

1st DAE-BRNS

TROMBAY SYMPOSIUM ON LIFE SCIENCES

(TSLS-2026)

ABSTRACT BOOK

NOVEMBER 25-28, 2026

DAE CONVENTION CENTRE,
ANUSHAKTINAGAR,
MUMBAI - 400094, INDIA

Organised by

BHABHA ATOMIC RESEARCH CENTRE (BARC), MUMBAI

TROMBAY SOCIETY FOR BIOLOGICAL SCIENCES (TSBS)

1st DAE-BRNS

TROMBAY SYMPOSIUM ON LIFE SCIENCES - 2026
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November 25 – 28, 2026
DAE Convention Centre, Anushaktinagar, Mumbai

Abstract Book

Organized by
Bhabha Atomic Research Centre, Mumbai
and
Trombay Society for Biological Sciences, India

TSLS-2026

1st DAE-BRNS TROMBAY SYMPOSIUM ON LIFE SCIENCES - 2026

Abstract Book

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व
सचिव, परमाणु ऊर्जा विभाग
Chairman, Atomic Energy Commission
&
Secretary, Department of Atomic Energy



MESSAGE

I am delighted to know that the Bio-Science Group, Bhabha Atomic Research Centre is organizing the 1st DAE-BRNS "Trombay Symposium on Life Sciences – 2026 (TSLS-2026)", which marks a significant step towards strengthening the scientific ecosystem of life science research at BARC. It is a welcome initiative towards creating a dedicated platform for promoting scientific interaction and collaboration among life science researchers.

The Bio-Science Group at BARC has a rich and longstanding tradition of multidisciplinary research in the field of life sciences. This approach is well aligned with the broader scientific mandate of the Department of Atomic Energy to pursue research on peaceful uses of nuclear sciences for societal impact. I am happy to note that significant milestones have been achieved by Bio-science Group in the areas of nuclear agriculture, food technology, radiation biology, cancer research and microbiology. The outcome includes release of 79 crop varieties developed using radiation-induced mutation breeding, shelf-life extension of perishable food commodities using radiation technology and release of Aktocyte tablets for preventing side effects of cancer radiotherapy.

TSLS-2026 provides an opportunity to bring together eminent scientists, academicians, clinicians, researchers and students from diverse scientific backgrounds. Such interactions are essential for sharing knowledge, identifying emerging research directions and fostering collaborations that transcend traditional disciplinary boundaries.

I am particularly pleased that the symposium provides significant opportunities for young researchers and students to interact with established scientists and present their research in front of peers. Nurturing scientific curiosity, encouraging independent thinking and providing young researchers with exposure to diverse areas of research are essential for building a strong scientific workforce for the future. I am confident that TSLS-2026 will contribute meaningfully towards this objective. I congratulate Bio-Science Group, BARC for taking this initiative and appreciate the efforts of all members of the organizing and scientific committees, invited speakers and participants who have contributed to making this symposium possible.

I am confident that TSLS-2026 will establish a strong foundation for a continuing scientific forum in life sciences at BARC. I extend my warm greetings and best wishes to all the participants and wish TSLS-2026 a grand success.

Ajit Kumar Mohanty
(Ajit Kumar Mohanty)

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Director, Bhabha Atomic Research Centre
सदस्य, परमाणु ऊर्जा आयोग
Member, Atomic Energy Commission



MESSAGE

It is a matter of great pleasure to extend my warm greetings and welcome to all the participants of the 1st DAE-BRNS "Trombay Symposium on Life Sciences - 2026 (TSLS-2026)", being organized by Bio-Science Group, Bhabha Atomic Research Centre.

Life sciences today stand at the interface of several rapidly advancing disciplines, encompassing molecular biology, biotechnology, cancer research, immunology, cell biology, computational biology and emerging areas of biomedical science. The convergence of these diverse fields with advanced technologies is opening new avenues for understanding complex biological processes and translating scientific discoveries into solutions of relevance to human health and society.

The multidisciplinary life science research at Bio-science Group, BARC encompasses diverse and emerging areas such as nuclear agriculture, food technology, radiation biology, cancer biology, microbiology, molecular biology, structural biology, biotechnology and advanced genomics. These programmes span fundamental understanding of biological processes as well as the development of innovative technologies and applications in areas of national relevance. The integration of nuclear science and technology with modern biological approaches provides unique opportunities for addressing complex scientific challenges. These endeavours are closely aligned with the broader mandate of the Department of Atomic Energy to harness nuclear science and technology for the benefit of the nation and society. I strongly believe that organization of the 1st DAE-BRNS "Trombay Symposium on Life Sciences (TSLS-2026)", will provide a valuable platform for bringing together scientists, academicians, clinicians, young researchers and students to exchange ideas, share emerging discoveries and foster scientific collaborations.

I congratulate the organizers of TSLS-2026 for this important initiative. I wish TSLS-2026 great success and hope that it marks the beginning of a sustained and vibrant scientific forum that will contribute significantly to the advancement of life science research and deployment of affordable technologies for the benefit of society.

09.11.2026

(Vivek Bhasin)

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सत्यमेव जयते

डॉ. पी. ए. हसन
Dr. P. A. Hassan
निदेशक, जैव-विज्ञान वर्ग
Director, Bio-Science Group



MESSAGE

It gives me immense pleasure to welcome all the distinguished scientists, academicians, clinicians, researchers and students to the "1st DAE-BRNS Trombay Symposium on Life Sciences – 2026" (TSLS-2026) being organized by Bio-Science Group, Bhabha Atomic Research Centre (BARC).

Life sciences research is witnessing an extraordinary period of discovery, driven by rapid advances in molecular biology, genomics, biotechnology, imaging, computational approaches and biomedical technologies. At the same time, many of the most important scientific questions of our time increasingly lie at the interface of diverse disciplines. Creating opportunities for scientists from different disciplines to interact, exchange ideas and explore common research interests is therefore essential for advancing scientific knowledge and translating it into meaningful societal impact.

TSLS-2026 is particularly significant as the inaugural scientific meeting of the Trombay Society for Biological Sciences (TSBS). The symposium brings together researchers working across a broad spectrum of life sciences, with particular emphasis on emerging areas of fundamental and applied research. The participation of eminent scientists from leading institutions in India provides an excellent opportunity to discuss recent advances, identify new directions and establish collaborations.

A special feature of any scientific meeting is the opportunity it provides to the younger generation of researchers. I hope that the students and early-career scientists participating in TSLS-2026 will take full advantage of the scientific discussions and interactions with senior researchers. Their questions, ideas and perspectives are an important part of building the future of life sciences.

The symposium also reflects the strong tradition of multidisciplinary research and commitment of the Department of Atomic Energy towards advancing biological sciences through fundamental research, technological innovation and translational applications. I am confident that TSLS-2026 will build upon this tradition and provide a platform for sustained scientific interaction within the life sciences community.

I express my sincere appreciation to all the invited speakers, delegates, organizing committee members, supporting agencies and colleagues whose contributions have made this symposium possible. I am confident that the scientific deliberations and interactions during these four days will be intellectually stimulating and will lead to new ideas and opportunities.

I extend my warmest wishes to all participants and hope that TSLS-2026 marks the beginning of a continuing tradition of excellence, collaboration and innovation in life sciences.

(P. A. Hassan)
Chairman, TSLS-2026

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1st DAE-BRNS

TROMBAY SYMPOSIUM ON LIFE SCIENCES - 2026 (TSLS - 2026)

Day 1: 25th November 2026	
09:30 AM-10:30 AM	**INAUGURAL CEREMONY,** followed by High Tea
10:30 AM-11:15 AM	**Keynote Lecture** **Chair: Dr. Sudeep Gupta, Director, Tata Memorial Centre, Mumbai** **Prof. Kumarasamy Thangaraj, Padma Shri** **CSIR-Centre for Cellular and Molecular Biology, Hyderabad** Our origin, culture and consequences
11:15 AM-12:40 PM	**Session 1: Cancer & Radiation Biology** **Chair: Prof. Kumarasamy Thangaraj, CCMB, Hyderabad** **Co-Chair: Dr. P. A. Hassan, Director, Bio-Science Group, BARC**
11:15 AM-11:45 AM	**PL-1: Dr Sudeep Gupta, Tata Memorial Centre, Mumbai** Clinical and translational research in gynecological and breast cancers - Improving outcomes
11:45 AM-12:15 PM	**PL-2: Dr. Sudhir Chandna, INMAS, DRDO, Delhi** Post-radiotherapy second primary or secondary malignancies- Deciphering the etiology and mechanisms
12:15 PM-12:40 PM	**IL-1: Dr. Vidita Vaidya, Tata Institute of Fundamental Research, Mumbai** Early stress and accelerated aging
12:40 PM-1:10 PM	**Session 2: Molecular Biology** **Chair: Dr. S. K. Apte, Ex-Director, Bio-Science Group, BARC** **Co-Chair: Dr. Neetu Singh, IIT, Delhi**
12:45 PM-01:10 PM	**IL-2: Dr. Radha Prasanna, ICAR-Indian Agricultural Research Institute, New Delhi** Cyanobacteria as climate-smart inputs to sustain healthy microbiomes in soil and produce across crops
01:10 PM-02:00 PM	**LUNCH**
02:00 PM-04:00 PM	**POSTER SESSION - I (PP 1 - PP 54)**
04:00 PM-05:35 PM	**Session 2: Molecular Biology (Continued)**
04:00 PM-04:25 PM	**IL-3: Dr. Neeti Sanan Mishra, International Centre for Genetic Engineering and Biotechnology, New Delhi** miRNAs: Master modulators of multigenic stress responses in plants

04:25 PM-04:50 PM	**IL-4: Dr. Dipshikha Chakravortty, Indian Institute of Science, Bengaluru** Formate's Whisper- How a metabolite can decide the bacteria's response to antibiotics
04:50 PM-05:05 PM	**OP-1: Dr. Arvind Kumar Mishra, Bhabha Atomic Research Centre, Mumbai** Molecular insights into double strand break repair in the radioresistant cyanobacterium *Nostoc* PCC 7120
05:05 PM-05:20 PM	**OP-2: Dr. Vinay Jain, Bhabha Atomic Research Centre, Mumbai** Understanding biological responses to radiation: From nature's own laboratory to cancer therapy and radiation protection
05:20 PM-05:35 PM	**OP-3: Dr. Sanjana Negi, National Agri Food and Biomanufacturing Institute** Unravelling the MYB regulatory network governing anthocyanin biosynthesis in banana
07:00 PM	**CULTURAL EVENING & DINNER**
Day 2: 26th November 2026	
09.15 AM-10:45 AM	**Session 3: Cancer Biology** **Chair: Dr. Punit Kaur, AIIMS New Delhi** **Co-Chair: Dr. S. K. Sandur, Head, RB&HSD, BARC**
09.15 AM-09:45 AM	**PL-3: Dr. Pankaj Chaturvedi, TMC- Advanced Centre for Treatment, Research & Education in Cancer, Navi Mumbai** Affordable cancer care - Role of Tata Memorial Centre, Department of Atomic Energy
09.45 AM-10:10 AM	**IL-5: Dr. Sib Sankar Roy, CSIR-Indian Institute of Chemical Biology, Kolkata** Mitochondrial association with oncogenesis: Impact of its deregulated bioenergetic function and beyond
10:10 AM-10:35 AM	**IL-6: Dr. Rakesh S. Laishram, BRIC-Rajiv Gandhi Centre for Biotechnology, Kerala** Untranslated RNA dynamics in anti-oxidant and radiation response: Implications in cardiac hypertrophy and failure
10:35 AM-10:45 AM	**TT 1: Dr. Gagan Deep Jhingan, VProteomics, New Delhi** Clinical mass spectrometry and its applications in personalized medicine
10:50 AM - 11:20 AM	**Session 4: Agriculture** **Chair: Dr. Anand Badigannavar, NA&BTD, BARC** **Co-Chair: Dr. Neeti Sanan Mishra, ICGEB, New Delhi**

10:50 AM-11:20 AM	**PL- 4: Dr. Anil Kumar Tripathi, Indian Institute of Science Education and Research, Mohali** Deciphering the repertoire of mechanisms of rhizocompetence in a plant growth promoting Rhizobacterium
11:20 AM-11:30 PM	**TEA**
11:30 AM-1:10 PM	**Session 4: Agriculture (Continued)**
11:30 AM-11:55 AM	**IL-7: Dr. Ajay Kumar Pandey, BRIC-National Agri-Food and Biomanufacturing Institute** Bioengineering genes to generate iron rich wheat grains using genome editing
11:55 AM-12:20 PM	**IL-8: Dr. Girdhar K. Pandey, University of Delhi South Campus, New Delhi** Interplay of calcium and ROS in regulating mitochondrial retrograde signaling under oxidative stress in plants
12:20 PM-12:45 PM	**IL-9: Dr. Santosh Satbhai, Indian Institute of Science Education and Research, Mohali** From plant science to public health: Innovating for iron security and sustainable agriculture
12:45 PM-1:10PM	**IL-10: Dr. Shilpi Sharma, Indian Institute of Technology Delhi** Rewiring the rhizosphere: Next-Generation solutions for resilient agriculture
01.10 PM-02.15 PM	**LUNCH**
02:15 PM-04:00 PM	**POSTER SESSION (PP55 - PP106)**
04:00 PM-05:45 PM	**Session 5: Bioinformatics and Structural Biology** **Chair: Dr. Anil Kumar Tripathi, Director, IISER, Mohali** **Co-Chair: Dr. Mukesh Kumar, Head, PCS, BARC**
04:00 PM-04:25 PM	**IL-11: Dr. B. Anand, Indian Institute of Technology, Guwahati** Waking up bacteria from stress-induced slumber
04:25 PM-04:50 PM	**IL-12: Dr. Punit Kaur, AIIMS, New Delhi** Structural insights into the function of a carbohydrate-active enzyme, GH43
04:50 PM-05:15 PM	**IL-13: Dr. Sangram Bagh, Saha Institute of Nuclear Physics, Kolkata** Towards AI bacteria: Genetically engineered E.coli networks identifies prime numbers, vowels and answer math questions
05:15 PM-05:30 PM	**OP-4: Ms. Rimanshee Arya, Bhabha Atomic Research Centre, Mumbai** Structural biology research at BARC: An overview
05:30 PM-05:45 PM	**OP-5: Dr. Chitra S Misra, Bhabha Atomic Research Centre, Mumbai** Genomics-based approaches for diagnosis of infectious and non-infectious diseases
07.30 PM	**DINNER** Buses will leave from the venue at 6:45 PM

Day 3: 27th November 2026	
09.15 AM-11:35 AM	**Session 6: Food Technology** **Chair: Dr. Dipshikha Chakravortty, IISc, Bengaluru** **Co-Chair: Dr. S. Gautam, Head, FTD, BARC**
09.15AM-09:45 AM	**PL-5: Dr. Narottam P Sahu, Central Institute of Fisheries Education, Mumbai** Valorisation of agro-industrial residues for sustainable protein resources and nutrient-enriched aquatic foods
09.45 AM-10:15 AM	**PL-6: Dr. Alka Rao, CSIR-Institute of Microbial Technology, Chandigarh** Microbes on our plate: Safety, standards and strains
10:15 AM-10:40 AM	**IL-14: Dr. Ashutosh Upadhyay, National Institute of Food Tech. Entrepreneurship & Management, Sonipat** Bioactive molecules at biological interfaces: engineering natural coatings for protection against oxidative and microbial stress
10:40AM-11:05 AM	**IL-15: Mr. Subray Pavar, Marine Products Export Development Authority Regional Division, Mumbai** Role and functions of MPEDA, registration procedure of seafood processing plants and marine products exports
11:05 AM-11:20 AM	**OP-6: Dr. Nilantana C. Bandyopadhyay, Bhabha Atomic Research Centre, Mumbai** From safe and healthy food to global trade: Expanding applications of radiation processing in India
11:20 AM-11:35 AM	**OP-7: Ms. Indu Pant, Bhabha Atomic Research Centre, Mumbai** Exploring fundamental research in food safety and nutrition: Insights from the Food Technology Division
11:35 AM-11:45 AM	**TEA**
11:45 AM-01:10 PM	**Session 7: Biomaterials** **Chair: Dr. Alka Rao, Director, CSIR-IMTech, Chandigarh** **Co-Chair: Dr. B. N. Pandey, RB&HSD, BARC**
11:45 AM-12:15 PM	**PL-7: Dr. Sandeep Verma, Indian Institute of Technology Kanpur** Therapeutic gases in chemical neuroscience and development of biomicrofluidic platforms
12:15 PM-12:45 PM	**PL-8: Dr. Neetu Singh, Indian Institute of Technology Delhi** The Chemistry-Biology nexus: Shaping the future of healthcare
12:45 PM-01:00 PM	**OP-8: Dr. Priyadarshi Chakraborty, Indian Institute of Technology Hyderabad** From supramolecular assembly to tissue regeneration: Peptide-based hybrid hydrogels

01:00 PM-01:10 PM	**TT2: Mr. Sriram Parameswaran, Chief Scientific Officer, Theracues Innovations Pvt Ltd** Unlocking Precision Medicine: Multi-Omics Integration and AI-Driven Biomarker Discovery
01:15 PM-02:15 PM	**LUNCH**
02:15 PM-04:00 PM	**POSTER SESSION (PP 107 - PP 152)**
04:00 PM-06:15 PM	**Session 8: Health Sciences** **Chair: Dr. Sandeep Verma, IIT, Kanpur** **Co-Chair: Dr. B. S. Patro, Head, BOD, BARC**
04:00 PM-04:25 PM	**IL-16: Dr. Agneyo Ganguly, Indian Institute of Technology Kharagpur** RECQ1-RPA interaction promotes fork restoration and facilitates efficient recovery from replication stress following DNA damage induced by topoisomerase inhibitors
04:25 PM-04:50 PM	**IL-17: Dr. Kamalesh D Mumbrekar, Manipal School of Life Sciences, Manipal** Individual radiosensitivity revisited: Fixed and modifiable determinants of normal tissue response
04:50 PM-05:15 PM	**IL-18: Dr. Ruchi Anand, Indian Institute of Technology Bombay** Can we reverse antibiotic resistance: a glimpse into molecular mechanism and drug design
05:15 PM-05:30 PM	**OP-9: Dr. Mahesh Kumar Padwal, Bhabha Atomic Research Centre, Mumbai** Deconvolution based 'other cells': A prognostic alternative to circulating tumour cells in Neuroendocrine tumours
05:30 PM-05:45 PM	**OP-10: Dr. Ananda Guha Majumdar, Bhabha Atomic Research Centre, Mumbai** Targeting DNA repair vulnerabilities and autophagy to overcome therapeutic resistance in cancer
05:45 PM-06:00 PM	**OP-11: Dr. Himanshi Narang, Bhabha Atomic Research Centre, Mumbai** Dissecting the cancer: Molecular networks, microenvironmental dynamics, and vulnerabilities in precision therapeutics
06:00 PM-06:15 PM	**OP-12: Dr. Sucheta Chatterjee, Bhabha Atomic Research Centre, Mumbai** Functional organic materials for cancer therapy
08.00 PM	**DINNER**
Day 4: 28th November 2026	
09.30 AM-11:00 AM	**Session 9: Health Sciences** **Chair: Dr. A. C. Bhasikuttan, Director, Chemistry Group, BARC** **Co-Chair: Dr. Devashish Rath, Head, AGS, BARC**
09.30 AM-9:55 AM	**IL-19: Dr. Bushra Ateeq, Indian Institute of Technology, Kanpur** DKC1-mediated sphingolipid dysregulation drives colorectal cancer and therapy resistance

09:55 AM-10:20 AM	**IL-20: Dr. Mohankumar K. Murugesan, Christian Medical College, Vellore** Targeted base editing for ELANE-associated severe congenital neutropenia
10:20 AM-10:45 AM	**IL-21: Dr. Siddharth Jhunjhunwala, Indian Institute of Science, Bengaluru** Altered neutrophil pool mediates tissue injury in chronic inflammatory disease
10:45 AM-11:00 AM	**OP-13: Dr. Cuckoo Mahapatra, MSCB University, Odisha** Amphibian resilience under radiation stress
11:00 AM-11:15 AM	**TEA**
11:15 AM-01:20 PM	**Session 10: Plant Biology** **Chair: Dr. Anand Ballal, Head, NA&BTD, BARC** **Co-Chair: Dr. Ajay Saini, MBD, BARC**
11:15 AM-11:45 PM	**PL-9: Dr. Alok Sinha, National Institute of Plant Genome Research, New Delhi** MAPKs beyond stress: Rewiring plant growth and photosynthesis
11:45 PM-12:10 PM	**IL-22: Dr. P. V. Shivaprasad, National Centre for Biological Sciences, Bengaluru** Epigenetic regulation of rice genomic imprinting
12:10 PM -12:35 PM	**IL-23: Dr. N. K. Dhal, Institute of Minerals and Materials Technology, Bhubaneswar** Phytoremediation of ^{137}Cs and ^{90}Sr at nuclear power plant sites: From site-specific strategies to sustainable remediation
12:35 PM -12:50 PM	**OP-14: Dr. Himanshu Tak, Bhabha Atomic Research Centre, Mumbai** Transgenic approaches for vascular wilt in banana
12:50 PM- 01:05 PM	**OP-15: Dr. Vikash Kumar, Bhabha Atomic Research Centre, Mumbai** Integrating mutation breeding and molecular approaches to enhance rice productivity, climate resilience and nutritional security in India
01:05 PM- 01:20 PM	**OP-16: Dr. Keithellakpam Sanatombi, Manipur University, Imphal** Strains and SynCom: Shaping *Capsicum chinense* cv. 'Umorok' chilli seedling performance
1:20 PM-02:30 PM	**LUNCH**
02.30 PM-03.30 PM	**CLOSING CEREMONY AND VALEDICTORY FUNCTION**

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Keynote Lecture

Our origin, culture and consequences

K. Thangaraj

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Indian subcontinent is a region of remarkable cultural, linguistic, and genetic diversity with over 4,500 anthropologically well-defined groups. We have been studying various South Asian populations to understand their origin, affinities, and impact of endogamy. Our genetic study revealed that the enigmatic tribal populations of Andaman Islands are the first modern humans, who migrated out of Africa (*Science*, 2005). Subsequently, we demonstrated that the contemporary Indian populations have descend from two divergent groups (*Nature*, 2009), and these two groups have admixed during the past 2000 – 4000 years (*Am. J. Hum. Genet*., 2013). Since then, almost all the populations in Indian subcontinent have been practicing endogamy. To assess the impact of endogamy, we have analysed 275 distinct South Asian groups and found 81 groups with strong founder event (*Nat. Genet*., 2017). Further, we revisited the populations that have strong founder event, and found that they have high prevalence of recessive and pathogenic mutation (*J. Genet. Genomics*, 2025), leading to population-specific diseases (unpublished). Our strategy is to provide prenatal and premarital counseling to such populations and reduce disease burden.

Plenary Lectures (PL)

PL-1

Clinical and translational research in gynecological and breast cancers - Improving outcomes

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Gynecological and breast cancers together constitute the most incident cancers among women in India and worldwide. Although significant progress has been made in the diagnosis and treatment of these cancers, there continues to be substantial morbidity and mortality. Clinical research in Tata Memorial Centre has documented the response to various treatments, survival outcomes, evaluated novel diagnostic and treatment strategies and cost-effective interventions. Additionally, a major focus of research has been to elucidate mechanisms of resistance and find novel targets. The invited presentation will share some of these findings with the audience.

PL-2

Post-radiotherapy second primary or secondary malignancies- Deciphering the etiology and mechanisms

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Over the past couple of decades, modalities of cancer radiotherapy have taken major development strides, and technological advancements have helped in the overall improvements in cure rates and patient survival. Combined with concurrent development/ improvisation of the other treatment regimes, the overall patient survival rates for various malignancies have improved quite significantly. However, certain reports have also been indicating the occurrence of post-therapy second primary malignancies (SPMs) or secondary malignancies/ metastasis, necessitating the assessment of potential transformation or potentiation by various treatment regimes, especially radiotherapy and chemotherapy. The conventional regimes of radiotherapy used previously have largely been replaced by the modern modalities and technologies. While the precision for focal irradiation has been enhanced significantly by the development of image guided (IGRT) or intensity modulated (IMRT) modalities, reports have also suggested that occurrence of SPMs/SMs remains a challenge. In our laboratory, we have observed that low doses of gamma-radiation (in the range of few cGy) can enhance the migration of cancer cells *in vitro*, raising the potential of secondary malignancies. Molecular mechanisms deciphered in the study indicated the involvement of MAPK mediated pathways. Clinical database from Massachusetts hospitals has also been analyzed recently by our laboratory, and we found nearly 4.5% incidence of secondary malignancies post-radiotherapy. Analysis of various cellular and systemic inflammatory molecular pathways and crosstalks have further suggested a molecular cascade switchover that might be responsible for the late SPMs or secondary malignancies and metastasis. In this presentation, different studies from our laboratory as well as published reports from various other laboratories in this important field will be deliberated. Development of new preventive and therapeutic strategies for reducing post-radiotherapy / post-chemotherapy occurrences and recurrences might greatly help in extending the much-needed improvement in patient survival.

PL-3

Affordable cancer care - Role of Tata Memorial Centre, Department of Atomic Energy

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The Tata Memorial Centre, Department of Atomic Energy serves as the cornerstone of affordable, equitable, and high-quality oncology services in India, mitigating the profound economic catastrophe frequently faced by cancer patients. Established originally in 1941 through private philanthropy and later merged with the government under the Department of Atomic Energy (DAE) in 1966, TMC stands as a sterling example of a government institution dedicated to service, education, and research. As cancer incidence escalates across low- and middle-income demographics, the institution addresses a critical public health priority by implementing structural, clinical, research and economic strategies designed to deliver high-quality, evidence-based care to the masses. Annually, TMC registers over 170,000 new cancer patients across its expanding national network, which spans multiple states including Maharashtra, Punjab, Uttar Pradesh, Assam, and Andhra Pradesh. Remarkably, approximately 60% to 70% of these patients receive primary oncology care free of charge or at heavily subsidized cost. This prevents vulnerable populations from severe financial distress or abandoning life-saving treatments due to out-of-pocket costs. Beyond individual hospital subsidies, TMC achieves systemic cost reductions through macro-level interventions. A prominent initiative is the National Cancer Grid (NCG), a vast network initiated by TMC that connects over 300 cancer centres, research bodies, and patient advocacy groups across India. By facilitating pooled drug procurement through the NCG, TMC has managed to drastically lower the costs of essential oncology medicines, achieving a median price reduction of 82%. This standardizes treatment protocols nationwide while unlocking immense financial savings for both institutions and individuals. Furthermore, TMC actively counteracts geographical barriers and urban overcrowding through its Distributed Cancer Care Model. Recognizing that travelling to its hubs in Mumbai and Navi Mumbai strains the livelihood of rural families, projects like "Access to Affordable Cancer Care for One and All" have decentralized treatment. By establishing community-level cancer day care centres, early screening program and conducting capacity-building workshops across districts, TMC brings preventive and therapeutic oncology closer to the society. Concurrently, the center drives affordable innovation through clinical trials targeting cost-effective interventions. From pioneering low-cost public health screening methods for breast, cervical and oral malignancies to integrating state-of-

the-art technologies like proton therapy within a public framework, TMC ensures that financial limitations do not dictate clinical outcomes. In conclusion, the Tata Memorial Centre is not merely a tertiary hospital but a transformative ecosystem. Through institutional subsidies, pooled procurement networks, decentralized infrastructure, and implementable clinical research, TMC provides a sustainable blueprint for scaling affordable cancer care across the developing world.

PL-4

Deciphering the repertoire of mechanisms of rhizocompetence in a plant growth promoting Rhizobacterium

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Bacteria of the genus *Azospirillum* colonize roots of a large number of plants and promote their growth by several mechanisms including phytohormone production, nitrogen fixation, siderophore production etc. Since rhizosphere is a zone of intense competition among microorganisms for the root exudates, successful rhizobacteria possess several traits that help them survive and outcompete other microbes. Swimming motility through polar flagellum with the help of which they display chemotaxis towards root exudates. Very efficient mechanisms to cope with oxidative and photooxidative stress as plant roots respond to bacterial colonization through oxidative burst leading to the production of lethal reactive oxygen species. The ability to produce β-lactamase enables them to protect themselves from microbes producing β-lactam antibiotics. They induce Type 6 Secretion system (T6SS) to kill other rhizosphere bacteria by a contact-dependent mechanism through which they inject toxins in the neighbouring bacteria. Mechanisms to produce and uptake siderophores enable them to survive and thrive under iron deficient conditions. They possess efficient transporters to use dicarboxylates present in the root exudates of C4 plants as preferred source of carbon and energy. We have studied mechanisms of chemotaxis, tolerance to oxidative and photooxidative stress, dicarboxylate utilization, resistance to β-lactam antibiotics, siderophore biosynthesis, and T6SS in one of the most rhizocompetent bacterium, *Azospirillum brasilense.* It also lacks the ability to utilize glucose as a carbon source resulting in the poor colonization of rice roots as the exudates of rice roots contain very low levels of dicarboxylates but high levels of glucose. We have engineered *A. brasilense* with a set of genes from *Azospirillum lipoferum* to enable *A. brasilense* to grow well on glucose. We have shown that glucose utilizing *A. brasilense* colonizes rice roots efficiently and promotes growth of rice plants.

PL-5

Valorisation of agro-industrial residues for sustainable protein resources & nutrient-enriched aquatic foods

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Feeding the world's population, projected to reach 9.7 billion by 2050, presents a major challenge to sustainable food production and nutritional security. Agro-industrial residues and food-processing by-products represent underutilized sources of proteins, bioactive compounds, dietary fibre and micronutrients, offering considerable opportunities for circular-economy-driven valorisation into functional ingredients for food and aquafeed applications while reducing resource wastage and environmental burdens. Our research encompasses systematic nutritional and anti-nutritional profiling of non-edible oilseed cakes, optimization of protein extraction processes and development of a protein extraction prototype. Technologies have also been developed for recovering bioactive-rich extracts and protein hydrolysates from diverse plant-based residues. Solid-state fermentation is employed to enhance the nutritional quality and feed value of conventional and unconventional plant-based ingredients, thereby improving their suitability for aquafeeds and contributing to the nutritional enrichment of fish as a food source. These valorised ingredients and processing technologies are further integrated into fish nutrition strategies, particularly micronutrient supplementation and nutritional biofortification with essential amino acids, selenium, zinc and iron, to enhance the nutritional value of aquatic foods for human consumption. Alongside technology development, ICAR-CIFE emphasizes entrepreneurship, industry linkages, technology scale-up and commercialization. The lecture highlights an integrated approach combining food technology, waste valorisation, fish nutrition and nutritional biofortification to transform underutilized agricultural resources into value-added feed ingredients and nutrient-enriched aquatic foods, contributing to resource efficiency, sustainable food systems and human nutritional security.

PL-6

Microbes on our plate: Safety, standards and strains

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Microbes occupy a dual position in the food chain. Beneficial species underpin fermented foods, probiotics, enzymes, natural colourants and vitamins, whereas pathogens cause an estimated 600 million food-borne illnesses and 420,000 deaths each year (WHO, 2015). Regulation must therefore control the former and define safe use of the latter. Microbial standards for food are analysed globally and nationally. The Codex Alimentarius framework is reviewed, covering the General Principles of Food Hygiene, microbiological criteria, commodity standards that specify starter cultures, and FAO/WHO guidance on probiotics. This is compared with the European Qualified Presumption of Safety (QPS) list and the United States GRAS pathway. In India, microbiological limits and provisions for probiotics, health supplements and food additives under the Food Safety and Standards Authority of India (FSSAI) are examined, and gaps are identified in strain identification, safety data, claim substantiation and reference cultures. Regulators increasingly expect authenticated, traceable strains supported by whole-genome data and screened for toxin genes and transferable antimicrobial resistance. National culture collections are central to meeting this. The Microbial Type Culture Collection and Gene Bank (MTCC), CSIR-IMTECH, holds over 14,500 cultures, has described about 100 novel taxa, and has been India's first International Depository Authority under the Budapest Treaty since 2002. Its food-relevant resources include lactic acid bacteria showing about 48% cholesterol reduction in laboratory studies, over 100 pigment-producing strains, vitamin B12-producing phototrophic bacteria, and fungi for fermentation, food enzymes, functional mushrooms and mycoprotein. Linking such validated resources to Codex-aligned safety assessment can strengthen evidence-based regulation and food innovation.

PL-7

Therapeutic gases in chemical neuroscience and development of biomicrofluidic platforms

Sandeep Verma

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My lecture will touch upon certain aspects of our ongoing research to develop peptide-based systems for delivering gaseous neuromodulators to transgenic and in ovo ischemic/reperfusion injury models. With the advantage of easy chemical manipulations, stimuli-responsiveness, and biocompatibility, we have tried to break new grounds with useful applications in chemical neuroscience. We will describe a nitric oxide–releasing, β-sheet–disrupting peptide, which exhibits dual anti-amyloidogenic and neuroprotective activity in Alzheimer's disease models. It suppresses NLRP3–ASC–caspase-1 inflammasome assembly, attenuates IL-1β/IL-18 secretion, oxidative stress, and neuronal loss. It supports cognitive enhancement and reduces amyloid-β accumulation, establishing its therapeutic potential against inflammasome-driven neurodegeneration. We will also present our efforts in engineered design and fabrication of biomicrofluidic platforms for creating organ-on-a-chip systems.

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2. J. Proteome Res., **2026**, 25, 1492-1506.
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PL-8

The Chemistry-Biology nexus: Shaping the future of healthcare

Neetu Singh

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Among myriad of health issues of global populace today, the problems associated with better means of diagnosis, and repair and regeneration of organs, bones, cartilages, etc. remain a big challenge. The prospect of using nanoscience and nanotechnology as a tool to answer questions arising out of these healthcare issues are exciting and form the basis of this talk. Nanostructures, due to their similar size scale as bio-macromolecules and cellular components, provide an unprecedented opportunity to target and potentially modulate important biological processes. Some of the key nanotechnology based scientific and technological contributions from our laboratory that will impact future healthcare strategies impacting disease diagnostics, better therapeutics delivery and tissue engineering will be discussed. Particular emphasis will be placed on our electrochemical sepsis detection platforms developed for rapid and sensitive diagnosis of bacterial infections. Sepsis remains a major cause of mortality worldwide, and current diagnostic approaches are often dependent on time-consuming blood cultures and multiple laboratory tests. To address this challenge, we developed a microgel/microscaffold-based electrochemical sensing platform incorporating carbon nanodots as redox-active probes. The system detects bacterial growth-associated metabolic changes through cyclic voltammetry, enabling classification of sepsis-positive patient plasma samples within approximately two hours. Clinical studies demonstrated superior diagnostic performance compared with conventional biomarkers such as procalcitonin, while also enabling discrimination between different bacterial classes through characteristic electrochemical signatures. Building on this work, we have further developed electrochemical immunosensor platforms for simultaneous detection of host and pathogen-derived sepsis biomarkers, including procalcitonin (PCT), interleukin-6 (IL-6), C-reactive protein (CRP), and lipopolysaccharide (LPS). Utilizing biofunctionalized screen-printed electrodes and three-dimensional microgel architectures containing electroactive carbon-dot nanoprobes, the platform achieves highly sensitive measurements from small sample volumes with analysis times as short as 10 minutes, providing a promising route toward pointof-care sepsis diagnosis. Together, these examples demonstrate how advances in chemical sciences, biomaterials, and nanotechnology can be translated into practical healthcare technologies for early disease detection, precision therapeutics, wound management, and tissue regeneration, ultimately contributing to improved patient outcomes and next-generation healthcare solutions.

PL-9

MAPKs beyond stress: Rewiring plant growth and photosynthesis

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Mitogen-activated protein kinase (MAPK) cascades are central signaling modules that enable plants to translate environmental and developmental cues into coordinated physiological responses. Over the past decade, our laboratory has uncovered diverse roles of MAPK signaling in submergence tolerance, light signaling, thermomorphogenesis, cell cycle regulation, miRNA biogenesis, and crop productivity. In this lecture, I will present these discoveries with a particular focus on our latest finding that reveals an unexpected role of MAPKs in regulating photosynthesis. We demonstrate that the cytosolic MAPK MPK3 controls chloroplast protein import by modulating the activity of the Raf-like kinase ACTPK1, which phosphorylates the transit peptide of the Rubisco small subunit (RbcS). This reversible phosphorylation acts as a molecular checkpoint governing RbcS import, Rubisco accumulation, and CO_2 assimilation. Together, these findings establish MAPK signaling as a master integrator linking environmental perception to chloroplast function and provide new opportunities for engineering climate-resilient, high-photosynthetic crop plants.

Invited Lectures (IL)

IL-1

Early stress and accelerated aging

Vidita Vaidya

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Growing evidence suggests that early-life stress history can shape biological aging, yet the pathways through which this lifelong vulnerability manifests remain unclear. Using a maternal separation (MS) rodent model of early-life stress, we show that MS history evokes persistent cognitive, inflammatory, neurovasculature and bioenergetic changes that can accelerate aging trajectories. MS animals exhibit premature decline in object recognition memory in middle-aged life, accompanied by elevated peripheral inflammation, blood-brain barrier (BBB) compromise, heightened neuroinflammasome and microglial reactivity, and deteriorated mitochondrial health in the hippocampus. Notably, we demonstrate that adult-onset systemic supplementation with Nicotinamide (NAM), a NAD+ precursor, prevents the emergence of peripheral and central inflammatory signatures, protects BBB integrity, maintains hippocampal mitochondrial health and mitigates cognitive decline in middle-aged MS animals. Collectively, these findings provide mechanistic insights into how early-life stress shapes brain aging, while highlighting NAM supplementation as a gerotherapeutic strategy to prevent premature aging driven by early adversity.

IL-2

Cyanobacteria as climate-smart inputs to sustain healthy microbiomes in soil and produce across crops

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Cyanobacteria, a diverse group of omnipresent oxyphototrophic prokaryotes are well recognized for being the earliest and most ancient organisms on our planet, hence befitting candidates to link biological activities to soil and crop productivity. In agriculture, cyanobacteria have been investigated as rice biofertilizers, mainly for their ability to supply biologically fixed nitrogen, contributing to the enduring fertility and sustainability of the rice production systems. In the last few decades, their role in plant growth stimulation, along with savings of 20-30% N as well as enriching micro- and macronutrients or other quality attributes in the produce, besides enhancing yields, has been demonstrated in several other cereals, besides rice, and in flowers, vegetables and legumes. The efficacy of cyanobacterial treatments through different modes in enhancing the quality of tomato fruits was investigated to understand the underlying mechanisms using shotgun metagenomics- transcriptomics of soil and fruit, along with fruit metabolomics. Stimulated nitrogen-carbon metabolism, phenylpropanoid metabolism and sugar transport in the fruits was found to be associated with improved fruit weight, lycopene and flavonoid content, while elevated CO_2 enhanced fruit yield and nutritional and quality traits. By developing multispecies biofilms using cyanobacteria, delivery system as seed coatings was optimized and its resource-efficiency and methane mitigating potential validated in wet direct seeded rice (DSR) vs flooded transplanted mode of cultivation (TPR). 16S rRNA amplicon sequencing illustrated cultivation- and treatment-dependent bacterial restructuring and associated functional rewiring, leading to improved crop yield, grain quality, water productivity with lower GHGs using cyanobacteria-coated rice seeds. This highlighted their significance as climate-resilient options in tomato and rice crops.

IL-3

miRNAs: Master modulators of multigenic stress responses in plants

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The microRNAs (miRNAs) comprise a novel class of regulatory molecules that have added a new dimension to the genetic management module within living cells. The regulatory action of the miRNAs is typically inhibitory in nature and it may operate at both transcriptional and post-transcriptional levels. The miRNAs are involved in regulating the vital and specialized aspects of plant biology including growth of cells, development of organisms and maintaining the integrity of genomes. The development programming of plants is greatly influenced by a wide range of environmental factors. Among these increasing temperatures and drought have emerged as the primary cause for limiting crop production. Rice miRNA profiles in response to different stresses were captured and compiled in a web server, ARMOUR. Analysis is being performed with selected molecules to undrerstand their regulatory functions in plants. The studies have indicated novel outcomes that can be utilized to prepare climate resilient crops, as an enduring step to fight stress mediated decline in crop yields.

IL-4

Formate's whisper- How a metabolite can decide the bacteria's response to antibiotics

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Formate, a host-associated short-chain fatty acid, plays a critical role in regulating Salmonella enterica serovar Typhimurium virulence. Although extracellular formate enhances invasion, the contribution of intracellular formate generated by pyruvate-formate lyase has remained unclear. Our work demonstrates that intracellular formate maintains cytoplasmic pH, membrane integrity, and envelope homeostasis, thereby supporting flagellar production, motility, adhesion, intestinal colonization, epithelial-cell invasion, and systemic dissemination. Loss of the formate-generating enzyme pflB depleted intracellular formate, induced envelope stress and RpoE-dependent regulatory pathways, reduced flagellar gene expression and motility, and simultaneously enhanced SPI-1-associated invasion programs. These findings reveal that formate availability functions as a metabolic signal that coordinates the transition between motility and invasion, enabling Salmonella to adapt to changing host microenvironments. Together, the study identifies intracellular formate homeostasis as an important metabolic determinant of bacterial physiology and pathogenesis, and highlights thepyruvate-formate lyase–formate axis as a potential target for limiting Salmonella infection.

