulent *Klebsiella pneumoniae* of environmental origin

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Abstract:

Background:

Klebsiella pneumoniae, a Gram-negative bacterium, is increasingly recognized as a significant contributor to antibiotic resistance and public health concerns. While often associated with healthcare settings, these pathogens are often reported from environmental reservoirs. This study aimed to investigate the antibiogram pattern of *K. pneumoniae* isolated from environmental origin.

Materials & Methodology:

A total of 25 environmental samples were collected from various water bodies including lakes and ponds from different locations of Silchar town. Isolation and identification of *K. pneumoniae* were achieved through biochemical characterization. From those 25 samples, 6 samples were identified as *K. pneumoniae*. Further Antibiotic susceptibility testing was carried out for those 6 confirmed *K. pneumoniae* isolates using the Kirby-Bauer disk diffusion method, in accordance with Clinical and Laboratory Standards Institute (CLSI) guidelines.

Results & Discussion:

All the *K. pneumoniae* isolates from the environmental sources harbored virulence genes and found to be susceptible towards tested antibiotics. These findings underscores environment as a potential reservoir for virulent *K. pneumoniae*. Although observed to be susceptible in nature, a thorough study with larger sample is required to establish their potential of carrying resistance determinants.

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P - 17

Prevalence and Antibiotic Susceptibility Pattern of MRSA in Blood Cultures in a Tertiary Care Centre of South Assam

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Abstract

Background:

Methicillin-resistant *Staphylococcus aureus* [MRSA] is a bacterium which is capable of producing a varied array of infections in humans ranging from mild skin infections to severe systemic diseases. Simultaneous resistance to multiple antibiotics in MRSA is a cause of serious concern. As per WHO report of November 2021, people with MRSA infections are 64% more likely to die thanpeople with drug- sensitive infections.

Methods and methodology:

A retrospective study was carried out from January 2023 to September 2023 inDepartment of Microbiology, Silchar Medical College and Hospital. Antibioticsusceptibility testing of blood culture samples was carried out on Mueller Hinton Agar using Kirby Bauer disc diffusion method. Phenotypic detection of MRSA was done using Cefoxitin 30 µg disc. The zones of antibiotics were measured and interpreted as per CLSI 2023 guidelines.

Results:

A total of 259 blood culture samples showed the presence of *Staphylococcusaureus* of which, 143 [55.21%] were MRSA and 116 [44.79%] were MSSA. MRSA was found to be more common in males [61.54%] as compared to females [38.46%] and also more common in paediatric age group [66.43%]. Majority of isolates were from ICU. Amongst MRSA, highest resistance was observed against Erythromycin [81%] followed by Azithromycin [76%], Ciprofloxacin [68%], Levofloxacin [65%], Cotrimoxazole [49%], Clindamycin [45%], Amikacin [24%] and Doxycycline [15%]. However, all isolates were sensitive to Linezolid.

Discussion:

Similar prevalence observed in studies by Devarsi Choudhury et al [61.88%], Sangeeta Joshi et al [48%],Haji Mohammad Naimi et al [56%]. MRSA pose a serious threat in terms of patient care due to its property of multi-drug resistance. Thus, there should be strict adherence to infection control practices such as adopting standard precautions like hand hygiene, avoiding misuse/overuse of antibiotics, de-escalation strategies, using combination drugsto combat the emergence of MRSA and thereby reduce patient morbidity and mortality.

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P - 18

Surveillance of Healthcare-associated bloodstream infections in the Neonatal Intensive Care Unit of a tertiary care hospital in Varanasi, north India

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Abstract

Background and objective:

Health-care-associated infections (HAIs) are a serious threat to patient safety. They cause substantial morbidity and mortality across various healthcare settings including neonatal intensive care units (NICU). This study was undertaken to determine the incidence of HA bloodstream infection (HA-BSI) in the NICU of a tertiary care hospital in Varanasi, north India.

Methodology:

Data were collected in a systematic manner based on the Centers for Disease Control and Prevention (CDC) guidelines for surveillance of HAI for a period of one year (Jan-Dec,2022). HAI rate was calculated using the formula: No. of cases/No. of patient days × 1000.

Result:

Among 1085 admitted newborns, the incidence of HA-BSI was 15.80/1000 patient days. HAI was seen in neonates having mean birth weight 1,722.5 ±113.906 g, mean gestational age 29.6 ±1.38, and mean duration of hospital stay 13.8 ±4.081day. Among the 80 cases of HA-BSI, recognized pathogens were 22 (27.5%) *Klebsiella pneumoniae*, 16 (20%) non-albicans *Candida*, 13 (16.25%) methicillin-sensitive *Staphylococcus aureus*, 10 (12.5%) *Candida albicans*, 10 (12.5%) *Acinetobacter baumannii*, 4 Coagulase-negative staphylococci, 3 (3.75%) Methicillin-resistant *Staphylococcus aureus*, 1 (1.25%) *Escherichia coli* and 1 (1.25%) *Enterococcus*. Mortality was 56.78%.

Conclusion:

HAI rate was comparable to the existing data in NICU in India. Besides, strict implementation of fully complied hand hygiene, surface disinfection and surveillance trainings of infection control measures should be prioritized.

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P - 19

Prevalence of ESBL producers in family *Enterobacteriaceae* isolated from pus samplesin a tertiary care hospital of southern Assam.

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Abstract

Background:
Extended Spectrum Beta Lactamases (ESBL) producing Gram Negative Bacilli is a worldwide problem being the most common causes of nosocomial pathogens. Increasing number of ESBL producers reduce the treatment options resulting in emergence of multidrugresistant strains, treatment failure and increased mortality.

Method & Methodology:
Total 100 isolates of *Enterobacteriaceae* had been taken from pus samples. All *Enterobacteriaceae* isolates from pus samples are received from hospital for gram staining, manual culture. Antibiotic susceptibility testing of these isolates were performed by disk diffusion method on Mueller-hinton agar as per CLSI guidelines. All isolates resistant to Cefoperazone and ceftriaxone were confirmed phenotypically for ESBL production by using combined disk synergy test. Cefoperazone and Cefoperazone-Sulbactum disk were used for the detection of ESBL production. A difference of ≥ 5 mm between diameters of zone of inhibition of Cefoperazone and Cefoperazone-Sulbactum disk were regarded as confirmatory for ESBL production.

Result:
100 different isolates of *Enterobacteriaceae*. 87(87%) ESBL producers and 13(13%) non-ESBL producers were isolated. Among the ESBL producers *E.coli*(52) was the most common organism followed by *Klebsiella spp.*(16), *Proteus spp.*(13), *Enterobacter spp.*(4) and*Citrobacter spp.*(2).

Discussion:
ESBLs are becoming increasingly complex and diverse, and increasing challenges for those creating guidelines for the detection of ESBLs in the clinical microbiology laboratory. The increasing prevalence of antibiotic-resistant bacterial infections seen in clinical practice stems from antibiotic use within medicine.

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P - 20

Identification of potential key genes linked to Hepatitis B Virus-induced Hepatocellular Carcinoma: A Bioinformatics Approach

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Abstract

Background:

Hepatocellular carcinoma (HCC) is a prevalent form of liver cancer with a significant global health burden. Chronic infection with the hepatitis B virus (HBV) is a major risk factor for the development of HCC. Understanding the potential key genes underlying hepatitis B virus –induced hepatocellular carcinoma is crucial for effective diagnosis, treatment, and prevention strategies.

Method:

This study employed bioinformatics methods using Gene Expression Omnibus datasets to identify differentially expressed genes (DEGs) in HCC. DEGs were analyzed with R packages, and Gene Ontology and KEGG enrichment analyses were conducted using the DAVID database. A protein-protein interaction (PPI) network was built in STRING, leading to the identification of hub genes through cytoscape tool -cytoHubba. These findings were verified in GEPIA, TNMplot and the protein levels of hub genes assessed using the Human Protein Atlas. Prognostic values of hub genes were analyzed with GEPIA, and a drug-gene interaction network was constructed with the Comparative Toxicogenomics Database (CTD).

Results and Discussion:

The result showed 1263 DEGs in which 670 were upregulated and 593 were downregulated, enriched in complement activation, DNA packaging complex, antigen binding. The PPI network analysis highlighted P53 signalling pathway and the cell cycle for module analysis. Nine hub genes were identified, significantly upregulated in HCC, and connected to poor patient survival. Additionally, toxicogenomics analysis suggested specific drugs that could reduce expression levels of these hub genes. Overall, this study unveiled key genes and pathways relevant to HCC pathogenesis, potentially informing future targeted therapies and prognosis assessments for HCC.

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Phyto-compounds as inhibitors of lipopolysaccharide biosynthesis: therapeutic implications in gut dysbiosis and Parkinson's disease

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Abstract

Background:

The association of disturbed intestinal microenvironment and Parkinson's disease (PD) is a well speculated and appreciated area of research. The dishomeostasis in the quantity and quality of intestinal microorganisms is a considered factor to contribute in the pathogenesis of PD, plausibly through the modulation of the host body immune system. In the recent years, several case studies as well as animal models have suggested the role of Gram negative bacteria in releasing the endotoxin lipopolysaccharide (LPS) from the outer membrane of their cell envelope which is a crucial initiator of the inflammatory cascade of host body. Despite several investigations being carried out to devise synthetic inhibitors for LPS biosynthesis, lesser solubility and risk of side effects hamper the therapeutic potential of these synthetic inhibitors. Besides, antimicrobial resistance is a crucial factor to be considered that lowers the pace of treatment of diseases associated with microbial dysbiosis. Thus, there prevails the need for devising more potential inhibitors of LPS biosynthesis which would come with better pharmacology and lesser toxicity.

Method & methodology:

The present study investigated the potential of selected phyto-compounds to inhibit the biosynthesis of LPS through computational approach.

Results and discussion:

This study presents the potential of a number of phyto-compounds (namely berebrine, cabucine, santiaguine, etc.,) to inhibit the biosynthesis of LPS and highlights their prospects to be considered for PD treatment through their antimicrobial and anti-inflammatory abilities, however, further investigations are warranted.

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Carbapenem Resistance in Gram Negative Bacilli in a Tertiary Care Hospital of South Assam

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Abstract

Introduction:

The rapid emergence and variations of antibiotic resistance among common gram negative bacteria has caused a significant concern specially in India and all over the world because of high mortality and morbidity rates. Carbapenem resistant among gram negative bacilli is an emerging threat and substantial hazard.

Aims and objectives:

1. To determine Carbapenem resistance in Gram Negative Bacilli obtained from clinical isolates in a tertiary care hospital of South Assam
2. Phenotypic detection of Carbapenem resistance using Modified Hodge method

Methodology:

This retrospective study was done in the Department of Microbiology, Silchar Medical College and Hospital from the month of January, 2023 to the month of June 2023. A total of 1239 isolates of Gram-negative bacteria from different clinical samples were included in the study. The clinical samples included in the study were pus, urine and blood collected from various patients admitted in wards and those coming to OPDs of the hospital. The bacterial isolates were identified according to standard microbiological procedure.

Antbiotic susceptibility testing of Gram-negative isolates was done by Kirby Bauer`s disc diffusion method. Carbapenemase detection was done by Modified Hodge Method (MHT).

Results:

Out of 1239 isolates, 23 (1.8%) showed resistance to carbapenem by disc diffusion. Maximum number of carbapenem resistant isolate were found in urine(n =5,out of 113) yielding 4.4% ,followed by blood samples (n= 3 out of 211) yielding 1.4% and pus (n=8,out of 715) yielding 1.1%.Carbapenemase production was maximum for *Klebsiella* spp. followed by *Pseudomonas* spp. and *Escherichia coli* spp. among all other gram negative bacilli.

Conclusions:

Carbapenem resistance due to production of carbapenemase is prevalent in our hospital. MHT is a simple test in the routine lab for detection of carbapenemases.

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P - 23

Screening of endophytic microorganisms from *Plectranthus amboinicus* for its antimicrobial activity

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Abstract

Background:

The current problem which is emerging globally is the increase of antimicrobial resistance (AMR) and it refers to the ability of the microorganisms like fungi, bacteria, viruses etc. to stop the action of antimicrobial agents thereby increasing the risk of pathogens. Several reports showed the probable dangers of AMR to global public health. *Plectranthus amboinicus* has many medicinal uses, especially for the treatment of common illnesses such as, of cough, stomachache, headache, skin infection, asthma, and urinary conditions.

Method and methodology:

A variety of relationships exist between endophytes and their host plants, ranging from mutualistic or symbiotic to antagonistic or slightly pathogenic. As the species *P amboinicus* have medicinal values and some antimicrobial properties hence we understand that the microorganisms residing in the host plant is having the capability of mimicking the characteristics of the host. Therefore, the present study was planned to look for antimicrobial activity of the organisms residing in the plant, screening relevant bioactive compounds with the help of GCMS analysis, from the endophytes.

Results and discussion:

The results showed capacity of the isolated endophytes to inhibit the growth of the pathogenic organisms, *Mycobacterium smegmatis* and *Escherichia coli*. GCMS analysis of the *P amboinicus* isolates proved the presence of cycloserine and furfural showing good antimicrobial activity. The antimicrobial properties of the samples against the selected strains indicates the potential usefulness of endophytes in treatment of various pathogenic diseases which in future may develop as a potential antimicrobial agent with perhaps reduce toxicity and adverse effect.

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Role of sub-inhibitory concentrations of carbapenem in transcriptional response of *bla*$_{OXA-232}$ in carbapenem-resistant *Escherichia coli* of clinical origin

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Abstract

Background

OXA-232 is a five amino acid substitutions variant of OXA-48. With recent reports of this emerging variant from India, the study characterizes *bla*$_{OXA-232}$ in *Escherichia coli* and investigate their transcriptional response against sub-inhibitory levels of carbapenems.