IL-5

Mitochondrial association with oncogenesis: Impact of its deregulated bioenergetic function and beyond

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It is well established that tumour cells exhibit numerous metabolic alterations. Further, mitochondrial structural and functional alterations are evident in tumor cells, and an obvious relationship exists between these two phenomena. The oncogenic transcription factor, ETS1, induces mitochondrial dysfunction in ovarian cancer by upregulating Drp1, leading to mitochondrial fragmentation. Our recently published data suggest that pharmacological or molecular inhibition of Drp1 can significantly curtail ETS1-associated EMT and metastasis in ovarian cancer cells. These studies underscore the intricate link between metabolic pathways and cancer progression, with a particular emphasis on how mitochondrial functionality influences oncogenesis, presenting new avenues for targeted cancer therapy. Metabolic alterations are increasingly recognized as fundamental features of cancer. Recent studies have highlighted altered fatty acid oxidation (FAO) at different stages of tumour development. CPT1, a rate-limiting enzyme of FAO, plays a crucial role in these metabolic adaptations in cancer cells. We showed that CPT1A, a variant of CPT1, is significantly upregulated in ovarian cancer (OC) and correlates with poor prognosis. Inhibition of CPT1A, either by siRNA-mediated knockdown or by etomoxir, reduces the migratory and invasive properties of the OC cells. The growth factor TGFβ, enhanced the FAO rate by enhancing CPT1A expression and its enzymatic activity in OC cells through an AMPK-dependent pathway. Cumulatively, our study underscores the role of CPT1A-mediated FAO in facilitating ovarian cancer progression through TGFβ-induced EMT. Thus, mitochondrial modifications at different levels are directly linked with the metabolic function of the tumour cells.

IL-6

Untranslated RNA dynamics in anti-oxidant and radiation response: Implications in cardiac hypertrophy and failure

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Eukaryotic messenger RNAs (mRNAs) undergo processing at the 3′-untranslated region (UTR) in two concerted steps - endonucleolytic cleavage followed by addition of a poly(A) tail (PA-tail). Unlike the polyadenylation step, the endonucleolytic cleavage is considered imprecise and random that leads to heterogeneity of cleavages (CSH). Contrary to this belief, we show that the cleavage imprecision is tightly regulated, that centres around a primary site, followed by several subsidiary cleavages. This regulates gene expression in anti-oxidant an UV-response. Globally and using reporter antioxidant mRNA, we discovered an inverse relationship between the CSH and the gene expression. Under oxidative stress, there is a decrease in CSH and an increase in the primary CS usage to induce antioxidant gene expression. We establish that oxidative stress induces affinity/strength of cleavage complex assembly, increasing the fidelity of cleavage at the primary CS, thereby reducing CSH inducing antioxidant response. This regulation is critical in cardiovascular conditions such as cardiac hypertrophy (CH) where oxidative stress is critical in the pathogenesis. CH is hearts response to pathological stress leading to cardiac remodelling increasing the cardiomyocyte size and ventricular wall thickness. Hypertrophic stimulus induces oxidative stress in the heart that is countered by cellular antioxidant response. However, at a later stage, notwithstanding the persistent oxidative stress, anti-oxidant response get diminished resulting in hypertrophied heart. We demonstrated that CSH is compromised at the late state but not at the early sate on hypertrophy induction and a compromised CSH from polyA polymerase down regulation diminishes antioxidant response leading to pathogenesis of hypertrophy in the heart.

IL-7

Bioengineering genes to generate iron rich wheat grains using genome editing

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Iron (Fe) is a crucial micronutrient for both human health and plant development. Enhancing grain iron content through biofortification is a primary strategy to combat micronutrient malnutrition in developing nations. While the molecular mechanisms governing Fe uptake and transport are well established in model plants like *Arabidopsis*, their counterparts in major crop species remain insufficiently characterized. A comprehensive understanding of how plants sense, transport, and partition Fe into edible tissues is therefore imperative. Bread wheat (*Triticum aestivum* L., AABBDD, 3x2n=6x=42, is an allohexaploid formed by three ancestral diploid genomes, grain iron and zinc concentrations remain sub-optimal despite its major role as a global staple. Our research elucidates the key molecular responses and signalling pathways mediating Fe mobilization. Transcriptomic analyses revealed temporal, asymmetric, and heterogeneous expression patterns among sub-genome homoeologous genes in roots under Fe starvation. Furthermore, integration of root-tip transcriptomes with single-cell datasets uncovered coordinated cell-type-specific responses to Fe stress. Our lab also used functional genomics approach such as CRISPR/Cas9 and TILLING mutant lines to provide the first insights into the molecular and biochemical machinery to enhance Fe loading in grains. Together, these findings establish and provided a much needed foundation and framework to develop genetic resources to optimize micronutrient uptake, remobilization, and bioavailability in wheat.

IL-8

Interplay of calcium and ROS in regulating mitochondrial retrograde signaling under oxidative stress in plants

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Calcium (Ca^{2+}) is a critical signaling molecule regulating a diverse range of biological processes. Intracellular Ca^{2+} signatures generated in response to stress stimuli affect a variety of cellular processes, including gene expression, hormone signaling, and ROS signaling which ultimately determine the physiology of the plant under stress conditions. The decoding and relay of the signal to different organelles have been reported, with mitochondria being the most crucial. As hubs of energy metabolism and signaling, mitochondria are also both generators and targets of Ca^{2+}-mediated regulation. These 'signatures' originating from mitochondria are signals as well as responders for initiating the mitochondria-to-nucleus retrograde signaling pathway; a key sensor for mitochondrial dysfunction status determination, energy metabolism and ATP levels modulation, and proteostasis. Building upon this work on calcium signaling and ROS signaling converging at MRS to maintain cellular homeostasis, we unravel a Ca^{2+}-dependent phosphoregulatory switch that controls the gating of these MRS signals from mitochondria to the cytosol and ultimately to the nucleus. Two key kinases, CIPK3 and CIPK9, of the CBL-CIPK family phosphorylate VDAC3, a beta-barrel protein at the outer mitochondrial membrane, thereby gating ROS flux and regulating the Mitochondrial Dysfunction Stimulon (MDS) genes. CIPK9 positively regulates VDAC3 by phosphorylating its C-terminus and allowing the passage of ROS from mitochondria to the nucleus. This ROS acts as a signal to elicit CIPK3-mediated phosphorylation of the N-terminus of VDAC3, thereby preventing further mETC overreduction, promoting alternative respiratory pathways, and limiting ROS accumulation. Hence, ROS gating through VDAC3 is a pivotal node and a critical checkpoint in oxidative stress tolerance in plants. Our detailed *in silico* analysis identified OsVDAC1 as the closest rice orthologue of AtVDAC3, suggesting a potentially conserved role for VDAC proteins in rice and Arabidopsis. To investigate the functional conservation of OsVDAC1, we performed yeast complementation assays using the VDAC-deficient mutant, Δpor1. The successful complementation suggests that OsVDAC1 may share functional properties with AtVDAC3 in maintaining ROS homeostasis and mitochondrial membrane potential. Building on these findings, our current research focuses on elucidating the regulatory role of rice CIPK3 and CIPK9 as potential phosphoregulatory switches governing OsVDAC1 function. Ultimately, this research aims to establish OsVDAC1 as a candidate for engineering stress-resilient crops and to elucidate the molecular mechanisms underlying mitochondria-to-nucleus communication in maintaining cellular redox homeostasis.

IL-9

From plant science to public health: Innovating for iron security and sustainable agriculture

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Iron deficiency anemia remains a major public health challenge in India, disproportionately affecting women and children while compromising cognitive development, maternal health, and economic productivity. Conventional interventions, including iron supplementation and soil-applied fertilizers, face persistent limitations due to poor compliance, high costs, and the widespread prevalence of alkaline and calcareous soils that restrict iron availability to crops. Addressing this interconnected nutritional and agricultural challenge requires scalable, biology-driven solutions that enhance iron acquisition across the food system. This initiative translates discoveries in plant iron biology into three complementary innovations. First, a light-mediated biofortification platform harnesses blue-light signaling to enhance plants' natural iron-acquisition pathways, enabling the production of iron-enriched microgreens and leafy vegetables without chemical treatments or genetic modification. Second, precision genome editing targets PROPEP2, a negative regulator of iron-deficiency responses, to improve root architecture, rhizosphere acidification, and iron accumulation, with potential applications in Indian mustard and other crops. Third, a climate-resilient biostimulant derived from extremophiles from Lonar Lake aims to improve crop performance, soil health, and nutrient availability under alkaline and saline conditions. Together, these innovations establish an integrated soil-to-plate strategy that connects fundamental biological discovery with agricultural applications and improved dietary iron supply. By combining non-transgenic cultivation technologies, precision crop engineering, and beneficial microbial resources, the initiative seeks to reduce dependence on chemical inputs, strengthen crop resilience, and expand access to nutrient-rich foods. Potential deployment pathways include controlled-environment agriculture, smallholder farming systems, local vegetable markets, and public nutrition programmes. Building on promising proof-of-concept findings and ongoing intellectual property development, this initiative aims to accelerate the translation of plant science into scalable, India-relevant solutions. Ultimately, it seeks to connect laboratory innovation with farmer livelihoods, sustainable food production, and improved nutritional outcomes, advancing a healthier and more iron-secure India.

IL-10

Rewiring the rhizosphere: Next-generation solutions for climate resilient agriculture

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Global food security is increasingly threatened by population growth and the degradation of arable land. Traditional eco-friendly interventions, such as conventional bioinoculants, often yield limited success in variable field environments. With the establishment of the plant-associated microbiome as a driver of host health, emphasis has shifted toward harnessing these complex microbial interactions as more effective and sustainable solutions. Rhizosphere microbiome engineering represents a transformative approach to enhancing crop fitness and resilience. The talk will showcase our group's research in developing top-down and bottom-up rhizosphere engineering strategies, including their translation from lab to field. Through select case studies, we examine how decoding the soil-plant-microbiome nexus allows us to leverage microbial communities for stress mitigation in key model crops. The talk underscores the strategic role of soil microbiome engineering in advancing long-term soil health, while critically discussing the current challenges in its broader adoption.

IL-11

Waking up bacteria from stress-induced slumber

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Bacterial cell adapts to changing environmental conditions by modulating growth-related processes to enhance the survival fitness. However, the molecular mechanism that governs the processes responsible for cellular homeostasis is not clearly understood. Here, we have investigated the interplay between two antagonistic pathways: ribosome biogenesis, which promotes growth, and the stringent response, which induces dormancy through the alarmone (p)ppGpp. We identified a new role for the conserved GTPase Era, an essential protein in Escherichia coli, as a key regulator of cellular resuscitation from dormancy. We found that Era is selectively upregulated during the lag phase, a critical transition period when cells exit dormancy and re-enter active growth. Beyond its established role in 30S ribosomal subunit maturation, we showed that Era exhibits a previously uncharacterized function in modulating stringent response signalling. Mechanistically, we showed that Era binds to RelA, which is a (p)ppGpp synthetase that inhibits the 70S ribosome and this Era-RelA interaction facilitates the release of RelA from the 70S ribosome, thereby alleviating translational repression. This promotes ribosome activation and restores protein synthesis, enabling efficient cellular recovery and growth. Our findings uncover a temporal and epistatic interaction between ribosome assembly and stringent response pathways, mediated by Era-RelA cross-talk. This study highlights a ribosome-centric regulatory mechanism that links RNA-dependent processes, ribosome maturation and translation, with stress signalling. Given that the dormant bacterial populations contribute to antibiotic tolerance, understanding this regulatory axis offers new insights into potential strategies to target persister cells.

IL-12

A Tetramer with a twist: Structural and functional insights into a carbohydrate-active enzyme, GH43

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β-1,4-Xylosidases are carbohydrate-active enzymes that contribute to lignocellulosic biomass degradation by releasing xylose from xylan-derived oligosaccharides. In this study, the structural and functional properties of a Glycoside Hydrolase family 43 enzyme, a β-1,4-xylosidase from *Pseudopedobacter saltans* (PsGH43) were investigated using X-ray crystallography and complementary biochemical approaches. The crystal structures of the wild-type enzyme and its xylose-bound complex were determined to examine molecular architecture, substrate interactions and potential catalytic mechanisms. Site-directed mutagenesis was employed to generate the A95P variant, enabling investigation of the contribution of the WAP element to enzyme function. Kinetic properties, pH and temperature optima, and metal-ion effects were evaluated. Time-dependent LC-MS/MS analysis was also performed to monitor the hydrolysis of xylobiose, a natural substrate. Structural analysis revealed a distinct tetrameric assembly. Both wild-type and A95P enzymes displayed optimal activity at pH 7.0 and 30°C. Notably, the A95P variant exhibited enhanced catalytic efficiency which suggested that the structural environment of the WAP element influenced the enzyme performance. The xylose-bound structure provided insights into product stabilization within the active site and suggested a possible contribution to product-release limitations. Together, these findings establish a structural and functional framework for understanding PsGH43 and provide insights into enzyme architecture, substrate recognition and catalytic activity. This has potential relevance to the development of improved biocatalysts for biomass conversion.

IL-13

Towards AI bacteria: Genetically engineered *E. coli* networks identifies prime numbers, vowels and answer math questions

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Performing cellular computations with engineered bacteria has enormous importance in biocomputer technology development at the micron scale, where microprocessor-based computers have limitations due to energy, cost, and technological constraints. Here, we designed and built Artificial Neural Networks (ANNs) with genetically engineered bacteria that can identify prime numbers, vowels, and even determine the maximum number of pieces of pizza or pie that can be obtained from a given number of straight cuts. In addition, the 'intelligent' bacteria can answer mathematical questions such as whether a number n's factorial is divisible by $n \times (n + 1)/2$ OR whether a number n's square can be expressed as the sum of three factorials. To build such "intelligent" bacteria, we created ANNs with *E. coli* by introducing synthetic gene regulatory networks such that each bacterium behaves like an artificial neuro-synapse. When these 'bacterial neurons' are mixed in a liquid culture, they create ANNs within themselves to perform human-designed computation. The questions were asked by adding or not-adding chemicals in binary pattern and the answers were obtained by specific patterns of multiple fluorescent reporter proteins. All those above solved problems by *E.coli* are classic abstract computational problems. Such problems are solved by a computer by writing codes in Python or C. Introducing such abstract computational capability in living cells, will be a step forward in biocomputer and bio-AI technology development.

IL-14

Bioactive molecules at biological interfaces: Engineering natural coatings for protection against oxidative and microbial stress

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Biological interfaces represent dynamic sites of interaction where oxidative reactions, microbial activity, moisture transfer and environmental stress collectively influence the stability, functionality and quality of biological materials. In fresh fruits and vegetables, these processes are particularly important in determining postharvest deterioration, nutritional losses and shelf life. Natural bioactive molecules, particularly plant-derived phenolics, flavonoids, essential oils and other phytochemicals, offer considerable potential for controlling such deterioration. However, their practical application is often constrained by volatility, chemical instability, limited aqueous solubility, sensitivity to environmental conditions and variable bioavailability. Engineering these molecules within natural edible coating matrices provides an opportunity to overcome these limitations while developing multifunctional protective systems. This is to explores the scientific principles and technological advances underlying the development of bioactive edible coatings, drawing substantially upon research undertaken at NIFTEM-K on polysaccharide-based, composite and active coating systems. Experimental investigations involving xanthan gum incorporated with pomegranate peel extract, mango kernel starch functionalised with lemongrass essential oil, muskmelon seed flour-based coatings containing oregano essential oil, and chitosan-based composite systems encapsulating clove nanoemulsions illustrate the potential of combining naturally derived matrices with functional bioactive agents. Further developments involving guar gum–almond gum composites, starch-based nano-edible coatings and ultrasound-assisted formulation approaches demonstrate how matrix composition and processing conditions can influence coating characteristics and their postharvest performance. The underlying mechanisms are discussed in terms of interfacial interactions, polymer network formation, mass-transfer regulation, antioxidant activity and antimicrobial action. Particular emphasis is placed on the capacity of phenolic compounds to mitigate oxidative stress through radical scavenging and related mechanisms, while essential oil constituents can interfere with microbial membrane integrity and cellular functions. Encapsulation, nanoemulsion formation and ultrasound-assisted processing offer additional opportunities to improve the dispersion, stability and functional delivery of these compounds within coating matrices.The presentation further examines the transition from passive barrier coatings towards engineered, multifunctional biological interfaces, highlighting the importance of bioactive–matrix compatibility, controlled release, coating integrity, sensory acceptability, food safety and scalability.

IL-15

Role and functions of MPEDA, registration procedure of seafood processing plants and marine products exports

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The Marine Products Export Development Authority (MPEDA) was established in 1972 under the Ministry of Commerce and Industry, Government of India, to promote and develop marine product exports. It plays an important role in improving the quality, safety and international competitiveness of Indian seafood. Its major functions include registration of exporters, seafood processing plants, fishing vessels and pre-processing centres, along with promoting aquaculture, infrastructure development, research and training. MPEDA also organizes trade fairs and promotional activities to explore international markets. Registration of seafood processing plants ensures compliance with prescribed hygiene, sanitation and food safety standards. The registration procedure involves submitting an online application, required documents and fees, followed by inspection of the processing facility. After satisfactory verification, registration is granted by the competent authority. India exports various marine products such as frozen shrimp, fish, squid, cuttlefish, crab and other seafood. Major export destinations include the USA, China, Japan, European Union countries and Southeast Asian countries. During 2024–25, India exported approximately 16.98 lakh metric tonnes of marine products worth US$7.45 billion. These exports contribute significantly to foreign exchange earnings, employment generation and the economic development of coastal communities. Thus, MPEDA plays a vital role in promoting sustainable fisheries, maintaining export quality and strengthening India's position in the global seafood market.

IL-16

RECQ1-RPA interaction promotes fork restoration and facilitates efficient recovery from replication stress following DNA damage induced by topoisomerase inhibitors

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Interaction between Replication Protein A and RECQ1 helicase stimulates the unwinding activity of RECQ1 on long DNA duplexes *in vitro*. However, the biological relevance of this association of RPA and RECQ1 in DNA damage response remains poorly understood. RECQ1 has been reported to restore stalled replication forks following topoisomerase I poisoning. We hypothesize that the RECQ1-RPA interaction might play a critical role in fork restoration and replication restart following genotoxic challenges. From structure based docking studies, we identified two acidic residues in the helicase core domain 2 (D2) of RECQ1 which are essential for its interaction with RPA. Biochemical and biophysical evidences demonstrate that, substitution of these residues with alanine significantly impaired RPA binding and diminished the stimulatory effect on helicase unwinding activity *in vitro*. When expressed in RECQ1-depleted cells, the RECQ1-2A mutant exhibited compromised replication fork progression and defective restoration of regressed forks following topoisomerase inhibition by camptothecin or etoposide. The decreased replication kinetics in RECQ1-2A expressing cells is associated with enhanced accumulation of double-strand breaks as observed from gamma-H2Ax foci. Overall, this study provides a structural basis of RECQ1-RPA interaction as well as insights into how the RECQ1-RPA partnership safeguards genomic stability by ensuring efficient fork restart following replication stress induced by topoisomerase inhibitors.

IL-17

Individual radiosensitivity revisited: Fixed and modifiable determinants of normal tissue response

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Normal tissue toxicity remains the principal constraint on radiotherapy dose escalation, yet patients receiving identical prescribed dose, volume, and fractionation display markedly divergent reactions. Two decades of radiogenomics have established that germline variation in DNA damage response, oxidative stress, and fibrotic signaling pathways contributes to this variance, but individually associated variants explain only a modest fraction of it, and the field has plateaued. Radiosensitivity has been modelled as a fixed host property, when it is more accurately described as the product of dose, germline capacity, and a modifiable microbial–metabolic state. Evidence is presented from three complementary strands of our work. First, candidate variant associations with acute and late toxicity endpoints, interpreted alongside regulatory-layer analyses indicating why genotype under-predicts functional repair capacity. Second, a functional double-strand break repair assay that converts static genotype into a measurable phenotype and quantifies the residual variance genotype fails to capture. Third, evidence that this residual variance - microbiota, pelvic irradiation in a rodent model - induces reproducible dysbiosis, metabolite depletion, mucosal barrier compromise, and notably out-of-field neuroinflammatory and hippocampal molecular changes, all attenuated by probiotic intervention.

IL-18

Can we reverse antibiotic resistance? A glimpse into molecular mechanisms and drug design

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Antibiotic resistance is a global pandemic that has emerged as a silent killer. Synthesizing newer antibiotics is an uphill task and so does unravelling new targets. Hence, we delve into resistance mechanisms such as drug target modification, a highly efficient strategy utilized by pathogenic systems to render themselves resistant to antibiotics. To understand origins of resistance we unravel the mechanism of resistance aquired by pathogens against macrolide lincosamide and streptogramin B (MLS_B) class of antibiotics. The enzyme Erythromycin-resistance methyltransferases (Erms),[1] exclusively harboured by several multi-drug resistant (MDR) pathogens can site specifically methylate a ribosomal base (A2058, *E. coli* numbering) in the nascent peptide exit tunnel of the 50S ribosomal subunit which then renders the MDRs resistant to MLS_B class of drugs. Interestingly, we show that Erm is an opportunistic enzyme that exclusively targets ribosomal precursors. Using Cryogenic Electron Microscopy (Cryo-EM) we have trapped the Erm-precursor complex and showed how in a complex environment, during ribosomal biogenesis, Erm can methylate its substrate selectively. Moreover, corroborating single molecule FRET measurements were performed to understand the dynamic nature of these interactions and decipher states that the enzyme charters to achieve catalysis. Our work dwells into the unique dual base flipping mechanism employed by Erms to achieve catalysis and its evolutionary implications in the design of these enzymes that induce resistance in pathogenic strains.[3,4] Furthermore, the findings help in the identification of allosteric sites distal from the catalytic site of Erm which can serve as druggable targets[5]. Subsequently, we have ongoing efforts towards AI-based drug design to specifically target Erm-based resistance thereby, facilitating ways of reversal of resistance. Overall, we draw a holistic picture of Erm's action and delineate methods of curbing its pathogenic function.

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IL-19

DKC1-mediated sphingolipid dysregulation drives colorectal cancer and therapy resistance

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Colorectal cancer (CRC), the second leading cause of cancer-related deaths worldwide, often exhibits poor response to first-line therapies due to drug resistance and molecular heterogeneity. This study identifies Dyskerin pseudouridine synthase 1 (DKC1) as a key oncogenic driver in CRC, with elevated expression linked to aggressive disease, poor recurrence-free survival, and resistance to FOLFOX/FOFIRI regimens. Functional assays reveal that DKC1 promotes cell cycle progression, inhibits apoptosis, and induces stem-like traits, aligning with Consensus Molecular Subtype 2 (CMS2). A positive feedback loop between DKC1 and canonical WNT signaling sustains its tumorigenic activity. Integrated lipidomic and transcriptomic profiling uncovers disrupted sphingolipid metabolism and enrichment of very-long-chain ceramides in DKC1-high tumors. Mechanistically, we show that DKC1 and SOX2 together drive the expression of SGPP2, modulating sphingolipid biosynthesis, and targeting SGPP2 in DKC1-positive CRC alleviates oncogenic properties. Moreover, dual inhibition of DKC1/WNT signaling suppresses the growth of patient-derived organoids and tumor burden in preclinical CRC mice models. These findings position the DKC1/WNT axis as a promising therapeutic target and highlight complex sphingolipids as potential plasma biomarkers for non-invasive diagnosis of advanced CRC.

IL-20

Targeted base editing for ELANE-associated severe congenital neutropenia

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Severe congenital neutropenia (SCN) caused by dominant ELANE mutations is characterized by impaired granulopoiesis and recurrent life-threatening infections. Current treatments, including granulocyte colony-stimulating factor and hematopoietic stem cell transplantation, have significant limitations. We developed a targeted base-editing strategy to disrupt ELANE without introducing DNA double-strand breaks, offering a potentially safer therapeutic approach. Three complementary strategies were evaluated: premature termination codon generation, splice-site disruption, and promoter disruption. Screening of guide RNAs using cytosine and adenine base editors achieved editing efficiencies of up to 97%, with minimal indels and substantial suppression of neutrophil elastase expression. Clinically relevant ELANE mutations were introduced into CD34+ hematopoietic stem and progenitor cells (HSPCs), successfully recapitulating SCN-associated defects in granulocyte maturation and cellular persistence. Therapeutic ELANE disruption in normal donor HSPCs achieved editing efficiencies of up to 94% while preserving granulopoiesis and neutrophil differentiation. Long-term evaluation in the NBSGW xenograft model demonstrated stable editing following 18 weeks of engraftment, robust human hematopoietic reconstitution, and comparable multilineage differentiation without lineage skewing. Furthermore, a nuclease-deficient dABE8e editor achieved 60–92% editing efficiency across selected ELANE targets, eliminating nick-associated DNA damage and further improving genomic safety. Together, these findings establish targeted ELANE base editing as a promising, mutation-independent therapeutic strategy for SCN. The approach combines efficient gene disruption, preservation of hematopoietic stem cell function, and sustained in vivo editing, supporting further preclinical development toward clinical translation for patients with ELANE-associated SCN.

IL-21

Altered neutrophil pool mediates tissue injury in chronic inflammatory disease

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Chronic inflammatory disorders shorten healthy lifespan and increase susceptibility to secondary insults such as infection or trauma. Identifying which immune populations drive this excess morbidity is challenging because few preclinical systems allow selective interrogation of individual cell types. I will describe experimental strategies from my laboratory that pair disease relevant mouse models with biomaterial implant-associated inflammation to test causality. Across models of type 2 diabetes and sterile implant inflammation, we find a population of altered neutrophils, driven by increase in immature neutrophils, that mediates inflammationlinked tissue damage. By combining singlecell RNA sequencing, highparameter flow cytometry, and ex vivo functional assays, we define a distinct immature neutrophil program associated with heightened tissuedestructive functions. Mechanistic experiments demonstrate that inhibiting specific neutrophil effector pathways reduces injury in chronically inflamed hosts while preserving overall antimicrobial defence. These results suggest that the altered neutrophil pool is a driver of immunopathology in chronic inflammatory settings and support targeted neutrophil modulation as a therapeutic approach to limit collateral tissue injury after infection or trauma. I will also discuss translational opportunities, candidate biomarkers for patient stratification, and ongoing efforts to develop selective inhibitors that maintain host defence while preventing neutrophilmediated damage in clinical contexts.

IL-22

Epigenetic regulation of rice genomic imprinting

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Small (s)RNAs are a group of key molecules resulting from RNA silencing pathways across eukaryotes. These 20-24 nt RNA molecules associate with specific protein partners called Argonautes to target nucleic acids having high base-pair complementarity. Among most eukaryotes, sRNA targeting might result in degradation of target RNAs or their translational repression or repression of their transcription by transcriptional silencing. Among plants, sRNAs generated from specific genomic regions induce DNA methylation and histone modifications in specific target genomic regions, often referred to as epigenetics. This pathway regulates repeats and transposons and commonly referred to as RNA-directed DNA methylation (RdDM). Our lab focuses on various aspects of sRNA biogenesis and their functions, using genetic, molecular, bioinformatic and biochemical approaches in a number of model systems. I will be discussing novel sRNA-mediated pathways that played crucial roles in genomic imprinting and endosperm development in rice. I will be also discussing how silencing-associated master regulators played crucial roles in chromatin architecture, induction and maintenance of histone marks and chromatin boundary formation in rice.

IL-23

Phytoremediation of ^{137}Cs and ^{90}Sr at Nuclear power plant sites: From site-specific strategies to sustainable remediation

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Nuclear power plant (NPP) sites need low-cost, low-disturbance options to manage accidental or legacy ^{137}Cs and ^{90}Sr contamination, as conventional excavation, washing and solidification are expensive, degrade soil and generate secondary waste. This AERB-supported project developed site-specific phytoremediation for Indian NPP sites. Soils from IGCAR-Kalpakkam, Kudankulam and Narora were characterised and found suitable for plantation. More than 12 fast-growing, non-edible species were screened in hydroponics with stable Cs and Sr (100-1000 ppm), and six were shortlisted: *Catharanthus roseus*, *Abutilon indicum*, *Ricinus communis*, *Vetiveria zizanioides*, *Cymbopogon flexuosus* and *Alstonia scholaris*. *A. scholaris* showed the highest Sr uptake and translocation, *A. indicum* the highest Cs uptake, and *C. roseus* transfer factors above 1 for both elements. The species tolerated gamma irradiation and $^{137}Cs/^{90}Sr$ spiking, including actual low-level radioactive waste at BARC Facilities, Kalpakkam; in nutrient-free medium *V. zizanioides* removed ~75% of ^{137}Cs and 74% of ^{90}Sr in four days. Aquatic *Eichhornia crassipes* and *Monochoria hastata* removed Cs and Sr from water. The project helped NPP sites by providing a soil-matched plant palette: vetiver, lemon grass, castor and periwinkle (Kalpakkam); *A. indicum*, castor and periwinkle (Kudankulam); *A. scholaris*, *A. indicum* and periwinkle (Narora). These non-edible plants limit radionuclide transfer to animals and humans, and validation under irradiation and with real low-level waste supports preparedness for accidental contamination. Future work: field-scale trials at NPP sites, post-harvest management of contaminated biomass by pyrolysis to biochar (84-88% volume reduction in follow-up work), and microbe-assisted uptake enhancement. The work contributes to UN SDGs 3 (Good Health and Well-being), 6 (Clean Water and Sanitation), 12 (Responsible Consumption and Production) and 15 (Life on Land).

Oral Presentations (OP)

OP-1

Molecular insights into double-strand break repair in the radioresistant cyanobacterium *Nostoc* PCC 7120

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The nitrogen-fixing heterocystous cyanobacterium *Nostoc* sp. PCC 7120 exhibits remarkable radioresistance, with an LD50 of approximately 6 kGy, attributed largely to its efficient DNA repair capacity, as evidenced by rapid restoration of fragmented genomic DNA within 2–3 days of recovery. The absence of a functional RecBCD complex, as a consequence of the absence of RecC and a full-length RecB, together with the absence of Ku/Ku-like proteins, suggests that both RecBCD-mediated homologous recombination and non-homologous end joining (NHEJ) are non-functional. Consequently, the RecF pathway has been proposed as the major DSB repair mechanism in this organism. Multiple SSBs, RecA, RecF, RecO, RecR, and RecQ, together with, may collectively facilitate DSB repair through synthesis-dependent mechanisms. Tight regulation of these proteins by LexA and additional cis- and trans-regulatory mechanisms, along with the flexible formation of binary and ternary RecF–RecO–RecR complexes, may contribute to efficient DNA repair. Efficient synthesis-dependent repair, however, requires not only these repair proteins but also a sustained supply of deoxynucleoside triphosphates (dNTPs) for DNA synthesis. Maintaining dNTP-pool homeostasis is therefore an essential metabolic component of RecF-mediated repair, linking nucleotide metabolism to genome maintenance. Nucleoside monophosphate kinases (NMPKs) and nucleoside diphosphate kinase (Ndk) support dNTP production, and in *Nostoc* PCC 7120, Ndk overexpression enhances recovery from γ-irradiation and increases phosphorylation of RecA and other repair-associated proteins. Thus, coordinated regulation of NMPKs, Ndk, dNTP homeostasis, and RecF-mediated repair may provide the metabolic and enzymatic support for synthesis-dependent DSB repair and underpin the exceptional radioresistance of *Nostoc* PCC 7120.

OP-2

Understanding biological responses to radiation: From nature's own laboratory to cancer therapy and radiation protection

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Biological responses to radiation are diverse and heterogeneous, influenced by dose, dose rate, radiation quality, acute versus chronic exposure, and biological context, including species and experimental models. These responses range from radio-adaptation and genome maintenance to bystander effects, tissue injury, and tumor radio-resistance. While the mechanisms underlying low-dose and chronic low dose-rate radiation responses remain incompletely understood, tumor radio-resistance following therapeutic irradiation remains a major clinical challenge. Understanding these diverse responses requires investigation across the full spectrum of radiation biology.The Radiation Biology and Health Sciences Division addresses these challenges through an integrated research program spanning human population chronically exposed to natural radiation, experimental radiobiology, cancer research, and clinical trials. A major focus is the long-term study of the population residing in Kerala's high-level natural radiation areas, investigating health outcomes, genomic stability, mutation burden, epigenetic changes, telomere maintenance, and molecular mechanisms potentially associated with adaptation and healthy ageing.Translational research is another key component of radiobiology program. A dedicated initiative to develop radiation mitigators for planned radiation-exposure scenarios has advanced chlorophyllin-based interventions into clinical evaluation in cancer patients. Preclinical studies have also shown promise for probiotic-based strategies to mitigate radiation-induced intestinal injury. Complementary mechanistic investigations explore thorium-associated DNA damage, high-linear energy transfer (LET) alpha-particle effects, cold atmospheric plasma-induced bystander signaling, and cellular stress responses. Cancer research examines macrophage radio-resistance, immune regulation, cancer stem cell plasticity, and mechanisms underlying tumor radio-resistance. Together, these multidisciplinary efforts connect population-level observations with molecular mechanisms, experimental findings, and clinical outcomes, advancing our understanding of radiation biology and informed strategies for radiation protection, mitigation of radiation-associated injury and improved therapeutic outcomes.

OP-3

Unravelling the MYB regulatory network governing anthocyanin biosynthesis in banana

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Banana cv. Rasthali, valued for its taste and texture, lacks anthocyanin accumulation in the edible pulp, indicating tight transcriptional regulation of the pathway. In this study, five Musa R2R3-MYB transcription factors—*MusaUP1, MusaUP2, MusaMA2, MusaMA4,* and *MusaMA8*—were functionally characterised as regulators of flavonoid and anthocyanin biosynthesis. Their overexpression induced visible anthocyanin pigmentation in banana embryos and vegetative tissues, demonstrating strong transcriptional activation. Co-expression with *MusaTT8* revealed gene-specific regulatory patterns, with *MusaMA2* and *MusaMA8* showing enhanced activation of late biosynthetic genes through MBW complex formation. Yeast one-hybrid assays confirmed direct binding of MusaUP1 to the *CHS* and *ANS* promoters and MusaUP2 to the *CHS* and *LAR* promoters. Consistently, *MusaUP1* and *UP2* strongly induced *CHS* (>200-fold), *ANS,* and *UFGT* expression. Heterologous complementation in *Arabidopsis* further supported their regulatory functions, with all MusaMYBs restoring anthocyanin pigmentation in the *myb90* mutant. Notably, *MusaUP1* and *MusaUP2* induced exceptionally high anthocyanin accumulation (~500-fold), causing phytotoxicity and limiting whole-plant regeneration (Thakur et al., 2026). In contrast, the negative regulation of anthocyanin biosynthesis in banana remains poorly understood. To identify potential repressors, transcriptomes of anthocyanin-rich and white banana bracts were comparatively analysed, leading to the identification of two MYB transcription factors as candidate negative regulators. Phylogenetic and homology-based analyses across crop species identified an additional candidate regulator. Transgenic knockout and overexpression lines were generated, and genome editing in knockout lines was confirmed by sequencing. Notably, enhanced anthocyanin pigmentation was observed exclusively in knockout lines, predominantly at leaf margins, leaf bases, and discrete patches on the leaf blade, supporting the role of these MYBs as negative regulators of anthocyanin biosynthesis in banana.

OP-4

Structural biology research at BARC: An overview

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Three-dimensional atomic structures of biological macromolecules is crucial for understanding their functional mechanisms and developing potential applications in biotechnology and human health. Our research encompasses structural and functional investigations of diverse proteins, including plastic-degrading enzymes, cancer-related proteins, viral proteins and gut microbial enzymes, with an emphasis on understanding their structural features crucial for their function, molecular interactions and catalysis. In environmental biotechnology, PET-degrading enzymes, including several variants of *Is*PETase and PHL7, have been characterized. PHL7m (L93F/Q95Y) exhibited enhanced catalytic efficiency and thermostability compared with the *Is*PETase variants studied, alongside improved PET degradation. Its crystal structure, determined at 1.67 Å resolution, provided detailed insights into the architecture of the substrate-binding groove and catalytic performance. Cancer-related studies encompass KRAS variants, thyroglobulin-targeting nanobodies and enzymes involved in cellular metabolism. Wild-type KRAS and its G12C and G12D mutants exhibited differences in their oligomeric behaviour. The thyroglobulin-targeting nanobodies KT75 and KT76 showed nanomolar binding affinity, with their crystal structures determined at 1.35 and 1.6 Å resolutions, respectively. Cryo-electron microscopy of the KT75-thyroglobulin complex revealed structural features underlying molecular recognition. Expression, purification and biochemical characterization have also been optimized for WDR5, SHMT1, SHMT2, MTHFD2, PHGDH and ACSS2, which are important cancer targets. Research on SARS-CoV-2 papain-like protease (PLpro) has explored its catalytic mechanism, substrate recognition and inhibition. Aurintricarboxylic acid was identified as a noncompetitive inhibitor, with an IC_{50} of approximately 30 μM and a binding dissociation constant of 11.3 μM. Investigations have also examined the contribution of the ubiquitin-like domain to PLpro function. Studies of clinically relevant PLpro mutants revealed substrate-dependent differences in activity, particularly enhanced deubiquitinating activity of the K232Q mutant compared with wild-type PLpro. Studies of gut microbial β-glucuronidases focus on enzyme inhibition as a potential strategy to mitigate drug-associated toxicity. Organodiselenides was identified as reversible covalent inhibitors of *Escherichia coli* β-glucuronidase involving Cys449. Several new gut microbial GUS enzymes were identified, characterized and a new classification framework based on domain organization has been proposed. Crystal structure of human gut symbioint *Akkermansia*

muciniphila GUS was determined at 1.91Å resolution, exhibiting an uncommon monomeric architecture and a distinctive loop configuration potentially involved in drug-glucuronide processing. Collectively, these investigations demonstrate how structural biology can reveal molecular determinants of protein function.

OP-5

Genomics-based approaches for diagnosis of infectious and non-infectious diseases

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The accurate and timely diagnosis of diseases is fundamental to effective clinical management, disease surveillance, and the development of personalized therapeutic strategies. Advances in genomics have transformed the diagnostic landscape by enabling the precise identification of genetic variations, pathogen-specific nucleic acid sequences, and molecular signatures associated with a wide range of infectious and non-infectious diseases. Cell-free DNA (cfDNA) consists of extracellular DNA fragments that circulate in the blood, and it can be used as a non-invasive liquid biopsy to detect actionable mutations in lung cancer by sequencing. In our analysis, cfDNA testing and tissue biopsy agreed in about 80% of cases for actionable targets, including single-nucleotide variants, fusions, and indels. Fragmentomic analysis also revealed clear differences in fragment length between mutant and wild-type reads for some variants.

Complementary to sequencing, is the CRISPR-based diagnostic method that provides programmability, relatively simple assay design, and compatibility with portable detection systems for point-of-care testing. A CRIPSR-based detection method was developed for SARS Cov-2 virus and validated using 47 patient samples, achieving a sensitivity of 95% and a specificity of 100%. The method was coupled to a portable, cost-effective battery-operated instrument, CRISPR-CUBE to run the assay and visualize the outcome in resource-limited condition. The work flow has subsequently been adapted for detection of monkey pox, blood pathogens and Mycobacterium. The aforesaid technologies will be extended for early cancer detection and differentiation from other diseases that mimic their symptoms such as TB and lung cancer, in the future.

OP-6

From safe and healthy food to global trade: Expanding applications of radiation processing in India

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Radiation processing has expanded into new food applications with changing dietary habits and growing health consciousness. Beyond food safety and security, research at the Food Technology Division (FTD) supports ready-to-eat and ready-to-cook (RTE/RTC) products, emergency rations, military supplies, space food and hospital diets. A shelf-stable nasogastric feed with undetectable microbial load has been developed for immunocompromised patients, and an irradiated, shelf-stable fruit-puree-based infant food protects another vulnerable group. Safety studies on cells cultured in media from irradiated foods (25 kGy) showed no induced mutations.For healthy lifestyle fibre-rich, preservative free foods were developed by combining irradiation with hurdle technologies, including fruit cubes, dried jamun pulp, strawberry rolls, chikoo bites, mint-coriander and date palm sauces. Beverages include an enzymatically produced banana health drink without added sugar, colour or preservative, beetroot juice, low-sugar fermented pomegranate juice and de-bittered karela juices. Fermented millet-based RTE products and low-glycaemic-index, fibre-fortified wheat flour add to this range. Along with a number of shelf-stable flesh food based products, a radiation-hygienized fish spread, dehydrated fish based soup, and several whole fish varieties with extended shelf life has been developed. Radiation-treated chickpea sprouts, hurdle-processed mushrooms and vegetable fillers remain acceptable for 20 days, reducing spoilage and food safety concerns. Radiation processing also benefits industry and trade. India's first commercial trial of radiation-processed potatoes (28 tonnes) showed sprout inhibition at 75 Gy with chip-making quality retained for 8 months, and sprout suppression was linked to reduced expression of auxin-related genes. Irradiation at 60 Gy followed by cold storage preserved onions for 7.5 months (Approx. 1500 tonnes). Research on Indian mangoes enabled commercial phytosanitary treatment, and an integrated delayed-ripening protocol supported sea shipment (16 tonnes) to the US. Fumigant-free Makhana technology has also been developed for export. Looking ahead, novel low temperature marine food irradiator has been commissioned at BRIT and high throughput onion-irradiator as well as continuous flow grain-irradiator are being designed to scale these technologies commercially, strengthening export competitiveness and global trade.