Materials & Methodology

A carbapenem non-susceptible *Escherichia coli* (BJD_EC25199) isolated from urine was received in January, 2022 from Silchar Medical College and Hospital, Silchar, Assam, India. Identified through VITEK® 2 Compact automated System (Biomerieux, France); BJD_EC25199 was investigated for carbapenemase production *via* Rapidec® Carba NP test (Biomerieux, France). Susceptibility testing against carbapenems were performed through Kirby-Bauer Disc Diffusion and agar dilution method as per CLSI, 2022 guidelines. PCR targeting *bla*$_{OXA-232}$ was performed followed by investigation of horizontal gene transferability and PBRT. Transcriptional expression of *bla*$_{OXA-232}$ in wild, transformant and transformant under one-week carbapenem exposure; against sub-inhibitory carbapenem stress were investigated by Quantitative Real-time PCR.

Results & Discussion

The carbapenem-resistant *Escherichia coli* (MIC ≥64 µg/ml) was harbouring *bla*$_{OXA-232}$ gene located in a conjugatively transferable I1-Iy Inc type plasmid. With increase in meropenem pressure, the expression level of *bla*$_{OXA-232}$ was increased in the experimental strains. The expressional level of *bla*$_{OXA-232}$ increased with the increase in imipenem pressure in the wild strain, however, the level was found to decrease in the transformant and transformant under one-week carbapenem exposure. Sub-inhibitory meropenem pressure induces *bla*$_{OXA-232}$ expression which could lead to inducible resistance during therapy. The conjugatively transferable I1-Iy Inc type plasmid harbouring *bla*$_{OXA-232}$ can be a potential source for horizontal expansion of this carbapenem resistance determinant and warrants urgent monitoring.

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Expressional analysis of *sdiA* gene with Acyl Homoserine Lactone (AHL) and carbapenem exposure

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Abstract

Background

Numerous bacteria rely on a cell density-dependent communication system known as quorum sensing (QS) to regulate several bacterial functions. The QS system described for *E.coli* include the orphan SdiA regulator which can sense AHL from other bacteria in the surrounding environment and regulate the expression of virulence factors, pathogenic gene expression, toxin production and extracellular polysaccharide synthesis. Due to the emergence of carbapenem resistant *E.coli* in this region, a more thorough understanding of its virulence control mechanisms is essential. Therefore, in this study the transcriptional response of *sdiA* gene was checked under exogenous AHL and sub inhibitory concentration Imipenem exposure.

Materials & Methodology

20 clinical isolates of *E.coli* was obtained from Silchar Medical College and hospital as secondary sources. The presence of bla_{NDM} was checked in the isolates by PCR. The bla_{NDM} harbouring isolates were then subjected to treatment with 10% SDS for 20 consecutive days for elimination of plasmid. The transcriptional response of *sdiA* gene was checked in the wild as well as the cured isolate under AHL and subinhibitory concentration imipenem exposure by quantitative real-time Polymerase Chain Reaction (PCR).

Results & Discussion

Seven clinical isolates were phenotypically found to be carbapenem resistant among which two isolates harboured the bla_{NDM} gene. Plasmid was successfully eliminated from one isolate after 18th treatment with 10% SDS. The transcriptional response of *sdiA* gene in the wild and cured isolates revealed that the expression of *sdiA* gene was enhanced when the isolates were grown with exogenous AHL, imipenem and in combination with AHL and imipenem at 1µg/ml concentration, respectively. The data obtained in the present study showcased that imipenem at sub-inhibitory concentration may act as a signal molecule to enhance the expression of quorum sensing receptor *sdiA* gene in *E.coli*.

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Occurrence of diverse aminoglycoside acetyltransferase (*aac*) genes in *Escherichia coli* with aminoglycoside resistant phenotype

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Abstract

Background-

The aminoglycosides are potent, broad-spectrum, bactericidal antibiotics. These are commonly prescribed for infections caused by Gram-negative pathogens. They were among the first group of antibiotics to be used in clinical practice. Aminoglycoside antibiotics act by inhibiting protein synthesis. They bind to the A- site on the 16S ribosomal RNA of the 30S ribosome. The current study highlights the prevalence of different aminoglycoside acetyltransferase (*aac*) genes in the aminoglycoside resistant *Escherichia coli*.

Methodology-

Fifty bacterial isolates were isolated from the different clinical samples and cultured in different agar media. Biochemical tests were performed to determine the isolates to be *Escherichia coli*. Antibiotic susceptibility test (AST) was done by Kirby-Bauer disc diffusion method using different aminoglycoside antibiotics like Amikacin, Netilmicin, Gentamicin, Tobramycin and Kanamycin. Molecular characterisation of the isolates of the confirmed *E. coli* were done by PCR for aminoglycoside acetyltransferase (*aac*) gene.

Result and discussion-

On performing Kirby-Bauer disc diffusion method, the study isolates showed maximum resistance to Tobramycin antibiotic followed by Gentamicin, Amikacin, Kanamycin and Netilmycin. Also on molecular characterisation, most of the resistant isolates harboured *aac(6')Ib* gene followed by *aac(3)-IIc, aac(3)-I* and *aac(6')II.* Presence of multiple variants of *aac* genes in a single centre signifies diverse source of origin and acquisition mechanism within the study isolates.

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Assessing the prevalence of SCC*mec* Type II and Type V in MRSA: Tracking the Genetic Environment for Enhanced Infection Control

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Abstract

Background: Understanding the significant diversification of mobile genetic elements, such as Staphylococcus cassette chromosome (SCC*mec*), is crutial for escalation of antibiotic resistance trait. The genetic composition of the 12 publicly accessible SCC*mec* elements, along with their genetic content, has been associated with the adaptation and evolution of MRSA in diverse environments, including hospitals, communities, and livestock which creates a significant reservoir with the potential for widespread infection transmission.

Methods: We conducted a study with a cohort of 150 MRSA isolates. These isolates underwent SCC*mec* typing through multiplex PCR followed by sequencing of the amplified products. Furthermore, we screened all isolates with SCC*mec* types for the presence of antibiotic resistance pattern. To gain insight into clonal relatedness, MLST was carried out for isolates with different antibiotic resistance determinants among SCC*mec* types.

Results & Discussion: The study confirmed the presence of SCC*mec* types I, II, III, IV, V, VI, VII, VIII, and XII among 84 MRSA isolates. Notably, SCC*mec* type II with ST1551 and type V with ST2416 were identified as strongly associated with multidrug resistance and were highly prevalent in the study area. Through hierarchical analysis of the antibiotic resistance profiles among these SCC*mec* types, the study identified eighteen distinct combinations of antibiotic resistance patterns. Notably, SCC*mec* types I, II, III, V, VI, VII, VIII, and XII displayed resistance to a broad spectrum of antibiotics. Among these, SCC*mec* types II and V demonstrated the highest number of unique antibiotic resistance patterns.

Conclusion: This study provides valuable insights into a novel and simplified detection technique for the SCC*mec* cassette chromosome, primarily focusing on SCC*mec* types II and V. The findings from this epidemiological investigation offer significant assistance in tracking and tracing the genetic environment of these resistance determinants, ultimately contributing to more effective strategies for infection control and antibiotic resistance management.

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Transcriptional Expression of *vanG* regulon in *Staphylococcus aureus*

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Abstract

Background: Therapeutic options for staphylococcus infections have been raised due to the emergence of VISA and VRSA. *vanG* is one of the genes that is responsible for moderate vancomycin resistance and reported from enterococci by producing modified peptidoglycan precursor D-Ala-D-Ser. The current investigation was designed to study transcriptional expression of three regulatory genes of *vanG* operon under sub inhibitory glycopeptide stress.

Materials & Methodology: *Staphylococcus aureus* of clinical origin which were previously confirmed to carry *vanG* were selected for this study. Antimicrobial susceptibility was performed by disc diffusion method. The expression of *vanG* operon genes in response to glycopeptide stress was done quantitative real-time PCR assay.

Results & Discussion: Presence of *vanG* was pre confirmed in all the six isolates. Kirby Bauer disk diffusion showed that all the isolates were resistant to all tested antibiotics expect tigecycline and imipenem. In the present study Quantitative relative PCR results showed that there was down regulation of *vanG* when vancomycin, teicoplanin stress was applied. A previous study has reported inducibility of *vanG* in the presence of vancomycin which reported a three-to-five-fold increase in expression. In the current investigation it was seen that $vanU_G$ was expressed more than threefold under teicoplanin exposure. $vanR_G$ showed a significant enhancement in expression when exposed against vancomycin. In case of teicoplanin expression was inversely proportional with increasing concentration of the antibiotic. $vanS_G$ showed down regulation against 0.5 µg/ml stress of vancomycin and teicoplanin. Teicoplanin exposure at 1 µg/ml showed a ten-fold increase in $vanS_G$ expression. However, the previous study showed that the expression of P_{UG} remained unchanged in the absence of *vanR* and *vanS*. The present study underscored that expression of *vanG* and its regulatory gene operons are dependent on concentration of vancomycin and teicoplanin exposure on *S.aureus.* The inducibility of different regulatory genes under vancomycin and teicoplanin exposure will help to design targets for future antimicrobials.

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Presence of *Transposon* (*Tn1546*) and *Insertion Sequence (IS1216V)* elements in Vancomycin non-susceptible *Staphylococcus aureus*

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Abstract

Background:

Vancomycin-resistance *Staphylococcus aureus* (VRSA) possess a significant threat to public health due to limited treatment options. Presence of mobile genetic elements in these pathogens further expand horizontal spread of resistance determinants. In the present study, occurrence of mobile genetic elements in *S. aureus* was determined.

Methodology:

In this study, a total of 67 isolates were studied. Then phenotypic screening done by vancomycin screen agar with 6 µg/ml. PCR was performed to detect *Transposon* (*Tn1546*) and *Insertion Sequence (IS1216V)* elements among study isolates.

Results and Discussion:

Out of 67 isolates 36 were confirmed as *S. aureus*. Twenty-one isolates were found to be vancomycin non-susceptible. Among them *Tn1546* was observed in eight isolates and *IS1216V* was found in six isolates. This study highlighted that mobile genetic elements can be potential carrier for expansion of vancomycin resistance in *Staphylococcus aureus.*

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P - 30

Transcriptional response of *sdiA* gene in *Escherichia coli* co-cultured with *Pseudomonas aeruginosa* of carbapenem resistant phenotype

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Abstract

Background

Pseudomonas aeruginosa is a model Quorum sensing organism and it synthesizes signal molecule, known as acyl-homoserine lactone (AHL). *E. coli*, which is an orphan quorum sensing organism, does not code for any synthase gene but codes for a receptor which is known as *sdiA*. In the present study, *E. coli* was co-cultured with *Pseudomonas aeruginosa* and the expression of *sdiA* gene in *E. coli* was checked.

Methodology

A total of 20 isolates were obtained as secondary sources from Silchar Medical College and Hospital. Antibiotic susceptibility test and Minimum inhibitory concentration determination test were performed and then the presence of bla_{NDM} gene in the resistant isolates was checked by PCR. Plasmid elimination was performed by treating the resistant isolates using 10% SDS. The wild and the cured isolates were co cultured with *Pseudomonas aeruginosa* with imipenem exposure at 1 µg/ml and then the transcriptional response of *sdiA* gene in the wild as well as cured mutant was checked by Quantitative Real-Time PCR.

Results & Discussion

Among 20 isolates, 7 isolates were found to be carbapenem resistant. Among the 7 resistant isolates, 2 isolates were found to harbour bla_{NDM} gene. After 18th passage, PCR analysis revealed the successful elimination of bla_{NDM} gene from one isolate. The MIC of the cured isolate reduced from 64 µg/ml to 8 µg/ml concentration. The transcriptional response of *sdiA* gene was found to be increased in both the cured and mutant isolate when these isolates were co-cultured with *Pseudomonas aeruginosa* with imipenem exposure at 1 µg/ml concentration. The enhanced transcriptional response of *sdiA* gene infers that imipenem at 1 µg/ml concentration may act as signal molecule to enhance the quorum sensing phenomenon in *E.coli*.

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Anti-virulence property of Linoleic acid against multidrug resistant hypervirulent *Klebsiella pneumoniae*

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Abstract

Introduction: Antimicrobial resistance is a global threat and the situation becomes more critical as no new groups of antimicrobials are on pipeline. Anti-virulence seems to be the most promising alternate strategy to tackle this global threat and block the virulence factors within a bacterium thereby limiting its pathogenic behaviour. This strategy is found to be advantageous as emergence resistance against anti-virulence compounds is very low. The rise in antimicrobial resistance among the bacterial pathogens is a global concern. In the present study, anti-virulence activity of Linoleic acid was assessed in multi-drug resistant (MDR) hypervirulent *Klebsiella pneumoniae.*

Materials and methods: Modelling of the proteins, ligand binding and molecular docking were performed by in-silico analysis using different bioinformatics tool and software. Minimum Inhibitory Concentration (MIC) was determined for all the anti-virulent compounds by standard protocol. All the isolates were tested for the presence of ESBL genes, as well as carbapenemase and aminoglycoside resistance-encoding genes. Quantitative Real-Time PCR was performed selecting two isolates harboring *rmpA*, *rmpA2* and *iroC*.

Results: In-silico analysis observed that linoleic acid could be the best fit in comparison with the other compounds. None of the compounds showed any inhibitory activity. All the study isolates were carrying bla_{SHV}, bla_{CTXM}, and *aac(6')-Ib* whereas, bla_{NDM} and bla_{OXA-48} was present in 4 isolates. Transcriptional expression pattern of both the isolates harboring *rmpA* was marginally increased when linoleic acid stress was given.

Conclusion: This study documented that linoleic acid have anti-virulence property without any antimicrobial activity. This study also lays the platform for further studies on this aspect of curbing or tackling virulence and morbidity and mortality thus caused by hypervirulent *K. pneumoniae* strains.

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Transcriptional response of *bla*$_{OXA-48}$ under sub-inhibitory carbapenem exposure

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Abstract

Background: OXA-48 is one of the big five carbapenemases and is frequently reported in Carbapenem Resistant Enterobacteriaceae (CRE) which are categorized as pathogen of "critical priority" by the World Health Organization (WHO). With the recent reports of *bla*$_{OXA-48}$ harbouring *E. coli* from this region, this study aimed to analyse transcriptional response of *bla*$_{OXA-48}$ with and without sub-inhibitory concentration of carbapenem exposure.