OP-7

Exploring fundamental research in food safety and nutrition: Insights from the Food Technology Division

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Research at the Food Technology Division (FTD) focuses on addressing critical challenges in functional foods, industrial bioprocessing and food safety to strengthen national food security. A healthy gut and balanced microbiome are essential for efficient nutrient absorption and overall well-being. To promote gut health, FTD explores the application of prebiotics, probiotics, symbiotic and strategies to reduce food allergies. Its research includes the use of radiation-treated fibres, such as inulin and psyllium, to regulate blood glucose levels. Industrial enzyme development represents a key research domain advancing sustainable bioprocessing. Key focus areas include advancements in fermentation technology, biofuel production, ACE inhibitory peptides, onion skin-derived potential anticancer compounds, antiviral therapeutic formulations, and xanthan gum synthesis. In parallel, FTD prioritizes food safety through the application of gamma irradiation. Accurate radiation dose assessment is ensured through the characterization of physical and chemical dosimeters and the use of Monte Carlo simulations to model radiation absorption. Ongoing research also addresses the elimination of foodborne pathogens, the detection of spice adulteration and the mitigation of antibiotic residues in seafood. Gamma irradiation is investigated as a means of degrading antibiotics, pesticides and textile industry contaminants, while artificial intelligence (AI)-based models are being developed to identify food adulterants. Combining gamma irradiation for microbial decontamination with investigations into bacterial survival genes supports the development of innovative food preservation strategies. Furthermore, targeting CRP-mediated energy regulation in *Salmonella* and programmed cell death mechanisms in *Xanthomonas* offers promising approaches to controlling significant human and plant pathogens. Therefore, R&D at FTD aims to enhance food quality, safety and wholesomeness.

OP-8

From supramolecular assembly to tissue regeneration: Peptide-based hybrid hydrogels

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The development of biomaterials that simultaneously provide structural, mechanical, biochemical, and functional cues remains a major challenge in tissue engineering. Self-assembling peptides hydrogels with tunable properties can be integrated with functional or tissue-derived components to address the requirements of specific tissues. Herein, we demonstrate two complementary strategies for engineering peptide-based hybrid hydrogels for regenerative applications. First, a self-healing electroconductive peptide–polyaniline hydrogel was developed via peptide-directed confined polymerization of aniline within the supramolecular network, in which the peptide serves as both a structural scaffold and a dopant. The resulting hybrid hydrogel exhibited enhanced electroconductivity, self-healing capability, and cytocompatibility, promoting cardiomyocyte adhesion and proliferation, neurite outgrowth, and improved cardiac–neuronal co-culture. Enhanced expression of cTnT, Cx43, and MAP2, together with organized F-actin and vinculin, further demonstrated improved cellular organization and cell–matrix interactions. In a second approach, decellularized cartilage extracellular matrix (dECM) was integrated with a self-assembling dipeptide hydrogel to generate a mechanically reinforced and biologically instructive scaffold for cartilage regeneration. While OSMODECEL-derived dECM retained native collagen architecture and sulfated glycosaminoglycans, the resulting hydrogel was mechanically weak. Incorporation of the dipeptide produced a stable hybrid network and increased the stiffness by approximately three orders of magnitude, while maintaining physiologically relevant mechanical properties. The hybrid scaffold additionally supported sustained chondrocyte viability and metabolic activity, and the preservation of the chondrogenic phenotype. These studies establish peptide self-assembly as a modular strategy for integrating structural reinforcement with tissue-specific biochemical or functional cues, enabling the design of multifunctional hybrid hydrogels for diverse regenerative medicine applications.

OP-9

Deconvolution-based other cells: A prognostic alternative to circulating tumor cells in neuroendocrine tumors?

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Circulating tumor cells (CTCs) predict outcome in neuroendocrine tumors (NETs), but their rarity and the cost of capture keep them out of routine care. This study evaluated the proportion of "other cells" (OC%), estimated by RNA-Seq deconvolution, as a prognostic biomarker in NET patients receiving ^{177}Lu-DOTATATE peptide receptor radionuclide therapy (PRRT). We deconvoluted pre-treatment blood RNA-Seq profiles of 81 healthy donors and 137 NET patients with the Kassandra-B algorithm and used the healthy-donor median (0.18) to define OC-Low and OC-High groups. NET patients had significantly higher OC% than healthy donors (median 0.26 vs 0.18; p = 0.0018). Patients with high tumor grade, high disease burden or low ^{68}Ga-DOTATATE avidity had significantly higher OC%. Patients with progressive disease on PRRT had significantly higher OC% (median 0.41) than those with stable disease (0.24) or objective response (0.22). Patients in the OC-Low group achieved disease control above 90% even with high grade, heavy burden or low avidity, whereas disease control was only 25% in OC-High G3 tumors and 56% in OC-High low-avidity tumors. OC-High patients had a 3.2-fold higher hazard of progression (95% CI 1.32–7.75), and all 17 deaths occurred in this group. The poorest outcomes were seen in patients combining well-differentiated tumors, high disease burden, low avidity and high OC%. OC% is a low-cost readout from the same RNA-Seq data used for other blood biomarkers and may offer an alternative to CTC counting for risk stratification before PRRT with a prospective validation in larger cohort

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OP-10

Targeting DNA repair vulnerabilities and autophagy to overcome therapeutic resistance in cancer

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Cancer cells frequently acquire defects in DNA repair pathways, compromising genomic stability while creating a heightened dependence on compensatory mechanisms that sustain their survival. Exploiting these vulnerabilities through synthetic lethal strategies offers a promising avenue for enhancing the efficacy of chemotherapy and radiotherapy. Our research focuses on understanding the molecular mechanisms underlying DNA double-strand break repair, replication-associated genomic instability, and autophagy, with the broader aim of identifying actionable vulnerabilities that can be exploited to overcome therapeutic resistance in cancer. We have investigated how DNA repair and replication-associated processes safeguard genome integrity and influence cancer cell survival. Our recent studies have uncovered a CHK1-mediated phosphorylation switch that suppresses human topoisomerase I-associated genomic instability (*EMBO Journal*, 2026), and demonstrated that targeting replication fork processing synergizes with PARP inhibition to potentiate lethality in homologous recombination-proficient ovarian cancer cells (*Advanced Science*, 2025). Earlier work revealed a non-catalytic function of the WRN helicase in the removal of topoisomerase I–DNA covalent complexes and the activation of NF-κB signalling (*Aging Cell*, 2022). In parallel, we are investigating the role of autophagy and organelle quality control in cancer cell adaptation and resistance to therapeutic stress. Our recent work has identified a novel chloroquine-derived lysosome-targeting molecule, Lysostilbene, that induces irreversible lysosomal damage and disrupts autophagosome–lysosome assembly in cancer cells (*Autophagy*, 2026). In another ongoing study, we further explore an unexpected role of WRN helicase in regulating mitophagy through the resolution of an intricate network of G-quadruplex structures, R-loops, and ATG7 pre-mRNA maturation. This presentation will discuss selected findings from these studies to illustrate how defects in DNA repair, replication-associated genome maintenance, and autophagy create exploitable dependencies in cancer cells.

OP-11

Dissecting the cancer: Molecular networks, microenvironmental dynamics, and vulnerabilities in precision therapeutics

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Oncology is undergoing a paradigm shift driven by the integration of multi-omic data and a deeper understanding of the tumor ecosystem. Despite therapeutic advancements, tumor resistance remains a critical barrier to the long term patient survival. At Radiation Biology & Health Sciences Division, Bhabha Atomic Research Centre, we are trying to explore various aspects of tumor biology. The studies range from identifying fundamental molecular alterations in tumor cells and its microenvironment to developing intervention strategies against such resistance. Our studies aimed at acquired radioresistance in cancer cells have shown role of epigenetic remodeling, enhancer reprogramming and altered DNA repair pathways in driving this phenomena. Mechanistic role of TRXRD1, thioredoxin reductase, in driving radioresistance through epigenetic regulation, histone modifications, and enhanced antioxidant capacity has been proven in lung cancer. Peroxiredoxin 6 (PRDX6), a multifunctional enzyme involved in phospholipid repair and redox regulation, was shown to play role in radioresistance via remodeling of cellular proteome and knocking it down led to ferroptosis-driven radiosensitivity. Our studies on tumor's immune microenvironment established immunosuppressive role of TGF-β-producing B regulatory cells in PTGS2-high malignancies and Peptide based PTGS2-siRNA nano-particles could sensitize breast cancers to immunotherapy. We also examined formation of macrophage mediated tunneling nanotubes (TNTs) in breast cancer cells and established its role in tumor progression and resistance. Further, our studies on effect of altered metabolism on tumor progression have shown role of leptin antagonists in reversing obesity-induced tumor progression via reducing C-reactive protein (CRP). In-house next-gen precision strategies using targeted magneto-liposomes (T-LMD) to deliver doxorubicin showed precision in drug delivery to tumors, induced immunogenic cell death and reduced side effects in triple-negative breast carcinoma (TNBC). Studies on Mitocurcumin, a mitochondria targeted derivative of curcumin found it to be highly effective than curcumin in killing MDA-MB-231 TNBCs and cisplatin resistant lung cancer cells. Inhibitors targeting specific pathways such as c-Met receptor have also shown promising results in targeting pancreatic adenocarcinoma. Together, these findings map out key molecular vulnerabilities that can be exploited to overcome tumor resistance and optimize targeted therapies.

OP-12

Functional organic materials for cancer therapy

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Functional organic materials, viz. small molecules, peptides, polymers, frameworks etc., are advanced cancer drug development tools by virtue of their abilities towards targeted drug delivery, stimuli responsive releases, tumor-microenvironment modulation and combination or synergistic strategies, with improved treatment outcomes and minimal side effects. Bio-Organic Division in BARC has been instrumental in developing various photodynamic agents including a photosensitizer NbB, which sequentially targets the endoplasmic reticulum and lipid droplets in pancreatic cancer cells, causing organelle stress, lipid peroxidation and light-induced apoptosis. A BODIPY–NHC–silver complex was also developed which combines BODIPY imaging, silver-based chemotherapy and light-activated photodynamic therapy resulting in synergistic cancer cell death by disrupting mitochondrial networks. Exploiting the high drug loading capacities and pH/GSH responsiveness of porous metal-organic frameworks (MOF), a nanocomposite (CaO_2-Dox@Cu-MOF@PEG) was successfully synthesized as a combined chemo-chemodynamic therapy agent. Further advancement was achieved via developing a prostate cancer targeting chemo-chemodynamic agent via post-synthetic surface modification of a MOF using a PSMA-targeted ligand. A robust, pH-responsive hydrogen bonded organic nano-framework (nanoHOF) was developed as a biocompatible anti-cancer drug delivery vehicle. Small molecule based chemotherapeutic agents, actively targeted to neuroblastoma (mIBG-Dox) and prostate cancer (PSMA-Dox) were also developed, which showed selective cytotoxicity to target cells. In an endeavor to provide affordable healthcare, in-house synthesis of important radiopharmaceutical ligands including PSMA-617, PSMA-11, mIBG hemisulfate, $[Cu(MIBI)_4]BF_4$, FAPI-2286, tetrofosmin have been achieved. These have benefitted thousands of patients across various hospital pan India.

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OP-13

Amphibian resilience under radiation stress

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Amphibians inhabiting naturally radioactive coastal placer deposits serve as a key model for understanding ecological stability under long-term environmental stress. We studied communities at ten sites within the Chatrapur placer deposits in Ganjam district, Odisha, an area with high background radiation (HBRA), and compared them to a nearby reference area (NBRA) about 50 km away with similar habitats (Mahuri Kalua). Our research involved measuring radionuclide levels in soil and water, analysing water ionic content, soil texture and assessing amphibian species richness and composition. Additionally, we examined the effects of natural radiation on blood cytology, morphology, oxidative stress, and proteomic and transcriptomic profiles of the liver and kidney in the toad *Duttaphrynus melanostictus*. Findings show that amphibian communities in these radioactive coastal areas remain stable—species richness, occupancy, and abundance are comparable to those in the reference sites. Redundancy analyses identified water chemistry, particularly Ca, K, Na, and Mg, as the main factors influencing community differences, while radionuclide levels and soil texture had minimal direct effects. Despite ionic gradients shaping community structure, frogs from high-radiation zones displayed stress signs, including the presence of poikilocytes in their blood. Biochemical and histological analyses of liver and kidney tissues confirmed stress-related changes. Moreover, transcriptomic and proteomic data suggest that high background radiation triggers cellular responses linked to stress, tissue remodelling, and altered cellular functions. This study is the first to report amphibian responses to elevated natural radiation in coastal placer deposits, revealing that stable communities can coexist with stressed physiological states. Our results emphasise the importance of integrating ecological, physiological, and molecular assessments to understand the impacts of natural radiation exposure.

OP-14

Transgenic approaches for vascular wilt in banana

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Musa spp. cultivation is under continuous threat by *Fusarium oxysporum f. sp. cubense* (Foc) infection, which results in vascular wilt or Panama disease. Modulation of xylem which act as a battle ground for Foc infection and plant immunity can prove vital in controlling Foc penetration. Herein, different strategies like expressing cell death inducing effectors in xylem and modulating xylem thickness was studied to analyze the Foc infection. Xylem-specific promoters (P_{VND7} or P_{VND2}) were employed to express three cell death-inducing proteins (*FocSIX1A*, *FocSIX6* or *TvSm1*) of fungal origin and the regenerated plants were healthy, showed improved resistance to Foc infection and developed systemic resistance-like symptoms. Using a novel positive feedback loop using VND genes, banana lines with thicker xylem devoid of any ectopic lignification were developed. Enhanced disease resistance of these lines against Foc strains, increased expression of defense genes, elevated jasmonic acid content and quantitative elevation of phenolic compounds provide evidence that elevation in xylem wall thickness does indeed contribute to the systemic resistance by playing a crucial role in regulating immune responses. Thinner xylem banana (*vnd2*, *vnd6*, and *vnd7*-lines) regenerated using CRISPR-Cas9 approach also develop strong Foc resistance by actively potentiating immune-signalling. Despite partial overlap in transcriptional responses, thinner xylem lines maintained a more balanced JA/SA profile, while thick-walled lines showed exaggerated hormonal accumulation.

OP-15

Integrating mutation breeding and molecular approaches to enhance rice productivity, climate resilience and nutritional security in india

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Rice *(Oryza sativa L.)* is a staple food for a large proportion of India's population and plays a pivotal role in national food and nutritional security. However, increasing climate variability, emerging biotic and abiotic stresses, stagnating productivity, and the need for improved grain quality and nutritional value pose major challenges to sustainable rice production. Integrating radiation-induced mutation breeding with molecular approaches offers an effective strategy for generating and utilizing novel genetic variability to address these challenges. The rice improvement programme at Bhabha Atomic Research Centre (BARC) focuses on developing improved rice varieties through induced mutagenesis, systematic screening of mutant populations, and evaluation of promising mutants for desirable agronomic, stress-tolerance, and grain-quality traits. India has highest diversity for aromatic and scented rice but is becoming extinct due to its poor yield and undesirable agronomic traits. Radiation induced mutation breeding has been instrumental in improving these landraces. Rice varieties viz, TKR Kolam, TCDM-1, CGJT, TCVM and CTLM have been released with better grain quality, high aroma and better grain yield. Salinity and drought stress are major abiotic stress affecting more than 15mha land in India and causing significant yield losses. Gamma ray induced mutation breeding have resulted in improved salt tolerant rice selections which will benefit farmers in coastal region on India. Trombay Konkan Khara, a highly salt tolerant rice variety, was released for coastal regions with very high salt tolerance (EC>7.0 dS/m) and higher grain yield under salt stress (3.5-4.0t/h). Similarly, Vikram TCR, an improved mutant of Luchai landrace, rice variety was released having low water requirement (drought tolerant), early maturity, very high yield (6.0 t/h) and good murmura making quality. Late monsoon cyclonic rains in coastal India is another threat resulted from Climate change over past few decades resulting complete crop failure in many parts of India. One mutant rice variety, Trombay Konkan Mahan, has been recently released which can withstand severe cyclonic late monsoon showers and give very high yield (6.0 – 6.5 t/h) and prevent farmers' losses. Currently, multi-stress tolerance for abiotic and biotic stress and biofortification in rice are major priorities and advance mutant breeding lines are in testing for future releases. Characterization of rice landraces/genotypes for resistance to biotic stresses, tolerance to abiotic stresses, and medicinal properties can provide valuable genetic resources for future rice improvement programmes at

BARC. Understanding the molecular basis for salt tolerance and biotic stress tolerance, and beneficial bioactive compounds in medicinal rice viz, Gathuwan have helped us in incorporating these traits into improved rice varieties through mutation breeding and molecular approaches. This integrated strategy will contribute to the development of high-yielding, climate-resilient, nutritionally enriched rice varieties, thereby strengthening sustainable agriculture and food and nutritional security in India.

OP-16

Strains and syncom: Shaping *Capsicum chinense* cv. 'umorok' chilli seedling performance

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Beneficial bacteria offer promising opportunities for sustainable crop production, but individual strains and microbial communities may influence plant performance in fundamentally different ways. This study evaluated four beneficial bacterial strains (*Azotobacter* sp., *Ochrobactrum* sp. and two *Bacillus* spp.) individually and as a defined synthetic microbial community (SynCom) for their effects on seedling growth and physiological responses of *Capsicum chinense* cv. 'Umorok'. All strains were compatible in vitro, supporting their combination into the SynCom. Bacterial inoculation markedly influenced seedling establishment, growth, photosynthetic pigments and antioxidant responses, with clear differences among individual strains and the SynCom. Among the single-strain treatments, RKH1 showed the strongest growth-promoting effect, recording the highest seedling survival (79%), shoot length (2.778 cm), root length (9.607 cm), leaf number (3.299) and fresh weight (0.254 g). In contrast, the SynCom produced distinct physiological responses, including the highest chlorophyll *a* content (1.753 μg mg^{-1} fresh weight), enhanced catalase and peroxidase activities, and reduced malondialdehyde accumulation. Thus, the SynCom did not consistently outperform the most effective individual strain in morphological growth, indicating that greater microbial complexity does not necessarily translate into greater growth promotion. Instead, the contrasting responses suggest complementary functional roles of single strains and microbial communities, with RKH1 particularly effective in promoting early seedling establishment and biomass accumulation, while the SynCom enhanced physiological attributes associated with photosynthetic performance and oxidative stress regulation. These findings highlight the importance of functional microbial selection and rational community design for developing targeted bacterial inoculants and sustainable strategies for improving chilli seedling performance.

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PP-1

Yield and nutraceutical quality enhancement in dragon fruit through micronutrient and hormonal foliar application

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Dragon fruit (*Hylocereus* spp.) is gaining importance as a functional fruit crop for its antioxidant and nutraceutical potential; however, yield and biochemical quality are strongly influenced by nutritional and hormonal regulation. This study evaluated foliar-applied micronutrients [boron 0.3%, zinc 0.5%, boron+zinc; (Kumari & Deb, 2018)] and growth regulators [NAA 200 ppm, (Baidya *et al*., 2022); GA_3 50 ppm, (Shariah *et al*., 2014)] on yield and biochemical attributes of *Hylocereus costaricensis* and *H. undatus* under a Factorial Randomized Block Design over two seasons (2023-2024). Boron+zinc produced the highest yield response, increasing flowers per plant by 23.33% and 35.56%, fruits per plant by 15.01% and 28.64%, and fruit weight by 24.10% and 27.02% in *H. costaricensis* and *H. undatus*, respectively, over control. NAA improved fruit retention, whereas GA_3 enhanced fruit size via cell elongation. Biochemically, boron+zinc recorded the highest soluble sugar, available carbohydrate, and soluble protein, rising by 14.31% and 16.33%, 14.84% and 16.34%, and 38.96% and 24.26%, respectively. Flavonoid content increased by 29.38% and 15.96%, while antioxidant capacity via DPPH, ABTS, and FRAP assays also improved, with FRAP rising by 20.21% and 19.44%; NAA showed the least biochemical improvement, and boron alone gave the lowest response. This synergism was attributed to boron's role in pollen viability and zinc's role in auxin biosynthesis (Kumar *et al*., 2014; Ullah *et al*., 2015). Overall, foliar boron+zinc emerged as the most effective strategy to enhance yield, biochemical composition, and antioxidant potential of dragon fruit as a functional food crop.

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PP-2

Optimisation of bacterial biopriming technology for enhanced seed germination of threatened plant (*Pterocarpus marsupium* Roxb.): A sustainable conservation approach

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Pterocarpus marsupium Roxb., a threatened medicinal tree with high ecological and pharmacological importance, exhibits poor and erratic seed germination, limiting its natural regeneration and large-scale propagation. Recent studies have reported low and variable germination in *P. marsupium* and shown that pre-sowing treatments can overcome dormancy-associated constraints (Behera et al., 2026). This study aimed to develop and optimise a bacterial biopriming strategy to enhance germination using Response Surface Methodology (RSM). Seeds were subjected to dormancy-breaking treatments, followed by biopriming with selected beneficial bacterial isolates obtained from cow dung. The bacterial isolates were characterised for plant growth-promoting attributes, including indole-3-acetic acid production, phosphate solubilisation, siderophore production and ACC deaminase activity. These microbial functional traits can contribute to improved seed germination, seedling vigour and plant establishment (Fiodor et al., 2023). Among the bacterial treatments, individual isolates achieved germination rates of 65-82%, while the bacterial consortium achieved approximately 80% germination, indicating the potential of microbial biopriming to overcome dormancy-associated constraints (Ahmad et al., 2022a). To systematically optimise the biopriming conditions, a Box-Behnken experimental design was employed, considering key process variables and germination responses. The developed model was used to determine the optimum combination of biopriming parameters for maximising germination performance and was subsequently evaluated through validation experiments (Sasani et al., 2026). The optimised bacterial biopriming approach while reducing dependence on conventional chemical dormancy-breaking treatments. The study demonstrates the potential of beneficial microorganisms as a sustainable biotechnological intervention for restoration and conservation programmes aligning with Sustainable Development Goal 15 (Life on Land).

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PP-3

Gaining molecular insights into the stress-responsive GLYIII enzymes in wild and cultivated rice

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In the face of a rapid global climatic change and the growing demand to produce food, ensuring sustainability, the concerted efforts of researchers across the globe are to significantly improve the yield of the major staple food crop, rice. This warrants that rice grows optimally even under stress conditions. Wild relatives of rice are known for their tolerance to various biotic and abiotic stresses, serving as an invaluable resource for crucial stress-tolerant alleles. Methylglyoxal (MG) is a reactive dicarbonyl compound ubiquitously synthesized as an offshoot of glycolysis, primarily detoxified by the glyoxalase pathway. In addition to the classical glyoxalase pathway comprising the GSH-dependent glyoxalase I (GLYI) and glyoxalase II (GLYII) enzymes, which act to convert cytotoxic MG to pyruvate, there exists a shorter route of detoxification catalyzed in a single step by the GSH and metal ion-independent glyoxalase III (GLYIII) enzymes. These enzymes are of utmost importance to living systems owing to their cytoprotective multifunctional roles. In this study, we have carried out a comprehensive genome-wide search to identify the *GLYIII* genes in the 11 rice genomes known so far. We found the GLYIII proteins to be conserved across the wild rice species and their number to have expanded during domestication, driven by gene duplications. Most of the *GLYIII* genes were found to be syntenic. Notably, we found wild rices' *O. punctata, O. meridionalis,* and *O. nivara* to be stress-tolerant attributed to higher endogenous GSH levels, TAC, % free radical scavenging activity, and most importantly, higher GLYIII activity. Interestingly, qRT-PCR analysis revealed a significant transcript abundance of selected *OpGLYIII, OmGLYIII, OnGLYIII,* and *OsJGLYIII* genes in response to different abiotic stresses, specifically salinity. Interestingly, we report that all the selected purified GLYIII proteins, especially OmGLYIII-3, have high catalytic efficiency. Abiotic stress tolerance assay showed overexpression of these proteins to impart maximum stress resilience to the transformed *E. coli* cells in response to multiple stresses, especially salinity, possibly via ROS mitigation in addition to MG detoxification.

PP-4

Characterization of a gamma ray induced fused compound leaf mutant identified *KNOTTED1-like homeobox* as a key regulator of compound leaf development in chickpea (*Cicer arietinum* L.)

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Chickpea, a widely grown pulse crop, ranks second in terms of global production. Leaves are the primary photosynthetic organs, contributing to the crop productivity. Chickpea generally possess pinnately compound leaf with 9-15 leaflets. We characterized a gamma ray induced mutant with fused compound leaf (*fcl*) of cultivar RSG888 (WT). The mutant shows age dependent fusion of leaflets that results in their appearance as 'simple leaves'. The petiole and rachis were reduced in length to near absence. The mutant exhibited significantly reduced leaf, pod and seed size, 100 SW than WT. The leaf epidermal peels showed increased circularity in the pavement cells and significantly higher stomatal density (269.94 ± 27.8 stomates/mm^2) than WT (202.05 ± 39.2 stomates/mm^2; P=2.42 x E^{-10}). To identify the causative mutation(s), whole genome resequencing analysis of the mutant and WT was conducted. The clean reads were aligned to the chickpea reference genome assembly. Variant calling was carried out for identification of SNPs, InDels and larger SVs. A targeted read-depth analysis identified a structural deletion on chromosome 8 of the mutant. The region contained 11 candidate genes. RT-PCR showed their compete loss of expression indicating their possible role in regulating mutant phenotype. Expression analysis of candidate genes in other *fcl* mutant and genotypes of varying genetic architecture has identified *KNOTTED1-like homeobox* as the candidate gene regulating compound leaf and petiole development in chickpea. So far, mechanism of action of this gene in regulating leaf development is currently unknown in legumes and will be explored in the future studies.

PP-5

Synergistic effect of irradiated chitosan and thiourea on enhancement of bioactive phenolic acids and flavonoids in sugarcane juice

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Gamma-irradiated chitosan (GIC) and thiourea (TU) are emerging plant biostimulants that capable of modulating secondary metabolisms and enhancing bioactive compounds in crops. However, their combined potential improving the phytochemical quantity in of sugarcane juice remains insufficiently explored. This study evaluated the effect of GIC–TU on co-stimulation on phenolic acids and flavonoids in sugarcane juice using HPLC based metabolite profiling. The analysis identified several bioactive phenolics including 4-hydroxybenzoic acid, *p*-coumaric acid, syringic acid, and ferulic acid, together with flavonoids such as rutin, quercetin-3-O-galactoside, quercetin glycosides, and glycosylated flavones. Comparison of their relative abundance between control and treated (GIC 100 ppm + TU 500 ppm) substantially enhanced accumulation of several metabolites., Quercetin-3-O-galactoside showed highest increase (81.8%), followed by syringic acid (42.9%), 4-hydroxybenzoic acid by 39.2%, and ferulic acid (33.3%), *p*-coumaric acid (11.11%) and 4- hydroxy benzoic acid (29.24%). These findings demonstrate that GIC–TU can redirect sugarcane secondary metabolism towards valuable phytochemical enrichment proving practical route for improving the compositional quality of sugarcane juice, such biofortified juice could provide foundation for developing value added functional beverages and other sugarcane derived products there by expanding the value of sugarcane beyond sugar production with potential benefits for growers, processors and emerging functional-food markets

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PP-6

Decoding promoter architecture: ACGT and AAAG motif patterns across resilient crops

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Cis-regulatory elements (CREs) and their spatial organization are important determinants of stress-responsive gene regulation in plants. ACGT and AAAG containing motifs are key regulatory elements associated with transcription factor binding and responses to environmental stress. However, the extent to which their pairing, spacing, and spacer sequence conservation contribute to promoter architecture across stress-tolerant crops remains poorly understood. In this study, we developed an open-source, genome-agnostic computational pipeline for comparative analysis of ACGT and AAAG cis-element pairs in plant promoters. The pipeline was applied to 214,746 promoter sequences from five stress-tolerant crops: chickpea, pigeon pea, sorghum, cassava, and quinoa, with *Arabidopsis thaliana* as a reference. Four motif pair combinations: ACGT–ACGT, ACGT–AAAG, AAAG–AAAG, and AAAG–ACGT were analyzed for promoter enrichment, spacer length, GC composition, and nucleotide-level conservation. Motif pairs showed promoter enrichment across species, with the strongest enrichment observed in chickpea and pigeon pea. Spacer thermodynamic profiling revealed localized GC divergence from the global promoter baseline (31.7%), with specific structural preferences such as 30.95% GC for the 24-bp Dof-Dof spacer and 34.52% GC for the 20-bp bZIP-Dof spacer. These findings provide insights into promoter organization associated with stress-tolerant crops and establish a framework for identifying candidate regulatory regions. This supports the development of stress-responsive promoters and informs future crop improvement strategies to enhance resilience to environmental stresses, thereby contributing to sustainable agriculture and long-term food security.

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PP-7

Optimization of gamma radiation dosage in Soybean (*Glycine max* L. Merr.) through LD_{50} and GR_{50} analysis

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Mutation breeding is an important breeding method for improving the crops by using mutagens such as physical/chemical mutagens for inducing heritable genetic variations (Prasad and Kumar, 2025) However, it demands precise implementation and thorough screening to promote higher mutation frequencies without excessive lethality. The present investigation includes 09 different doses (viz. 100, 150, 200, 250, 300, 350, 400, 450, 500 Gy) of gamma radiation which were employed to evaluate the mutagenic sensitivity of soybean seeds to physical mutagen, to estimate optimum doses of GR_{50} and LD_{50} in soybean. The treated seeds, along with an untreated control, were assessed for germination and subsequent seedling survival for LD_{50} while seedling height reduction for GR_{50} under controlled laboratory conditions. The study showed dose dependent negative correlation with dose of gamma radiation. To work out the LD_{50} and GR_{50} values, probit analysis was performed. Under the experimental laboratory conditions, the estimated LD_{50} was 396.25 Gy which was **c**omparable with the findings reported by Padavai and Dhanavel (2004) and Singh & Kole (2005). While the estimated GR_{50} was 241.68 Gy. Marroquín *et. al.* (2017) reported similar results of GR_{50} in case of gamma rays treated soybean. The LD_{50} and GR_{50} estimate provides useful benchmarks for determining an appropriate mutagenic treatment range for subsequent mutation-breeding experiments.

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PP-8

Deciphering floral biology of annual flowers for efficient breeding and seed production

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Genetic improvement of annual flowers through breeding programs is essential to develop novel flower colours, shapes, sizes and stress-tolerant varieties. This study focuses on study floral biology in important annual flowers (celosia, gaillardia and ornamental sunflower), aiming to provide a framework for effective hybridization and future varietal development. *Celosia argentea* has a feathery inflorescence bearing small, tubular flowers arranged on a spike. Emasculation and pollination should be performed when the flower is 3 mm in length and 1 mm in thickness, whereas natural pollination occurs when the flower reaches 5 mm in length and 2 mm in thickness. The flower has 5 perianth segments, which are petaloid and united at the base; 5 stamens; a bicarpellary gynoecium; a superior ovary; a long style; and a 2-fid stigma. The fruit is an utricle, and the seed is black, shiny and albuminous. Gaillardia having capitulum (head) type inflorescence, head has two kinds of florets: outer ray florets (female) and inner disc florets (bisexual). Disc florets are tubular and fertile, producing ovules and pollen. Flower type is bisexual, symmetry: actinomorphic, zygomorphic (ray florets), perianth modified into pappus (absent in ray florets), 5 anthers, inferior ovary, bicarpellary, fruit type is achene, non-endospermi. Further ornamental sunflower produces a capitulum-type inflorescence consisting of peripheral ray florets and central disc florets. The ray florets form the prominent ornamental portion of the flower head, whereas the disc florets are tubular and contain the reproductive structures. The male floral structures include anthers, while the female reproductive structures consist of the ovary and style. The capitulum is borne on a peduncle and surrounded by hairy bracts.

PP-9

Development and identification of novel sources of genetic resistance against powdery mildew *(Erysiphe cruciferarum)* disease of *Brassica juncea*

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Powdery mildew (PM), caused by *Erysiphe cruciferarum*, is an economically important disease of rapeseed-mustard, occurring under moderately warm and dry conditions. Currently, the changing climatic conditions further favor its early development and spread which can cause significant yield and oil losses in *Brassica juncea.* Development and identification of novel sources of genetic resistance is most viable and ecofriendly option for sustainable plant disease management. Therefore, the present study was undertaken to develop and identify PM resistant mutants in *B. juncea* through induced mutagenesis. Two *B. juncea* cultivars, NRCHB101 and GDM4 were subjected to induced mutagenesis using gamma (γ) irradiation and ethyl methane sulfonate (EMS) treatments (γ- irradiation-1400 Gy, EMS- 0.75% & combined-1200 Gy + 0.5%), based on calculated GR_{50} & LD_{50} values. For screening M_2 & M_3 population, spray inoculation method & staple leaf inoculation was used respectively and disease rating scale (0-9) was used for percentage disease severity calculation (Kumar et al., 2023). Approx. one lakh M_2 plant population for NRCHB101 & GDM4 were screened during 2024-25 & 2025-26 respectively. NRCHB101 M_3 population of 39 plants (plant to row) were screened at BUAT, Banda U.P.; ICAR-NBPGR, Issapur Farm, New Delhi; and Agriculture University, Jodhpur, Rajasthan. In M_2 generation, 39 & 59 plants for powdery mildew-resistant/tolerant mutant plants were selected for NRCHB101 and GDM4 respectively. Two promising NRCHB101 M_3 mutant lines, PMR-N-710 and PMR-N-291were identified from the 1400 Gy and 1200 Gy + 0.5% EMS treatments, respectively based on selection at all the locations. Purple and light-yellow stem pigmentation was found to be associated with PM resistance. The stable mutant lines with immune/highly resistant reaction across location can be exploited as novel genetic resources for strengthening PM resistance breeding in *B. juncea*.

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PP-10

Evaluation and selection of promising watermelon (*Citrullus lanatus l.*) genotypes for kharif season cultivation

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Watermelon [Citrullus lanatus (Thunb.) Matsum. & Nakai] is an important warm-season cucurbit crop widely cultivated in tropical and subtropical regions for its sweet, juicy, and refreshing fruits. In India, it is commonly known as tarbooj or mateera and is extensively grown in Uttar Pradesh, Andhra Pradesh, Tamil Nadu, Odisha, West Bengal, Madhya Pradesh, and Haryana. Although watermelon is predominantly cultivated during the summer season, there is considerable potential for its production during the kharif season under suitable agro-climatic conditions. Therefore, the present investigation was undertaken to identify promising watermelon genotypes adapted to kharif season cultivation. Forty-five genotypes were evaluated in a randomized block design with two replications for various phenological, morphological, and fruit quality traits. VRW-12-3-1 and VRW-515 recorded the earliest male flowering (22.0 days), while VRW-606 and VRW-511 exhibited the earliest female flowering (27.5 days). The lowest node number for first male flower was recorded in VRW-515 and VRW-38 (3.2 nodes), whereas VRW-507-1 produced the first female flower at the lowest node (8.4 nodes). VRW-54-2 recorded maximum leaf length (18.58 cm), while VRW-58-2 exhibited maximum leaf width (22.32 cm). The highest fruit diameter (70.0 cm) was observed in VRW-91-1, whereas VRW-12-3-1 recorded maximum flesh thickness (19.40 cm) and fruit weight (5.50 kg). The highest total soluble solids content was recorded in VRW-514-1 (13.80 °Brix), followed by VRW-604 (13.30 °Brix). Based on overall performance across the evaluated traits, VRW-514-1, VRW-604, VRW-605, and VRW-603 were identified as promising genotypes for kharif season cultivation.

PP-11

Combining resynthesis and induced mutagenesis to develop diverse genetic stocks in *Brassica juncea*

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Climate change poses a major challenge to food security by adversely affecting crop productivity and stability, highlighting the need to develop genetically diverse and climate-resilient crop varieties. *Brassica juncea* is an important oilseed crop; however, its amphidiploid nature and relatively narrow genetic base limit the availability of genetic variability for crop improvement. Broadening its primary gene pool through interspecific hybridization, resynthesis, and mutagenesis can generate novel variability and facilitate the introgression of useful traits. In the present study, an innovative approach combining interspecific hybridization and mutagenesis was employed to generate novel genetic variability in resynthesized *B. juncea*. The diploid progenitors, *B. rapa* (2n=20) and *B. nigra* (2n=16), were crossed to generate amphihaploids (AB, n=18). The resulting F_1 amphihaploid seeds were subjected to gamma irradiation at BARC, Mumbai. Radiation doses ranging from 700 to 1400 Gy were evaluated to determine the GR_{50} based on seedling growth and biomass-related traits. A dose of 900 Gy was identified as the LD_{50} and subsequently used for irradiation. Germinated irradiated amphihaploid plants (F_1) were chromosome-doubled and selfed to develop mutant-derived resynthesized *B. juncea* lines. A total of 123 plants exhibiting substantial variation in plant morphology, plant height, siliqua length, seeds per siliqua, seed colour, and seed size were obtained. Pollen viability indicated high fertility, whereas cytogenetic analysis revealed variable chromosome numbers, suggesting chromosome elimination/rearrangement in the mutated resynthesized *B. juncea* (MRBJ) lines. The lines were subsequently selfed and advanced through successive generations with selection for phenotypic stability. SSR-based characterization further confirmed substantial genetic diversity among the MRBJ lines. These lines represent valuable resources for studying mutagenesis-induced chromosome variation and genetic improvement of *B. juncea*.

PP-12

Decoding the disordered landscape of salt stress-responsive genes of soybean

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Intrinsically disordered proteins (IDPs) are devoid of well-defined tertiary structures under physiological conditions and are increasingly recognized as modulators of cellular flexibility, signalling, and environmental acclimatization. The present study provided a genome-wide landscape of IDPs associated with NaCl stress responses in soybean. The identified IDPs were distributed across all the 20 chromosomes, with functional overrepresentation in regulatory classes including kinases, phosphatases, transcription factors, and transporters. Cross-analysis with the NaCl-responsive transcriptome identified a broad set of salt-responsive IDPs, and a combined disorder–expression scoring framework prioritized GmPM9, GmPM16, and GmDAPH3 as key candidates. The NaCl-dependent upregulated expression of these genes was validated through time-course qPCR, which highlighted 'shoot-first followed by root' type transcriptional response. The prioritized NaCl-responsive IDPs were consistently enriched across independent drought-responsive transcriptomic datasets, supporting their broader involvement in abiotic stress responses. Analysis of 115 agronomically diverse, genome-sequenced soybean accessions revealed substantial haplotypic diversity, particularly for GmDAPH3. Major haplotypes encompassed accessions across all sensitive as well as tolerant categories, whereas minor haplotypes showed clearer phenotypic differentiation. Together, these findings established a genome-scale framework for the soybean disordome and identified evolutionarily conserved NaCl-responsive IDPs as promising candidates for understanding environmental stress adaptation.

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PP-13

Characterization of radiation-induced genetic variability and selection of promising mutants in blackgram (*Vigna mungo* (L.) Hepper)

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Blackgram (*Vigna mungo* (L.) Hepper) is an important self-pollinating pulse crop with a narrow genetic base, necessitating the generation and exploitation of additional genetic variability for crop improvement. In the present investigation, the blackgram genotype TJU-130 was subjected to gamma-ray and electron beam (EB) irradiation at doses ranging from 100–400 Gy to compare dose- and trait-based morphological and phenotypic responses. Generation advancement was carried out up to the M_2 generation for the identification and characterization of putative mutants and evaluation of genotypes based on 12 morphological and yield-related traits. Significant variation was observed for several traits, including days to 50% flowering, number of secondary branches, clusters plant^{-1}, pods plant^{-1}, plant height, pod yield, pod length, 100-seed weight, and seed yield, indicating substantial phenotypic variability induced by radiation treatment. High heritability coupled with high genetic advance was recorded for days to 50% flowering (99.09%, 21.16), number of clusters plant^{-1} (94.05%, 14.49), number of pods plant^{-1} (99.60%, 40.03), pod yield plant^{-1} (99.91%, 14.31), and yield plant^{-1} (99.97%, 13.56), suggesting their potential utility as selection criteria. Diverse mutant phenotypes were identified, including profuse branching with high yield, short pods, large leaves, chlorina, trailing, green-seeded, narrow-leaved, and dwarf types. EB-induced mutants generally exhibited increased branching and pod number, whereas gamma-irradiated mutants showed reduced pod length and plant height compared with the parent. The diverse phenotypic variation generated demonstrates the effectiveness of mutation breeding in broadening genetic variability and provides valuable genetic resources for the selection of desirable traits and future improvement of blackgram.

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PP-14

Molecular analysis of GTE-type bromodomain (BRD)-containing epigenetic regulators from *Arabidopsis thaliana*

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Gene expression in plants is highly complex and spatio-temporally regulated by genetic and epigenetic mechanisms. Among various DNA and histone modifications (involved in epigenetic regulation), histone acetylation/deacetylations are associated with chromatin accessibility. A large and diverse family of proteins, referred to as bromodomain (BRD)-containing proteins, reads acetylation marks on lysine residues on histones. The BRD-proteins along with associated 'readers' and 'writers' are central to histone-lysine-acetylation-mediated epigenetic regulation in physiological conditions and stress responses. In humans, several BRD-members have been studied for molecular-biochemical characteristics, and involvement in cellular functions and disease conditions. The plant BRD-families are also large and diverse, but relatively less explored. Model plant *Arabidopsis thaliana* contains 28 BRD-members (12 are originated due to duplication events), however many of these remain poorly characterized for functional significance. In this study, a duplicated gene-pair (AtBRD22-AtBRD28) was investigated for expression pattern, sub-cellular localization, and biochemical characteristics. The two AtBRDs (BET-Type), originated due to a block-duplication event, displayed variations in promoters, gene and protein structure, and protein-protein association/interaction network. RT-qPCR analysis showed differences in tissue-specific expression, transcript stability, and response to environmental factors, and phytohormones. Cloning of AtBRDs in pCAMBIA1302 (as GFP-fusion), and sub-cellular localization analysis in onion epidermal cells showed that both localize to nucleus. Both the AtBRDs were over-expressed in *E. coli* and purified. Analysis by far-western blotting showed that the AtBRDs recognize multiple histones. The present study provided several insights into functioning and characteristics of a duplicated AtBRD pair, which will be useful for understanding their epigenetic functions.