Materials & Methods: A total of 140 clinical isolates of *E. coli* was obtained from Silchar Medical College and Hospital, Silchar, Assam, India as secondary sources during January 2023 to April 2023. Susceptibility testing followed by determination of minimum inhibitory concentration (MIC) for carbapenems was performed using Kirby-Bauer disc diffusion method and agar dilution method as per CLSI, 2022 guidelines respectively. Rapidec® Carba NP test (Biomerieux, France) was used to investigate carbapenemase production. PCR targeting *bla*$_{OXA-48}$ was performed followed by investigation of horizontal gene transferability of *bla*$_{OXA-48}$ and plasmid based replicon typing (PBRT). Transcriptional expression of *bla*$_{OXA-48}$ in wild, transformant and transformant under one-week carbapenem exposure; against sub-inhibitory carbapenem stress were investigated by Quantitative Real-time PCR.

Results & Discussion: Among 140 multidrug resistant *E. coli* isolates, sixty isolates exhibited resistance towards carbapenems. Rapidec® Carba NP test detected carbapenemase activity in fifty-five carbapenem resistant *E. coli* and five among them were harbouring *bla*$_{OXA-48}$ within conjugatively transferable I1-Iy Inc type plasmid. The transcriptional response of *bla*$_{OXA-48}$ in wild, transformant and transformant under one-week carbapenem exposure revealed that the expression of *bla*$_{OXA-48}$ gene was enhanced under imipenem exposure. This present study highlights that imipenem exposure increases the expression of *bla*$_{OXA-48}$ and I1-Iy Inc type plasmid can act as a carrier for horizontal transfer of this carbapenem resistance determinant and warrants urgent monitoring.

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Transcriptional expression analysis of *ItaTR* toxin-antitoxin system in aminoglycoside resistant *Escherichia coli*

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Abstract

Background:

The toxin-antitoxin (TA) systems are systems in which an unstable antitoxin inhibits a stable toxin. The toxin-antitoxin systems are well known to have many functions like bacterial stress response, biofilm formation, intestinal colonisation, virulence, antibiotic tolerance and persister cell formation. There are various types of TA system, and the type-II module is the most widely studied class. In this module, both toxin and antitoxin are small proteins. The *ItaTR* toxin–antitoxin *is a* type II TA module found in *Escherichia coli*. *ItaT* forms a tight complex with the *ItaR* antitoxin, which represses the transcription of the *ItaTR* operon. The current study emphasizes on the transcriptional expressional pattern of the *ItaTR* TA system in aminoglycoside resistant *Escherichia coli*.

Methodology:

50 confirmed *Escherichia coli* isolates were subjected to antibiotic susceptibility test with different aminoglycoside antibiotics and molecular characterisation was done to see the prevalence of *ItaT* and *ItaR* genes. Both the wild and mutant types were given 1µg/mL and 2µg/mL concentration stress of Gentamicin antibiotic to observe the change in transcriptional expression pattern.

Results & Discussion:

10 isolates were found harbouring *ItaTR* genes after molecular characterisation and were also found resistant to all the aminoglycoside antibiotics, i.e., Amikacin, Gentamicin, Netilmycin, Kanamycin and Tobramycin. The isolates were cured giving 10% SDS treatment for consecutive 10 days and then the transcriptional expression for *ItaT* and *ItaR* genes were observed for both wild and mutant types and it was seen that with the increasing concentration of Gentamicin, the isolates showed an enhanced expressional pattern in both the cases. This implicates that the *ItaTR* TA system can act as a future endogenous biomarker for AMR detection.

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Detection of resistant *Salmonella* spp. and their pathogenicity island from drainage water

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Abstract

Background:

Pathogenicity islands in *Salmonella* spp. from drainage water is a crucial aspect of understanding the potential public health risks associated with this pathogen. *Salmonella* spp. is the causative agent of typhoid fever, and its presence in drainage water can pose a significant threat to the surrounding population.

Materials & Methodology:

A total of 30 samples were collected from different sites of Silchar town. Biochemical test was performed to confirm the isolates. Multiplex PCR was performed for the detection of *sipA, sipB, ssefF, misL, pipA, safD, STY2876, sefA, envE*, and *narP* genes. Further antimicrobial susceptibility testing of the positive isolates was done.

Result & Discussion:

Out of 30 samples, *Salmonella* spp. was found in all the samples. Among 30 isolates 16 were found to have the *safD* gene, 15 *narP* gene, 15 *pipA* gene, 14 *MisL* gene, 9 *sipA* gene, 9 *sseF* gene, 4 *sipB* gene, 4 *envE* gene, and 1 *STY2876* gene. Among 30 isolates most susceptibility rate was against Co-trimoxazole [n=24], followed by Norfloxacin [n=17], Ceftriaxone [n=16], Ampicillin [n=5], Cefepime [n=2]. In this study Presence of *Salmonella* spp. in drainage sample underscores presence of asymptomatic typhoid carrier within the community.

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P - 35

Carriage of *bla*$_{TEM}$ and *bla*$_{NDM}$ *via* Inc X replicon type plasmid within multidrug resistant *Escherichia coli* and *Klebsiella* spp. of environmental origin

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Abstract

Background:

Beta-lactam antibiotics are preferred treatment regime in treating infections caused by multidrug resistant Enterobacteriaceae. However, the enzymatic inactivation of these antibiotics through beta-lactamases plays a major role in beta-lactam resistance and pose an imminent threat to global public health. Current study reports the presence of the beta-lactamases *bla*$_{TEM}$ and *bla*$_{NDM}$ within Enterobacteriaceae isolated from drainage water samples.

Materials & Methodology:

Drainage water samples were collected from nearby healthcare settings of Silchar town. Carbapenemase and ESBLs production were investigated through Rapidec® CarbaNP test and combined disc diffusion method. Susceptibility testing was performed using Kirby-Bauer disc diffusion method and agar dilution method (CLSI, 2022). PCR targeting carbapenemase and ESBLs genes were performed followed by investigation of horizontal transferability, PBRT and SDS treatment of the isolates at various concentrations.

Results & Discussion:

A total of forty-eight Enterobacteriaceae consisting of 28 *Escherichia coli* and 20 *Klebsiella pneumoniae* were isolated from the drainage water samples. Among them nine isolates were carbapenemase producers while thirteen were ESBLs producers. Twenty isolates were resistant to cephalosporins and seven were carbapenem-resistant. *bla*$_{TEM}$ was identified in three *Escherichia coli* and one *Klebsiella* spp. carried by a conjugatively transferable Inc X type plasmid while *bla*$_{NDM}$ was identified in a sole *Escherichia coli*. This study findings highlight that this replicon type can be a potential source for horizontal expansion of this resistance gene and warrants urgent monitoring. SDS can be used as an anti-plasmid compound along with disinfectants to halt the dissemination of these resistance determinants within hospital and clinical settings.