PP-15

Molecular basis of antagonistic Arsenic–Cadmium interactions in rice

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Arsenic (As) and cadmium (Cd) frequently co-occur in paddy soils and accumulate in rice grain, posing a major threat to food safety. The present study investigated the nature of interaction between As and Cd stress in rice, either alone or in combination. At the seedling stage, the shoot biomass was maximally reduced under Cd stress (0.52-fold) compared with those of control, while the phenotype of As (0.75-fold) and As+Cd (0.86-fold) were comparable. The heavy metal accumulation under As+Cd were also reduced than those under As or Cd alone treatments. However, the observed growth antagonism under As+Cd treatment was limited to 50 µM concentration of As and Cd at 1:1 ratio, beyond which synergistic toxicity was observed. Additionally, the antagonism in terms of growth and heavy metal accumulation was also validated at the mature plant stage. Interestingly, the grain ionome analysis mirrored this antagonism even in terms of essential nutrients. To unravel the molecular basis, RNAseq analysis was performed that revealed a clearly distinct transcriptomic signatures under As and Cd treatments, while As+Cd clustered close to As stress. The whole genome co-expression network analysis supported modules were used to identify genes showing maximal expression antagonism ($Exp_{As\text{-}Cd}$) in shoot (AsCd-Shoot: 9) and root (AsCd-Root: 46). While metabolic enzymes and transporters were present in both the tested organs, four transcription factors (AsCd-TFs) were identified from AsCd-Root, that included *OsWRKY76* ($Exp_{As\text{-}Cd}$: 2.23), *OsbHLH042* ($Exp_{As\text{-}Cd}$: 1.95), *OsC2H2* ($Exp_{As\text{-}Cd}$: 7.9) and *OsbZIP16* ($Exp_{As\text{-}Cd}$: 1.72). The contrasting expression of AsCd-TFs was validated using real-time PCR analysis, which substantiated them as potential molecular regulators for mediating the "Tug-of-war" between As and Cd induced antagonistic expression in rice. Taken together, the growth and heavy metal antagonism highlighted the need to develop specialized agronomic solutions to deal with As+Cd based co-contamination scenario in rice.

PP-16

Genome scale identification of early salt stress-responsive intrinsically disordered proteins (eIDPs) in rice

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In recent years, there has been a growing understanding regarding the role of intrinsically disordered proteins (IDPs) as central regulators of cellular signaling. However, their contribution to salt stress adaptation remains poorly understood. In this study, we conducted the first genome-scale survey of IDPs in rice and its transcriptomic responses under NaCl stress. Genome-scale survey of 48,444 rice proteins, revealed that nearly half of the rice proteome consists of intrinsically disordered proteins, particularly enriched with transcription factors and kinases. One-hour NaCl induced transcriptome identified a subset of early-responsive IDPs (eIDPs), among which highly disordered proteins were significantly associated with RNA metabolism and abscisic acid-responsive pathways, suggesting their important roles as regulatory hubs during rapid stress adaptation. Temporal expression profiling showed varied transcriptional dynamics, supporting a transient "hit-and-run" regulatory model where eIDPs function as early signaling proteins before the expression declines. By integrating combined disorder-expression score and broad transcriptional data across multiple abiotic stress datasets, three eIDPs, OsEnS53, OsEnS49, and OsSMP1 were prioritized. Comparative phylogenetic analyses of these eIDPs, showed that the intrinsic disorder remained highly conserved within the prioritized eIDP homologs, implying that conformational plasticity may be more evolutionarily constrained than sequence identity. This study provides a comprehensive genome-scale survey of eIDPs and identified promising candidates for developing salt tolerant varieties.

PP-17

Redesigning the canopy: High-yielding small leaf mutants of Indian mustard (*B. juncea*) via radio-mutagenesis

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Rapeseed-mustard is one of the top three oilseed crops in the world, with Indian mustard (*Brassica juncea*) being predominantly grown in India. A major challenge in *B. juncea* breeding programs is narrow genetic base that can be addressed using induced mutagenesis. Leaf mutants are of particular significance because leaf morphology & physiology directly affect photosynthetic efficiency & yield. The present study aimed to characterize a gamma ray induced dwarf & early mutant (*tjd1*) with small leaves. Significant reduction in leaf length (19.46%,31.87%), width (16.15%, 45.31%) & area (31.63%, 53.32%) of mutant were observed at seedling & full-grown stage respectively. Further transcriptomic analysis of SAM revealed differential expression of genes regulating leaf growth (*GRF4* & *SPK*), cell expansion (*SPIRAL1-like*, *Kinesin*), auxin & GA (*WAT1* & *LOG5*) hormonal pathway between parent & *tjd1*. Expression analysis for the hormonal pathway genes showed downregulation of *GA20ox* (2.62-fold), *ARF3* (1.62fold). Mutant *tjd1* had similar yield as parent despite small leaves. Baseline chlorophyll fluorescence analysis revealed non-significant variations for non-photochemical quenching (NPQ) between parent & mutant and maintained maximum quantum yield (Fv/Fm = 0.83. Anatomical studies suggested significant increase of 47.87% in stomata per 1000µm^2 & a higher cell density in mutant (5144.75 cells/mm^2) as compared to parent variety (3163.13 cells/mm^2). Increased number of stomata in mutant may contribute to improved gaseous exchange & may support efficient carbon assimilation in *tjd1*. A mutant with no yield penalty will be of great significance for crop improvement programme to develop semi-dwarf high yielding recombinants.

PP-18

Multi-scale morphometric changes associated with reduced seed size in a gamma-ray-induced cowpea mutant

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Seed size in cowpea is a complex trait whose cellular basis remains poorly understood [1]. A preliminary comparison of TC901 (Parent) and PLM211 (petioleless, small-seeded mutant) revealed concordant phenotypic changes at organ, cellular and organelle levels. Sixty iodine-stained storage-parenchyma cells and approximately 1,500 amyloplasts per genotype were evaluated from transverse cotyledon sections of soaked seeds using compound microscopy and ImageJ software. Morphometric traits were compared using non-parametric tests, while size distributions were assessed using density histograms, kernel density estimation (KDE), empirical cumulative distribution functions (ECDFs), and quantile analysis. The mutant showed significant reductions in storage-cell area (25.8%), amyloplast area (21.8%), and major and minor axes (>11%), accompanied by marked differences in amyloplast size distribution. Quintile analysis revealed enrichment of mutant amyloplasts in lower size classes (Q1–Q3) and depletion in the upper classes (Q4–Q5), with a highly significant association between genotype and size class ($\chi^2 = 276.03$, df = 4, $P < 0.0001$; Cramér's $V = 0.296$). Starch area fraction and granule number were significantly reduced, whereas packing density increased. The proportional reduction in storage-cell major and minor axes, together with the preserved aspect ratio, suggests largely isometric cell expansion without major alteration of cell shape [2]. Overall, the coordinated reductions in storage-cell and amyloplast size, coupled with redistribution toward smaller amyloplast classes, support a coherent developmental model in which the mutation limits storage-tissue expansion and potentially reduces starch storage capacity, contributing to smaller seeds [2,3]. The concordance of these traits suggests a shared developmental basis underlying the observed phenotype.

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PP-19

Gamma radiation-induced genetic variability for pod-related traits in cluster bean (*Cyamopsis tetragonoloba* (L.) Taub.)

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Cluster bean commonly known as guar, is an economically important legume valued primarily for its endospermic galactomannan gum, which has extensive industrial applications and considerable export potential. However, genetic improvement of cluster bean is constrained by its limited genetic variability and the inherent difficulties associated with conventional hybridization, particularly due to its small and delicate floral structure. In this context, mutation breeding provides an effective strategy for generating novel genetic variability and broadening the available genetic base for the improvement of desirable agronomic and pod-related traits. In the present investigation, seeds of the cluster bean variety HG 884 were subjected to gamma irradiation at doses of 200 Gy, 300 Gy, and 400 Gy. The M_2 population exhibited considerable phenotypic diversity in pod length, pod width, pod number plant^{-1}, pod shape, pod colour, and other pod attributes. Five mutant lines exhibited significant improvement in single-plant seed yield, with TCBM-005 showing the highest performance (97.61 g), nearly twice that of the control (48.9 g). This increase was associated with higher primary branching (17) and pod number plant^{-1} (417) compared with the control (9 branches and 158 pods). Mutants TCBM-17 and TCBM-18 also recorded increased seed yield, associated with higher seeds pod^{-1} and pod numbers of 202 and 445, respectively, despite their shorter pod length. The occurrence of distinct pod phenotypes, including desirable variants with improved pod characteristics, provided an opportunity for the identification and selection of promising mutants for subsequent generations. The observed variability in the M_2 generation highlights the potential of gamma irradiation as an effective tool for broadening the genetic variability available for pod and yield improvement in cluster bean. These induced variabilities will serve as important genetic material for molecular studies such as gene discovery, marker development and functional genomics, thereby underscoring their potential for advancements in breeding programs.

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PP-20

Gamma-irradiated mustard cake based liquid fertilizer for plant growth improvement

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Mustard cake (MC) is used as an organic soil amendment for crops. However, due to its slow nutrient release property, its efficacy is limited. In the current work, we have investigated the effects of gamma radiation on the biochemical properties of MC and evaluated its potential in promoting growth of rice plants. In this regard, MC was subjected to various doses of gamma radiation (0 to 10 kGy), aqueous extract (liquid fertilizer) was obtained and characterized for changes in biochemical composition. Among the irradiation treatments, 5 kGy resulted in the highest amino acid content (196.5 µg/mL), representing a marked increase compared with unirradiated MC (134.67 µg/mL). The growth-promoting potential of liquid fertilizer was evaluated under hydroponic conditions using rice as the model crop. Rice plants receiving 5 kGy-irradiated liquid fertilizer showed improved growth and biomass yield. The findings demonstrated that gamma radiation effectively enhanced the nutrient bioavailability, resulting in improved rice growth under hydroponic conditions. These results highlight the potential of gamma radiation as a simple and sustainable strategy for adding value to MC, enabling its more efficient utilization as an organic nutrient amendment for sustainable rice cultivation.

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PP-21

Identification of QTL-seq derived InDel and SNP markers for late leaf spot resistance in cultivated groundnut (*Arachis hypogaea* L.)

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Groundnut late leaf spot (LLS) disease caused by *Cercosporidium personatum* (Berk. & M.A. Curtis), is very prevalent in India and bring heavy losses for both seed and fodder. Genetic resistance acquired from wild groundnut is a main source of resistance against this devastating disease. A recombinant inbred line population (164 lines) derived from TAG 24 X VG 9514 was used to identify the major QTL through QTL-Seq analysis. The analysis revealed a major significant delta SNP index peak at 400 kb (3.8 to 4.2 Mb) interval of A02 chromosome of groundnut. This particular region harbors 27 genes. Of which, seven genes code for disease resistance protein based on the annotation available in Peanutbase. Based on the CDD search in PDB database, six genes with typical CC-NBS-LRR domain were identified. The InDel data obtained within this significant sliding window was used to design PCR-based InDel markers. Of them, two InDel markers, InDel-A02_3075036 and InDel-A02_4286471 represented the true difference between resistant and susceptible groups in terms of LLS field score and percent defoliation. A 'G' to 'A' mutation at 4,172,480 bases of A02 chromosome was detected in annotation of QTL-Seq analysis. Based on this SNP, an ARMS-PCR genotyping assay was developed, that could clearly distinguish between resistant and susceptible groups. These InDel markers combined with ARMS-PCR genotyping assay showed very promise in efficient selection of LLS resistant genotypes in marker assisted breeding.

PP-22

Evaluation of gamma radiation-induced mutation frequency in *Trichoderma virens* and selection of improved biocontrol mutants

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Gamma irradiation was evaluated as a tool for generating useful genetic variability in the biocontrol fungus *Trichoderma virens*. Conidial suspensions were exposed to 75, 125, 250, 500, 750 and 1000 Gy, and radiation sensitivity was assessed by growth response and conidial survival. The D10 dose was estimated to be approximately 240 Gy from the survival curve. To assess the frequency of selectable point mutations, irradiated conidia were plated on benomyl-containing medium. Since benomyl resistance in filamentous fungi is associated with point mutations in the β-tubulin gene, resistant colonies were used as a marker for radiation-induced mutagenesis. The highest frequency of benomyl resistant mutants was observed at 125 Gy, while mutant recovery declined at higher radiation doses. Sequencing of the β-tubulin gene from five randomly selected resistant mutants confirmed mutations at the expected target site. Mutant population was further screened for tolerance to oxalic acid, an important virulence factor produced by S*clerotium rolfsii*. Of 42 putative mutants screened, five showed higher oxalic acid tolerance than the wild-type strain. These mutants also exhibited enhanced aggressiveness in confrontation assays, overgrowing *S. rolfsii* approximately 1–2 days earlier than the wild type. The study shows that low dose gamma irradiation coupled with selection can be used for recovery of point mutants in *T. virens*. Subsequent screening for oxalic acid tolerance identified mutants with improved antagonistic performance against *S. rolfsii*, indicating the potential of this approach for strain improvement in fungal biocontrol. Together, these findings indicate that gamma irradiation coupled with selectable mutation-frequency screening can be used to identify potentially improved *T. virens* strains.

PP-23

Persistence of *Bacillus thuringiensis var. israelensis ISPC 12* (Bti) based biopesticide against *Aedes* aegypti and *Culex quinquefasciatus vectors*

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Increasing occurrence of insecticide resistance and the need for environmentally friendly mosquito-control strategies have stimulated interest in biopesticide based on *Bacillus thuringiensis* var. *israelensis* (*Bti*). The present study evaluated the mosquito-larvicidal efficacy and persistence of *Bti* ISPC-12 against larvae of *Aedes* and *Culex* mosquitoes. Laboratory bioassays were conducted using a small-cup assay following an ICMR-aligned protocol (WHO, 2005), with different concentrations of ISPC-12 tested against mosquito larvae and mortality assessed at defined exposure periods. Dose response relationship assays were evaluated to determine the lethal concentration (LC_{50}/LC_{90}) values of *Bti* ISPC-12 against the two mosquito genera. Both mosquito species found susceptible to the *Bti* based biopesticide formulation, with LC_{50} values of 0.242 mg/L for *Aedes* and 0.199 mg/L for *Culex*. The persistence of the different concentrations of biopesticide formulation was subsequently assessed at Anushaktinagar, Mumbai and RRCAT, Indore. Larval mortality was monitored for six weeks by introducing larvae at weekly intervals. Results indicated that residual activity of *Bti* ISPC-12 formulation was dose dependent and 50% larval mortality (0.5 mg/L) was retained against *Aedes* and *Culex* larvae for four weeks. Moreover, *Bti* ISPC-12 formulation demonstrated consistent larvicidal activity in both locations and persisted significantly across varying temperature and environmental conditions. These findings have demonstrated the potential of *Bti* ISPC-12 based biopesticide for the management of mosquito larvae and providing information regarding the concentration, application interval and field use against *Aedes* and *Culex* larvae.

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PP-24

Purification of Txp40 protein and its insecticidal activity against lepidopteran insects

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The widespread use of *Bacillus thuringiensis* (Bt)-based biopesticides has resulted in the development of resistance among several insect pest species. This increasing resistance necessitates the development of insect pest-specific toxins with novel modes of action for effective insect pest management. Gram-negative bacteria like *Xenorhabdus* and *Photorhabdus*, which are symbionts of *Steinernema* and *Heterorhabditis*, have demonstrated high pathogenicity towards insect pests. These bacteria produce multiple insecticidal proteins, including Txp40, a ~42 kDa toxin (Kinkar et al., 2024). In the present study, Txp40 protein from *Xenorhabdus* was purified using affinity chromatography (Ni-IMAC) and yielded 13 mg/L. The different concentrations (10-1000 ng/larva) of purified protein were delivered into the hemocoel of lepidopteran insects (*Helicoverpa armigera* (Hübner), *Spodoptera litura* (Fabricius) and *Spodoptera frugiperda* (Smith)). Dose-response relationship of purified Txp40 was established by determining LD_{50} and LT_{50} values. Delivery of Txp40 protein into the haemocoel of caterpillars resulted in 90-100% mortality after 24 hours. Moreover, dose response assays revealed LD_{50} of 230 ng/larva, 312 ng/larva and 185 ng/larva for *H. armigera, S. frugiperda* and *S. litura*, respectively. Fourteen hours (LT_{50}) were required to observe 50% mortality of *H. armigera* and *S. litura* larvae, while *S. frugiperda* required 16 hours. The moribund caterpillars showed strong melanization within 14 hours of delivery and suggests Txp40 may disrupt the immune pathways of insects and affect its hemocytes. Txp40 altered cellular morphology by inducing swelling and vacuolization in hemocytes across all three insect larvae. Herein, the insecticidal activity and potential mechanism of action of the Txp40 protein will be discussed, providing insights into its role as an effective pest management strategy.

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PP-25

Evaluation of Carbonic anhydrase assay from mice kidney and its application in DTC fungicide biosensor

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Dithiocarbamates (DTCs) are organo-sulfur compounds, among the widely used broad-spectrum contact fungicides for protection of fruits and vegetables against a wide range of fungal infections across the world. Statistically, India accounts for approximately one-third of the worldwide dithiocarbamate fungicide market according to market reports. These fungicides reportedly cause serious health hazards for living beings, soil contamination, and bioaccumulation. Henceforth, their detection and monitoring are essential. Carbonic anhydrase, a zinc-containing metallo-enzyme was explored for its inhibitory interaction in the presence of DTCs fungicide. Further cost effective and natural source of carbonic anhydrase from mice kidney was investigated for the biosensor development. To study the potential application of carbonic anhydrase (CA) in DTC fungicide biosensor, initially *in silico* molecular docking were conducted with carbonic anhydrase pdb structure sourced from RCSB and propineb, a DTC fungicide. The docking interactions demonstrated significant binding of propineb fungicide with CA with binding energy -6.6 kcal mol-1. Based on the *in silico* findings, CA was experimentally investigated for the enzyme-inhibition based detection of propineb. A protocol was optimized for extraction and estimation of CA in the crude extract using p-Nitrophenyl acetate as substrate. Optimum activity of CA was observed at pH 7.6. Biochemical determination of CA activity using Michaelis Menten plot exhibited classic hyperbolic saturation kinetics for the extract acting on pNPA, consistent with esterase-like CA activity. Inhibition studies of extracted CA by propineb were carried out in the range 1–25 ppm for biosensor calibration.

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PP-26

Screening natural variation reveals aleurone layer thickness as a predictive marker for grain phytic acid accumulation in rice

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Micronutrient deficiency remains a critical global health concern. One contributing factor is the high concentration of phytic acid in rice grain that chelates essential divalent cations like zinc and iron, severely limiting their bioavailability. Hence, there is a growing need to either identify or develop low-phytic acid accumulating rice through breeding approaches. In view of this, the present study screened a panel of 125 agronomically diverse genotypes for phytic acid and inorganic phosphate (Pi) accumulation, using both brown and white rice grains. Based on the spectrum, we classified them under low- (brown rice ≤ 9.0 mg/g, white rice ≤ 0.45 mg/g), medium (brown rice 9.0-10.5mg/g, white rice 0.45 -0.65mg/g) or high (brown rice >10.5mg/g, white rice >0.65mg/g) phytic acid category. The top-ranked low phytic acid genotypes included IR-64-21 (7.19 mg/ml), CG-1919 (7.83 mg/ml), and IRRI-154 (8.10 mg/ml), while JAMIR (11.12 mg/ml), CT-11291-2-2-7(11.16 mg/ml) and MOROBEREKAN (11.17 mg/ml) were identified as high phytic acid genotypes. In addition, the Pi levels also coincided with those of total phytic acid in the tested genotypes. Incidentally, many of the widely cultivated mega varieties of rice fall under high- (SWARNA, MTU-1001, VANDANA), medium - (VIKRAM TCR, JAYA, MTU-1010), low (IR-64, IRRI 154, C.G. 19-19) -phytic acid accumulation category. The X-ray fluorescence spectrometry data reveled the phytic acid accumulation overlaps with the loss of essential nutrients, mainly zinc, in the rice grains, however, the overall cooking quality remained unchanged. The overall spectrum of major agronomic traits (height of plant, 50% flowering, panicle length) did not show any significant correlation with the grain phytic acid accumulation, suggesting the difficulty for field-site identification of low-phytic acid genotypes, Since, phytic acid is primarily synthesized and localized within the aleurone layer, histological staining was attempted to measure aleurone layer thickness as a direct structural determinant of phytate accumulation in grains. The data revealed a direct correlation between aleurone thickness and phytic acid concentration, as all the tested lower phytic acid genotypes exhibited significantly reduced aleurone layer thickness. Therefore, aleurone thickness can be considered as a predictive histological marker for breeding low-phytate rice lines of rice.

PP-27

Radiation assisted extraction of biosilica from rice straw and its functionalisation with silver nanoparticles

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Agricultural residues such as rice straw are an abundant but underused source of silica. The use of waste-derived biosilica to bind and stabilize different bioactive components has received comparatively less attention. In this study, a radiation-assisted approach was used for extraction of biosilica from rice straw and instantiated investigated its potential agricultural and biotechnological applications. Raw rice straw was exposed to gamma irradiation at 25 and 50 kGy, followed by water or acid leaching and calcination for biosilica recovery. Straw irradiated with 25 kGy gamma radiation resulted yield of 19.4% with water extraction while with acid yield of 21.0% was achieved. The recovered material showed characteristics of amorphous, porous biosilica. Further, the as prepared biosilica was used for in-situ reduction of silver nitrate using plant extract and immobiolisation of silver nanoparticles. Rapid AgNP formation was observed in the presence of biosilica, along with binding of the nanoparticles to the silica matrix. The resulting biosilica–AgNP systems showed antimicrobial activity against Escherichia coli and Staphylococcus aureus. These results indicate that radiation-assisted treatment followed by water leaching can be used to recover biosilica and functionalized with nanoparticles for biotechnological application.

PP-28

Biopolymer coating for improved seed germination and growth under abiotic stress

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Seed germination and early seedling establishment are highly vulnerable to unfavourable environmental conditions, including salinity, heavy-metal toxicity, moisture fluctuations, and other abiotic stresses. Conventional seed treatments may provide limited and short-term protection, hence there is a need for sustainable and multifunctional approaches that can protect seeds while promoting germination and early plant growth. This study focuses on the development and optimization of a biopolymer-based seed coating to enhance the germination, vigor, and abiotic stress tolerance of Trombay Mung (TM 96-2) seeds. Sodium alginate was used as the primary coating material, and different concentrations and calcium chloride cross-linking durations were evaluated to determine the most effective formulation. The optimized coating, particularly 3% sodium alginate with 15-minute calcium chloride cross-linking, was further enhanced by incorporating functional additives, including silver nanoparticles, zinc sulphate, and biosilica obtained from gamma-irradiated rice straw. These modifications were designed to improve seed resilience under salinity and cadmium stresses. The results demonstrated that the optimized biopolymer coating, particularly when combined with functional additives, improved seed germination, vigor, and stress tolerance. Overall, this multifunctional seed-coating approach provides a promising and sustainable strategy for improved seed germination and growth under stressful environmental conditions.

PP-29

Generating genetic variability by induced mutagenesis for improving agronomically important traits in soybean

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Soybean [*Glycine max* (L.)] is one of the most economically important crops because of its high protein (40%) and oil content (20%). Due to rich nutritional and biochemical composition, soybean is widely utilized as a protein source for human diets, poultry feed, aquaculture feed and biofuel production. Soybean ranks first among oilseed crops in India and contributes 40% to total oilseed production and 25% to edible oil production. However, high demand for soybeans has spurred widespread use of few elite genotypes as parents in breeding programs, creating a severe genetic bottleneck. Mutation breeding is an effective approach for generating novel genetic variability in crop plants, particularly when natural variation is limited and plays a crucial role in improving agronomically important traits in crop plants to sustain food production. In the present study, gamma ray induced mutagenesis of soybean genotype SL958 was used to generate genetic variability. Approximately 9,000 M_2 plants were raised and 94 putative mutant plants showing distinct phenotypic variation compared to parent were selected. The selected mutant plants exhibited variation for many agronomically important traits including plant height, maturity, yield etc. Four dwarf mutants and two mutants for early maturity were identified. The seeds of all putative mutants were collected individually and were screened for phytic acid content. Three mutants having reduced phytic acid content (11.8–12.8 mg/g) compared with the parent genotype SL958 (15.32 mg/g) were also identified. All putative mutants were advanced to the M_3 generation for further confirmation and study of breeding behaviour. These mutants would serve as important genetic resource for the improvement of soybean crop.

PP-30

Comparative radiosensitivity of elite late-maturing safflower (*Carthamus tinctorius L.*) varieties to gamma-ray and electron-beam irradiation for developing early-maturing cultivars for rice-fallow ecosystems

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Safflower (*Carthamus tinctorius* L.) is an important oilseed crop; however, its narrow genetic base and the predominance of late-maturing cultivars limit genetic improvement through conventional breeding. Chhattisgarh predominantly follows rice–fallow system, creating a need for early-maturing safflower varieties to utilize residual soil moisture effectively. Despite the availability of superior elite safflower cultivars with good agronomic features, their longer maturity duration restricts their feasibility in rice-fallow condition. Utilizing mutation breeding, an effective approach for creating new genetic diversity while preserving the desired characteristics can facilitate the development of early-maturing safflower variety suitable for rice-fallow condition. Optimizing mutagen doses is a prerequisite for efficient mutation breeding to generate useful genetic variability while minimizing biological damage. This study determined and compared the Lethal Dose 50 (LD_{50}) and 50% Growth Reduction dose (GR_{50}) of gamma rays and electron beam irradiation in two elite safflower varieties of Chhattisgarh, IGKV Kusum and CG Kusum 2, to establish optimum doses for mutation breeding. Dry seeds were exposed to nine irradiation doses (100-900 Gy at 100 Gy intervals) of gamma rays and electron beam. Germination, shoot length, root length, total seedling height, and vigour index were recorded at 36 and 85 days after sowing in a factorial randomized complete block design with two replications. LD_{50} was estimated using probit analysis, whereas GR_{50} values were derived from dose–response relationships of seedling traits. Gamma rays exhibited greater biological effectiveness than electron beam irradiation. The estimated LD_{50} for gamma rays was 319.78 Gy in both varieties, whereas electron beam LD_{50} values were 342.00 Gy for IGKV Kusum and 326.46 Gy for CG Kusum 2. GR_{50} values ranged from 300-402 Gy for gamma rays and 329-416 Gy for electron beam, depending on growth stage and trait evaluated. Vigour index consistently produced lower GR_{50} estimates (254-275 Gy), indicating its greater sensitivity for assessing radiation-induced damage. Relative Biological Effectiveness ranged from 0.935-0.980 for electron beam (gamma rays = 1.00), while analysis of variance revealed

highly significant dose effects on all measured traits. The lower LD_{50} and GR_{50} values of IGKV Kusum indicate comparatively greater radiosensitivity and lower radio-tolerance than CG Kusum 2 for both the physical mutagens. Overall, an optimum mutagenic dose range of 300-400 Gy was identified for both irradiation sources. These findings provide a robust foundation for developing early-maturing, high-yielding, and high-oil safflower mutants adapted to the rice-fallow ecosystems of Chhattisgarh through mutation breeding.

PP-31

Alginate-based delivery systems for sustained iron release: From biopolymer to smart fertilizer

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Alginate, a biodegradable and biocompatible polysaccharide derived from natural sources, offers excellent gel-forming ability, high loading capacity and tunable release characteristics, making it a promising material for advanced nutrient delivery systems. Iron (Fe) is an essential micronutrient required for numerous physiological and biochemical processes in plants, including chlorophyll synthesis, electron transport, enzyme activation, and overall growth and development. However, limited Fe availability in soils, particularly under alkaline and calcareous conditions, often leads to Fe deficiency, reduced crop productivity, and poor nutritional quality. Conventional iron fertilizers frequently suffer from low use efficiency and nutrient losses, necessitating the development of sustainable strategies for controlled and efficient Fe^{2+} delivery. In this study, the development of alginate-based Fe^{2+} carrier aims to regulate Fe^{2+} release through diffusion-controlled mechanisms, thereby maintaining prolonged nutrient availability. A protocol was optimized for preparing alginate-based composite in form of bead with various concentrations (1 - 7%) of alginate. Based on swelling index and stability, alginate bead (2%) was selected and exhibited pH dependent swelling in the range of pH 3-9. Also, crosslinking with glutaraldehyde (GA) was optimized, 2% GA further improved the stability and controlled release property of the bead. Further, dual nutrient delivery system of alginate beads loaded with Fe^{2+} and zinc was developed and characterized for its release under varying pH and salinity conditions. The developed alginate-based carrier represents a sustainable advancement toward nutrient management and next-generation smart fertilizers.

PP-32

Development of high yielding, blast-resistant rice through gamma-ray-induced mutation breeding and genetic analysis using MutMap

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Rice blast, caused by *Magnaporthe oryzae*, is a major disease affecting rice production worldwide. Developing and understanding the genetic basis of blast resistance is important for breeding resistant rice varieties [1]. In this study, the genetic basis of blast resistance in Vikram-TCR, a gamma-ray-induced mutant derived from the susceptible rice landrace Safri-17 and released for cultivation, was investigated using genetic analysis, whole-genome resequencing and MutMap. Under uniform blast nursery conditions, Vikram-TCR showed higher resistance than Safri-17, with stable resistance observed across repeated and multilocation evaluations [2,3]. Genetic analysis of the F_2 population derived from Safri-17 × Vikram-TCR showed a 3:1 susceptible-to-resistant ratio, indicating that resistance is controlled by a single recessive locus. Whole-genome resequencing identified genetic differences between Vikram-TCR and Safri-17, despite their high overall genomic similarity [4,5]. MutMap analysis identified a candidate region on chromosome 4 containing two nonsynonymous mutations, including a G14R substitution in *OsPiPR1* (Os04g0621700), a previously reported blast-resistance-associated gene. Further evolutionary and computational analyses suggested that the substitution may influence local protein properties without substantially altering its overall structure. Based on the genetic mapping and supporting analyses, *OsPiPR1* was identified as the strongest candidate gene associated with blast resistance in Vikram-TCR [6]. However, further functional studies are required to confirm the role of the identified mutation in resistance. This study demonstrates the application of mutation breeding and genome-based approaches to investigate disease resistance in rice and provides a candidate gene and variant for further research and potential use in blast-resistance breeding [7,8].

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PP-33

A DREB-NAC cross talk modulates abiotic stress tolerance by orchestrating hormone biosynthesis and senescence in banana plants

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Dehydration Response Element Binding (DREB) and NAC transcription-factors are crucial for stress tolerance in plants. While their specific roles are well-defined in model plants, the cross-regulation between these factors remained unexplored. In this study, we report that MusaDREB1G of banana interacts with MusaATAF2, a NAC transcription factor, to regulate stress tolerance. MusaDREB1G is strongly responsive towards drought and cold stress and $Pro_{MusaDREB1G}$-$_{GUS}$ activity thought confined to vascular tissues is expanded to non-vascular tissues under environmental insults. Despite development of a stunted-growth phenotype in MusaDREB1G-overexpressing banana lines, they exhibited tolerance towards cold and drought. RNAseq-data revealed a positive shift in phytohormone-related genes and MusaATAF2 transcription factor. Specific DRE-elements associated with MusaDREB1G was identified through EMSA assay with purified MusaDREB1G protein were also detected in promoters of MusaATAF2 and ABA-biosynthetic genes. Furthermore, MusaDREB1G affinity and positive modulation of Pro-MusaATAF2 and Pro-ABA genes was corroborated with dual-luciferase assays. Surprisingly, MusaATAF2-Ox lines developed precocious-senescent phenotype with strong induction of chlorophyll catabolic genes and significant ROS accumulation indicating that senescence is intricately associated with stress-responses. Collectively, our findings unveil a unique molecular mechanism for drought and cold tolerance driven by MusaDREB1G and MusaATAF2 cross-talk leading to a strategic foundation for developing genetically-engineered, stress-resistant banana crops.

PP-34

Multi-target phytochemical strategies for factors orchestrating thrombotic microangiopathy: An IMPPAT-based network study

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Transplantation-associated thrombotic microangiopathy (TA-TMA) and hepatic veno-occlusive disease (HVOD) are severe, life-threatening endothelial damage syndromes following hematopoietic stem cell transplantation (HSCT). Current clinical countermeasures, such as defibrotide and eculizumab, face critical hurdles including high cost, restricted global access, and suboptimal outcomes in severe presentations. Indian medicinal plants offer an untapped polypharmacological reservoir capable of addressing the complex, multi-factorial etiology of post-transplant vascular toxicity. Pathological target repertoires for TA-TMA and HVOD were gathered from DisGeNET. Phytochemical compounds from Indian medicinal herbs were screened via IMPPAT 2.0 and Binding DB. Intersecting disease–phytochemical targets were evaluated by constructing high-confidence protein-protein interaction (PPI) networks in STRING (confidence score ≥ 0.7) and analyzed via Cytoscape (cytoHubba) using degree centrality. Functional gene ontology (GO) and pathway over-representation (KEGG and Reactome) were mapped using the DAVID platform ($p < 0.05$). Target retrieval captured 62 TA-TMA and 37 HVOD disease-associated genes, which mapped to 11 and 12 consensus targets across 15 high-ranking Ayurvedic herbs, including *Terminalia arjuna*, *Phyllanthus emblica*, *Mangifera indica*, and *Camellia sinensis*. Topological hub screening pinpointed MMP9, IL6, TNF, ALB, and F3 as top regulatory nodes in TA-TMA, while MMP9, IL6, TNF, IGF1, and ALB governed HVOD interactomes. Pathway mapping revealed significant modulation of AGE-RAGE signalling, hemostasis, complement/coagulation cascades, and extracellular matrix (ECM) remodelling. Quercetin, ellagic acid, mangiferin, beta-sitosterol, and epigallocatechin gallate (EGCG) were identified as master polypharmacological drivers. This study establishes a systems-biology paradigm demonstrating that Indian medicinal plants mitigate post-transplant microvascular and hepatic injuries by concurrently attenuating inflammation, hypercoagulation, and ECM breakdown. These findings identify high-priority phytochemical candidates for immediate translational and preclinical validation.

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PP-35

In silico and molecular analysis of bromodomain (BRD)-containing epigenetic regulators from *Arabidopsis thaliana*

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Regulation of gene expression in plants is highly complex and multi-layered, where epigenetic regulators have emerged as key players of stress adaptive mechanisms. Epigenetic regulation operates in a sequence independent manner, via modification of DNA and/or proteins. Post-translational modification (PTM) of histones in chromatin is regulated by interplay of 'Writer', 'Eraser' and 'Reader' proteins for different PTM marks. The bromodomain (BRD)-containing protein family contain epigenetic 'readers', which recognize and bind to acetylated lysine residues on histones, and facilitate gene expression. The human BRD- members play roles in physiological and pathological processes via involvement in chromatin remodeling, alternative splicing, transcriptional regulation and protein-scaffolding. Model plants like Arabidopsis and Rice contains small BRD-families, with some members shown to be involved in development, stress responses, and physiological processes, however functional significance of many members still remains unknown. This study aims to explore the characteristics of AtBRDs from Ortholog Group 2, which harbors four members (AtBRD2a, AtBRD2b, AtBRD2c, AtBRD2d: due to two block duplication events), using *in silico* and wet-lab analysis. *In silico* analysis was done to: 1) identify closest members in other organisms, 2) infer evolutionary relationships, 3) comparison of promoter, gene and domain-motif architecture, and 4) interaction network. Analysis of RNA-Seq data from databases and RT-qPCR assays revealed expression pattern in different tissues, development stages, and abiotic-biotic stresses. The BRD-region of AtBRD2c was cloned, optimized for over-expression and solubility, and successfully purified. The study provided insights into important features of AtBRD2-group members, and purified bromodomain of one member for further functional characterization.

PP-36

Plant responses to metal stress: Interplay of physiology, redox homeostasis, and molecular adaptation

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Metal stress is a major abiotic constraint that profoundly influences plant growth, metabolism, and ecological fitness in contaminated environments. Excess accumulation of potentially toxic metals, including cadmium (Cd), lead (Pb), chromium (Cr), nickel (Ni), copper (Cu), and mercury (Hg), disrupts plant homeostasis through interconnected effects on metal uptake and transport, mineral nutrition, cellular redox balance, and metabolic activity. After root uptake, metals may compete with essential nutrients or interfere with their transport, causing nutrient imbalance and impairing fundamental processes such as photosynthesis, respiration, water relations, and biomass production. A central consequence of metal exposure is excessive generation of reactive oxygen species (ROS), particularly in chloroplasts and mitochondria, which can disturb membrane integrity, proteins, nucleic acids, and photosynthetic machinery when ROS production exceeds the cellular scavenging capacity. In response, plants activate an integrated defence network involving enzymatic antioxidants such as superoxide dismutase (SOD), catalase (CAT), peroxidases (POX), ascorbate peroxidase (APX), and glutathione reductase (GR), together with non-enzymatic antioxidants and redox-buffering metabolites. Concurrently, metal chelation by phytochelatins and metallothioneins, cell-wall binding, intracellular compartmentalisation, and vacuolar sequestration restrict the cytotoxic effects of accumulated metals. Metal stress also signals through calcium- and MAPK-dependent pathways, phytohormonal networks, transcription factors, and stress-responsive genes, coordinating physiological and molecular adaptation. The outcome of metal exposure therefore reflects a dynamic balance between metal accumulation, toxicity, and the capacity of plants to activate protective and detoxification mechanisms. Understanding these interconnected responses provides a mechanistic basis for identifying metal-tolerant plants and exploiting their adaptive traits for phytostabilisation and phytoremediation of contaminated ecosystems.

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PP-37

Interactive effects of heat stress and radiofrequency radiation on growth, anatomy, and physiology of *Vigna radiata* L.

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Plants are increasingly exposed to multiple environmental stressors, yet their interactive effects on plant growth and physiological functioning remain poorly understood. This study investigated the individual and combined effects of heat stress and radiofrequency (RF) radiation on *Vigna radiata* L. seedlings under controlled conditions. Seedlings were exposed to heat stress (42 °C), continuous-wave RF radiation (2.6 GHz), or their combination for 4 h day^{-1}, and responses were evaluated in terms of growth, stem anatomy, stomatal characteristics, and biochemical attributes. Heat stress markedly inhibited plant growth, reducing plant height by 56.3% at 15 days, whereas RF radiation alone caused a moderate reduction of 20.0%. Combined exposure resulted in a 58.8% reduction, comparable to heat stress alone, indicating a predominantly heat-driven and non-additive effect on growth. Anatomical observations revealed greater structural disruption under combined stress, including epidermal damage and poorly differentiated xylem elements. Stomatal pore area decreased from 28.87 μm² in controls to 19.98 μm² under heat and 17.54 μm² under combined exposure, whereas RF alone increased pore area to 56.34 μm². Biochemical responses showed greater impairment under combined stress, with relative water content declining from 88% in controls to 65% under heat and 52% under combined exposure. Carbohydrate and protein contents also decreased substantially under combined stress. Overall, heat predominantly governed growth, anatomical, stomatal, and pigment responses, whereas combined exposure intensified metabolic impairment. These findings highlight the importance of considering multiple environmental stressors when assessing plant responses under changing environmental conditions.

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PP-38

Recombinant expression, purification, and biophysical analysis of cancer-associated metabolic enzymes MTHFD2 and PHGDH

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Cancer cells undergo extensive metabolic reprogramming to meet the increased demands of proliferation, biosynthesis, and redox homeostasis. Among the metabolic pathways dysregulated in cancer, one-carbon metabolism and de novo serine biosynthesis have emerged as promising therapeutic targets[1]. Methylene tetrahydrofolate dehydrogenase 2 (MTHFD2), a key mitochondrial enzyme in folate-mediated one-carbon metabolism, contributes to nucleotide biosynthesis and redox regulation and is frequently overexpressed in cancer[2]. Similarly, phosphoglycerate dehydrogenase (PHGDH), the rate-limiting enzyme of de novo serine biosynthesis, supports tumor progression by supplying serine and downstream metabolites required for nucleotide biosynthesis and redox homeostasis. The recurrent dysregulation of MTHFD2 and PHGDH highlights their potential as metabolic vulnerabilities and candidate targets for anticancer drug development. In the present study, recombinant expression constructs encoding human MTHFD2 and PHGDH with His-tags were designed and codon-optimised for heterologous expression in *Escherichia coli*. The corresponding plasmids were synthesized and transformed into *E. coli* BL21(DE3), followed by optimization of recombinant protein expression and purification to obtain proteins suitable for downstream biophysical and structural studies. The conformational properties of the purified proteins were evaluated using circular dichroism spectroscopy, while dynamic light scattering was employed to assess solution homogeneity and aggregation behaviour. Size-exclusion chromatography was used to investigate oligomeric states, and differential scanning fluorimetry was performed to evaluate protein thermal stability. In addition, initial crystallization conditions for PHGDH were identified through systematic crystallisation screening. Collectively, these studies establish a foundation for the structural and functional characterisation of MTHFD2 and PHGDH and their further evaluation as potential therapeutic targets in cancer.

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PP-39

AI-driven *de novo* design and experimental validation of miniprotein binders targeting GRP78

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Effective cancer diagnosis and treatment require molecular targets that are minimally expressed in normal tissues but strongly upregulated in tumors, providing high target-to-background contrast and minimizing off-target effects. Glucose-regulated protein 78 (GRP78; ~69 kDa), an endoplasmic reticulum chaperone aberrantly overexpressed and displayed on the cell surface of aggressive and therapy-resistant cancers, represents a promising target for cancer-directed therapeutics. Here, we developed an integrated AI-driven and structure-based computational pipeline for the de novo design of high-affinity miniprotein binders targeting GRP78. Using RFdiffusion, three complementary design strategies—full-length diffusion, partial diffusion, and motif scaffolding—were employed to generate and refine candidate binder architectures targeting the GRP78 nucleotide-binding domain (NBD). BindCraft was additionally used for energy-based design and conformational optimization of structurally stable binders. Top-ranked candidates were evaluated using AlphaFold3 with stringent structural criteria (pAE < 7.5, pLDDT > 90, and ipTM > 0.75). The integrated workflow generated more than 200 diverse candidate miniprotein binders with favorable predicted structural and binding properties. Experimentally, 20 GRP78-targeting miniproteins were successfully expressed and purified. Size-exclusion chromatography was performed to assess their oligomeric state and solution behavior, followed by initial ELISA-based screening using ScFv positive controls (MAb159 and PAT-SM6). Surface plasmon resonance demonstrated that Gpx84 binds the GRP78 NBD with nanomolar affinity. Circular dichroism spectroscopy further confirmed the expected secondary structure and high thermal stability of the characterized miniprotein. Overall, this integrated AI-driven computational and experimental platform provides a rapid and scalable strategy for developing structurally stable GRP78-targeting miniproteins with potential applications in cancer imaging, diagnosis, and targeted therapy.

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PP-40

Structure-guided design of NS2B peptide mimics for inhibiting dengue NS2B-NS3 protease

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Dengue virus is a deadly human pathogen that has been causing immense socioeconomic burdens to global health for ages, and no antiviral drugs have been approved for it to date [1,2,3]. The dengue NS2B-NS3 protease-helicase is a heterodimeric multifunctional protein complex in which the protease domain catalyses the cleavage of the flavivirus polyprotein precursor into mature viral proteins, while the helicase domain unwinds viral dsRNA intermediates and hands them off to RdRp for viral mRNA synthesis. NS2B functions as an integral membrane protein, in which its central cytosolic domain acts as a vital cofactor for NS3 protease activity. Its transmembrane domains, located at the N- and C-terminal ends, are integrated into the host cell's endoplasmic reticulum (ER), where viral RNA synthesis occurs [4,5]. The N-terminal region of cytosolic NS2B acts as a structural stabiliser for the NS3 protease and membrane anchor for the NS3 protease-helicase complex, while its flexible C-terminal region, when bound by substrate, wraps around the protease and acts as a functional effector by becoming part of its active site [6,7]. Decades of research have failed to identify a suitable, safe drug for the NS2B-NS3 protease, largely because of its shallow, charged, featureless active site and off-target concerns [8]. Here, we present a peptidomimetic strategy targeting the NS2B-NS3 interface, in which we designed several high-affinity peptides that mimic the N-terminal region of NS2B, thereby preventing the C-terminal region of NS2B from interacting with the NS3 protease's active site, ultimately inhibiting the protease. Moreover, as the NS2B-NS3 interface is largely native to the virus, off-target interactions are less likely to occur, thereby offering the potential for enhanced specificity and safety.

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PP-41

Gut microbial β-glucuronidase inhibitors as anti-cancer adjuvants: Discovery of proton pump inhibitors as covalent inhibitors of *E. coli* β-glucuronidase

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Gut microbial β-glucuronidases (GUS) hydrolyse SN38-glucuronide (SN38-G), the inactive metabolite of the anticancer drug irinotecan, regenerating cytotoxic SN38 in the intestine. This exposure to reactivated SN38 damages the intestinal mucosa and causes irinotecan-induced diarrhea. Targeted inhibition of bacterial GUS is therefore a promising strategy to mitigate this side effect. *Escherichia coli* GUS (EcGUS) is among the most catalytically efficient enzyme in the metabolism of SN38-G. To identify potential EcGUS inhibitors, we screened ~1800 compounds from an FDA-approved drug library identifying ~15 compounds with >80% inhibition at 10 μM. Among these, proton-pump inhibitors (prazoles) used to manage GERD-related gastrointestinal symptoms, emerged as a notable chemical class with rabeprazole (IC_{50} = 2 μM) and omeprazole (IC_{50} = 5 μM) as the most potent hits. Time-dependent inhibition and jump dilution assay indicated a slow, irreversible inhibition mechanism for rabeprazole. Prazoles inhibit proton pumps through allosteric covalent inhibition by forming disulfide bonds with specific cysteine residues. A reducing environment diminishes rabeprazole's EcGUS inhibition, indicating that PPIs inhibit EcGUS via the same mechanism. To identify target cysteine residue in EcGUS, site-directed mutagenesis of cysteine residues were performed. Interestingly, mutation of Cys449 to serine abolished rabeprazole inhibition suggesting Cys449 as likely site of covalent adduction. Differential Scanning fluorimetry showed decreased thermal stability of EcGUS in the presence of rabeprazole while circular dichroism revealed local conformational changes upon rabeprazole binding, consistent with a cysteine-targeted covalent mechanism. Together, these findings identify prazoles as lead compound to develop adjuvants to irinotecan chemotherapy to reduce its dose-limiting gastrointestinal toxicity.

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PP-42

Small molecules target a conserved RNA-binding vulnerability in the coronavirus nucleocapsid protein

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The Nucleocapsid (N) protein of coronaviruses is essential for genome packaging and replication, and its high sequence conservation across the Coronaviridae family makes it an attractive but pharmacologically underexploited antiviral target — in contrast to rapidly mutating proteins such as spike, against which most current therapeutics are directed. This raises a central question: does the N protein harbor a druggable site that is not only functionally critical but also structurally conserved enough to support broad-spectrum inhibition? To address this, we screened 1,813 FDA-approved compounds against the RNA-binding N-terminal domain (N-NTD) of SARS-CoV-2 using differential scanning fluorimetry, and validated functional inhibitors by electrophoretic mobility-shift assays, identifying ceftazidime, sennoside A, and tannic acid as compounds that abolish N protein–nucleic acid interaction. Surface plasmon resonance and [1H,15N]-HSQC NMR chemical shift perturbation, corroborated by HADDOCK docking, showed that ceftazidime (KD ~407 nM) and sennoside A (KD ~21 nM) act through a common mechanism, both engaging the basic "palm–finger" groove that the N-NTD uses to bind RNA — indicating that inhibition is not incidental but targets the protein's core nucleic-acid-binding architecture. If this pocket is indeed a conserved feature of coronavirus biology rather than a SARS-CoV-2-specific vulnerability, the same inhibitors should retain activity against divergent coronaviruses. Testing this directly, we found that 95% of the inhibitor-contacting residues are invariant across SARS-CoV-2, SARS-CoV, and MERS-CoV despite considerable divergence in the N protein overall, that all three recombinant N proteins bind RNA with comparable high affinity (KD 105–145 nM), and that both compounds inhibit RNA binding across all three homologs (IC_{50} 45–78 μM) through a conserved docking pose at the equivalent site in each N-NTD structure. Taken together, these results support a model in which the N-NTD RNA-binding groove is a structurally conserved, druggable vulnerability shared across human coronaviruses, and identify ceftazidime and sennoside A as pan-coronavirus inhibitors acting through this common mechanism — establishing a rational, mechanism-based foundation for broad-spectrum antiviral development against current and future coronavirus threats.

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PP-43

Integrative peptidomic and mass spectrometric analysis of post-translational modifications in a novel contryphan variant from marine cone snail

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Marine cone snails (*Conus betulinus*) secrete a complex cocktail of bioactive peptides known as conotoxins, which undergo extensive post-translational modifications (PTMs) to achieve structural rigidity and high target selectivity. This study details the mass spectrometric identification and structural characterization of a novel contryphan peptide variant isolated from the venom duct of *Conus betulinus*. Crude venom samples were processed via reduction (dithioerythritol) and alkylation (iodoacetamide), followed by high-resolution LC/ESI-MS/MS analysis. Utilizing a complementary workflow integrating transcriptomics, *de novo* sequencing, and chemical synthesis, a novel contryphan-like peptide sequence (ZSGCO^{D}*W*K$_{Ac}$PWC*; where native peptide M:1228.58Da, reduced and alkylated peptide M: 1344.54 Da; where M: Mass, *: C-terminal amidation, Ac: acetylation, O: hydroxyproline, ^{D}: D configuration of W, Z: N-terminal pyroglutamic acid) was successfully characterized alongside other variants ZSGCP^{D}*W*KPWC*; M: 1170.48 Da. High-resolution accurate-mass spectrometry overcame significant analytical hurdles posed by cyclic constraints and labile neutral losses, enabling the precise localization of an intricate suite of PTMs. These modifications include N-terminal pyroglutamic acid, hydroxyproline, lysine acetylation, and conserved disulfide bonding and *D* configuration of W. Experimentally chromatographic profile of synthesized peptides confirmed the structural identity at D-configuration of tryptophan. Additionally, integrating proteomics and transcriptomics data from Conus venom ducts confirms the presence of specialized conoenzymes responsible for executing these complex PTMs. Contryphan peptides function by binding to and inhibiting neuronal calcium (Ca^{2+}) and potassium (K^{+}) ion channels. These findings underscore the sophisticated enzymatic tailoring utilized by marine venom systems and establish a robust analytical framework that advances marine natural product peptidomics and targeted drug discovery.

PP-44

Structure-function analysis of globally circulating SARS-CoV-2 PLpro variants reveals gain-of-function in gamma mutant

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The emergence of SARS-CoV-2 variants during the COVID-19 pandemic altered viral transmissibility, immune evasion, and pathogenicity, emphasizing the need to understand the structural and functional consequences of viral mutations. Here, we investigated mutations in the papain-like protease (PLpro), a domain of Nsp3 that processes the viral polyprotein and suppresses innate immune responses via deISGylation and deubiquitination activities. We previously identified five circulating PLpro variants (P77L, P77S, A145D, V187A, and K232Q) from ~17 million Nsp3 sequences (Arya et al., 2023). Mutants were generated by site-directed mutagenesis and purified for biochemical, biophysical, and structural characterization. Steady-state kinetic assays with three fluorogenic substrates (RLRGG-AMC, ISG15-AMC, Ub-AMC) showed wild-type-like activity for all mutants except K232Q, a Gamma-VOC mutation showing a ~4-fold increase in deubiquitination activity toward Ub-AMC. K232Q was crystallized and its structure was solved by molecular replacement using WT PLpro structure (PDB: 9VAO), refined to R_{work}/R_{free} of 0.17/0.21 and submitted to PDB (PDB: 26ZO) which revealed localized conformational changes relative to wild-type. At the mutation site, a water-mediated K232–Y207 hydrogen bond in wild-type was replaced by a direct bond in K232Q, indicating increased local rigidity for ubiquitin engagement. Molecular dynamics simulations of the PLpro–ubiquitin complex (PDB: 7RBR) revealed interface remodeling in K232Q, including new hydrophobic and electrostatic contacts and a more favorable, enthalpy driven, MM/GBSA binding free energy ($\Delta\Delta G$ = −13.26 ± 6.23 kcal/mol). These findings provide a mechanistic basis for K232Q's enhanced deubiquitination activity and underscore the functional significance of naturally occurring PLpro mutations in viral evolution and pathogenicity.

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PP-45

Intrinsically disordered protein as stress shield: Protective mechanisms of chaperone-like disordered protein in cyanobacteria

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Intrinsically disordered proteins (IDPs), which lack stable tertiary structures, play important roles in cellular regulation and stress adaptation through their flexible and dynamic interactions. However, their specific contributions to photosynthetic physiology, including in cyanobacteria, the evolutionary ancestors of plant chloroplasts, remain poorly understood. Proteome of the N_2-fixing cyanobacterium *Anabaena* PCC 7120 showed the presence of 688 proteins containing intrinsically disordered regions (IDRs), including 130 predicted IDPs (>30% overall disorder). Transcriptomic analysis under salt stress revealed differential expression of 41 IDP genes, with six conserved IDPs induced under multiple stress conditions. Protein-protein-interaction network analysis suggested that these proteins function as interaction hubs linking diverse cellular pathways[1]. Among these proteins, Alr0806, which displayed 70% disorderedness was strongly induced under NaCl stress and was studied further. Experimental analyses revealed that the expressed Alr0806 protein corresponds to a shorter form than the one annotated in databases. Recombinant Alr0806 displayed hallmark features of intrinsically disordered proteins (IDPs), such as anomalous electrophoretic mobility, high thermal stability, and low secondary structure content. Furthermore, the protein underwent disorder-to-order transitions at low pH near its pI and exhibited molecular chaperone-like activity, effectively shielding target proteins from stress-induced aggregation. Consistent with this role, the Alr0806-deficient *Anabaena* strain displayed impaired growth and reduced photosynthetic performance under normal as well as salt or heat stress conditions[2]. Together, these findings establish IDPs as important contributors to cyanobacterial stress tolerance and provide new insights into their physiological roles within photosynthetic organisms.

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PP-46

Conservation of a diverse butterfly population in the Bhabha botanical garden: Insight into niche requirement and sustainability

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The present study aims to document the diversity of butterfly species in the Butterfly Garden of Bhabha Botanical Garden, BARC, Trombay, Mumbai, Maharashtra. Butterflies play an important role as pollinators and are also considered valuable biological indicators of environmental health, habitat degradation and pollution. Selective plantation was promoted over an area of approximately 5 acres in the Bhabha Botanical Garden, comprising important larval host plants and nectar-producing plant species. In addition, *Heliotropium indicum* and *Crotalaria retusa*, which serve as sources of pyrrolizidine alkaloids for certain butterfly species, were incorporated to promote butterfly diversity. Comprehensive field surveys were conducted from September 2024 to August 2026 using the line transect method, a standardized sampling technique (Pollard, 1979). A total of 55 species of butterflies were recorded during the study period, belonging to five families. Family Nymphalidae (20 species) comprised the highest number of species followed by, Pieridae (13 species), Lycaenidae (08 species), Papilionidae (08 species) and Hesperiidae (06 species). The abundance of these species stated in terms of very common (VC), common (C) and rare (R). The Nymphalidae family was dominant among the five families, with 20 (36%) species observed during this survey. Common Crow (*Euploea core*), Striped tiger (*Danaus genutia*) and Common grass yellow (*Eurema hecabe*) are the most dominant butterfly species, followed by Tailed Jay (*Graphium agamemnon*) and Common mormon (*Papilio polytes*). Crimson rose (*Pachliopta hector*) and Danaid egg fly (*Hypolimnas misippus*) species are protected under Schedule II of the Wild Life (Protection) Act, 1972 as amended in 2022, is also observed. The study area included grassland, open scrub, forest edge, dense forest, and horticultural zones. Open scrub and forest-edge habitats had higher butterfly diversity, likely due to more nectar, larval host plants, sunlight, and varied vegetation. The present survey helps to the documentation and systematic classification of butterfly fauna for future study.

PP-47

Optimization of a dual-target RPA–CRISPR–Cas12 platform for rapid tuberculosis diagnosis

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Rapid, sensitive, and point-of-care-compatible detection of *Mycobacterium tuberculosis* (Mtb) is critical for timely diagnosis and effective disease management. Here, we developed and optimized a multiplexed isothermal amplification-based RPA–CRISPR–Cas12 assay targeting low-copy microbial DNA, mimicking circulating cfDNA in blood. This approach provides a minimally invasive alternative to conventional sputum-dependent testing and may improve applicability in extrapulmonary and sputum-scarce cases. Two genomic targets were incorporated to improve assay sensitivity and robustness: the conserved single-copy gyrB gene and multicopy insertion sequence IS6110. Target-specific RPA primers generating ~200 bp amplicons were systematically optimized for balanced co-amplification. Higher total primer concentrations resulted in inefficient amplification or failure of one or both targets during multiplexing, whereas reducing primer concentrations below the conventionally recommended 960 nM markedly improved amplification. This may arise from excess single-stranded primers sequestering single-stranded DNA-binding (SSB) proteins required to stabilize displaced DNA strands during RPA. The optimized total primer concentration was therefore maintained at ≤480 nM, with higher IS6110: gyrB primer ratios compensating for lower IS6110 amplification efficiency. Multiple target-specific gRNAs were designed, and the best-performing gRNAs were selected for Cas12-based detection. Surprisingly, their predicted secondary structures were inconsistent with literature-described requirements for efficient Cas12 complexes. Under optimized conditions, a limit of detection below 3.5 copies/μL was achieved for both targets in singleplex and multiplex formats using synthetic samples. Multiplexed detection functioned as an OR gate, whereby detection of either target resulted in a positive signal, improving assay robustness and reducing false negatives and dependence on just one marker.

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PP- 48

Epigenetic control of RNA binding protein, RBM10 expression and its cytoplasmic mislocalization: Implications in cardiac hypertrophy

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RNA-binding motif proteins are largely a family of proteins having one or more structurally conserved RNA recognition motifs controlling almost all co/post-transcriptional mRNA processing events. One such protein, RBM10 is a well-established splicing factor that regulates apoptotic genes associated with different cancers. Additionally, in a non-canonical function, RBM10 regulates cardiac hypertrophy in a splicing independent function along with a variant poly(A) polymerase Star-PAP. RBM10 is downregulated during hypertrophy leading to compromised expression of anti-hypertrophy regulators. Yet, how expression or sub-cellular features RBM10 is regulated in disease conditions is still unknown. Our data reveals its connection with the mitogen-activated protein kinase extracellular signal-regulated kinase (ERK) pathway. We show that ERK inhibition decreased methylation status of RBM10 promoter such that induced ERK activity during hypertrophy results in RBM10 downregulation. Among the DNA methyltransferases, we identify DNMT1 as the enzyme that enables RBM10 promoter methylation. Further, knockdown of different transcriptional factors showed CTCF being capable of binding to RBM10 promoter and regulate its expression. CTCF binding sites were mutated to resemble the effects of methylation, which can further show how methylation affects CTCF binding to promoter. Experiments carried out in cardiac cells and Wistar rat heart models show RBM10 is downregulated upon hypertrophy induction which was rescued on ERK inhibition. We also generated AAV9-RBM10 construct cTNT promoter to overexpress RBM10 in animal heart. Knockdown of RBM10 showed downregulation of NAD^+dependent enzymes (SIRT1, SIRT2, SIRT6), critical proteins for hypertrophy induction in the heart. Our study indicates a novel epigenetic control of RBM10 that can act as a potential target in heart failure therapeutics.

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PP-49

Comparative mutational spectra in the genome of groundnut due to gamma ray and electron beam mutagenesis

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Induced mutagenesis creates genetic variability in groundnut (*Arachis hypogaea* L.), and the choice of mutagen influences the mutational spectra and mutagenic effectiveness. The present study compared mutational spectra induced by gamma rays and electron beam irradiation in a high yielding Trombay groundnut breeding line, TG 67. Seeds were irradiated with gamma rays and electron beams at doses of 150 and 200 Gy. A total of 25,000 M_2 plants were screened, from which 33 gamma ray derived and 28 electron beam derived mutants with variations in different traits were isolated. Of these, four mutants derived from each mutagen, along with the parent were subjected to whole genome resequencing at 30X to 40X coverage. Small nuclear variants and structural variants were identified using two complementary variant calling tools for each and filtered against the parent genome. Small nuclear variants constituted 93–96% of the detected variants, whereas structural variants accounted for 4–7%. About 99% of annotated variants fell outside exons, and 84-85% were located in intergenic, upstream and downstream regions. Among the treatments, 150 Gy gamma irradiation resulted in the highest number of exonic variants. Gamma ray mutants showed higher number of small nuclear variants whereas electron beam mutants showed higher number of structural variants. Electron beam derived mutants exhibited a higher transition to transversion ratio (1.56) than gamma ray derived mutants (1.44), indicating differences in the substitution spectra associated with the two radiation sources. Structural variants were predominantly represented by breakends (44 to 50%) and deletions (21 to 32%). The distribution of structural variant sizes showed a bimodal pattern, with rearrangements exceeding 10 kb accounting for 31–50% of the mutagenic events, while moderate sized indels (101–500 bp) constituted 18–52% of the events. A significant sub-genome asymmetry was observed for structural rearrangements, with the B sub-genome carrying a higher representation of structural variants. Although, the total mutant specific structural variants were comparable across treatments, electron beam derived mutants showed a greater representation of breakends and insertions across most chromosomes. These findings indicate that gamma rays and electron beams generate distinct profiles of small nuclear variants and structural genomic variants in groundnut.

PP-50

Recombinant expression and biophysical characterization of *Plasmodium falciparum* Ribosomal protein P2

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Ribosomal protein P2 (P2) is an essential component of the ribosomal stalk, which facilitates interactions with translation factors and supports efficient protein synthesis. In *Plasmodium falciparum*, the causative agent of malaria, the parasite's translational machinery represents a potential avenue for therapeutic intervention. Characterizing P2 protein structural properties, oligomeric behaviour and molecular interactions is important for understanding its function and evaluating its potential as an antimalarial target. In this study, recombinant *P. falciparum* P2 was characterized using size-exclusion chromatography (SEC), circular dichroism (CD) and intrinsic fluorescence spectroscopy. Full-length P2 exhibited heterogeneous solution behavior and substantial recovery of its CD profile following thermal perturbation, whereas its C-terminally truncated construct showed a predominant SEC peak consistent with a putative dimer. The addition of DNA induced concentration-dependent fluorescence quenching, suggesting changes in the protein's local environment upon DNA addition. These findings provide a foundation for further investigation of P2 structure-function relationships and its potential relevance to antimalarial drug discovery.

PP-51

Integrative characterization of translin mutations and its functional association with radiation response

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Translin (TSN) is a conserved nucleic-acid-binding protein involved in RNA metabolism and protein-RNA complex formation. In-vitro activities of Translin protein are well documented, the functional significance of clinically reported Translin variants and their contribution to cellular responses to genotoxic stress remain poorly understood. Here, we investigated the role of Translin using an integrated computational and experimental approach, focusing on mutation-associated structural changes and radiation response. Ten clinically reported Translin variants were characterized using structure-based computational analyses and molecular dynamics (MD) simulations to investigate alterations in protein stability, flexibility and conformational dynamics. Selected variants were generated by site-directed mutagenesis and characterized following recombinant expression and purification. Native PAGE, dynamic light scattering, circular dichroism and electrophoretic mobility shift assay were employed to evaluate oligomeric organization, structural properties and DNA-binding activity. To establish cellular relevance, radiation-induced responses of Translin were investigated in multiple cellular models. Distinct temporal and cell-type-dependent changes in Translin expression and subcellular localization were observed following ionizing radiation. In addition, MCF7 cells expressing GFP-tagged Translin were subjected to 2, 4 and 8 Gy irradiation, followed by assessment of cellular viability and long-term survival using MTT and clonogenic assays. Radiation exposure resulted in dose-dependent changes in cellular survival. Collectively, these findings integrate mutation-associated structural dynamics with biochemical characterization. Cellular radiation responses, providing insights into the potential involvement of Translin in cellular adaptation to genotoxic stress. This study established a basis for further investigation of its role in DNA damage response pathways.

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PP-52

Expression, purification and biophysical characterization of human SHMT1 and SHMT2 isoforms as anticancer targets

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Cancer cells, characterized by their uncontrolled proliferation, undergo significant metabolic reprogramming to sustain their rapid growth and division. This metabolic rewiring often involves an increased dependence on one-carbon metabolism to meet the heightened demands for nucleotide synthesis, amino acid production, and maintenance of redox balance. Serine hydroxylmethyl transferases (SHMTs), key enzymes of one carbon metabolism, play a crucial role in supplying one-carbon units, which is critical for tumour growth and survival, making SHMTs promising targets for anticancer drug discovery. The present study aims to establish a structural biology-driven approach to investigate potential inhibitors targeting both cytosolic (SHMT1) and mitochondrial (SHMT2) isoforms for cancer therapeutics. As an initial step, genes encoding human SHMT1 and SHMT2 were cloned into the pET28A expression vector and transformed into *Escherichia coli* DH5α for plasmid propagation, followed by expression in *E. coli* BL21(DE3). Recombinant proteins were expressed and purified using Ni-NTA affinity chromatography. Expression and purification conditions were systematically optimized by varying induction temperature, IPTG concentration, and buffer composition to obtain proteins suitable for biochemical, biophysical, and structural studies. Purified proteins were characterized using circular dichroism (CD), differential scanning fluorimetry (DSF), dynamic light scattering (DLS), and size-exclusion chromatography to assess secondary structure, thermal stability, homogeneity, and oligomeric state, respectively. The effect of the PLP cofactor on protein stability was also investigated. Crystallization trials for both isoforms are currently underway. Details will be presented.

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PP-53

Structure–function analysis of polyethylene-degrading enzymes: Insights from kinetics, docking and molecular dynamics

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Accumulation of commonly used plastics, polyethylene(PE) and PET, generate 350 (western countries) and 30 (India) gms/person/day of recalcitrant wastes, which poses a severe global environmental challenge (1). The discovery an insect-derived arylphorin-like enzyme, Demetra, has opened promising avenues for the enzymatic degradation of non-hydrolyzable PE (2). However, its mechanism of action and scalable production is needed for technological translation. Here, we report successful gene cloning in pET vector, heterologous expression of Demetra in *Escherichia coli* and its biophysical characterization. Recombinant Demetra was expressed in the soluble fraction after several optimizations, and purified via two-step purification combining Ni-NTA immobilized metal affinity chromatography with size exclusion chromatography (SEC). SEC profiles confirmed a monodisperse enzyme preparation, effectively removing trace contaminants and high-molecular-weight aggregates. Analysis by SDS-PAGE verified high purity and the monomeric mass of ~76 KDa was confirmed by ESI-MS. The structural integrity of purified Demetra in solution was probed using circular dichroism (CD). The optimum pH and temperature were determined for PE degradation assays and protein crystallization. Demetra is stable within 50-55°C. To gain insight into its solution structure and flexibility, Demetra was characterized using Small-Angle X-ray Scattering (SAXS). SAXS data analysis, including radius of gyration (Rg) and dimension (Dmax) from real-space distance distribution function, revealed that Demetra adopts a compact globular shape in solution at room temperature. Together, these results demonstrate an efficient production pipeline for active recombinant Demetra in *E. coli* and establish crucial structural benchmarks in solution.

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PP-54

Structure studies of *Acinetobacter baumannii* FtsA

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Bacterial cell division proteins represent promising targets for the development of novel antibiotics to combat the escalating global threat of antimicrobial resistance (1). The bacterial divisome is nucleated by the tubulin homolog FtsZ, which polymerizes into a membrane-tethered ring through its interaction with the actin-fold protein FtsA(2,3). Disrupting the FtsZ-FtsA interaction effectively inhibits cell propagation, rendering this interface a viable target for structure-guided drug design. In this study, we determined the crystal structure of FtsA from the multidrug-resistant pathogen *Acinetobacter baumannii* (AbFtsA) to a resolution of 1.8 Å using molecular replacement with diffraction data collected at the INDUS-2 synchrotron (R-factor/R-free ≈ 19.5/22.8%). Structural comparison revealed that despite sharing only 29.8% sequence identity, AbFtsA superimposes on *Escherichia coli* FtsA with a Root Mean Square Deviation (RMSD) of 1.039 Å across 265 C-alpha atom pairs. This highlights a remarkable conservation of the protein fold across evolutionarily distant species, suggesting broad-spectrum potential for targeting this protein.To further elucidate the interaction mechanism, the 17-residue C-terminal tail of *A. baumannii* FtsZ was docked onto AbFtsA using HADDOCK based on homology-mapped residues. The highest-scoring cluster (Z-score: −1.7; HADDOCK score: −65.9 ± 8.8) revealed a buried interface area of 1181.7 ± 64.0 Å², driven largely by electrostatic interactions (−241.0 ± 17.6 kcal/mol). These results confirm a conserved FtsA-FtsZ recognition mode in *A. baumannii*. Together, these findings provide a comprehensive structural template for the FtsZ-FtsA interface, establishing a critical foundation for the structure-guided screening and design of novel broad-spectrum inhibitors to disrupt bacterial cell division.

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PP-55

Surfactant based fluorogenic dye assembly enables detection of cancer biomarker in 100% urine matrix

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This study presents a promising approach for the detection of a cancer biomarker (spermine, Sp), utilizing fluorescence signal amplification from a red emitting dye, quinaldine red (QR) in combination with a negatively charged surfactant, sodium dodecyl sulfate (SDS). The QR–SDS assembly itself exhibited very weak fluorescence; however, with the introduction of spermine, the assembly demonstrated a significant magnification in its fluorescence intensity, offering an effective "turn-on" fluorescence response towards spermine. This fluorescence magnification has been ascribed to the formation of a ternary assembly (QR–SDS–Sp), where spermine encouraged self-assembly of SDS, facilitating efficient hydrophobic interactions between dye and SDS. Consequently, there was a large magnification in fluorescence intensity, which enabled detection of Sp with a remarkably low limit of detection (LOD) of 65 nM in buffer and 1.35 μM in 100% urine matrix, highlighting high sensitivity of the probe even in complex biological environments. This strategy offers a simple, fast, cost-effective, and highly reliable technique for real-world applications, including clinical diagnostics. Given the crucial role of spermine as a biomarker in various pathological conditions including cancer, this fluorescence-based detection method holds significant potential for the early diagnosis and monitoring of life-threatening diseases in 100% urine matrix.

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PP-56

Gut microbiome profile of immunotherapy receiving lung cancer patients.

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Immune checkpoint inhibitors have significantly improved clinical outcomes in advanced non-small cell lung cancer. However, response rates remain heterogeneous, and reliable predictive biomarkers are still needed. While the gut microbiome has emerged as a key modulator of systemic antitumor immunity, population-specific compositional and functional signatures, particularly within underrepresented Indian cohorts, remain largely uncharacterized. We collected faecal samples from non-small cell lung cancer patients undergoing a combination of chemotherapy and immunotherapy treatment before therapy initiation and sequenced via high-throughput shotgun metagenomic sequencing. We stratified patients into responders and non-responders according to RECIST 1.1 criteria. Bioinformatic and statistical analyses were performed to evaluate composition, alpha & beta diversity, and differential taxonomic abundance of gut microbial flora. Analysis of faecal microbiome profile of patients at baseline exhibited distinct community clustering. Taxonomic profiling displayed marked enrichment of known short-chain fatty acids producing commensals featuring members of *Lachnospiraceae*, and *Agathobacter rectalis* in patients showing favourable clinical responses. Elevated levels of *Veillonellaceae, Pseudomonadota* and *Dialister succinatiphilus* in non-responders may demonstrate dysbiosis, characterised by a depletion of beneficial obligate anaerobes and a pronounced overabundance of opportunistic, pro-inflammatory pathogenic taxa. Differential abundance analysis identified significantly upregulated levels of *Phascolarctobacterium faecium* and *Phascolarctobacterium succinatutens* in responders, and *Cronobacter malonaticus, Kosakonias sp. and Enterobacter oligotrophicus* in non-responders, reflecting species-level discriminators between response phenotypes. Our findings delineate distinct baseline gut microbial signatures associated with ICI efficacy in Indian lung cancer patients. Expansion of facultative pathobionts suggests a dysbiosis-driven resistance that undermines therapeutic response. Given that this study is limited by sample size, a further expanded study with more samples is warranted to establish the potential translational utility.

PP-57

Functional organic molecule-based neuroprotection against paraquat-induced parkinsonian phenotypes in *Drosophila melanogaster*: therapeutic potential of ambroxol and citicoline

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Paraquat (PQ), a redox-cycling herbicide structurally analogous to MPP^+, induces dopaminergic neuronal damage through oxidative stress, mitochondrial impairment and reproduces several pathological features of sporadic Parkinson's disease (PD). The present study investigated the neuroprotective and therapeutic potential of Ambroxol and Citicoline, individually and in combination, against PQ-induced Parkinsonian phenotypes in Drosophila melanogaster. Wild-type Canton S flies of both sexes were exposed to PQ and subsequently treated with Ambroxol, Citicoline, or two combination regimens comprising lower and higher doses of both agents. Survival, locomotor performance assessed by negative geotaxis, olfactory cognition evaluated using the T-maze preference index, biochemical parameters including reduced glutathione (GSH), lipid peroxidation (MDA), superoxide dismutase (SOD), catalase, and dopamine, along with RT-qPCR analysis of GBA1b and SIRT1 expression, were evaluated. PQ exposure resulted in significant locomotor impairment, olfactory dysfunction, oxidative stress, dopamine depletion, and downregulation of GBA1b and SIRT1. Ambroxol preferentially improved GBA1b expression and antioxidant enzyme activities, whereas Citicoline primarily reduced lipid peroxidation and restored SIRT1 expression. Notably, combined treatment produced the most pronounced neuroprotective effects, with greater recovery of locomotor and olfactory performance, dopamine levels, antioxidant defense, and expression of both target genes. Overall, these findings highlight the therapeutic potential of Ambroxol and Citicoline as functional organic molecules for mitigating PQ-induced Parkinsonian phenotypes and suggest that their complementary actions on lysosomal and mitochondrial pathways may provide a promising strategy for neuroprotection in PD.

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PP-58

Dioxazolium desferrioxamine as a cell permeant chelator of intracellular labile iron

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Iron overload has been associated with several types of cancer, and needs immediate treatment via iron chelation. Desferrioxamine (DFO, **1**) is a clinically used iron chelator, but its high hydrophilicity and molecular size restrict cellular uptake and limit its ability to remove intracellular labile iron. In this study, a dioxazolium masking strategy was developed to improve the cell permeability of DFO while retaining its iron-chelating activity. One hydroxamate group of DFO was masked as a dioxazole[1] to generate Dioxazolium-DFO prochelator (PC, compound **2**), resulting in a substantial reduction in hydrophilicity and a predicted improvement in membrane permeability. The masked chelator underwent selective deprotection in the presence of Fe^{2+}/ Fe^{3+}, regenerating the hydroxamate group and producing the hexadentate Fe–DFO complex. Compound **2** retained antioxidant and iron-binding properties comparable to DFO and showed reduced cytotoxicity in U2-OS cells. Compound **2** was also able to protect iron overloaded cells from iron-toxicity in a better way than DFO. Importantly, fluorescence imaging using the in-house prepared BODIPY-TEMPO probe[2] demonstrated that Dioxazolium-DFO removed intracellular labile Fe^{2+} more effectively than DFO in iron-overloaded cells. Overall, these findings established dioxazolium masking as a promising prochelator strategy for converting poorly cell-permeable hydroxamate chelators into iron-responsive, cell-permeable agents with enhanced intracellular labile iron chelation.

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PP-59

Organocatalyzed deuteration of enones/ketones and pharmaceutical drugs

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Deuterium labeling of organic molecules has garnered attention from synthetic chemists to medicinal chemists due to the myriad applications of the deuterium-labeled molecules in various research fields.[1] For examples, (i) to understand the mechanistic pathway of the organic reactions,[1] (ii) to elucidate the metabolic pathway of drug molecules,[1] (iii) synthesis of organic OLEDs,[1] (iv) in the synthesis of heavy drug molecules,[1] etc. Due to the said applications, there is stark increase in the development of methods for deuterium labelling of organic molecules/building blocks. Enones/ketones are not only important motifs present in many naturally occurring molecules, pharmaceuticals, and flavoring products but also versatile building blocks in the synthesis of complex molecules including, natural products and drugs.[2] Despite their vast applications, the synthetic methods for the deuteration of enones are limited in literature. Controlled regioselective deuteration of enones poses significant challenges due to the presence of multiple reactive site. On the other hand, there are few reports on deuteration of ketones under orgnocatalytic conditions. Herein, we present highly regioselective deuteration of enones at either the α'-position or at both the α-and α′-positions and deuteration of ketones using D_2O as an environmentally friendly deuterium source by amine based organocatalysts[3]. Moreover, the method has been successfully applied to the late-stage deuteration of enones/ketons derived from drugs and natural products.

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PP-60

α-Amination at BODIPY core via metal-free regiospecific cross dehydrogenative coupling reaction toward the development of Lysotracker

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Lysosomes are membrane-bound organelles that serve as the "digestive system" of the cell, playing a crucial role in the degradation, recycling, and removal of cellular components to maintain cellular homeostasis. Lysosomes are dense cellular organelles due to their high concentration of digestive enzymes and other proteins. Higher acidity in the interior of lysosomes also contributes to their density. Considering those, the development of lysosome-targeted fluorescent probes is therefore of significant importance for investigating lysosomal function and monitoring its dynamic chemical microenvironment. Such probes provide valuable tools for the early diagnosis, real-time monitoring, and therapeutic investigation of diseases associated with lysosomal dysfunction, including cancer and neurodegenerative disorders. We know BODIPY is emerging fluorescence candidates for therapeutic as well as theranostic applications. Morpholine is well known lysosome targeting moiety. Attachment of morpholine with BODIPY core is big challenge for development of Lysosome targeting BODIPY probe. Thus, a metal free, efficient and quick cross dehydrogenative coupling (CDC) methodology was developed using PIDA as an oxidant to synthesize regiospecific α -amino BODIPYs. Apart from morpholino-BODIPY several coupled products were synthesized using different primary/secondary amines and commercial drug molecules. As anticipated, both 3b and 3t exhibited strong lysosomal affinity. Compound 3t displayed robust green florescence localized within lysosomes, as evidenced by the significant spatial overlap, high Pearson's correlation coefficient (R = 0.76), and notable correlation scatter diagram with LysoTracker Red in the merged images. These findings underscore the excellent lysosomal targeting efficiency of 3t, rendering it a promising candidate for applications in probing lysosomal dynamics, including pH monitoring and homeostasis under both physiological and pathological conditions.

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PP-61

Development of fluorometric dosimeter for low dose gamma radiation

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Gamma (γ) radiation is widely used in food, blood, and sludge irradiation, as well as in radiodiagnosis and radiotherapy.[1,2]Accurate γ-dose measurement is essential for ensuring safety and controlling irradiation processes; however, conventional dosimeters can be expensive and have practical limitations. Fluorescence-based sensors offer high sensitivity, selectivity, and low-cost operation, but their application in γ-dosimetry remains relatively unexplored. In this work, a BODIPY–Leucomalachite Green (BLMG) dye was developed as a highly sensitive low-dose γ-dosimeter. BLMG was synthesized through a multistep process involving the preparation of leucomalachite green aldehyde, followed by condensation with pyrrole, DDQ oxidation, and $BF_3 \cdot OEt_2$ complexation. In $CHCl_3$, BLMG exhibited absorption maxima at 263 and 501 nm with weak fluorescence at 524 nm. Upon γ-irradiation, the 263 nm absorption decreased, while a new band at 638 nm appeared, accompanied by enhanced fluorescence at 524 nm. A linear fluorescence response was observed from 0–11 Gy, with a detection limit of 0.006 Gy. The solution changed from yellow to green and from nonfluorescent to green fluorescent. By varying BLMG concentration, the dynamic range could be tuned to 0–25 Gy (40 μM) and 5–45 Gy (80 μM), making the latter suitable for blood irradiation. To overcome limitations of solution-based dosimeters, a solid-supported BLMG dosimeter was developed using superporous hydrophobic polyHEMA grafted with GMA through γ-radiation-assisted grafting. BLMG-loaded SPH showed a light-yellow-to-green color change and blue-to-green fluorescence over 0–50 Gy. RGB analysis demonstrated linear green fluorescence enhancement and blue fluorescence reduction between 5–45 Gy, indicating its potential as an accurate, user-friendly, and commercially viable dosimeter for low-dose γ-radiation monitoring, particularly in blood irradiation.

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PP-62

Development of BODIPY based fluorometric dosimeter for low dose gamma radiation

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Gamma radiation is ionising radiation which is hazardous to life, in spite of that it finds many useful applications in various fields e.g. disinfections of medical accessories, irradiation of blood, food and sludge as well as cancer diagnosis and therapy. Various available γ-detectors are either costly or have their own drawbacks which restrict their uses. Highly sensitive γ-dosimeter is essential for accurate measurement of γ-dose received by human tissue and the material exposed. Fluorescence based sensors are highly sensitive, but underexplored for γ-radiation. Hence the aim was to develop a fluorescence-based dosimeter for low dose γ-radiation. Thereby substituted BODIPY based dyes we synthesized and were exposed to γ-radiation (0-300 Gy) in $CHCl_3$. The radiolytic degradation of these dyes was evaluated by monitoring changes in the fluorescence intensities of post irradiated samples. PM-567 showed promising results and its potential as a dosimeter was further evaluated. The dye concentration of 12.57μM in $CHCl_3$ followed linear relationship with increase in gamma dose upto 35 Gy, also the dynamic range of this dosimeter can be changed by changing the concentration of dye. Mechanistic study revealed that the radiolytic degradation is due to interaction of PM-567 with the radicals formed due to radiolysis of $CHCl_3$ during irradiation. Also, PM-567 loaded superporouspoly (HEMA) (SPH) beads demonstrated potential as a simple visual fluorometric indicator for monitoring gamma irradiation in the dose range of 25–50 Gy. Highly sensitive liquid dosimeter and solid fluorometric visual indicator for low dose range have been developed, which can find application in blood irradiation.