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P - 36

Occurrence of *FosA* mediated fosfomycin resistance in *Escherichia coli*

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Abstract

Introduction:

The primary cause of urinary tract infections (UTIs), including cystitis, is *Escherichia coli*. Fosfomycin is the drug of choice for the treatment of UTI infections in many countries due to widespread resistance to other antibiotics. Globally, there has been a growing identification of plasmid-mediated fosfomycin resistance in *Escherichia coli* isolates, which poses challenges to treatment. The purpose of this study was to identify the plasmid-mediated fosfomycin resistance genes among the *Escherichia coli* isolates from urinary tract infections in India.

Methodology:

A total of 134 *Escherichia coli* isolates were collected from secondary sources of Silchar Medical College and Hopitals, Assam from patients of urinary tract infections cases. All isolates were tested for fofomycin resistant using Kirby Bauer Disk Diffusion method and MIC was performed according to the CLSI, 2022 guidelines. All fosfomycin resistant isolates were screened for the presence of the fosfomycin modifying enzyme gene by polymerase chain reaction. Horizontal mobility and spreading of these genes were confirmed by transformation and PCR-based replicon typing was determined to know the plasmids type. Transcriptional expression of the resistant isolates was studied by performing RT-PCR and Ct value of the tested isolates was interpreted and compared with fosfomycin stress and wild type of the test isolates.

Results:

The present study revealed that out of the 134 *Escherichia coli* isolates 55 (41%) isolates were resistant to fosfomycin. By performing simplex PCR, it was found that out of 55 resistant isolates 6 isolates were harboured *FosA* gene. MIC was performed for the 55 isolates and it was observed that 28 isolates showed MIC above breakpoints and rest 5 isolates showed intermediate range and 4 isolates showed susceptible. *FosA* gene appeared to be transferable by transformation and it is found to be carrying *FIC* Inc type of plasmids having 262bp. Expression of fosfomycin enhanced transcriptional expression of *FosA* gene.

Conclusion:

The study highlights the presence *FosA* gene in *Escherichia coli* within single study centre. The presence of this gene further increases the burden of fosfomycin resistance complicating treatment option. Further molecular investigation should be carried out to detect the source of acquisition of these gene.

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Occurrence of multidrug resistant shiga toxigenic *E. coli* from environmental origin: A study from southern Assam

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Abstract

Background:
Shiga toxin-producing *Escherichia coli* (STEC) produces a potent toxin known as shiga toxin. STEC causes gastrointestinal illness in humans and even kidney failure. Sub-inhibitory dose of antibiotics alters a range of expression in bacteria and there are reports regarding the influence of sub-inhibitory dose of antibiotics in shiga toxin production. The sub-inhibitory concentration of antibiotics is easily achievable in wastewater systems as wastewater receives large amounts of antibiotic residues as hospital wastes. Thus, this study was undertaken to screen the wastewater samples for STEC and analyse the expressional pattern of shiga toxin under sub-inhibitory dose of antibiotic.

Material & Methodology:
31 *Escherichia coli* isolates were recovered from drain effluents which were collected from different sites of Silchar, India. PCR assay was done targeting the toxin and intimin encoding genes of STEC. Antibiotic susceptibility was performed with beta-lactams and non-beta-lactams and genes encoding ESBLs, aminoglycoside, tetracycline and quinolone resistance were detected. Transcriptional response of *stx1* in STEC isolates in presence and absence of antibiotic was measured by quantitative real-time PCR.

Results & Discussion:
Three STEC harbouring *stx1* were identified in the drain effluents. Two isolates (Se-91 and SR- 32) showed resistance to multiple beta and non-beta lactam antibiotics while one (Se-112) showed resistance to beta-lactams. All the three isolates harboured bla_{TEM} while Se-91 and SR- 32 also carried *tetK*. SR-32 additionally harboured bla_{SHV}. Ampicillin substantially upregulated the expression of *stx1* in isolates Se-91 and SR- 32 when compared to gene's response in control while *stx1* in Se-112 was downregulated. This study suggests that aquatic environments can serve as reservoirs for the maintenance of STEC and associated antibiotic resistant determinants. Further, the antibiotic resistant phenotypes of STEC can complicate the existing antibiotic therapy for gastrointestinal disorders and emphasizes the antibiotic profiling of the STEC strains due to the increase in toxin expression by these multidrug resistant pathogenic strains.

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Investigation and Characterization of Fungal Diseases in *Capsicum* Genus of Assam: A Botanical-Based Approach for Controlling Phytopathogens

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Abstract

Background:

The genus *Capsicum*, holds a paramount significance due to its extensive economic importance on a global scale. Nonetheless, these crops are often infected by pathogenic fungi causing severe fruit and foliar disease thereby decreasing the yield considerably. Hence, the use of synthetic chemicals to combat these fungal pathogens has increased, resulting in resistance development and elevated toxicity in food products. As a result, there's an increased demand for eco-friendly and non-toxic alternatives to synthetic fungicides. This has led to a surge in research focused on harnessing natural products like botanical-based extracts, which offer a sustainable and safe approach for controlling phytopathogens.

Method & Methodology:

Diseased *Capsicum* (Chilli) samples were collected from diverse locations in Assam. The pathogens were isolated, identified, and subjected to pathogenicity tests. Selected plants having bio-activity were used to create botanical extracts, which were then tested for antifungal efficacy against the pathogens. Pathogens with the highest inhibition rates underwent further analysis using SEM imaging to assess mycelial growth destruction in dual culture plates.

Results & Discussion:

A total of 8 fungal pathogens were isolated from various disease samples. All of them exhibited positive results in pathogenicity tests and were identified using a combination of morphological and molecular techniques. The botanical extracts displayed impressive effectiveness against all phytopathogens, leading to severe rupturing of their mycelial walls as observed in SEM imaging. These findings underscore the potential for developing novel, precise, and naturally derived fungicides to combat phytopathogens and protect *Capsicum* crops.

****

Assessing Inhibitors for Colibactin Synthetase ClbQ: Ligand-Based Screening, Docking, and Dynamics

Surajit Chanda and Diwakar Kumar

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Abstract

Background: Extraintestinal pathogenic *Escherichia coli* producing colibactin promotes various inflammatory disease in the colon by inducing DNA damage in the cells lining the colon.[1] ClbQ is one of the genes within the colibactin genomic island responsible for the synthesis and transport of colibactin.[2] Structure and functional insights to the respective gene was previously studied. [3] Inhibiting ClbQ, which is a part of the colibactin genomic island in certain strains of E. coli, may disrupt the biosynthesis and export of the genotoxin colibactin.

Method: The current study was performed to identify potential inhibitor phytochemicals by targeting Colibactin Synthetase ClbQ with the help of structure-based virtual screening. 3D structure of the protein [PDB: 5UGZ] was selected for this work after energy minimization, followed by docking; 46 phytochemicals from Traditionally used plants were docked with the target protein. The best-docked molecule was subjected molecular dynamic simulation and admet screeing.

Result: ClbQ structure was taken from PDB [PDB: 5UGZ] and refined by YASSARA web servers. Based on the docking score, lead molecules were selected for further studies. And followed by molecular dynamic simulations and ADMET screening.

Reference:

1) Nougayrède JP, Homburg S, Taieb F, Boury M, Brzuszkiewicz E, Gottschalk G, Buchrieser C, Hacker J, Dobrindt U, Oswald E. Escherichia coli induces DNA double-strand breaks in eukaryotic cells. Science. 2006 Aug 11;313(5788):848-51. doi: 10.1126/science.1127059. PMID: 16902142.