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PP-63

AI-guided dynamic modelling of the tumor ecosystem for next-generation precision oncology

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The tumor microenvironment (TME) is a dynamic, multiscale ecosystem in which malignant, immune, stromal, vascular, and metabolic compartments interact through spatially and temporally evolving regulatory networks. Static biomarker-centric approaches incompletely capture these emergent states, constraining mechanistic resolution of tumor evolution, immune plasticity, therapeutic response, and resistance. This study establishes an AI-guided computational systems oncology framework to reconstruct and model the dynamic tumor ecosystem states from multimodal biological information. The framework integrates single-cell and spatial multi-omics, digital pathology, molecular profiles, cellular communication networks, and immune-metabolic features through network biology and explainable machine-learning strategies. Multimodal data fusion enables identification of latent ecosystem states, reconstruction of intercellular regulatory circuits, characterization of immune-metabolic vulnerabilities, and mapping of adaptive immune-state transitions associated with therapeutic sensitivity and resistance. By shifting precision oncology from static molecular biomarkers toward dynamic ecosystem-state modelling, the framework provides a quantitative basis for the patient stratification, biomarker and therapeutic-target prioritization, response prediction, and rational optimization of immunotherapeutic strategies. Explainable AI further facilitates mechanistically interpretable links between computationally inferred network states and actionable biological hypotheses. Integration of longitudinal clinical data, spatially resolved biology, functional perturbation datasets, and interpretable AI could enable adaptive modelling of tumor evolution and immune-state plasticity, accelerating translational discovery and supporting biologically informed, clinically actionable precision oncology. Such integration may also reveal context-dependent vulnerabilities that remain obscured within conventional single-marker analyses and provide a principled basis for updating therapeutic hypotheses as tumor ecosystems evolve.

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PP-64

Distinct fragmentation profiles and conserved terminal motifs in extracellular cell-free DNA in lung cancer

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Circulating cell- DNA (cfDNA) fragmentomics is currently being studied as a promising approach to manage cancer without invasive procedures. Understanding the fragmentation patterns of extracellular DNA and how it changes in cancer is an important area of research. This study investigated the fragmentation patterns of cfDNA in different lung cell lines to check for differences in fragment length distribution and end-sequence motifs. Our results show consistent differences in cfDNA yield and fragment length across the tested cell lines. Specifically, lung cancer cells such as A549 and H460 released significantly higher amounts of cfDNA that were heavily enriched for shorter, mono-nucleosomal fragments. In contrast, normal cell line exhibited greater overall cfDNA integrity, showing a prominent abundance of longer di- and tri-nucleosomal fragments. Despite these clear variations in fragment length of cfDNA, terminal four-base motif profiles showed remarkable consistency across all groups. The DNA fragments displayed a universally strong preference for AT- and CT-rich ends, when compared against standard genomic references. Rigorous validation steps were performed, including sequencing depth normalization, genomic background comparisons, and cross-platform sequencing evaluations, to confirm that these terminal motif patterns are reliable and robust. Together, these findings indicate that while overall fragment lengths and yields vary depending on the specific cell line, terminal sequence motifs remain highly conserved, highlighting their strong potential as stable biomarkers for future liquid biopsy applications.

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PP-65

Understanding epigenetic mechanisms governing acquired radiation resistance in lung cancer cells

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Radio-resistance is a significant barrier to effective radiotherapy in lung cancers. Understanding the epigenetic mechanisms involved in determining the radiation resistance can help in devising novel strategies to restore radio-sensitivity in these cancer cells. In this study, a radioresistant (RR) subline of A549 lung adenocarcinoma was established that showed enhanced survival ability as compared parental cells (PT) against radiation. Further studies involving immunofluorescence assays, reporter plasmid analyses and qPCR demonstrated increased DNA repair by RR cells through upregulation of homologous recombination repair pathway. These RR cells also showed strong resistance to ferroptosis through upregulation of xCT proteins leading to the higher GSH synthesis and antioxidant response. To investigate epigenetic reprogramming contributing to radio-resistance, we performed CUT & Tag-seq for key histone modifications. H3K27ac enrichment data revealed genome wide epigenetic remodeling of many regions that are involved in antioxidant defense and DNA repair mechanisms. Motif enrichment analysis on the RR-enriched H3K27ac peaks revealed enrichment of binding motifs for specific transcription factors, notably TEAD1, within RR cells specific active regions. We also mapped enhancer elements across the genome based on the H3K27ac & H3K4me1 overlapping and ranked them based on differential activity between PT and RR cells and subset of enhancers that were poised in PT cells but became activated in RR cells. These findings showed the role of efficient DNA repair and ferroptosis resistance in acquired radiation resistance, and the epigenetic remodeling that could be mediating this resistance.

PP-66

Low-pass long read sequencing for detection of lung cancer using peripheral blood samples

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DNA methylation patterns are frequently altered in cancer with aberrant methylation changes often occurring in early stages of carcinogenesis and exhibiting cancer type specific profiles. Therefore, they can be used as a potential diagnostic biomarker for cancer detection and classification. However, current methods measuring global methylation patterns are limited by their relative lengthy processing time, high cost and less accuracy. Various studies have shown the utility of long read sequencing for characterization of genome-wide methylation patterns, tumor methylation classification, and plasma cfDNA based cancer detection, proving valuable method for molecular profiling of tumor. However, considerably less work evaluating whether nanopore sequencing of genomic DNA isolated directly from peripheral blood can discriminate cancer patients from non-cancer individuals using an integrated molecular signature. Low-pass nanopore sequencing offers a fast, rapid and cost-effective alternative approach that uses long-read technology at a minimal sequencing depth providing insights into epigenetic signatures. In this study, we evaluated the feasibility of low-pass nanopore sequencing for distinguishing cancer patients from healthy individuals based on genome-wide DNA methylation patterns. Peripheral blood samples from 4 healthy individuals and 4 lung cancer patients were collected followed by isolation of genomic DNA (from low input volume of 200 uL), nanopore library preparation and low-pass whole-genome long-read sequencing. Despite the low coverage, analysis of differentially methylated regions (DMRs) revealed distinct methylation profiles between the two groups. The principal component analysis (PCA) based on DMRs demonstrated clear separation of healthy and lung cancer samples into distinct clusters. This distinct clustering highlights the potential of low-pass nanopore sequencing as a fast and cost-effective approach for integrated genomic and epigenomic profiling of cancer.

PP-67

Mangrove-derived phytochemicals as potential anticancer agents: Cytotoxic and metabolomic investigations

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Mangroves are a rich source of bioactive phytochemicals having substantial pharmacological potential, especially for cancer treatment. While several mangrove species have been investigated for their therapeutic properties, many members of the Rhizophoraceae family remain relatively unexplored. This study investigates the anticancer activities, antimigratory potential, and phytochemical constituents of methanolic leaf extracts from *Rhizophora mucronata*, *Rhizophora apiculata*, *Bruguiera gymnorhiza*, *Bruguiera cylindrica*, *Kandelia candel*, and *Ceriops tagal*, representing four genera of the Rhizophoraceae family. The cytotoxic potential of the extracts was assessed against A549, AW 13516, and HeLa cell lines using the MTT assay, and the associated anti-migratory properties were monitored using the scratch wound healing assay. Toxicity against the HaCaT cell line was also performed to assess the selectivity of the extracts. Additionally, Orbitrap-LC-HRMS was used for the metabolite profiling of the extracts. Among the species studied, *B. cylindrica* exhibited the most prominent anticancer activity, with IC_{50} levels of 323.965 ± 1.417 µg/mL, 287.062 ± 1.127 µg/mL and 25.942 ± 2.048 µg/mL against A549, AW 13516, and HeLa cells respectively. Importantly, no cytotoxicity was observed against HaCaT cells, indicating selective anticancer activity. In addition, the results of the scratch wound healing assay on A549 cells underscored the anti-migratory potential of mangrove-derived extracts. LC-HRMS analysis showed the presence of 107 metabolites. Compounds with well-documented anticancer properties, such as chlorogenic acid, esculetin, phloroglucinol, caffeic acid, rutin, quercetin, naringenin, kaempferol, nobiletin, and luteolin, were detected. Our study lays down a groundwork for *B. cylindrica* as a promising candidate for exploring mangrove-derived bioactive compounds as potential oncological drugs, having combined cytotoxic and anti-migratory effects.

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PP-68

Harnessing LSPR-active CuS nanostructures for NIR-triggered doxorubicin delivery and tumor ablation

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Photothermal therapy (PTT) has received considerable attention as a minimally invasive cancer treatment owing to its low systemic toxicity, high spatial precision and selectivity. The integration of PTT with chemotherapy has emerged as a promising multimodal therapeutic strategy [1]. For effective chemo-PTT, photothermal agents (PTAs) should possess good biocompatibility, colloidal stability and suitable surface functionalities for therapeutic drug loading. In this study, water-dispersible, surface-functionalized CuS nanostructures (NSs) were developed using biocompatible ligands, including polyphosphates and amino acids, as surface-passivating agents. These ligands enhanced the long-term colloidal stability of the CuS NSs while facilitating stabilization of the desired crystallographic phase. The formation of nanocrystalline CuS was confirmed by XRD and TEM analysis, while successful surface functionalization was established through XPS, FTIR, DLS and zeta-potential measurements. Photothermal studies under 980 nm NIR irradiation demonstrated concentration and laser power dependent heating with excellent photostability, attributed to the localized surface plasmon resonance (LSPR) properties of CuS. The negatively charged CuS NSs enabled efficient loading of positively charged doxorubicin hydrochloride (DOX), with maximum loading observed at a drug-to-particle ratio of 1:10. The DOX-loaded system exhibited pH-responsive drug release. *In vitro* studies revealed dose-dependent cytotoxicity, which was significantly enhanced under NIR irradiation. Confocal microscopy confirmed efficient cellular internalization and localization of the DOX-loaded NSs in both the cytoplasm and nucleus. Furthermore, *in vivo* studies demonstrated efficient tumor ablation through the synergistic chemo-photothermal effect of DOX-loaded CuS NSs under NIR irradiation.

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PP-69

Development of surface functionalized carbon dots for cellular imaging

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Bioimaging is an indispensable tool in medical and biological research. Nanomaterials have received significant attention in cancer diagnostics and therapy [1,2]. However, many conventional nanomaterials face drawbacks such as high synthesis costs, poor biocompatibility, and long-term toxicity. Recently, carbon dots (CDs) have attracted growing interest for cancer diagnostics and therapy due to their unique physico-chemical characteristics, tunable optical properties, high drug loading and biocompatibility nature. In this aspect, amino acid derived CDs were developed by a modified hydrothermal method using malic acid and arginine as carbon sources. The successful formation of well-spherical nanostructured CDs of sizes about 5 nm was evident from XRD and TEM analysis. The appearance of $n \rightarrow \pi^*$ and $\pi \rightarrow \pi^*$ transitions in UV-Vis absorption spectrum further supported the formation of CDs. FTIR spectrum confirmed the presence of various functional groups on the surface of CDs. Dynamic light scattering (DLS) studies suggested good aqueous colloidal stability of developed CDs, which essential for biomedical applications. Further, these CDs exhibited both excitation and pH dependent tunable fluorescence properties. From MTT assay, it has been observed that the cell viability is more than 90% even after 24 h incubation with 75 µg/ml of CDs suggesting their good bicomapatibility nature. Furthermore, these CDs also showed good hemocompatibility (hemolysis < 10%). Thus, the developed CDs may serve as potential candidates for cellular imaging.

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PP-70

Investigation of *Terminalia bellirica* and nanocomposites-including antioxidant action

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Preparations based on Ayurveda and herbal origin are getting more into mainstream as they lead to very little or zero side effects. For the past almost five decades, herbal solution was dominantly used. Of late, it has become the most sought-after medical approach. It is very often the first attempted protocol and other fields like allopathy are only subsequently tried. It is worth mentioning that multiple formulations of plant products are being used as dietary supplements to avoid occurrence and relapse of numerous pathological conditions. One such preparation of *Terminalia bellirica* is the matter of investigation in this study. Combined protocols using plant based and chemical based preparation are being put to use. The study aims to find advantages over earlier methods. This is particularly of great application in diseases arising from excess uncontrolled and unwanted oxidations. These affect the microenvironment and membrane potentials of sub-cellular compartments especially the mitochondria. The superoxide dismutase enzymes and endogenous molecules are the first ones to be affected and recruited. Their levels and effective functioning determine the overall oxidative status of not only the cell but also the sub-cellular compartments. Results based on gamma radiation induced oxidative damages are included in this report. These findings can be put to use not only for clinical applications but also in cosmetic, commercial and industrial applications.

PP-71

HDACi-responsive genes associated with radioresistance in triple-negative breast cancer

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Triple-negative breast cancer (TNBC) is an aggressive breast cancer subtype having limited targeted therapeutic options, with radioresistance posing a major challenge. We integrated publicly available transcriptomic and epigenomic datasets to identify genes affected by the histone deacetylase inhibitor (HDACi) suberoylanilide hydroxamic acid (SAHA) and assess their association with radioresistance in TNBC cells. Four independent datasets were analysed to screen differentially expressed genes in SAHA-treated TNBC cells. The volcano plots, heatmaps, and pathway analysis were used to examine the biological processes enriched upon SAHA treatment. In order to identify SAHA-responsive genes associated with TNBC radioresistance, the resultant differentially expressed genes were compared with a published transcriptomic dataset of radiosensitive and radioresistant TNBC cells. The candidates showing downregulation in radioresistant cells but increased expression upon SAHA treatment were further evaluated by Kaplan-Meier survival analysis for their association with patient outcome. For experimental validation, a radioresistant (RR) TNBC cell model was generated using fractionated irradiation to a cumulative dose of 40 Gy. The effectiveness of SAHA treatment in RR cells was assessed by cell viability and cell-cycle distribution assays. Additionally, the expression of selected candidate genes, MAPT, ACADSB, and PARM1, and the H3K27ac enrichment in their promoter region upon SAHA treatment were validated by RT-qPCR and publicly available ChIP-seq datasets, respectively. Among others, MAPT showed a consistent response to SAHA and was associated with H3K27ac enrichment in TNBC cells. These results support further investigation of HDAC inhibition as a promising approach to modulate radioresistance in TNBC.

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PP-72

From photon resistance to proton sensitivity: Targeting Nrf2 in lung adenocarcinoma

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A subset of non-small cell lung cancers (NSCLC) harboring constitutive NRF2 activation exhibits poor therapeutic outcomes following conventional photon radiotherapy[1]. However, whether NRF2 activation similarly influences the response of NSCLC to proton beam therapy remains poorly understood. Here, we investigated the radiation response of KEAP1-mutant, NRF2-overexpressing A549 cells and isogenic NRF2-knockout (NRF2-KO) A549 cells following photon and proton irradiation. Corroborating with our earlier findings about the role of NRF2 in radioresistance[2], NRF2-KO cells exhibited greater sensitivity to photon (γ) irradiation than parental A549 cells. Interestingly, NRF2-overexpressing A549 cells exhibited significantly greater loss of viability following proton beam irradiation (70–120 MeV; IBA, Belgium) compared with an equivalent physical dose of photon irradiation. We subsequently evaluated pharmacological targeting of NRF2 as a strategy to enhance radiation response. Although the previously identified NRF2-modulating glucocorticoid clobetasol propionate (CP) sensitized NRF2-overexpressing NSCLC cells to photon irradiation[3], this effect was not observed following proton irradiation. However, pharmacological inhibition of NRF2 using a more specific inhibitor significantly enhanced proton-induced cytotoxicity in NSCLC, identifying NRF2 as a potentially actionable vulnerability during proton therapy. These findings demonstrate a differential, NRF2-dependent response of NSCLC to photon and proton irradiation and provide preclinical evidence that pharmacological NRF2 inhibition may enhance the efficacy of proton beam therapy in NRF2-driven, therapy-resistant NSCLC. To our knowledge, this is the first study to demonstrate that NRF2-overexpressing lung adenocarcinoma are preferentially sensitive to proton beam irradiation compared with an equivalent dose of photon irradiation, revealing a previously unrecognized therapeutic vulnerability associated with NRF2 activation.

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PP-73

Exploiting non-apoptotic cell death pathways via Shikonin and Rapamycin combination for advanced triple-negative breast cancer therapy

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Triple-negative breast cancer (TNBC) because of its highly invasive and metastatic nature and limited therapy options, continues to pose a serious clinical challenge. A potential approach to maximize cytotoxicity while limiting off-target damage is the use of drug combination techniques. This study investigates the mode of cell death and anti-cancer efficacy of a combination of Shikonin (Shk) and Rapamycin (Rapa) in TNBC cells. The effective combination dosages were determined using a graded concentration matrix via cell viability studies. Compared to the individual drugs, the drug combination resulted in a noticeably higher loss of cell viability and migratory capability. The decrease in viability was confirmed by flow cytometry-based cell death and cell cycle analysis, which also showed no phase-specific cell-cycle arrest. Western blot analysis indicated impaired autophagic flux impairment. The resulting cell death was subsequently verified to be a caspase-independent autophagic catastrophe. In order to advance cancer treatments, this study reveals the use of small compounds in combination as a potential strategy that exploits non-apoptotic cell death pathways to suppress aggressive and invasive TNBC.

PP-74

Reversing Taxol resistance in triple-negative breast cancer through bioengineered gold nanoparticle-mediated sensitization

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One of the biggest obstacles to the clinical management of triple-negative breast cancer (TNBC) is chemoresistance, which highlights the critical need for innovative treatment approaches that go past drug resistance. One of the ways to tackle chemoresistance is using compounds which can reverse resistance. This work examines the chemosensitizing ability and mechanism of surface-bioengineered gold nanoparticles, synthesized using green synthesis method made with phytochemicals from *Withania somnifera* (Ashwagandha) [A-GNPs] and characterised using various biophysical techniques like Energy-dispersive X-ray (EDX) spectroscopy, dynamic light scattering (DLS), transmission electron microscopy (TEM) and Fourier-transform infrared (FTIR) spectroscopy etc. against chemoresistant cancer cells. A highly Taxol-resistant subtype of MDA-MB-231 cells (CR) was developed via repeated exposure to Taxol and validated using cell viability, clonogenicity and migration assays, cell death studies, and evaluation of drug efflux-associated protein (MDR1) expression. The resistance was validated by a ~12-fold rise in the IC50 value (14±2nM to 180±2nM), prolonged clonogenic and migratory potential, and increased expression of multidrug resistance protein 1 (MDR1) in comparison to sensitive cells. Further, sensitization assay revealed significant sensitivity recovery (180±2 nM to 12±2 nM) of the CR cells after being pretreated with a sub-lethal dose of A-GNPs and subsequent exposure to Taxol. This work emphasizes the potential of phytofabricated gold nanoparticles as nanotherapeutics to improve the effectiveness of traditional chemotherapy and overcome therapy resistance.

PP-75

TPP conjugates of eugenol and isoeugenol as potential cancer therapeutics

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Cancer remains a major global health challenge, and the development of selective and effective therapeutic strategies continues to be a significant area of research. Natural plant phenylpropanoids, notably eugenol and isoeugenol, exhibit strong antiproliferative and pro-apoptotic effects in preclinical cancer research. However, their therapeutic application is often limited by poor bioavailability, low cellular uptake, and limited selectivity toward cancer cells. Because of its hydrophobic structure and positive charge, making it a promising pharmacophore for the intracellular delivery of bioactive compounds, triphenylphosphonium (TPP), a lipophilic delocalized cation, is frequently used as a molecular carrier. This study investigates the design and therapeutic potential of TPP conjugates of eugenol and isoeugenol as anticancer agents. Their phenolic functionality was utilised for incorporating a suitable linker, which was then coupled with TPP. The compounds were purified and structurally characterised using analytical and spectroscopic techniques. The synthesised compounds were evaluated for antibacterial activity against Gram-positive (*Staphylococcus aureus* and *Bacillus subtilis*) and Gram-negative bacteria (*Escherichia coli*). To assess their potential as bioactive therapeutic agents, the synthesised compounds were further evaluated for anticancer activity against selected cancer cell lines. The results of the antibacterial and anticancer activity of these compounds will be discussed in the conference poster.

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PP-76

Impact of post-translational modifications on anti-metastatic activity of kisspeptins

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Metastasis accounts for most cancer-related mortality and morbidity. Preventing the growth of disseminated tumor cells (DTCs) at secondary sites therefore requires a better understanding of the factors that regulate metastatic progression. Metastasis suppressor genes inhibit metastatic spread without preventing primary tumor formation and can act at multiple stages of the metastatic cascade, from invasion to colonization. Although more than 30 metastasis suppressor genes have been identified, the mechanisms underlying many of their effects remain poorly understood. Defining these mechanisms may reveal new strategies to control metastatic disease and improve patient survival. *KISS1* is a metastasis suppressor that limits metastatic outgrowth by maintaining DTCs in a dormant state at secondary sites. KISS1 encodes a 145-amino-acid protein that is constitutively secreted, and its secretion is essential for its anti-metastatic activity. Following secretion, KISS1 undergoes proteolytic processing by furin and ADAM-family proteases, including MMP-9, to generate kisspeptins (KPs). Several KPs, including KP54 and KP10, signal through the G-protein-coupled receptor KISS1R and can suppress metastasis. However, KISS1 also retains anti-metastatic activity in cells lacking KISS1R, indicating that additional KISS1R-independent mechanisms may contribute to its function. KISS1 processing appears to occur predominantly after secretion, suggesting that its proteolytic cleavage is differently regulated inside and outside the cell. Post-translational modifications such as glycosylation and phosphorylation can alter the accessibility and efficiency of cleavage by furin, related proprotein convertases, and ADAM-family proteases. We therefore hypothesize that site-specific PTMs on KISS1 regulate its susceptibility to proteolytic processing and control the generation of kisspeptins after secretion in the extracellular milieu. Defining this regulatory mechanism may clarify how KISS1 is processed in the extracellular environment and how specific kisspeptins contribute to its anti-metastatic activity.

PP-77

Thermo-responsive gold nanorods for targeted multi-modal therapy of triple-negative breast cancer

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Triple-negative breast cancer (TNBC) is an aggressive breast cancer subtype characterized by high recurrence and metastatic potential but with limited therapeutic options. Nanotechnology-based platforms offer potential for targeted delivery and multi-modal therapy. Amongst the nanoparticles, the gold nanoparticles (AuNPs) are of particular interest due to their tunable localized-surface plasmon resonance at near-infrared (NIR) suitable for photothermal therapy. This study evaluated the photothermal efficacy of spherical AuNPs and gold nanorods (AuNRs) for chemo-radiotherapeutic applications in cancer. Spherical AuNPs and AuNRs were synthesized using modified Turkevich [1] and one-pot method [2], respectively, exhibiting surface plasmon resonance peaks at 520 and 785 nm. Photothermal studies using an 808 nm NIR laser demonstrated superior heating efficacy of AuNRs compared with spherical AuNPs. To functionalize AuNRs with a biocompatible ligand, cytotoxic CTAB was replaced with citrate following a ligand exchange protocol. Fourier-Transform Infrared Spectroscopy showed reduced CTAB-associated CH_2 bands at 2920 and 2850 cm^{-1}, and the presence of citrate carboxylate bands at 1600–1700 and 1400 cm^{-1}. Citrate-functionalized AuNRs were further encapsulated into liposomes using thin-film hydration method [3,4] and characterized by transmission electron microscopy, zeta-potential, dynamic light scattering and UV–visible spectroscopy. Doxorubicin (DOX) was loaded using an active pH-loading approach, achieving 98.99% loading efficiency. Relative to 30 °C, external heating resulted in 36.2% higher DOX release at 40 °C, which was further increased to 48.9% at 45 °C, demonstrating temperature-responsive drug release [4]. The heating ability of nano-formulation and its anti-cancer efficacy in combination with hyperthermia in TNBC cells are being studied.

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PP-78

Diversity-oriented synthesis and study of triazole fused bicyclic iminosugars

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Triazole-fused bicyclic iminosugars were synthesized from D-glucose using intramolecular azide-alkyne cycloaddition (IAAC) as the key step for constructing a tetracyclic, diversity-oriented scaffold. The common scaffold enabled the synthesis of iminosugar analogues incorporating additional nitrogen atoms within the triazole and pyranose rings, thereby expanding the structural diversity of glycosidase inhibitor frameworks. The synthetic strategy incorporated one pot multistep transformations and water as a solvent/co-solvent in key steps, facilitating an efficient and sustainable synthesis. Molecular docking studies identified several compounds with strong predicted interactions with glycosidases, with binding energies of up to −10.1 kcal/mol. Enzymatic evaluation against seven glycosidases identified four triazole-fused bicyclic iminosugars with inhibitory activity (IC_{50} = 0.17–0.54 mM), showing partial agreement with the docking results. Among these, tetracyclic C5-azido compound 13 exhibited significant inhibition of α-glucosidase and α-mannosidase (K_i = 0.08–0.21 mM). Notably, enzyme inhibition did not directly correlate with cytotoxicity, as compounds 17 and 19 displayed selective cytotoxicity against MDA-MB-231, PC3, and WRL68 cells (IC_{50} = 0.13–0.50 mM). These findings suggest distinct biological mechanisms and identify separate lead structures for glycosidase inhibition and anticancer applications.

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PP-79

Methyl gallate functions as a PPA2 inhibitor to suppress mitochondrial fission signaling and trigger apoptosis in oral cancer cells

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Mitochondrial dynamics (a continuous cycle of mitochondrial fission and fusion) and mitophagy are two pivotal processes underlying homeostasis. However, mitochondrial fission is constitutively activated in oral cancer cells and is associated with high-grade malignancy, acquired chemoresistance, and metastatic propensity [1]. MTP18, an inner mitochondrial membrane protein, executes mitochondrial fission and LC3-dependent mitophagy [2]. Earlier, our study reported that PPA2, a mitochondrial pyrophosphatase, acts as an upstream regulator of MTP18 and mitochondrial fission [3] and has been reported to promote cancer growth and proliferation. This study identifies a potent natural compound, methyl gallate (MG), a methyl ester of gallic acid, and explores its role in inhibiting PPA2-associated signaling in mitochondrial fission. MG treatment inhibits PPA2 expression and PPA2 enzymatic activity in oral cancer cells. Interestingly, the drug treatment reduces the expression of mitochondrial fission proteins MTP18 and pDRP1 and increases MFN1 expression, promoting mitochondrial hyperfusion. Moreover, it induces apoptosis by impairing the engulfment of hyperfused mitochondria and mitophagy, thereby increasing ROS production. In addition to mitophagy, MG inhibits autophagy by reducing the expression of ULK1, Beclin1, ATG5, and LC3. PPA2 and MTP18 overexpression further reduces the drug's cytotoxic effect by restoring pDRP1 recruitment and mitochondrial fission. Altogether, this drug inhibits oral cancer proliferation without cytotoxic effects on healthy cells, as validated in an *in vivo* mouse model.

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PP-80

Butein coordinately activates mitophagy and mPTP opening to trigger oral cancer cell death

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Mitochondria are the key players in maintaining cellular health by critically regulating metabolic processes, stress adaptation through cellular survival, and redox balance. They regulate mitochondrial homeostasis through coordinated cycles of fission and fusion, which isolate dysfunctional mitochondria for either repair or clearance via mitophagy[1]. However, excessive stress also leads to their clearance via mitochondrial apoptosis and altered mitochondrial potential. In this study, we explored the mechanistic modulation of these phenomena through an antioxidant therapeutic compound, Butein, a flavonoid phytochemical found in the plant *Butea monosperma*[2]. We found significant upregulation of MTP18 and DRP1, mediating mitochondrial fission, along with an augmentation of the PINK1-PARKIN-dependent mitophagy pathway, as a primary response to initiate mitochondrial quality control. However, prolonged stress triggers the elimination of dysfunctional mitochondria via caspase-dependent increases in apoptosis and cytochrome c release, which are amplified by increased ROS and the opening of the mitochondrial permeability transition pore (mPTP)[3]. This altered the levels of its matrix component Cyclophilin D, with a concomitant decrease of mitochondrial calcium levels. Therefore, Butein orchestrates an intricate time-dependent mechanistic regulation of cell fate that preserves mitochondrial integrity via mitophagy while activating the mitochondrial apoptotic cascade. Thus, this balance was found to be a major driver for restraining oral cancer progression in a compromised environment of mitochondrial health.

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PP-81

Thymol- and carvacrol-based triphenylphosphonium derivatives: Design, synthesis and anticancer potential

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Cancer remains a major therapeutic challenge, creating a continuing need for the development of novel chemical entities with improved anticancer potential. Thymol and carvacrol, naturally occurring monoterpene phenols, possess diverse pharmacological properties, including antimicrobial, antioxidant, anti-inflammatory, antifungal, and anticancer effects. Triphenylphosphonium (TPP), a lipophilic delocalized cation, is widely employed as a molecular carrier because its hydrophobic character and positive charge facilitate cellular uptake and membrane permeation, making it an attractive pharmacophore for the intracellular delivery of bioactive compounds. The present study, thymol- and carvacrol-based TPP derivatives were designed to combine the bioactive phenolic scaffold with a lipophilic cationic pharmacophore. The synthetic approach involved functionalization of the phenolic hydroxyl group, followed by incorporation of TPP, enabling systematic structural modification of the parent scaffolds. The compounds were purified and structurally characterised using suitable analytical and spectroscopic techniques. To explore the biological potential of the synthesized compounds, primary antimicrobial screening was performed against selected Gram-positive and Gram-negative bacterial strains, namely *Staphylococcus aureus*, *Bacillus subtilis*, *Escherichia coli* and *Salmonella typhi*. Selected compounds were further investigated for their effect on extracellular glutathione (GSH) levels in *E. coli* to explore their potential influence on bacterial redox homeostasis. The synthesized compounds were also investigated for their anticancer potentialagainst cancer cell lines, providing an opportunity to assess the biological activity of these multifunctional conjugates across both cancer and bacterial models. Overall, the study demonstrates the potential of thymol- and carvacrol-derived TPP derivatives as multifunctional bioactive compounds and provides a basis for further structural optimization and biological investigation.

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PP-82

Design, synthesis and *in vitro* evaluation of a PSMA-targeted doxorubicin-conjugate

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Prostate specific membrane antigen (PSMA), often referred to as glutamate carboxypeptidase II (GCPII), is the primary focus of clinical treatment for prostate cancer, especially metastatic castration-resistant prostate cancer (mCRPC) [1]. Small molecule drug conjugates (SMDCs), which combine a chemotherapeutic with a PSMA targeting ligand, have become a significant targeted therapeutic tool in this regard [2]. Here, we have created 39 ligands with different targeting heads and linkers, and we have used molecular docking and molecular dynamics simulations to assess their effectiveness *in-silico*. A novel PSMA-Dox conjugate was produced by further synthesizing the best docking molecule and conjugating it with doxorubicin via an acid labile imine linkage. This conjugate was further evaluated *in-vitro* in PSMA-positive (LNCaP and C4-2 cells) and PSMA-negative (PC3 cells) to evaluate its selectivity towards PSMA, as well as to ascertain its selective cytotoxicity towards PSMA-positive cells. Further, cell cycle analysis confirmed the efficacy of the conjugate to induce apoptosis in PSMA-positive cancer cells [3]. Thus, this study demonstrated a new SMDC which can serve as a template for creating new analogs with enhanced targeting and anticancer efficacy.

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PP-83

Synergistic anticancer effect of doxorubicin and *Nyctanthes arbortristis* through ferroptosis induction in breast cancer

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Breast Cancer treatment is often limited by reduced sensitivity to conventional chemotherapy. Alterations in epithelial-mesenchymal transition, oxidative stress, and regulated cell death pathways have been associated with therapeutic resistance. However, the interplay between these processes during chemotherapy sensitization remains poorly understood. Therefore, this study investigated the potential of *Nyctanthes arbor-tristis* to enhance doxorubicin response in Breast cancer cells. MCF-7 cells were treated with *Nyctanthes arbor-tristis*, doxorubicin, either alone or in combination. Epithelial-mesenchymal transition (EMT)-associated cellular behavior, including cellular plasticity and invasiveness, were evaluated. Cell viability, Reactive oxygen species (ROS), clonogenic survival, apoptosis assay, and cell migration were assessed by cellular and fluorescence-based assays. Changes in subcellular localization were quantified using ImageJ. The combination treatment enhanced the cytotoxic response compared with individual treatments. The effect was accompanied by increased cellular stress, ROS generation, and apoptotic changes. The combined treatment also induced ferroptosis-associated and EMT-related cellular responses. Furthermore, it markedly reduced clonogenic survival and impaired the migratory potential of MCF-7 cells. Overall, the findings suggest that the *Nyctanthes arbor-tristis* enhances doxorubicin sensitivity by modulating oxidative stress, ferroptosis-associated responses, and EMT-related processes. These findings support further investigation of natural bioactive compounds as potential chemosensitizing agents in breast cancer.

PP-84

Micronucleophagy contributes to the cisplatin resistance through disposal of unresolved replication-associated DNA lesions

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Cisplatin remains a cornerstone of chemotherapy for several advanced malignancies, including head and neck, ovarian, and neuroblastoma etc. However, treatment failure frequently occurs due to tumor recurrence, metastasis, and the emergence of cisplatin resistance. Cisplatin exerts its cytotoxic effects primarily by forming bulky DNA adducts that interfere with DNA replication and transcription, thereby inducing replication stress and persistent DNA damage. Understanding how cells respond to transient cisplatin exposure is therefore important for identifying mechanisms of resistance and potential therapeutic targets. Most experimental studies investigate cisplatin responses using continuous, high-dose exposure for 24-72 h, which may not adequately reflect clinical drug exposure, where circulating cisplatin concentrations decline following administration and tumor cells experience transient drug exposure. Here, we established an 8-h cisplatin treatment followed by prolonged drug-free recovery to model transient exposure. U2-OS and Cal27 cells were analyzed for cell viability, cell-cycle progression, DNA damage and repair, and autophagy at different recovery time points. DNA damage was assessed by γH2AX and 53BP1 foci, while autophagy was evaluated using LC3 and p62. Transient cisplatin exposure induced substantial cell death, which became evident predominantly after four days of recovery. γH2AX and 53BP1 foci progressively increased for several days after cisplatin removal, indicating persistent DNA damage. Autophagy was also strongly induced following cisplatin treatment and gradually declined during recovery. Notably, inhibition of DNA replication after cisplatin removal markedly reduced cell death and attenuated γH2AX and 53BP1 accumulation. Our finding related to detail mechanism of cross-talk between cisplatin mediated DNA damage and micronucleophagy will be discussed in the conference.

PP-85

Surface functionalized metal-organic framework-based nanoplatform for combined chemo-chemodynamic therapy

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Chemodynamic therapy (CDT), using Fenton-like reaction for ROS generation, is an emerging anticancer approach. Metal-organic frameworks (MOFs), with high metal loading, stimuli-responsiveness, and drug-loading porosity, suit TME-targeted chemo-chemodynamic therapy (CT-CDT). Surface-functionalized, tumor-targeted CT-CDT agents are envisaged to reduce unwanted biodistribution, dosage, and toxicity. Treatment of prostate cancer, relies on its hallmark biomarker PSMA (Prostate Specific Membrane Antigen).[2] Towards targeted CT-CDT of prostate cancer, we designed copper-based metal-organic framework (Cu-MOF) nanoplatform with a free amine functionality, which was conjugated to the PSMA targeting peptide (DCL), and was loaded with chemotherapeutic drug Doxorubicin (29% w/w). Further conjugation with PEG_{2000} yielded the water-soluble nanocomposite Cu-MOF@DCL@Dox@PEG. The nanocomposite was found to release Dox upto 70% within 2 hours of treatment with high GSH conditions. Comprehensive *in vitro* investigations demonstrated that the PSMA-targeted nanocomposite exhibited selective uptake and potent cytotoxicity in PSMA-positive LNCaP prostate cancer cells, while showing minimal toxicity toward PSMA-negative PC-3 cells, other non-prostate cancer cell lines, and normal cells. Competitive binding assays further validated the specificity of PSMA-mediated targeting, and hemolysis studies established excellent hemocompatibility. Collectively, these findings demonstrated the potential of the developed targeted Cu-MOF platform as a safe, selective and effective PSMA-targeted chemo-chemodynamic therapeutic system for prostate cancer treatment. Parallelly, a meta-iodobenzylguanidine (mIBG) analogue was synthesized as a targeting ligand for MOF surface functionalization in neuroblastoma-targeted delivery. A four-step route regioselective iodination, benzylic bromination, nucleophilic substitution, and deprotection afforded the compound in 12% overall yield. Intermediates and product were characterized by FT-IR and NMR. This ligand will enable NET-targeted chemo-chemodynamic therapy.

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PP-86

Molecular design of heavy-atom-free photosensitizers for photodynamic therapy and theranostic imaging of cancer cells

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Heavy-atom-free triplet photosensitizers (PSs) are highly desirable for photodynamic therapy (PDT) because they can generate reactive oxygen species while minimizing the dark toxicity associated with heavy-atom substitution. Herein, we present a molecular design strategy that exhibits structural modifications (Twisted to Orthogonal to Planar conformations), efficient singlet oxygen ($^1O_2$) generation, and organelle targeting to develop efficient heavy-atom-free boron-based photosensitizers for theranostic applications. BODIPY–hetero[5]Helicene (BhH) conjugates were developed by integrating a twisted helicene framework with the BODIPY core, generating non-planar architectures that promote intersystem crossing (ISC), efficient triplet-state formation, and $^1O_2$ production. These dyes exhibited pronounced light-induced cytotoxicity toward cancer cells with minimal dark toxicity. In parallel, an organelle-targeted β-linked BODIPY–naphtholimine–BF_2 (NbB) dye was developed for precision PDT. NbB displayed orthogonal geometry, broad absorption, environment-sensitive dual-colour fluorescence, and efficient $^1O_2$ generation. Its simultaneous localization in the endoplasmic reticulum (ER) and lipid droplets (LDs) enabled enhanced reactive oxygen species production and synergistic phototoxicity against pancreatic ductal adenocarcinoma cells, while facilitating dual-colour intracellular imaging. Building on our earlier studies of indolocarbazole-based boron materials, we further introduced planar indolocarbazole–imine boron (IIB) complex with tunable optical properties. Computational and ultrafast spectroscopic investigations revealed strong spin–orbit coupling between S_1 and T_2 states, facilitating ISC and triplet formation. Remarkably, the complex showed enhanced singlet oxygen generation under light irradiation, leading to significant phototoxicity in cancer cells. Its inherent residual fluorescence additionally facilitated real-time assessment of cellular uptake and intracellular localization. Collectively, these findings establish structural modifications, excited-state engineering, and organelle targeting as complementary strategies for developing heavy-atom-free photosensitizers with combined imaging and PDT capabilities.

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PP-87

Synthesis, structure-activity relationship and biological evaluation of novel malabaricone analogues as potential anti-cancer agents

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Malabricones are naturally occurring polyphenolic diarylnonanoids derived from the edible spice Rampatri (*Myristicamalabarica*). This class of compounds exhibit potent anticancer activity against various cancer cell lines. However, the relationship between their specific structural features and biological potency has not been systematically investigated. To this end, a series of novel malabaricone analogues (ML-1 to 20) were synthesized towards lead optimization and structure-activity relationship (SAR) studies. The target compounds were synthesized via C-alkylation reaction of differently substituted phenyl β-ketoesters with ω-aryl alkyl bromides or alkyl bromides, followed by hydrolysis and subsequent decarboxylation of the ester moiety. All the compounds were evaluated for their anticancer potential against human breast adenocarcinoma cells using MTT and clonogenic assays. Amongst all the analogues, ML-20, devoid of the carbonyl group, was found to be the most potent, displaying a three-fold higher anti-proliferative activity than natural malabaricone-C. ML-20 induced dose-dependent apoptosis, DNA double-strand breaks, loss of mitochondrial membrane potential (MMP), and lysosomal membrane permeabilization (LMP). Furthermore, ML-20 inhibits autophagic flux and can act as a radiosensitizer, highlighting its potential as a promising lead compound for adjuvant cancer therapeutics.

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PP-88

Lysostilbene, a novel lysosomotropic agent, disrupts lysosomal homeostasis and impairs autophagosome-lysosome assembly in cancer

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Pancreatic ductal adenocarcinoma (PDAC) is highly therapy-resistant in part because of its dependence on lysosome-mediated nutrient recycling, metabolic adaptation, and stress tolerance for survival. Clinically explored lysosome-targeting agents such as chloroquine (CQ) and hydroxychloroquine (HCQ) have shown limited efficacy because of transient activity and dose-limiting toxicity. To overcome these limitations, we developed lysostilbenes, hybrid molecules combining the CQ pharmacophore with lysosome-disrupting stilbene analogs derived from the resveratrol scaffold. Among these compounds, lysostilbene-4 exhibited ~30-40-fold greater cytotoxicity against PDAC cells than the parent compounds while sparing nonmalignant cells. At nanomolar concentrations, lysostilbene-4 induced rapid and irreversible lysosomal membrane permeabilization (LMP), triggering cathepsin B (CTSB) release and a lysosome-mitochondria apoptotic cascade involving BID cleavage, BAX activation, and caspase-dependent cell death. Importantly, lysostilbene-4 also compromised lysosomal recovery by impairing lysosomal repair, lysophagy, autophagosome maturation, and TFEB-dependent transcriptional programs required for lysosome biogenesis. Reduced TFEB expression was associated with poorer overall and disease-free survival across cancer cohorts, particularly in pancreatic cancer. Using *TFEB*$^{+/+}$ and *TFEB*$^{-/-}$ PDAC cells, we further demonstrated that TFEB loss enhanced lysostilbene-4 cytotoxicity by promoting persistent lysosomal damage and disrupting autophagosome-lysosome assembly. These findings establish TFEB as a key determinant of lysosomal resilience and a potential predictive biomarker. Importantly, lysostilbene-4 was well tolerated in preclinical mouse models at supra-therapeutic doses without evident systemic toxicity. Collectively, our findings establish lysostilbene-4 as a potent lysosome-targeting agent that couples irreversible lysosomal damage with impaired adaptive recovery, providing a mechanistically precise strategy for targeting lysosomal dependence in PDAC.

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PP-89

Reciprocal tumor–leucocyte crosstalk drives breast cancer EO771 cell migration

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The interplay between tumor cells and macrophages is a critical determinant of tumor progression and metastasis (1,2) but remain poorly understood. In this study, we investigated the reciprocal interaction between EO771 breast cancer cells and leucocytes (macrophages and lymphocytes). The effect of tumor educated leucocytes was studied on tumor cell migration. Tumor-educated leucocyte conditioned media (CM) was generated by treating peritoneal macrophages, splenic macrophage and total spleen cells with EO771 CM. Tumor educated macrophage CM significantly enhanced the migratory potential of EO771 cells, mesenchymal marker vimentin expression compared with untreated controls. These tumors educated peritoneal and splenic macrophages produced high amount of interleukin-6 (IL-6). Furthermore, co-culture of EO771 cells with either peritoneal or splenic macrophages also increased EO771 cell migration and was associated with elevated transforming growth factor-β (TGF-β) levels. Because, adaptive immune cells are important regulators of the tumor microenvironment, we further examined the effects of EO771 TCM on total splenic immune cells. EO771 TCM significantly increased CD69 expression and splenocyte proliferation, indicating activation of splenic immune cells. This activation was IL-2 independent in contrast to mitogen induced activation. Treatment with an ERK inhibitor significantly reduced TCM-induced CD69 expression, suggesting that ERK signaling contributes to tumor-derived factor-mediated immune cell activation. These findings highlight the dynamic interplay among tumor cells, macrophages, and adaptive immune cells and suggest that IL-6 and TGF-β may be important mediators linking macrophage activation to enhanced tumor cell migration, providing a basis for further investigation of these pathways in breast cancer progression and therapy.

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PP-90

Bioisosteric redesign of 4,4′-dihydroxystilbene preserves replication stress induction and creates therapeutically exploitable checkpoint dependency in cancer

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Cancer cells experience chronic replication stress owing to their increased demand for DNA synthesis, rendering them dependent on replication stress response pathways for survival. We previously identified 4,4′-dihydroxystilbene (DHS), a rationally optimized analogue of resveratrol, as a potent replication stress inducer that sensitizes cancer cells to DNA damage response-targeted therapies. However, the stilbene scaffold is limited by its central ethylene (C=C) linker, which may restrict pharmacological optimization. Here, we investigated whether bioisosteric replacement of the C=C bond with an azo (N=N) linkage could preserve the biological activity of DHS while improving its drug-like properties. Screening of a focused library of azo-stilbene analogues identified AzB-6 as the lead compound and established the importance of the 4,4′-dihydroxyl substitution for anticancer activity. AzB-6 retained robust anticancer activity while demonstrating enhanced serum stability and improved *in silico* bioavailability. Molecular docking revealed similar binding affinities of AzB-6 and DHS to ribonucleotide reductase M2 subunit (RRM2). Mechanistically, AzB-6 induced profound replication stress, evidenced by FUCCI analyses, S-phase arrest, reduced EdU incorporation, shorter DNA fibers, and accumulation of phosphorylated RPA32 foci. Persistent replication stress resulted in enhanced DNA damage and apoptotic cell death. Furthermore, AzB-6 activated the Chk1-mediated checkpoint pathway, while Chk1 inhibition using SCH900776 or UCN-01 markedly potentiated apoptotic cell death, demonstrating a therapeutically exploitable checkpoint dependency. Collectively, these findings show that replication stress induction is a transferable property of the DHS pharmacophore and can be preserved through rational azo-bioisosteric redesign, establishing a mechanistically conserved class of replication stress-inducing molecules with improved development potential for checkpoint-targeted combination therapy.

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PP-91

Circulating exosomal thrombospondin-1: A potential biomarker of disease progression in breast cancer

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Breast cancer remains a leading cause of cancer-related mortality worldwide, due to disease progression and metastasis. This underscores the need for minimally invasive prognostic and diagnostic tools, highlighting the limitations of invasive tissue biopsies for diagnosis and prognosis.[1] Liquid biopsy approaches, particularly exosome-based, offer a minimally invasive alternative with substantial clinical potential.[2] Thrombospondin-1 (THBS1), a matricellular glycoprotein implicated in tumor progression,[3] has been associated with breast cancer aggressiveness, but its enrichment in circulating exosomes, relationship with disease progression [4], and its potential as a biomarker are poorly studied. In this study, we investigated the association of circulating exosomal THBS1 with breast cancer aggressiveness and disease progression. THBS1 expression was evaluated across breast cancer cell lines, while exosomes from breast cancer cell lines, preclinical mouse models, and patient plasma were characterized by NTA, TEM, and immunoblotting. We found marked enrichment of THBS1 in exosomal fractions, with the highest levels in MDA-MB-231 cells. *In vivo*, THBS1 knockdown delayed tumor onset and reduced circulating exosome burden, supporting the tumor as a major source of circulating exosomes. Isolated vesicles exhibited exosomal characteristics, including a size range of 100–130 nm and expression of exosomal markers. Importantly, patient samples showed a significant increase in circulating exosome burden with advancing disease stage across molecular subtypes, with the highest burden in Stage IV. THBS1 was predominantly enriched in exosomes rather than the soluble plasma fraction, and exosomal THBS1 increased with disease stage, particularly in TNBC, whereas soluble THBS1 showed minimal variation. Collectively, these findings identify exosomal THBS1 as a promising circulating biomarker associated with breast cancer aggressiveness and disease progression.

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PP-92

Reactive oxygen species-mediated bystander effects in multi-irradiated lung adenocarcinoma cells

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Cancer remains one of the leading causes of morbidity globally, with radiotherapy being a key treatment strategy. However, accumulating evidence has revealed that ionizing radiation can also exert effects on neighbouring healthy cells that are not directly exposed to radiation through a phenomenon known as 'radiation induced bystander effect (RIBE)' which may influence cellular stress responses and contribute to acquired radioresistance during repeated radiation exposure. Reactive oxygen species (ROS) are important mediators of radiation induced signalling and can regulate both oxidative damage and antioxidant responses. This study aims to characterize ROS-associated bystander effects in multi-irradiated A549 lung adenocarcinoma cells with a broader objective to understand their role in acquired radioresistance. A multi-irradiated population (A549-10F) was generated by exposing A549 cells to fractionated radiation of 10 doses of 4 Gy each. Clonogenic dose-response of A549-10F cells was studied by using increased doses of IR (2-10 Gy). Conditioned medium from irradiated 10F cells was transferred to non-irradiated A549 cells to study the bystander response. Proliferation and survival of the cells were investigated using MTT assay and clonogenic survival respectively. ROS and antioxidant status were evaluated using DCFDA, Amplex Red, ABTS and glutathione assays. DNA damage responses were studied using γH2AX, ATM, ATR, Chk1 and Chk2 while migration associated changes were studied using scratch assay. Multi-irradiated A549-10F cells showed increased clonogenic survival and increased oxidative stress responses compared with parental A549 cells. Bystander cells also exhibited increased survival and proliferation along with enhanced ROS levels, antioxidant capacity and increased migration and upregulated DNA damage signaling. The study thus, supports that ROS-associated signaling and antioxidant responses in multi-irradiated cells may mediate radiation-induced bystander effects and contribute to radioresistance.

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PP-93

Anticancer potential of 3-aminopyrrolidine derived from the marine bacterium *Streptomyces albidoflavus* CSEA02 against oral squamous cell carcinoma

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Marine microorganisms are a rich source of structurally diverse secondary metabolites with promising therapeutic potential. Their unique metabolic capabilities and adaptation to diverse marine environments enable them to produce bioactive compounds with antibacterial and anticancer properties [1]. In the present study, the marine-derived *Streptomyces albidoflavus* CSEA02, isolated from Chilika Lake, Odisha, India, was investigated for its potential to produce bioactive secondary metabolites with anticancer activity. The strain underwent primary and secondary screening, followed by cultivation under optimized culture conditions in ISP-2 medium at 30 °C and pH 6. The resulting metabolites were extracted using ethyl acetate and characterized by GC-MS [2]. Among the identified compounds, 3-aminopyrrolidine (3AP) significantly inhibited proliferation in oral cancer cells and increased caspase-3/7 activity and the expression of apoptosis-associated proteins, including cleaved PARP and BAX. While Caspase-3 knockdown attenuated these effects, supporting caspase-dependent apoptosis. In addition, 3AP induced autophagic responses, characterized by increased LC3 puncta, LAMP1-LC3 colocalization, and the expression of ULK-1, ATG-5, Beclin-1, and LC3. Chloroquine treatment further increased LC3-II accumulation following 3AP treatment, indicating enhanced autophagic flux [3]. Collectively, 3AP suppresses oral cancer cell growth by inducing caspase-dependent apoptosis, accompanied by enhanced autophagy.

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PP-94

Thorium-induced DNA-double strand breaks preferentially engages NHEJ repair over HR pathway in lung epithelial cells: *in vitro* and *in vivo* investigation

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Thorium (Th-232), a naturally-occurring actinide is widely encountered in rare-earth mining, processing, and Th-based nuclear fuel cycle. The molecular mechanisms underlying the repair of Th-induced DNA damage remain poorly understood. Present study investigated the role of homologous recombination (HR) and non-homologous end joining (NHEJ) pathways in the repair of Th-induced DNA double-strand breaks (DSBs) in human alveolar epithelial type-I (WI26) and type-II (A549) cells and validated the findings in mouse inhalation exposure model. Th exposure (0.1–10 µg/mL) induced a concentration-dependent increase in γH2AX foci and phospho-H2AX levels, confirming the formation of DNA-DSBs. Activation of DNA damage response (DDR) was evidenced by phosphorylation of ATM and ATR. Gene expression analysis revealed significant upregulation of NHEJ genes, including DNA-PK, Ku70/80, XRCC4, and Ligase-IV, whereas several HR genes, particularly BRCA1/2, Rad51 were downregulated. Remarkable activation of DNA-PK and its foci formation indicated preferential engagement of NHEJ pathway. In contrast, expression of key HR proteins, including BRCA1/2 and RAD51, was suppressed during early Th exposure, and RAD51 foci formation decreased at higher Th doses, compromising HR repair. DNA-PK inhibitors significantly enhanced Th-induced cell death and altered cell-cycle progression, demonstrating the protective role of NHEJ over HR pathways. Inhalation exposure of mice to Th-aerosols induced significant activation of DNA-PK, ATM, and ATR, increased DNA-PK foci, and reduced level of RAD51 in lung tissues, corroborating *in vitro* findings. Collectively, our results demonstrate that Th induces persistent DNA damage and activates ATM/ATR-dependent DDR signaling while preferentially promoting DNA-PK-mediated NHEJ repair and suppressing HR repair capacity. Such imbalance in repair pathways may contribute to genomic instability, lung toxicity, and the carcinogenic potential associated with Th-exposure.

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PP-95

Cold atmospheric plasma induces radiation-like bystander responses through non-canonical ATR signaling in A549 lung adenocarcinoma cells

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Cold atmospheric plasma (CAP) is gaining attention as a non-invasive therapeutic strategy for cancer; however, its capacity to induce biological responses in cells that are not directly exposed to plasma remains insufficiently characterized. In this study, we examined the induction and underlying mechanism of CAP-mediated bystander effects in human lung adenocarcinoma A549 cells. Cells were exposed to CAP for 5 min, following which conditioned medium was collected and transferred to untreated cells to generate a bystander population. Both directly exposed and bystander cells demonstrated a substantial reduction in clonogenic survival, accompanied by increased formation of γ-H2AX foci and activation of DNA damage response (DDR) signalling, indicating that CAP exposure can initiate non-targeted cellular effects. To investigate the signalling mechanism responsible for this response, pharmacological inhibition of the major DDR kinases ATR and ATM was performed. Treatment with the ATR inhibitor NU6027 markedly diminished the CAP-induced bystander response, whereas inhibition of ATM using KU-55933 produced no significant attenuation. These observations indicate that CAP-mediated bystander signalling is predominantly dependent on ATR rather than ATM, suggesting involvement of a non-canonical DDR pathway. The transfer of conditioned medium further supports the possibility that soluble factors released from CAP-exposed cells contribute to the propagation of stress signals to neighbouring untreated cells. Collectively, these findings demonstrate that non-ionizing CAP can generate radiation-like non-targeted effects and establish ATR-dependent signalling as an important mediator of the CAP-induced bystander response. Targeting this pathway may provide a potential strategy for modulating and enhancing the therapeutic efficacy of CAP-based cancer treatment.

PP-96

Gold nanoparticles encapsulated with erastin induced ferritinophagy through NCOA4-LC3B axis in radio-resistant breast cancer stem cells

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Radioresistance remains a major challenge in breast cancer treatment and is closely associated with the persistence of cancer stem cells (CSCs). Radioresistant tumor cells possess enhanced self-renewal and antioxidant mechanisms that facilitate survival following repeated radiation exposure. Since CSCs exhibit altered iron metabolism and dependence on antioxidant defense, ferroptosis represents a potential strategy to target radioresistant cancer cells. MDA-MB-231 and MCF-7 breast cancer cells were subjected to progressively increasing doses of ionizing radiation (Gy) to generate radioresistant clones. CSC populations were subsequently enriched from the radioresistant clones based on ALDH1A1 activity using the ALDEFLUOR assay. The stem-like phenotype was further evaluated by serial spheroid formation [1]. Erastin, a ferroptosis inducer drug was further encapsulated into gold nanoparticles (AuNPs). FTIR, UV-Vis spectrophotometer, DLS, and XRD were carried out to characterize the encapsulated nanoparticles. The effect of the system Xc^- inhibitor erastin loaded AuNPs on radioresistant CSCs was assessed using MTT assay. Flow cytometry, western blotting, enzymatic assays, immunofluorescence and RT-PCR were carried out to evaluate alterations in ferroptosis-associated and stemness-associated markers. Progressive radiation exposure resulted in enrichment of an ALDH1A1-positive population with enhanced stem-like characteristics in radioresistant breast cancer cells. The ALDH1A1-positive population increased from 0.6% to 5.2% in MDA-MB-231-derived radioresistant BCSCs while a gradual increase from 1.3% to 6.0% was observed in MCF-7 derived radioresistant BCSCs, accompanied by enhanced spheroid-forming capacity. Erastin loaded AuNPs reduced the expression of stemness-associated markers, including ALDH1A1, NANOG and OCT4. NCOA4 a cargo for ferritin recruitment into LC3B vesicles was also found to be elevated, together with depletion of intracellular glutathione and increased oxidative stress.

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PP-97

Chlorophyllin suppresses the growth of prostate cancer cells via induction of reductive stress and targeting the tubulin–microtubule system

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Cancer radiotherapy remains the major treatment modalities for most solid tumors, however, its clinical utility is frequently limited by radiation-induced normal tissue toxicities. Hence, there is a growing need for agents that not only reduce radiation-associated toxicity but also control tumor growth. The present study focuses on Sodium Copper Chlorophyllin (CHL), a water-soluble derivative of chlorophyll, which was recently reported by our group to protect against radiation-induced hemorrhagic cystitis, highlighting its potential as a radioprotective agent for patients undergoing pelvic radiotherapy [1,2]. However, its effect on growth of pelvic tumors and the mechanism of its anti-tumor activity are not completely explored. In the present study, the cytotoxic efficacy of Chlorophyllin was evaluated on prostate cancer cells and its mechanism of action was elucidated. The IC_{50} values of CHL in PC-3 and DU145 were found to be 23 μM and 15.69 μM, respectively. CHL also suppressed the clonogenic potential of cancer cells. Since CHL is a known antioxidant, its effect on cellular redox homeostasis was studied. CHL reduced cellular ROS levels and increased GSH levels, suggesting induction of reductive stress in cancer cells. Further, RNA sequencing was performed and CHL treatment led to enrichment of pathways associated with chromosome segregation, tubulin binding and kinetochore assembly in cancer cells, indicating a possible role of tubulin–microtubule system in the cytotoxic effects of CHL. In conclusion, the study provides preliminary evidence for a potential reductive stress–microtubule axis underlying CHL mediated inhibition of cancer progression.

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PP-98

Pathological screening of laboratory rodents bred in animal house facility, BARC

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Laboratory rodents play an indispensable role in biomedical research owing to their genetic similarity to humans, short reproductive cycles and well-characterized physiological characteristics. Maintaining high standards of animal health is essential to ensure the reliability, reproducibility and validity of experimental outcomes. The present study was undertaken to assess the pathogen status of laboratory rodents maintained in the Animal House Facility as part of a routine quality control program. A total of 120 animals, comprising adult and sentinel animals of both sexes, representing in-house bred BALB/c, Swiss, C57BL/6 and NOD.SCID mice, and Wistar rats, were screened during 2025-2026. Animals were subjected to routine physical health assessment and signs of morbidity or mortality. Parasitological screening of fecal samples was performed using standard microscopic techniques, including direct smear, flotation, sedimentation, and perianal tape test, for detection of common ecto- and endo-parasites. Serum samples were evaluated by enzyme-linked immunosorbent assay for serological evidence of selected pathogens. All animals examined were in good condition, with no apparent clinical signs suggestive of pain, illness or infectious disease. Serological screening revealed no detectable antibodies against Mouse Hepatitis Virus, Mouse Ectromelia Virus, Mouse Sendai Virus, Mouse Hantavirus and *Mycoplasma pulmonis*. Parasitological examination revealed no evidence of the common ectoparasites or endoparasites. In conclusion, laboratory rodents maintained in the facility had satisfactory health status during the study period. Regular health monitoring and pathogen surveillance are essential components of facility management and contribute to maintaining healthy colonies and minimizing potential confounding factors in biomedical research. These findings support the suitability of the screened colonies for research applications, subject to continued routine health surveillance.

PP-99

Stiff ECM-tuned integrated stress response (ISR) modulates radiation response in TNBC

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Extracellular matrix (ECM) stiffening is a peculiar feature of the breast tumor microenvironment that facilitates cancer progression. Stiff ECM is instrumental in potentiating survival, proliferation, contractility, invasion, and stemness of cancer cells. However, the role of ECM rigidity in regulating the radio-response of cancer cells remains largely unclear and warrants in-depth investigation. To recapitulate the stiffness of normal breast stroma (0.5kPa) and metastatic breast stroma (5kPa), stiffness-tunable hydrogels were fabricated. To assess how ECM stiffness affects the radio-response of cancer cells, we conducted functional and molecular assays, including cell survival, cell cycle analysis, apoptosis, migration, immunofluorescence, immunoblotting, RT-PCR, and RNA sequencing. The stiff scaffold-primed cells showed significantly decreased apoptosis, higher survival, and a sustained proliferation index post-IR compared to the soft ECM. Post-IR, the low levels of γH2AX and early recruitment of DDR proteins (pATM, pDNA-pk, and 53BP1) at DSBs showcase attenuated DNA damage in stiff ECM-primed cells. The transcriptomic profile of stiff ECM-primed cells revealed differential regulation of genes related to ribosome biogenesis, organelle assembly, and translation. Upon investigation, we found that rigid ECM activates the integrated stress response (ISR) as an adaptive mechanism, which further potentiates stiffness-acquired radio-resistance in breast cancer cells.

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PP-100

Clonal heterogeneity in cancer cells: Comparative characterization of holo-, mero-, paraclones and their response to radiation

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Cancer stem cells (CSCs) are a distinct tumor subpopulation with enhanced self-renewal, tumor-initiating capacity, and therapeutic resistance, contributing to tumor heterogeneity [1]. Clonal expansion of individual cancer cells generates phenotypically distinct holoclones, meroclones, and paraclones representing stem-like, intermediate, and differentiated states, respectively [2,3]. Here, we isolated these clonal populations from A549 non-small cell lung cancer cells and characterized them for stemness, radioresistance, and their association with topological features. Among these clonal populations, holoclones (~12%) were compact and densely organized, meroclones (~55%) showed intermediate morphology, and paraclones (~30%) were highly dispersed. Holoclones exhibited increased expression of OCT4 (2.3-fold), SOX2 (3.25-fold), and NANOG (1.87-fold) and greater clonogenic survival following γ-irradiation. At 8 Gy, holoclones showed ~1.31-fold higher survival than parental cells and ~2.1-fold higher survival than paraclones. Quantitative spatial analysis of nuclear centroids revealed distinct organizational patterns. At a 40-µm connectivity threshold, 99.46% of holoclone and 95.52% of meroclone nuclei were incorporated into the largest connected component, compared with 14.01% in paraclones. Holoclones and meroclones exhibited greater network connectivity, clustering, and global efficiency, whereas paraclones showed extensive fragmentation. Clones with a Largest Connected Component Fraction (LCF) ≥95% demonstrated small-world-like organization, with small-world coefficients (σ) of 14.46 ± 3.52 and 14.22 ± 2.79 for holoclones and meroclones, respectively. The clustering coefficient (CC) was significantly higher in holoclones than meroclones ($p = 0.0047$), whereas σ was comparable between the two populations ($p = 0.768$). These findings indicate that the cohesive spatial organization of holoclones is associated with their stem-like phenotype and enhanced radiation survival.

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PP-101

Radiation-induced bystander effect in human normal breast cells after low and high doses of radiation exposure

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Radiation-induced bystander effect (RIBE) is a phenomenon in which non-irradiated (bystander) cells exhibit biological response as a consequence of signals from the irradiated cells, which may contribute to either survival or killing of bystander cells [1]. RIBE is mediated through Inter-cellular Gap Junction Communication (GJIC) involving especially Connexin 43 (Cx43) and/or secretion of diffusible factors [2-3], which may show differential response at low and high doses of radiation. The present study is aimed to investigate RIBE and underlying mechanism in human normal breast cells (MCF10A) irradiated with low and high doses of γ-radiation. Out of the normal cells studied [mouse fibroblast (L929), human lung fibroblast (WI-38, WI-26) and human breast epithelium (MCF10A)], MCF10A cells showed highest level of lucifer yellow dye transfer (~225 μm) than other cells (~15 μm) suggesting higher functional GJIC in MCF10A cells. The expression of Cx43 and its phosphorylation is known to regulate GJIC, which was found to be higher in MCF10A than other cells suggesting suitability of MCF10 A cells for bystander studies. To optimize the radiation dose for RIBE studies, clonogenic survival assay of MCF10A cells was performed after gamma radiation (10-500 cGy). Results showed insignificant change in clonogenic survival at 10 and 50 cGy, which however was decreased at higher doses. Further RIBE experiments were conducted at 10 cGy, 200 cGy and 500 cGy using insert co-culture protocol. Our results showed damaging bystander effect at higher doses not at low doses. Role of soluble factors and GJIC in under RIBE mechanism at low and high doses is being studied.

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PP-102

Mechanistic insights into radiation-induced exosome biogenesis in cancer cells

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Exosomes are extracellular vesicles of endosomal origin that play an important role in intercellular communication [1]. Although ionizing radiation is primarily recognized for inducing oxidative damage to cellular macromolecules [2], it can also modulate extracellular vesicle release [3] and composition [4]. However, the molecular mechanisms underlying radiation-induced alterations in exosome biogenesis remain poorly understood. In this study, cancer cells maintained in exosome-depleted culture medium were exposed to 2 or 5 Gy X-rays (225 kV, 17 mA; dose rate: 1.86 Gy/min). Exosomes were isolated using a commercially available kit and characterized by nanoparticle tracking analysis (NTA), transmission electron microscopy (TEM), and immunoblotting. Radiation resulted in a dose-dependent increase in exosome production across cancer cells of different tissue origins, as determined by NTA, without appreciable changes in vesicle size. To investigate whether radiation alters intracellular exosome biogenesis, MDA-MB-231 cells were examined for lysophosphatidic acid (LBPA), a marker of multivesicular bodies (MVBs)/late endosomes [5]. Irradiation increased both the number of LBPA-positive puncta and their fluorescence intensity, indicating enhanced MVB formation. TEM analysis further demonstrated increased numbers of MVBs and intraluminal vesicles (ILVs), along with an increase in ILVs per MVB, supporting enhanced exosome biogenesis following irradiation. To identify the molecular pathway involved, proteins associated with ESCRT-dependent and ESCRT-independent mechanisms were evaluated by western blotting. While no appreciable alterations were observed in proteins associated with the canonical ESCRT-dependent pathway, the ESCRT-associated protein Alix and the tetraspanin CD63 were upregulated following irradiation. Collectively, these findings demonstrate that ionizing radiation enhances exosome production and intracellular MVB/ILV formation, with increased Alix and CD63 expression suggesting a predominant involvement of ESCRT-independent mechanisms in radiation-induced exosome biogenesis.

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PP-103

Alternative splicing as a therapeutic target for radiosensitisation in breast cancer

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Resistance to radiotherapy remains a major obstacle in the treatment of breast cancer [1]. Aberrant alternative splicing is known to influence multiple pathways involved in tumor survival and therapy response [2]. In this study, we investigated whether pharmacological perturbation of the splicing machinery could enhance the radiosensitivity of breast cancer cells. Transcriptome-wide comparison of MCF7 breast cancer cells with non-tumorigenic MCF10A breast epithelial cells identified altered splicing patterns across genes associated with cell-cycle regulation, mitosis, DNA-damage signaling and DNA repair. These observations prompted evaluation of splicing modulators as potential radiosensitisers. Among the compounds tested, the SF3B1-targeting agent H3B-8800 (H3B) produced the strongest radiosensitising effect in MCF7 cells, while causing comparatively limited cytotoxicity in MCF10A cells. Further analysis showed that combined H3B and radiation treatment altered cell-cycle dynamics, resulting in sustained accumulation of irradiated MCF7 cells in G2/M phase. H3B treatment also increased radiation-associated DNA damage and impaired its resolution, reflected by enhanced comet formation and persistence of γ-H2AX foci. Using a dual-splicing reporter, early exposure to H3B was found to perturb pre-mRNA splicing, whereas extended treatment caused global suppression of transcription, indicating a possible temporal link between disruption of RNA processing and transcriptional activity. Together, these findings demonstrate that pharmacological interference with SF3B1-dependent splicing can potentiate radiation response in MCF7 cells through coordinated effects on RNA processing, cell-cycle progression and DNA-damage repair. Targeting spliceosome function may therefore provide a potential strategy for enhancing breast cancer radiosensitivity.

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PP-104

Investigating the role of RECQL5 in DNA damage–induced G2/M checkpoint activation

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The G2/M cell cycle checkpoint acts as a critical safety mechanism after exposure to ionizing radiation (IR). It stops cells from entering mitosis with damaged DNA. The core target of this checkpoint is the CDK1/Cyclin B1 complex (also known as the Mitosis-Promoting Factor). To halt the cell cycle, the cell uses a highly coordinated cascade of sensors, transducers, and effectors to keep CDK1 phosphorylated. Though it is widely believed that ATM/ATR senses the damage to DNA after radiation and then transduces the signal by CHK1 and CHK2 ultimately inhibiting the function of CDC25C phosphatase (CDK1 remains phosphorylated and mitosis does not happen), it does not completely explain the process of arrest. Status of P53 also plays a role in manifestation of the duration of G2/M arrest. We have observed that lack of RECQL5 helicase leads to ineffective induction of G2/M checkpoint as RECQL5 knockout cells do not undergo G2/M arrest as robustly as WT cells after exposure to gamma radiation. We have established this phenomenon in U2OS osteosarcoma cells. Further our data revealed RECQL5 knockout cells are resistant to gamma radiation compared to WT cells. This is contrary to the expectation, where lack of a functional G2/M arrest leads to cells proceeding ahead with damages incurred culminating in mitotic catastrophe/ cell death. Flow cytometry data revealed substantial increase in G2/M population in a dose dependent manner in WT cells. However, in REQL5 KO cells substantially lower population were in G2/M compared to WT. We are currently investigating the role of RECQL5 in induction of G2/M arrest post irradiation.

PP-105

Glutathione depletion sensitizes lung cancer cells to Conoidin A by triggering disulfidoptosis

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Glutathione (GSH) and the thioredoxin reductase–thioredoxin–peroxiredoxin (TXNRD–TXN–PRDX) system constitute two major arms of the antioxidant defence network in cancer cells. Conoidin A, a cell-permeable peroxiredoxin inhibitor, was found to additionally inhibit upstream thioredoxin reductases, thereby disrupting the TXNRD–TXN–PRDX redox axis. Bioinformatic analyses revealed a strong association between cellular glutathione levels and sensitivity to Conoidin A. Consistent with this, pharmacological depletion of GSH using buthionine sulfoximine (BSO), or through GCLC silencing, markedly sensitized cancer cells to Conoidin A. Notably, cell death induced by the combination was refractory to a panel of established cell death inhibitors and reactive oxygen species scavengers. Combination treatment led to enhanced levels of disulphide based crosslinking of cellular proteins, including peroxiredoxins and cytoskeletal proteins. Loss of actin stress fibres and collapse of tubulin network was also noted. The combination also increased the NADP+/NADPH ratio, consistent with severe disruption of cellular reducing capacity and a disulfidoptosis-like phenotype. Accordingly, treatment with reducing agents rescued combination-induced cell death. Importantly, selective depletion of mitochondrial glutathione sensitized cells to Conoidin A, implicating mitochondrial redox disruption as a critical determinant. *In vivo*, combination treatment with Conoidin A and BSO enhanced antitumour efficacy of Conoidin A. This therapeutic interaction was further reproduced in patient-derived organoids and across cancer cell lines of diverse origins. Collectively, these findings identify glutathione depletion as a strategy to potentiate Conoidin A-mediated disruption of thiol redox homeostasis and establish coordinated collapse of the thioredoxin and glutathione systems as a disulfidoptosis trigger in cancer cells.

PP-106

Proton radiation-induced damage repair in POLQ deficient background

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Radiation therapy (RT) has long been used in conjunction with surgery and drugs to provide optimal cancer care. RT-induced cell death is mostly due to DNA damage, especially to double-strand breaks (DSBs). While double-strand break repair via classic non-homologous end joining and homologous recombination is well defined, the physiological contribution of Alternative End-Joining (Alt-EJ) to radiation-induced DNA damage remains under-characterized. Most mechanistic insights into Alt-EJ derive from site-specific, endonuclease-cleaved lesions; however, ionizing radiation—particularly charged particles such as protons—induces complex, clustered lesions with localized loss of sequence information. As space exploration expands and proton beam therapy becomes widespread, elucidating the pathways resolving charged-particle-induced complex lesions is essential for evaluating radiation risks and refining therapeutic strategies. Crucially, Alt-EJ and its key functional enzyme, Polymerase Theta (PolQ), are frequently overexpressed in specific oncological contexts, positioning PolQ as a prime target for targeted radio-sensitization. Here, we evaluated the functional requirement of PolQ in repairing gamma and proton radiation induced DNA damage using POLQ inhibitors or POLQ knockout cells. POLQ knockout cells showed increased γ-H2AX foci and elevated chromosomal fragments suggesting unrepaired DNA rather than chromosomal rearrangements in these HR and NHEJ proficient cells. Relatively higher fragments observed after proton irradiation suggested notable requirement of POLQ in repairing proton induced damage. Our studies therefore show that POLQ may be targeted for enhancing therapeutic index after proton irradiation.

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PP-107

Green chilli powder preparation, analysis and hygienization using gamma radiation

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Fresh matured green chilli procured from local market and dried in Infra-red drier at temperature of 60°C. Completely dried green chilli sample were used for powder preparation in domestic food processor. Powder was suitably packed in polypropylene bag and irradiated (gamma radiation at dose of 5 kGy) and further stored at ambient temperature (~28°C). Analysis including physicochemical characteristics like colorimetry, moisture content, aw activity and microbial count (Total Aerobic Plate Count, Coliforms) was carried out. Moisture content in the fresh green chilli sample before drying was 88 to 92%. However, Water activity (a_w) found in the prepared powder was in the range of 0.44 to 0.57 in the control, treated and market samples. However colorimetric values L, a* and b was in the range of 60-65, 1.5-2, 12-13.3 respectively. Microbial analysis results show the absence of coliforms in the prepared and packed green chilli powder. However total aerobic plate counts were well within acceptable limit. Conclusion: A well hygienized and nutritious good alternative for domestic use of green chilli powder over traditional red chilli powder.

PP-108

Catalytic steam reforming of Nisarguna biomass for H_2 production

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Hydrogen will play a key role in solving the requirement of the global energy requirement as it's a clean energy and can be utilized in fuel cell [1, 2]. Hydrogen generation from biomass can be an alternative solution as it is widely available, cost-effective and maintains carbon neutrality [3]. Incineration, composting and fermentation/biological processes, are currently used as thermal or biochemical waste conversion technologies. In this study, post-digested discarded effluent form Nisarguna Biogas plant is used as the feed for production of hydrogen using supported catalyst in a Fixed Bed Reactor (FBR). Ni dispersed Ceria (Ni/CeO_2) foam-based catalysts were synthesized by co-precipitation of $CeNi_xO_y$ using triethylamine (TEA) from the nitrate solutions. The precipitate was calcined at 500° C for 4 hours. Polyurethane (PU) foams were immersed in the thick slurry containing the catalyst, binder, dispersant and plasticizer. The catalyst loaded foams were then calcined at 700° C following slow heating rate (0.5° C min^{-1}) for 6 hours resulting in 3D foam structured catalyst. The catalyst was then reduced with H_2/N_2 mixture (10% v/v) at 350° C for 1 hour. The catalyst was evaluated for steam reforming of biomass at 500°C with 0.12 ml/min feed flow rate and 60 ml/min carrier (N_2) flow rate [GHSV = 26,611 h^{-1}]. The hydrogen yield of 18g/kg and 13g/Kg was obtained by catalytic steam reforming of post-digested discarded effluent from Nisarguna and model glucose solution, respectively.

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PP-109

Shelf-life extension of grains using ^{137}Cs-based gamma irradiation and comparative assessment with ^{60}Co-based gamma irradiation on rheological properties

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A ^{137}Cs-source-based Agro-Irradiation Facility (AIF), operating in a free-flow continuous mode, has been developed at BARC. Following its commissioning, a pilot-scale feasibility study was conducted to evaluate the efficacy of irradiation for shelf-life extension of wheat, rice, and chana dal. Approximately 60 kg of each commodity was irradiated at a minimum dose of 650 Gy and periodically evaluated. No significant differences were observed between the control and irradiated samples for proximate composition and antioxidant activity throughout the study. Rheological analysis indicated that irradiation resulted in greater paste breakdown during heating and lower retrogradation during cooling, suggesting reduced starch reassociation and improved paste stability. Microbiological analysis demonstrated significantly lower CFU in the irradiated samples compared with the controls after 0 and 3 months of storage. Furthermore, irradiated samples retained higher sensory scores and overall acceptability throughout the study. Notably, insect infestation was observed in control rice samples after two months of storage, whereas no infestation was detected in the irradiated samples. The rheological properties of grains irradiated with ^{60}Co γ-radiation were further investigated in comparison with ^{137}Cs γ-radiation. Preliminary results exhibited similar pasting and retrogradation characteristics for both radiation sources. The sensory quality and insect disinfestation of samples irradiated with ^{60}Co and ^{137}Cs were also comparable. Overall, the findings demonstrated the potential of the ^{137}Cs-based AIF for improving the shelf-life of the studied commodities without affecting their analyzed properties. The results were further substantiated using an established ^{60}Co-based irradiation facility with respect to rheological properties, disinfestation behavior, and sensory quality.

PP-110

Degradation of malachite green in fish using gamma irradiation

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Malachite green (MG) is a cationic dye used as parasiticide or fungicide in aquaculture. This compound has genotoxic and carcinogenic effects[1]. Hence, its utilization in aquaculture has negative impact for fish consumers. As per European Union guidelines, the minimum content of MG and its reduced form leucomalachite green (LMG) in a food of animal origin to be detected and confirmed is 2ppb (µg/kg)[2]. In present study, different concentrations of aqueous solution of MG (10-75 µg/ml) were irradiated at 2, 4 and 6 kGy gamma-irradiation. At 10 µg/ml, 55% of MG was found to be degraded at 2 kGy and complete degradation at 4 kGy. At 20 µg/ml, 78, 95 and 100% degradation were observed at 2, 4 and 6 kGy respectively. At 50 µg/ml, 81, 90 and 100% degradation were found at 2, 4 and 6 kGy respectively whereas, at 75 µg/ml, 64, 93 and 100% degradation were found at 2, 4 and 6 kGy respectively. This showed the degradation of MG as concentration dependent and dose dependent. Further, MG was also spiked in basa (*Pangasius bocourtii*) fish fillets at a concentration of 10 and 50 µg/kg followed by gamma-irradiation treatment at doses of 2, 4 and 6 kGy. At 10 ppb, 48, 68 and 80% MG degraded at 2, 4 and 6 kGy respectively whereas, at 50 ppb, 68, 74 and 87% degradation was observed at 2, 4 and 6 kGy respectively. Antimicrobial activity against *staphylococcus aureus* and *Escherichia coli* of aqueous solution of MG (2 ppb) was also lost after gamma-irradiation treatment (2 kGy). Hence, gamma-irradiation can be used as an effective method to degrade MG in fish.

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PP-111

Molecular-level investigation of lignin degradation by deep eutectic solvents using computational approaches

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Bioethanol from lignocellulosic biomass is renewable, cheap and free from food to fuel debate. However, release of fermentable sugar from such biomass is cumbersome due to presence of lignin. Deep eutectic solvent (DESs) based pretreatment could be an effective strategy for removal of lignin. Thus, a better understanding of the molecular level interactions between a DES and lignin is of important for preparation, selection, and optimization of DES. Such solvent mainly breaks β-O-4, an abundant chemical linkage between lignin monomers. Lignin is mainly composed of guaiacyl (G), syringyl (S), and p-Coumaryl (H). The predominant dimers of lignin are G-G, S-G and S-S.[1,2] In present study, representative G-G dimer was constructed using Avogadro and B3LYP D3BJ def2-TZVP was used to optimize the structure of dimer to ground state at 403.15 K. β-O-4 bond length of 1.436Å was observed between aromatic O and β-Carbon. After performing a relaxed Potential Energy Surface (PES) scan and transition-state analysis by stretching the β-O-4 bond from 1.436Å to 3.5Å in 20 steps, a cleavage at 3.06Å and threshold energy barrier of 202.06 kJ/mol were observed. Further, the dimer was stimulated in presence of 1:2 choline chloride to formic acid-based DES to determine how its interactions modify reaction energetics and facilitate lignin bond cleavage. Such computational analysis can help to identify the DES with greater potential for lignin bond cleavage and, consequently, guide the selection of a suitable DES for biomass pretreatment for bioethanol production.

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PP-112

Bioactive flavonoids of guar bean (*Cyamopsis tetragonoloba*): isolation, characterization and antioxidant potential

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Guar bean (*Cyamopsis tetragonoloba*) is an economically important legume widely utilized as a food and industrial crop and is increasingly recognized as a potential source of health-promoting phytochemicals. Despite its nutritional and antioxidant potential, information on the isolation, characterization, and biological significance of individual bioactive compounds from guar bean remains limited. Therefore, the present study was undertaken to isolate and characterize flavonoids and evaluate the antioxidant potential of guar bean extracts, thereby supporting its sustainable utilization as a natural source of bioactive compounds. An 80% aqueous methanol extract was fractionated using XAD column chromatography followed by preparative thin-layer chromatography. Twelve compounds were isolated in pure form, including kaempferol, quercetin, daidzein, and genistein in their free and glycosidic forms. Five major glycosidic compounds were tentatively characterized using UV, IR, NMR, and HPLC analyses; the proposed structures of the isolated compounds are shown below. The aqueous methanol extract demonstrated markedly higher antioxidant activity than the aqueous extract, exhibiting 76% anti-lipid peroxidation, 73% superoxide, and 61% hydroxyl radical scavenging activities. DPPH radical scavenging activity showed an IC_{50} of 8.24µg/mL compared with 20.15 µg/mL for the aqueous extract. Overall, the findings establish guar bean as a valuable source of structurally diverse flavonoids and potent antioxidant constituents, highlighting its potential for development into natural antioxidant ingredients for nutraceutical, functional food, and related applications and providing a scientific basis for its greater value-added utilization.

PP-113

Gamma irradiation: a sustainable preservation method for degradation of furazolidone residue in fish

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Furazolidone (FURA) is a broad-spectrum antibiotic with known potentially carcinogenicity and toxicity in sensitive individuals. Hence, present study focused on the effect of different processing methods on FURA. Heat treatment, Autoclaving and gamma irradiation were analysed for degradation of FURA. Heat treatment and autoclaving showed no significant degradation, while gamma irradiation at 4 kGy dose resulted in 73.3% degradation of FURA (50µg/ml). Six major compounds were identified with *m/z* 456, 330, 274, 246, 218 and 103 using LC-MS/MS. The degraded compounds showed lower antimicrobial activity when tested against different food borne pathogens. There was no resistance development in microbes when co-cultured and maintained with degraded compounds. Further, gamma irradiation could effectively degrade FURA in fish which was previously fed with antibiotics at optimized absorbed dose of 4 kGy. Findings suggest that gamma irradiation can be a sustainable preservation method for fish which can degrade the antibiotic residues present in it and assure food safety.