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3) Naga Sandhya Guntaka, Alan R. Healy, Jason M. Crawford, Seth B. Herzon, Steven D. Brune (2017) **Structure and Functional Analysis of ClbQ, an Unusual Intermediate-Releasing Thioesterase from the Colibactin Biosynthetic Pathway;** *ACS Chemical Biology* **2017** *12* (10), 2598-2608 DOI: 10.1021/acschembio.7b00479

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Antibacterial studies of NO donor triss-buffer based Schiff base ligand and some of its selected metal complexes

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Abstract

Salicylaldimine Schiff base ligand (HL) having pendant hydroxymethyl (CH_2OH) groups 2-((1,3-dihydroxy-2-(hydroxymethyl)propan-2-ylimino)methyl)-5-(tetradecyloxy)phenol and complexes with transition metals viz., zinc, copper, and vanadium have been synthesized. The synthesized compounds were characterised by FT-IR, ^{1}H NMR, ^{13}C NMR and UV-Vis spectroscopy. The ligand and metal complexes were studied for the antibacterial property against few selected bacteria viz., *Clinical Escherichia coli, Escherichia coli ATCC 25922, Pseudomonas aeruginosa, Clinical Pseudomonas aeruginosa* and *Clinical Staphylococcus aureus* bacterial strains using well diffusion method. The complexes showed significantly enhanced antibacterial activity against the selected microbial strains in comparison to the free ligand. The predominant effect of the metal complexes against the bacteria is attributed to the presence of the metal ions which increases the permeability through the cell membrane.

Reference:

[1] Harun A. R. Pramanik, Chiranjit Chanda, Pradip C. Paul, Chira R. Bhattacharjee, S. Krishna Prasad, D.S. Shankar Rao. *J.Mol.Struct.* 1180 **(2019)** 472

[2] Ibrahim Waziri, Tunde L. Yusuf, Eric Akintemi, Monsuru T. Kelani, Alfred Muller *J.Mol.Struct.* 1273 **(2023)** 134328

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P - 41

Survey of dairy farms for milk quality assessment and their antimicrobial resistance profile from mastitic milk in Barak Valley, Assam

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Abstract

Background-

The contamination of raw milk depends on the number and type of organisms present in milk that can cause health risks. This study evaluated bacterial contamination, the risk factor, and drug sensitivity patterns.

Methods-

A cross-sectional study was carried out on selected 122 raw milk sample. Data were collected using the structured pre-test questionnaire and the observation control list. Subsequently, milk samples were taken for laboratory analysis and diluted for the enumeration of total bacterial count. Biochemical and drug sensitivity tests have been done. The version 20 SPSS was used for analysis of the associated factors using logistical regression analysis and a *P* value less than 0.05 was considered as statistically significant.

Results-

The geometric mean of the total bacterial count was 5.38log cfu/ml (2.45×10^5). 58% of the samples had TBC counts that exceeded acceptable limit and thus graded as contaminated or poor quality. Dirty barns (0.006), dirty cows (0.026) Poor hygiene of the milker (0.03), use of cold water (0.00) and unclean milk utensil (0.026) were found to be significantly associated with bacterial contamination of milk. The bacteria isolated were E. coli (18.6%), Staphylococcus aureus (26.8%), and Klebsiella spp. (22.76%). Among isolated bacteria, above 50% were multidrug resistant, and 2.7% were resistant to all drugs tested in the current study.

Conclusion-

Appropriate hygiene practices during time of milking, clean barn, cow, udder, and containers reduced milk contamination. Doctors should consider drug resistance during the treatment of cows with mastitis.

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The Effect of Body Mass Index on Baroreceptor Sensitivity Evaluated Indirectly by Estimation of Mean Arterial Pressure Among The Undergraduate MBB Students And Paramedical Students of Silchar Medical College & Hospital - A Cross-Sectional Study

Dr. Chiradipta Ghosh, Prof. (Dr.) Jyotismita Deka

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Abstract

Background and Objective

Patients with obesity are at a major risk for development of hypertension and cardiovascular disease (CVD). Body Mass Index (BMI) is now widely accepted for defining obesity.

Change in Baroreceptor reflex sensitivity is associated with alternate change in parasympathetic activity and sympathetic activity that accompany the development and progression of hypertension.

Mean Arterial Pressure (MAP) can be used as an indirect tool for evaluating the Baroreceptor sensitivity (BRS)[1]**.** The study has been done to observe the effect of BMI on Baroreceptor sensitivity.

Materials and Methods

The study is a cross sectional study conducted in Department of Physiology, SMCH. For calculating BMI, the Weight (Kg) and Height(m) of the volunteers has been recorded. Blood pressure of the volunteers has been recorded in supine position after 10 minutes of complete rest. Mean arterial pressure (MAP) is obtained by using the formula: MAP= DBP+1/3rd (SBP-DBP)(SBP- Systolic blood pressure; DBP- Diastolic blood pressure).
Pearson's correlation coefficient was carried out to analyze the effect of BMI on Mean arterial pressure.

Results

Mean age of the participants was 20.54±1.22 years and Mean BMI was 23.11±3.57 Kg/m^2. The study revealed that there is a positive correlation between BMI and MAP (r = 0.9).

Conclusion

We found a significant association between BMI and Mean Arterial Pressure. Abnormal BMI causes deleterious effect on the Mean arterial pressure and therefore indirectly on the Baroreceptor sensitivity (BRS) in the human body.

Reference

1) Hesse C, Charkoudian N, Liu Z, Joyner MJ, Eisenach JH. Baroreflex sensitivity inversely correlates with ambulatory blood pressure in healthy normotensive humans. Hypertension. 2007 Jul 1;50(1):41-6.

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Studies on Chemical Composition and Antimicrobial Activities from Date Palm [*Phoenix dactylifera*] Barari Fruit

S.Mohamed Musthafa [1], A.Anbu Abubakkar Sidik [2], Mohamed Jasim[3]

Abstract

Background and purpose

Collection of sample-date fruit [*Phoenix dactylifera*] barai, extraction of phytochemical activities by solvent extraction method, Screening for phytochemicals, antimicrobial activity of extract, dpph assay, screening by paper chromatography, uv analysis, gc/ms analysis.

Methodology

Dates fruit of barari variety was purchased from the local grocery shop situated in tenkasi, first order, an acid hydrolysis was performed on 5g dry plant material blinded with 40 ml hydrocholoric acid [2n hcl].The mixture prepared was transferred into Erlenmeyer flasks and was boiled in water bath at 100 degree for 40 minutes.

Result and Discussion

1.**Terpenoid test**

Positive result is indicated by the formation of reddish brown layer at the interface.

2.**Saponin test**

Positive result is indicated by the froth appearance while shaking the tube.

3.**Tanin test**

The colour change was observed and read out OD values was observed in calorimeter. The positive observation is indicated by the development of blue green and blue black precipitate

4.**Cardiac glycoside test**

Positive result is indicated by a violet ring. In some case violet ring can be accompanied by a brown ring which will appear in the bottom layer of the tube

5.**Anthroquinone test**

Positive result is indicated by the pink, violet or red colour.

Conclusion

In the current work, to evaluate the antimicrobial activity of dates[barari] dates companies was checked by subjecting the selected products to diverse physical, chemical preservatives adulteration and biological test generally employed in dates industries as per FSSAI in addition to their antioxidant role.

The microbiological parameter recorded in the current work raises efficiency of antimicrobial activity employed during the production due to the growt of *E.coli sp, Streptococcus sp, Enterococcus sp, Pneumonia* sp, *Pseudomonas sp,*. There may be several reason for the poor microbial quality.

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Isolation and characterization of the probiotic microorganisms from the gut of different aquatic and terrestrial species

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Abstract

Probiotics are live microorganisms that confer health benefits to its host when consumed in an adequate amount. A comprehensive biochemical characterization of the isolated gut microbiota from different aquatic and terrestrial species was done using different advance analytical methods in three different types of media. Bacterial isolates were grown in media plates containing bile that indicated their tolerance to different bile concentration. Probiotic assessment of the bacteria was done by co-incubating them with pathogenic strains like *Salmonella typhi* and *Escherichia coli*. A greater proportion of strains were found to be resistant to *E. coli* as compared to *S. typhi*. The resistant microbes were further analyzed for the production of different extracellular enzymes by culturing them in protein and amylase rich media like Skim milk and Starch agar. Bacteria showing positive results for the production of both extracellular protease as well as amylase were found to be more in number in aquatic species as compared to the terrestrial species. These screened strains were then examined for their tolerance to different pH. Most of the bacterial isolates showed high survival rate in extreme basic pH. A few of them showed tolerance to extreme acidic pH. Culturing gut microflora in different conditions might help in predicting the niches of the microbes and their production at a larger scale, considering the ethical and regulatory aspects.

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Studies on antibiotic stress with reference to biofilm formation of *Staphylococcus sp.* from clinical samples

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Abstract

Background:

Antimicrobial resistance is an emerging issue in biofilm forming *Staphylococcus sp*. Biofilms are sessile community of microorganisms embedded in 3D extracellular matrix that acts as a barrier to protect against antibiotic agents. *Staphylococcus sp*. is a common cause of nosocomial , and Cystic fibrosis infections. *Staphylococcus sp*. colonization/infection, either by methicillin-susceptible or methicillin-resistant strains, will become chronic in about one third of CF patients. It has been postulated that compared to planktonic cells, cells in a biofilm are 10–1,000 times more resistant to antibiotics.

Methodology:

The present study aimed to analyse 70 clinical samples from Silchar Assam, India. Biofilm assay, antimicrobial susceptibility test, antibacterial susceptibility test, molecular characterization of *icaA* and *icaD g*enes(biofilm specific) were performed.

Results:

Of the analysed 70 samples , 34 were *Staphylococcus sp.* isolates. A total of 61% isolates were emerged as strong biofilm producers. Vancomycin showed 67% resistance, followed by methicillin. Molecular characterization of *ica A* and *icaD* genes revealed that both the genes are highly prevalent genes of *Staphlococcus sp.* Antibacterial susceptibility was performed for all the strong, intermediate, weak and non-biofilm producing strains against zinc oxide and silver nanoparticles of approximately size 30nm where *Staphylococcus sp.* exhibited different sensitivity pattern with the increased concentration of AgNPs and ZnO particles.

Conclusion:

The present study will provide insights in combating antimicrobial resistance in the biofilm producing organisms by understanding their virulence factors.

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Representation of antibiotic resistance using automated methods and molecular characterisation of carbapenemases in a tertiary care hospital of Eastern India

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Abstract

Introduction: Antibiotics are one of the greatest discoveries of the 20th century. However, there is a risk that we may return to post antibiotic era. The problem rampant in health care beginning with MRSA, ESBL, CRAB and CRE is multi drug resistant bacteria which may appear in local community acquired infections without health care associated risk factors.

Aims & Objectives: This is a pilot study to determine the antibiotic resistance using automated methods and molecular characterisation of carbapenemase mediated resistance.

Methodology: This is a cross-sectional study conducted in the Department of Microbiology, NRS Medical College for a period of 6 months between July 22 to December 22 in patients of all age groups and both sexes where blood cultures yielded 60 isolates of multi drug resistant (MDR) Gram negative bacilli using automated VITEK methods and molecular characterisation for carbapenemase detection was done using real time RT PCR.

Result: In our study all GNBs showed MDR pattern phenotypically. They were 100% resistant against carbapenems, quinolones and aminoglycosides. Genotypic characterization of carbapenem resistance revealed all were bla_{NDM} type (100%) followed by bla_{OXA48} (87.5%) and bla_{VIM} (50%) types. Better susceptibility were observed against tetracyclines (87.5%) and polypeptides (87.5%) group of antibiotics.

Discussion: This study highlighted alarming pattern of multi-drug resistance in GNBs. Phenotypically detected carbapenem resistance was accurately confirmed by molecular methods. The genomic analysis of antimicrobial-resistance (AMR) demonstrates a significantly high prevalence of bla_{NDM} and bla_{OXA48} carbapenem resistance genes among clinical isolates. Co-occurrence of bla_{NDM} with other carbapenem resistance genes was found in 50% isolates.

Conclusion: Thus this study highlighted the mechanism of carbapenem-resistance among drug-resistance bugs which would guide targeted antimicrobial therapy for better outcome.

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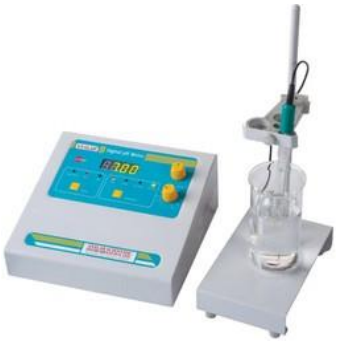

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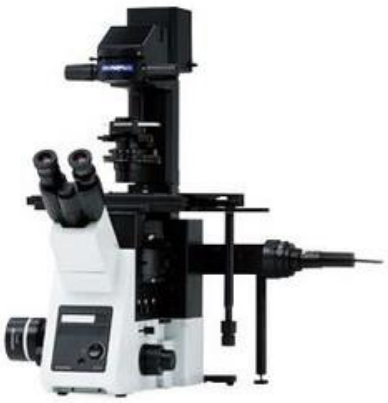

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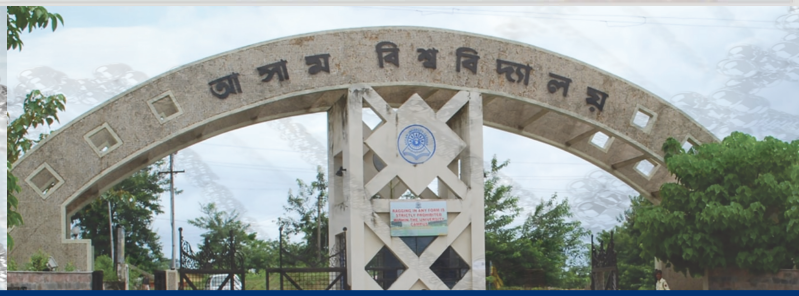

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