PP-114

Sugar reduction in apple juice using *Yarrowia lipolytica* fermentation

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Fruit juices offer several health benefits due to their very complex composition characterized by a large number of micronutrient and phytochemical content. However, due to their high sugar and fructose levels, these juices cause rapid blood sugar spikes that increase the risk of type 2 diabetes and non-alcoholic fatty liver disease. There is an urgent need for innovative sugar-reduction strategies and non-alcoholic yeast fermentation is a promising method which naturally metabolizes free sugars and converts them into low-calorie compounds and pleasant volatiles. In current study, the sugar reduction was attempted in apple juice using non-alcoholic fermentation using oleaginous *Yarrowia lipolytica*, which was known to consume sugar and produce lipids. Fresh apple juice was prepared from apple (red delicious var.) using pectinase treatment which was optimized by assessing different enzyme concentrations and incubation times at 50°C to obtain maximum juice yield. The juice was bottled and pasteurization condition was optimized (90°C, 5 min) by microbial analysis of different temperature and time combinations. The growth characteristics *Y. lipolytica* were determined in growth media. The fermentation of pasteurized apple juice performed using log phase *Y. lipolytica* culture for 7 days across different pH in range of 3.5–7.5. The sugar reduction along with ethanol and citric acid accumulation were quantitatively analyzed using HPLC. The maximum sugar reduction (31 ± 3) % was observed at pH 7.5 without ethanol production on day 7 of fermentation. The citric acid content was maintained in range of 17-26 g/L during fermentation.

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PP-115

AptamerDB: a comprehensive database for aptamers against small molecules

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Aptamers are short single-stranded DNA or RNA oligonucleotides that bind their targets with high affinity and specificity. Small-molecule aptamers are used in biosensing, diagnostics, food safety, and environmental monitoring, yet their data remain scattered across the literature. Existing general-purpose repositories mix small molecules with protein, cell, and virus targets. The largest of them, the UTexas Aptamer Database, holds 1,443 internally reviewed aptamer records across all target types, and AptaDB contains 1,350 experimentally validated aptamer–target interactions. We present AptamerDB, a database devoted exclusively to small-molecule binding aptamers. Approximately 18,000 Scopus records spanning years (2005-2027) were screened for small-molecule targets using two independent AI agents (Claude and NotebookLM), with manual verification of all flagged entries. A second screen retained only primary studies reporting novel aptamer sequences, excluding reviews, book chapters, and reused aptamers. Each entry was annotated with ligand chemical, predicted secondary structure with descriptors, functional domain, and experimental 3D structure information where available. AptamerDB contains more than 2000 curated small-molecule aptamer entries, over twice the size of the largest general aptamer database. In a preliminary analysis, RNA made up roughly 60% of entries and DNA about 40%, spread across 12 ligand classes led by metal and inorganic ions, nucleotides, and pharmacological agents. Aptamer lengths were mostly 30–90 nt, MFE values clustered between −15 and −5 kcal/mol, and most ligands had MW below 400 g/mol. This database can aid researchers in designing machine learning models aimed at rapid development of new aptamers.

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PP-116

Comparison of irradiation (gamma and E-beam) and fumigation for microbial decontamination of spices, and analysis of residual 2-chloro ethanol (2-CE)

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The Indian whole dry spices including black pepper, chilli, coriander, cumin and turmeric have the problem of higher microbial load and insect infestation affecting the storage shelf life and export quality. The physical treatments like Gamma irradiation, E-beam processing and chemical fumigation using Ethylene oxide (EtO) are known to be effective for microbial decontamination and insect disinfestation. However, the comparison of effectiveness of these three processing methods has not been reported earlier. In current study these three treatments were compared for their effectiveness during storage of the five spices for period of one year. The microbiological analysis showed a dosedependent reduction in microbial load and 6 kGy (Gamma and E-beam) samples were found to have residual microbial counts (<1 log cfu/g) throughout storage at ambient temperature. However, analysis of 12 month stored fumigated samples exhibited higher total viable counts (TVC), with approximately 2 log CFU/g in black pepper and chilli and up to 4 log CFU/g in turmeric. Ethylene oxide (EtO) fumigation of spices reported to result in formation of 2chloroethanol (2CE) as a stable residual byproduct, raising food safety concerns due to its carcinogenic potential (1). In this study, a QuEChERS extraction method (2) coupled with gas chromatography–mass spectrometry (GCMS) was employed for the quantitative determination of 2CE residues in fumigated spices (black pepper, chilli, coriander, cumin and turmeric) during extended storage up to one year. Immediately after fumigation, 2CE content in the treated spice samples ranged from 400 to 1100 mg/kg. Over one year of storage, 2CE levels decreased significantly to 90–170 mg/kg. As per FSSAI guidelines the permitted levels of 2-CE in spices is 0.1 mg/kg (FSSAI order dt 08.04.2024). The present study showed the advantageous effect of irradiation over EtO fumigation during storage of a year at ambient storage condition.

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PP-117

Shelf life extension of ready-to-drink beetroot (*Beta vulgaris* L.) Bulb juice using gamma irradiation

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The freshly extracted beetroot (*Beta vulgaris)* juice known to be beneficial for health but has very low shelf life of few hours after preparation (1). Gamma irradiation though effective for microbial decontamination and shelf-life extension of many food items but it's use for beetroot juice preservation has not been reported (2). In current study, the effectiveness of gamma irradiation was studied for shelf-life extension of bottled pure beetroot juice without any other physical processing and chemical additives. The bottled, gamma irradiated at absorbed dose of 12.5 kGy, was found to be shelf stable for 45 days at ambient temperature (26 ± 2^{o}C). The processing did not involve any thermal treatment and chemical preservatives. The microbial safety of irradiated beetroot juice was ensured by sterility testing during 45 days of storage. In addition, irradiated beetroot juice was also analyzed periodically for TSS, pH, sucrose, glucose, betalains, total phenol content, antioxidant activities, and organoleptic parameters during storage. Analysis of proximate contents (protein, fat, carbohydrate, sodium, cholesterol and energy) revealed no significant change after gamma irradiation. Additionally, a 1-month feeding trial in infant mice (5 days/week) revealed no differences in dietary intake, body weight (monitored 3×/week), complete blood count (CBC), or spleen index between irradiated and non-irradiated juice groups, confirming toxicological safety. The volatile aroma constituents of juice analysed using GC-MS was found to be not affected by irradiation. The current findings showed that the gamma radiation processing was found to be suitable for shelf-life extension of beetroot juice without use of any chemical additives and thermal processing.

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PP-118

Antimutagenicity of selected culinary fruits and class-based separation, enrichment and enhancement of their bioactive phytochemicals

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The antimutagenicity of selected culinary fruits such as Avocado, Blueberry, Dragon fruit (pink and white pulp), Grapes (black, green, and red), and Kiwi were evaluated in *Escherichia Coli* MG1655 based RNA polymerase B (rpoB) - rifampicin resistance assay and Human Lymphoblast TK6 Cell line - Thymidine Kinase (TK) gene mutation assay. Prior, an MTT assay was conducted to determine the optimal non-cytotoxic concentration of fruit extracts for antimutagenic analysis. The antimutagenic analysis revealed that green-grapes, blueberry, white-pulp dragon fruit and pink-pulp dragon fruit exhibited high (72-80%) activity. Avocado displayed moderate activity (43.8%), while red and black-grape along with Kiwi showed least activity i.e., < 30%. The correlation between antimutagenicity and antioxidant capacity [DPPH (2,2-diphenyl-1-picrylhydrazyl) and ABTS (2,2′-azino-bis (3-ethylbenzothiazoline-6-sulfonic acid) radical Scavenging, and FRAP (Ferric Reducing Antioxidant Power)] was found to be low (r = −0.24 to 0.13). This indicated that observed antimutagenicity was not primarily due to antioxidant activity in these fruits. Further, class-based bioactive phytochemicals were separated and enriched using solid-phase extraction with C-18 column for anthocyanin and phenolics, and silica column for naphthoquinones. Antimutagenicity of these class-based enriched extracts revealed that anthocyanin in blue berry and pink-pulp dragon fruit and naphthoquinones in green-grapes are the major bioactive phytochemical groups responsible for the observed antimutagenicity. Fourier-transform infrared (FTIR) spectroscopy was conducted for various class of phytochemicals showing high activity for validation where typical or specific peaks based upon their functional group were observed. Furthermore, approaches pertaining to extractability and bioactivity enhancement are being made.

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PP-119

Application of gamma irradiation for quality enhancement and shelf-life extension of yellow and black tofu

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Tofu is a protein-rich soy-based food with high moisture content, which makes it highly susceptible to microbial spoilage and limits its refrigerated shelf life. This study evaluated gamma irradiation as a non-thermal preservation strategy for extending the refrigerated shelf life of yellow and black tofu. Laboratory-prepared tofu was subjected to vacuum packaging, irradiation, followed by storage at refrigerated temperature (3-4°C). Physical and biochemical characteristics, including colour, texture, water activity, microbial quality, protein content, phytate content, total phenolic content (TPC), antioxidant activity, antimutagenic potential, and sensory attributes, were evaluated throughout the storage period. Protein content was higher in black tofu (54.69%) than in yellow tofu (25.16%). Water activity remained stable in both tofu varieties, with no significant differences between irradiated and control samples. The colour difference (ΔE) between irradiated and control samples decreased from 1.84 to 0.79 in black tofu and from 3.60 to 0.95 in yellow tofu over 65 days of storage. Irradiation reduced phytate content by 19% in black tofu and 11% in yellow tofu. Antioxidant activity was enhanced in black tofu following irradiation, with DPPH radical-scavenging activity increasing from 37% to 58% and FRAP values from 1.85 to 2.00 mg AAE/g. Similarly, TPC increased after irradiation, from 17.0 to 19.7 mg GAE/g in black tofu and from 9.0 to 11.0 mg GAE/g in yellow tofu; however, these values declined during storage to 4.5 and 2.5 mg GAE/g, respectively. Irradiated black and yellow tofu exhibited antimutagenic activities of 29.7% and 14%, respectively. Sensory acceptability remained high in both varieties throughout storage, with scores declining only slightly from 8 on day 0 to 7 on day 65. Overall, gamma irradiation at a dose of 1 kGy demonstrated potential as an effective preservation strategy for extending the refrigerated shelf life of tofu while maintaining its nutritional, antioxidant, physicochemical, and sensory quality.

PP-120

Passive MAP mediated shelf-life extension of pointed gourd (*Trichosanthes dioica* Roxb.) and radiation processing for overcoming quarantine barrier of trade

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The effect of irradiation as a phytosanitary treatment (D_{min} 400 Gy) on the storability of Pointed gourd vegetable remains unexplored. Additionally, pointed gourd incurs extensive moisture loss during extended storage which severely impacts its commercial appeal and consumer acceptance. The current study highlights an integrated approach including packaging and phytosanitary irradiation which simultaneously addresses various issues including moisture loss, shelf stability and quarantine concerns. Unprocessed Pointed gourd displayed extensive moisture loss & quality deterioration during storage. However, the integrated treatment extended the shelf life of the product by approximately 25-30 days under low-temperature storage conditions (4-6°C). Interestingly, the head-space gas analysis confirmed the development of passive modified atmosphere inside the package which also may be instrumental in maintaining the shelf-life. Microscopic analysis indicated loss of tissue integrity in unprocessed samples with surface wrinkling, seeds detachment, yellowing and significant textural loss. On the contrary, the processed samples remained fresh-like even after 25-30 days of storage under the same temperature while retaining the nutritional properties. The functional quality attributes including radical scavenging, reducing power as well as glucose uptake potential (in yeast-based assay) were observed to be substantially retained in the processed samples over the storage period. Besides, the activity of the enzymes involved in redox homeostatis including H^+-ATPase was found to be significantly maintained in processed samples indirectly indicating the integrity of plant tissue. Integration of the optimized procedure in the processing and supply chain of pointed gourd could be quite advantageous for stakeholders associated in production, marketing and trade of pointed gourd.

PP-121

Carbon uptake and growth analysis in different yeasts for non-alcoholic fermentation of juices

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The understanding of species-specific carbon uptake kinetics and yield is essential for optimizing parameters for non-alcoholic fermentation of juices for sugar reduction. This study systematically evaluated the physiological growth parameters of six yeast strains – *Saccharomyces cerevisiae*, *Kluyveromyces marxianus*, *Kluyveromyces lactis*, *Pichia fermentans*, *Debaryomyces occidentalis* and *Trichosporon cutaneum* cultured in Yeast Nitrogen Base (YNB) supplemented with 2% (w/v) glucose, fructose, sucrose and their combinations. Key kinetics parameters including final biomass concentration (X_{final}), biomass yield ($Y_{X/S}$), and substrate consumption rate (q_S) with specific growth rate (μ_{max}) were quantified. Results revealed distinct carbon preferences across species. *S. cerevisiae* produced maximal final biomass on fructose (15.91 g/L) and sucrose (15.76 g/L) driven by rapid growth (μ_{max}=0.53) for single-sugar conversion associated with undesirable formation of ethanol. *T. cutaneum* was the next strain in terms of consuming single-sugar glucose (8.94 $g.g^{-1}.h^{-1}$), fructose (7.90 $g.g^{-1}.h^{-1}$) and sucrose (8.39 $g.g^{-1}.h^{-1}$). When fermenting with mixed sugar feeds, *K. marxianus* was the most balanced strain for mixed sugar (Glucose and fructose) co-utilization, effectively avoiding catabolite repression (CI = 0.950) while sustaining rapid growth (μ_{max}=0.42) and stable biomass yields (0.20 $g.g^{-1}.h^{-1}$) which was ideal for mixed-sugar juices. The other strains *P. fermentans, D. occidentalis,* and *K. lactis* likewise could simultaneously consume sucrose and glucose mixtures (CI = 0.51, 0.56, and 0.96 respectively), enabling them optimal for sucrose-glucose rich juices. The carbon uptake kinetics and yield kinetics results showed the leads for tailored starter yeast selection for sugar reduction by fermentation in fruit juices of different sugar composition.

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PP-122

Dynamics and control of fungal spore bioaerosols in cold storage rooms

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Cold storage rooms are important for food quality, yet refrigerated conditions do not eliminate airborne fungal contamination. This study investigated fungal spore bioaerosol dynamics in cold storage environments and evaluated an integrated monitoring and control strategy combining microbiological, aerosol, molecular and computational approaches. Fungal loads were assessed in four cold rooms using passive air sampling. Viable fungal growth was detected in all rooms, with total counts ranging from 141 to 599 CFU/plate. CFD analysis revealed non-uniform airflow patterns and identified low-velocity regions associated with higher particle concentrations, thereby supporting the optimal placement of ionizers. The analysis also helped determine the suitable positioning and arrangement of stored produce within the cold room, considering differences between newly received and previously stored commodities, to promote uniform airflow and effective environmental control. The ionizer has been installed in the cold room, and pre/post-intervention OPC, Andersen impactor and PDA monitoring are ongoing. The study provides an integrated framework for profiling, understanding and mitigating fungal bioaerosols in refrigerated food storage environments overall.

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PP-123

Modulation of microbial dynamics in whole tilapia fish through irradiation-based hurdle technology

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Fish is highly perishable, leading to significant post-harvest losses and safety concerns (Sheng & Wang, 2021). This study evaluated an irradiation-based hurdle technology using high-throughput metagenomics to ensure the microbial safety and extend the shelf life of whole tilapia without compromising quality. Untreated control fish spoiled by day 7 (C_7_MX), shifting from initial dominance by Fusobacteria (19%; *Cetobacterium* 19%) and Actinobacteriota (12%; *Brachybacterium* 11%) to classical specific spoilage organisms (SSOs) dominated by Proteobacteria (33%) and Firmicutes (28%), primarily *Brochothrix* (15%), *Psychrobacter* (11%), *Shewanella* (11%), and *Acinetobacter* (9%). Conversely, irradiation suppressed initial SSO abundance (*Pseudomonas, Psychrobacter, Acinetobacter* to 0.2–0.4%) in treated fish (I_0_MX) while maintaining a diverse initial microflora comprising of beneficial gut microorganism *Cetobacterium* (6%), minor spoiler *Brachybacterium* (2%), and major aquatic and zoonotic pathogen *Streptococcus* (2%). Consequently, the hurdle treatment extended shelf life of whole tilapia to 30 days (I_30_MX), when spoilage finally occurred under the dominance of Proteobacteria (33%; *Psychrobacter* 33%) and Firmicutes (19%; *Romboutsia* 19%), alongside marked suppression of Actinobacteria. These metagenomic insights are in conformity with other studies and confirm that irradiation processing effectively curbs key spoilage-associated Proteobacteria, offering a viable strategy to mitigate post-harvest fishery losses (Mohamed, 2023).

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PP-124

CT-based three-dimensional modelling and microdosimetry for optimization of electron-beam irradiation of mango

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Achieving uniform dose distribution within individual food products is important for effective irradiation treatment of food. This becomes particularly relevant for electron-beam (e-beam) processing, where the particulate nature of the ionizing radiation results in finite penetration and characteristic build-up and depth-dose profiles, making dose deposition highly sensitive to product geometry, material boundaries, internal densities and heterogeneities. Some commonly irradiated fruits, such as mango, contain structurally distinct regions including skin, pulp, seed and internal air spaces, which differ in density and composition and can influence local energy deposition during e-beam irradiation. For such cases, microdosimetric assessment can provide information beyond conventional experimental dosimetry and aid in the identification of irradiation conditions suited to the treatment objectives for the particular food product. In this regard, radiation-transport simulations using realistic three-dimensional (3D) models of the food commodities provide a means of systematically investigating the influence of internal heterogeneity and optimizing irradiation protocols for varying beam energies and irradiation configurations. In the present work, X-ray CT datasets of three mango varieties – Banganapalli, Alphonso and Kesar – were reconstructed and segmented into their constituent anatomical regions, including skin, pulp, seed coat, embryo and internal air pockets, to develop realistic 3D models of the fruit. Both high-resolution voxel-based models and simplified ellipsoidal computational models representing the internal fruit structure were generated. These models were employed in radiation-transport simulations to obtain internal dose distributions for different e-beam energies and irradiation configurations. The resulting computational microdosimetry profiles reveal the influence of beam energy, irradiation geometry and internal fruit heterogeneity on dose deposition and enable irradiation conditions to be evaluated for different treatment objectives. Experimental microdosimetry using dosimetric films inserted at different locations within mango fruit was also performed under e-beam irradiation to complement and validate the computational findings. This work demonstrates the utility of CT-based microdosimetry for understanding internal dose distribution and guiding the optimization of e-beam irradiation protocols for heterogeneous food products.

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PP-125

Menaquinone-7 (vitamin K2MK-7) attenuates mineral metabolism imbalance and improves cardiovascular dysfunction in adenine-induced chronic kidney disease rats via modulation of the FGF-23 axis

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Chronic kidney disease (CKD) is associated with progressive renal dysfunction, disturbances in mineral metabolism, and cardiovascular complications. Fibroblast growth factor-23 (FGF-23) plays an important role in phosphate regulation and has been associated with cardiovascular remodelling in CKD. Vitamin K_2 menaquinone-7 (K2MK-7) has potential roles in mineral homeostasis and vascular health; however, its effects in CKD-associated cardiovascular dysfunction remain insufficiently explored. To investigate the effects of K2MK-7 on renal dysfunction, mineral metabolism imbalance, and cardiovascular alterations in an adenine-induced CKD rat model, with emphasis on the FGF-23 axis. Male Sprague-Dawley rats were divided into four groups (n=8): vehicle control, adenine-induced CKD, CKD treated with K2MK-7 (15 mg/kg), and CKD treated with K2MK-7 (30 mg/kg). CKD was induced using adenine (200 mg/kg/day, orally) for 28 days, followed by K2MK-7 treatment for 28 days. Renal function, serum and urinary biochemical parameters, FGF-23, NT-proBNP, blood pressure, ECG parameters, and histopathological changes in kidney, heart, and aorta were evaluated. Adenine administration produced marked renal dysfunction, characterized by increased serum creatinine and BUN, reduced eGFR, hyperphosphatemia, increased Ca×P, albuminuria, elevated FGF-23 and NT-proBNP, hypertension, and ECG alterations. K2MK-7 treatment improved renal and mineral metabolism parameters and reduced cardiovascular alterations. Greater improvement was generally observed in several parameters at 30 mg/kg. Histopathological examination showed attenuation of renal injury and fibrosis, with improvement in cardiac and vascular architecture following K2MK-7 treatment. K2MK-7 attenuated adenine-induced renal dysfunction, mineral metabolism disturbances, and cardiovascular alterations in CKD rats. These findings suggest that K2MK-7 may exert protective effects through modulation of the FGF-23–mineral metabolism axis and reduction of calcium-phosphorus imbalance.

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PP-126

Delineating the anti-inflammatory effect of Glycerophoshocholine (GPC) in gut-liver-brain axis of murine high-fat diet model

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The link between diet induced obesity (DIO), gut dysbiosis, and macrophage polarization remains poorly understood [1,2]. Glycerophosphocholine (GPC) was identified as an abundant metabolite in lean BALB/c mice as compared to obese C57BL/6 mice maintained on a high-fat diet. In this study, we investigate the anti-inflammatory effect of GPC in *in vitro* and *in vivo* conditions. The anti-inflammatory effect of GPC was confirmed in peritoneal macrophages which showed a switch from pro-inflammatory M1 (CD86) to anti-inflammatory M2 (CD163) phenotype. Further, *in vivo* experiments were carried out in both strains maintained on a high-fat diet. To assess inflammatory changes, gut (colon and caecum), liver and brain tissues were studied to differentiate tissue-specific resident (F4/80+ CD11b+) versus infiltrating (F4/80+ Ly6C+) macrophage population of both strains. It was observed that HFD group had decreased resident to infiltrating ratio as compared to ND group, which was restored with GPC supplementation (increased resident: infiltrating ratio). This suggests the role of GPC in shifting tissue niche towards anti-inflammatory phenotype. High fat diet also results in the gut barrier disruption, by decreasing short chain fatty acids (SCFAs; acetate, propionate, and butyrate), leading to gut dysbiosis. GPC supplementation restores this microbiota imbalance by restoring SCFAs to normal levels, hence improving gut health. These findings highlight GPC as a potential anti-inflammatory molecule, which may be an important mediator, linking DIO, gut dysbiosis and metabolic reprogramming, which might open up new targets for immune-modulatory treatments.

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PP-127

When chemotherapy compromises the heart: Can nature offer a solution?

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Despite significant advances in cancer therapeutics, treatment-associated cardiotoxicity remains a major challenge, particularly with anthracyclines such as doxorubicin (DX). Doxorubicin-induced cardiac injury, characterized by electrical disturbances, myocardial dysfunction, oxidative stress, inflammatory insult, and cardiac remodeling, can compromise long-term cardiovascular health leading to associated morbidity/mortality and limit its therapeutic outcomes. The identification of safe, naturally derived cardioprotective adjuvants that preserve anticancer efficacy is therefore of considerable clinical interest. In the present study, we investigated the therapeutic potential of allylpyrocatechol (APC), a bioactive molecule from *Piper betle*, in a syngeneic murine tumor model. Oral administration of APC in combination with DX significantly reduced tumor progression and overall tumor burden, with improved survival compared with DX monotherapy. Notably, APC co-administration attenuated DX-induced cardiac electrical abnormalities, including disturbances in cardiac rhythm. The combination improved atrio-ventricular conduction patterns, mitigated tachycardia-associated cardiac stress, and ameliorated alterations in cardiac contractile function. In addition, it enhances systolic ejection and diastolic filling with improved blood flow dynamic. Furthermore, APC significantly reduced DX-induced QTc prolongation, a marker associated with ventricular electrical instability, predisposing heart to failure. Importantly, it also attenuated cardiac hypertrophy. These cardioprotective effects were accompanied by improved redox homeostasis, enhanced antioxidant defense, (increasing the SOD, catalase, and reducing MDA levels) and modulation of inflammatory responses, as evidenced by alterations in pro- and anti-inflammatory markers (reducing TNF-α, IL-6, and increasing IL-10). Collectively, our findings demonstrate that APC exhibits promising cardioprotective, and antitumor-supportive effects *in vivo* and may represent a potential naturally derived adjuvant for mitigating DX-associated cardiovascular toxicity while preserving its therapeutic index.

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PP-128

Identification and characterization of a novel two exon *LAMC2* deletion in severe junctional epidermolysis bullosa

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Epidermolysis bullosa (EB) is a group of inherited skin fragility disorders characterized by blistering after minimal mechanical trauma. Severe junctional EB (JEB3B; OMIM #619786), is an autosomal recessive disorder caused by pathogenic variants in *LAMC2*, which encodes the γ2 chain of laminin-332, a critical component of the epidermal-dermal junction. We evaluated a neonate with severe blistering and aplasia cutis who had a rapidly progressive clinical course and succumbed at 46 days of age. Initial skin biopsy immunofluorescence raised the possibility of epidermolysis bullosa simplex. However, trio whole exome sequencing did not identify a plausible single-nucleotide or small insertion/deletion variant whereas BAM-based read-depth analysis revealed absent or reduced coverage across exons 18 and 19 of *LAMC2*, suggesting a structural variant. Long-range PCR confirmed a homozygous deletion in the proband and heterozygosity in both parents, consistent with autosomal recessive inheritance. Oxford Nanopore sequencing of the PCR product precisely defined the breakpoints of a novel 1609-bp deletion encompassing exons 18 and 19 and flanking intronic sequences, NC_000001.11:g.183237256_183238864del. The deletion is predicted to cause a frameshift and premature termination codon, resulting in the loss of functional laminin γ2 chain and disruption of functional laminin-332. Prenatal testing in the subsequent pregnancy confirmed the same homozygous deletion. Following genetic counselling the couple was offered a reproductive choice including adoption or IVF using donor oocyte and donor sperm. This study highlights the value of integrating BAM-based read depth, long range PCR and long read sequencing for detecting and resolving pathogenic structural variants that may be missed by conventional WES variant analysis.

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PP-129

The chimeric TLR2/NOD2 agonist CL429 drives macrophage activation and induces durable trained immunity that protects against systemic candidiasis

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Trained immunity is the durable functional reprogramming of innate immune cells by a primary stimulus, and it is coupled to metabolic shifts that supply substrates for chromatin modification. Most characterized inducers engage a single pattern recognition receptor. Here we show that CL429, a synthetic conjugate engaging TLR2 and NOD2 simultaneously [1], induces trained immunity [2] in human peripheral blood mononuclear cells and in mice. CL429 drove macrophage maturation with a cytokine output lower than that of LPS, sustained MAPK activation, and a metabolic shift characterized by reduced glycolytic capacity and reserve alongside accumulation of S-adenosylmethionine and depletion of acetyl-CoA. Human monocytes trained with CL429 at 5 ug/ml and restimulated with LPS six days later produced more IL-6 and TNF-alpha than untrained cells. This enhancement required PI3K, mTOR and HIF-1alpha during the training window but was independent of MyD88, NOD2 and NF-kB, which were required instead for the acute inflammatory response, and it survived inhibition of fatty acid oxidation, glutaminolysis, mitochondrial pyruvate import and glycolysis. Mice injected subcutaneously with CL429 retained an amplified bone marrow derived macrophage response for at least 60 days and survived systemic Candida albicans challenge that was lethal to untrained animals. H3K27ac ChIP-seq of trained bone marrow derived macrophages revealed widespread loss rather than gain of acetylation at signaling loci, consistent with the depleted acetyl CoA pool and pointing to methylation rather than acetylation as the carrier of the CL429 memory.

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PP-130

Mechanistic insight into the function of a cognate redox pair Alr2204-Alr2205 that enhances oxidative stress tolerance in cyanobacteria

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Cysteine-mediated catalytic reactions play a vital role in sustaining the overall cellular redox environment in photosynthetic organisms. In *Anabaena* sp. PCC 7120, the genes encoding thioredoxin reductase (TR, *alr2204*) and thioredoxin (Trx, *alr2205*) are located adjacent to each other. Interestingly, these two proteins are evolutionarily closer to the TR and Trx domains of the plant NADPH-thioredoxin reductase C (NTRC), respectively. This study focuses on the functional characterization of Alr2204 and Alr2205 from *Anabaena* and their roles in oxidative stress tolerance. Overexpression of either Alr2205 (An2205+) or Alr2204 (An2204+) in *Anabaena* conferred enhanced protection against H_2O_2, methyl viologen (MV), and cadmium (Cd), suggesting that the reductase functions of these proteins are essential for cellular protection. Biochemical analysis revealed Alr2204 to be a FAD-associated, predominantly alpha-helical protein with NADPH-dependent TR activity, whereas Alr2205, an atypical thioredoxin-containing a non-canonical 'CPSC' active-site motif, exhibited disulfide reductase activity. Given their genomic proximity and sequence similarity, it was pertinent to investigate whether Alr2204 and Alr2205 form a cognate redox pair, with Alr2204 capable of donating electrons to Alr2205. Our results indicate that Alr2204 not only physically interacts with Alr2205 but also establishes an Alr2204–Alr2205 redox couple that facilitates the activity of 2-Cys Prx, a key regulator of redox homeostasis in *Anabaena*. Furthermore, co-expression of Alr2204 and Alr2205 as a single polypeptide in *Anabaena* led to the *in vivo* reduction of 2-Cys Prx, emphasizing the functional coupling of these two proteins. Together, these findings demonstrate that Alr2204 and Alr2205 constitute a functional redox couple crucial for maintaining edox homeostasis in this organism.

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PP-131

Structure-based identification of small-molecule ERRα modulators with potential relevance to mitochondrial biogenesis

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Mitochondrial dysfunction is closely associated with impaired cellular energy metabolism and contributes to a range of metabolic and degenerative disorders. The estrogen-related receptor alpha-peroxisome proliferator-activated receptor gamma coactivator 1-alpha (ERRα-PGC-1α) axis is a key regulator of mitochondrial biogenesis and oxidative metabolism, making it a relevant target for identifying modulators of mitochondrial function. In this study, a multistep computational and cellular screening workflow was used to identify candidate small molecules targeting this pathway. A molecular library was generated using a transformer-based approach trained on chemical structures of reported modulators associated with ERR and PGC-1α signalling. Generated molecules were screened for predicted pharmacokinetic, drug-likeness, and toxicity properties, including mitochondrial membrane potential disruption. Candidates with the most favourable combined profiles were assessed for predicted binding orientations and interactions within the human ERRα ligand binding domain. AutoDock Vina docking scores and ligand efficiency values were used for prioritisation, followed by analysis of key receptor-residue interactions. Selected protein ligand complexes were further evaluated by molecular dynamics simulations for short-term conformational stability and by single-frame MM/GBSA for comparative energetic assessment. The biological suitability of the selected compounds was subsequently examined in C2C12 skeletal muscle cells. MTT analysis identified sub-cytotoxic concentrations suitable for further evaluation. Treatment with the selected compounds also modulated PGC-1α and mitochondrial transcription factor A (TFAM), indicating effects on molecular markers associated with mitochondrial biogenesis. Overall, this workflow integrated molecular generation, computational prioritisation, structural assessment, and preliminary cellular validation. The selected compounds represent promising candidates for further investigation of ERRα associated regulation of mitochondrial biogenesis.

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PP-132

Single cell clones of human T-lymphocytes for genomic integrity assessment in individuals chronically exposed to high level natural radiation

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Populations residing in high-level natural radiation areas (HLNRAs) of Keralam are exposed to chronic low-dose ionizing radiation for generations. However, the health effects of low-dose and low-dose-rate radiation exposure <100 mSv remain elusive, and their impact on genome integrity is poorly understood. Clones of human T-lymphocytes under long term culture *in vitro* may act as surrogate to assess genomic integrity in cells many generations after chronic low-dose radiation exposure. Single-cell clones were established from peripheral blood lymphocytes of individuals from normal-level (NLNRAs, n=8) and HLNRAs (n=6) in microtiter plates with irradiated TK6LLrrL feeder cells for about 30 days. Clonal descendants of NLNRA and HLNRA were examined using CBMN-cytome assay for micronuclei (MN), nucleoplasmic bridges (NPBs), and nuclear buds (NBUDs). Two-way ANOVA evaluated the effect of Culture Time (CT) and Area (NLNRA/HLNRA), and the Area × CT interaction. MN frequency increased from 11.9 to 22.4 in NLNRA and from 16.0 to 23.2 in HLNRA, with a significant effect of CT (p=0.002). Similarly, NPB frequency increased from 3.3 to 16.8 in NLNRA and from 3.3 to 12.9 in HLNRA, showing significant CT effect (p <0.001). However, Area × CT interactions were non-significant for MN (p=0.46) and NPB (p=0.22), indicating comparable increase in these markers over time in NLNRA and HLNRA. The NBUD frequency increased from 0.3 to 1.9 in NLNRA but decreased from 2.7 to 0.75 in HLNRA, with no significant CT effect (p=0.74) but with significant Area × CT interaction (p=0.018), indicating population-dependent difference. These results show that clonal expansion induces measurable changes in genomic integrity biomarkers. However, cytogenetic markers like NPB and MN are not influenced by chronic low dose radiation exposure. The study suggests the use of the clonally expanded T-lymphocyte system as a model for assessing genomic integrity in low-dose exposed cells after multiple cell cycles *in vitro*.

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Study on age dependency of chromosomal aberrations in humans from high level natural radiation areas of south-west coast of Keralam

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The population residing in the high-level natural radiation areas (HLNRA) of Keralam (with annual external gamma radiation levels of >1.5 mGy/year to over 150 mGy/year) offers a distinct potential to study the direct biological effects of chronic low dose exposure in humans. The aging pattern was investigated in whole blood samples of young (< 25 years) and aged (>60 years) individuals from normal-level (NLNRA) and HLNRA using dicentric chromosomal assay (DCA) and fluorescence in situ hybridization (FISH) based translocation analysis. Blood samples were collected from 23 healthy volunteers categorized into four groups: (i) Young HLNRA individuals (KHY: >15 mGy/y, n=6), (ii) Aged HLNRA individuals (KHA: >15 mGy/y, n=5), (iii) Young NLNRA individuals (KNY: <1.5 mGy/y, n=6), and (iv) Aged NLNRA individuals (KNA: <1.5 mGy/y, n=6). Lymphocyte cultures were established and slides for the DCA and FISH assays were prepared 51 hours post-culture initiation. The dicentric chromosomes showed a frequency (per 1000 cells) of 1.37 ± 0.41 in KHY, 1.53±0.62 KNY, 1.07 ± 0.42 KHA and 1.08 ± 0.34 in KNA individuals. Poisson regression analysis did not suggest any relationship between frequency of dicentrics and background radiation dose levels (P=0.69) or age of individuals (P=0.14). Chromosomal translocations detected by FISH showed a frequency of 3.45 ± 0.95 in KHY, 2.27±0.9 in KNY, 5.98 ± 2.36 in KHA, 6.79 ± 2.02 in KNA individuals. Poisson regression analysis did not indicate any relationship between frequency of stable translocations and background radiation dose levels (P=0.69). However, the age of individuals showed statistically significant difference in translocation frequency (p=0.0).

PP-134

Living with natural radiation for generations: Evidence from Kerala HLNRA reveals genomic stability, efficient DNA repair, and adaptive biological responses in chronically exposed individuals.

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Human populations living in the monazite-rich south-western coastal belt of Kerala, India, have been chronically exposed to elevated natural background radiation for generations, providing a unique model to investigate the biological effects of long-term low-dose radiation exposure. The High-Level Natural Radiation Areas (HLNRA) of Kerala, characterized by thorium-rich beach sand deposits and annual doses ranging from <1 to 45 mGy/year, have been the subject of multidisciplinary investigations for more than three decades. Large epidemiological studies in the High-Level Natural Radiation Areas (HLNRA) have consistently shown no increase in congenital abnormalities or cancer incidence, and comparable reproductive outcomes when compared with adjacent Normal-Level Natural Radiation Areas (NLNRA). Cytogenetic analyses revealed no significant increase in chromosome aberrations or other indicators of genomic instability with increasing radiation exposure. Molecular studies demonstrated no elevation in baseline DNA damage, mutation frequency, or germline mutational burden among chronically exposed individuals. In contrast, our investigations have identified evidence of radio-adaptive biological responses. Transcriptomic analyses revealed dose-responsive modulation of genes involved in DNA damage response, DNA repair, cell-cycle regulation, chromatin remodeling, apoptosis, and immune function. Telomere studies demonstrated preserved telomere length and adaptive regulation of shelterin and DNA repair genes. Functional investigations showed lower induction and more efficient repair of radiation-induced DNA double-strand breaks in HLNRA individuals, accompanied by enhanced expression of key DNA repair genes. Recent genomic, epigenetic, telomere, and transcriptomic studies further support enhanced genome maintenance mechanisms and possible *in vivo* radio-adaptive responses in this population. Collectively, findings from the Kerala HLNRA cohort indicate that chronic exposure to natural low-dose radiation, even over a lifetime, is not associated with detectable adverse health or genetic effects. Instead, the evidence suggests activation of protective metabolic and molecular pathways that promote genomic stability and biological homeostasis. These studies provide important insights into human responses to chronic low-dose radiation and contribute significantly to the global understanding of low-dose radiation biology and health risk assessment.

PP-135

Molecular cross-talk between microbial short-chain fatty acids and tryptophan metabolites in immune regulation

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The metabolites produced by the gut microbiome act as a complex language of chemistry through which microbes can interact with the immune system of their hosts. However, it is not well understood how metabolites belonging to different chemical families coordinate in terms of regulation through common signaling pathways. In this study, we used a comparative and integrative approach to study two key microbial signaling languages, short-chain fatty acids (SCFAs) and metabolites derived from tryptophan. SCFAs impact the physiology of their hosts through G-protein-coupled receptors and epigenetics, whereas metabolites derived from tryptophan by the gut microbiota target signaling pathways related to the aryl hydrocarbon receptor (AhR) and the pregnane X receptor (PXR). To compare these two different modes of signaling, docking, molecular dynamics, and network pharmacology were used to understand the mode of action of metabolites and identify potential convergent biological pathways. At the same time, physicochemical, pharmacokinetic, and ADMET properties of molecules were predicted to evaluate their potential biological availability. The network analysis also showed a convergent effect on the pathways of maintaining epithelial integrity, regulating inflammation, and the activity of immune cells, although there was considerable diversity among the metabolites based on their structural features. Notably, the computational approaches used here were followed up by an experimental validation of the impact of the individual and combined metabolites in a mouse lymphocyte system, thus setting a stage for evaluating the immunoregulatory functions of these metabolites. Taken together, our data indicate that the chemical language of host-microbiome interaction is not uniform. On the contrary, SCFAs and tryptophan metabolites comprise two different but interrelated chemo-languages.

PP-136

Valproic acid targets GSK-3β to promote WNT-dependent intestinal regeneration and radioprotection

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Radiation-induced injury to the gastrointestinal tract continues to be a major toxicity for radiotherapy of abdominal and pelvic tumours due to the loss of epithelium, disruption of barriers, inflammation, and stem cell failure to regenerate epithelial structures. Glycogen synthase kinase-3β (GSK-3β), a critical repressor of Wnt/β-catenin signaling, plays a significant role in controlling intestinal stem cell fate and epithelial regeneration. In this study, we showed valproic acid (VPA) as a GSK-3β regulator to improve regeneration of irradiated intestines employing an *in silico*, *in vitro*, and *in vivo* approach. Molecular docking studies suggested a stable binding of VPA with GSK-3β ATP binding site (ΔG = −4.7 kcal/mol; Ki ≈ 0.36 mM) through interaction with ATP coordinating residues (Val139, Gly67, Lys89, Asp137, Tyr138). A 200-ns MD trajectory showed a stable VPA-GSK-3β complex and persistent hydrogen bonding, supporting electrostatic stabilization. MM/PBSA binding energies for VPA (-34.16 kcal/mol) were favorable than the native ligand and known inhibitor (native: -35.09 kcal/mol, known inhibitor: -26.99 kcal/mol). Principal component analysis highlighted ligand-dependent shifts in GSK-3β conformational dynamics. Network modelling connected GSK-3β inhibition to β-catenin stabilization and dampening of NF-κB–driven inflammatory circuits. *In vivo*, VPA (100 mg/kg. b. wt) significantly improved survival after whole-body irradiation (66% vs. 33% in irradiated controls), reduced intestinal permeability, and preserved jejunal crypt–villus architecture. VPA also mitigated colon shortening following abdominal irradiation. Together, these results support a model in which VPA exerts moderate, indirect inhibition of GSK-3β, nuclear translocation of β-catenin that favors Wnt-mediated regeneration, and reduces inflammatory responses in the irradiated intestine.

PP-137

Reprogramming lymphocytes *in vivo* with an injectable scaffold provides therapeutic radioprotection and promotes tissue recovery

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Peripheral blood lymphocytes consist of various lineages of B cells and T cells. Subsets of regulatory T cells and cytotoxic T cells have been shown to support tissue regeneration in the kidney, liver, brain, skeletal muscle, heart, and bone marrow. Conversely, allogeneic lymphocytes can exacerbate tissue toxicity and cause graft-versus-host disease (GvHD). The use of lymphocytes for the treatment of radiation-induced injury has not been systematically examined. In this study, we evaluated allogeneic, xenogeneic and TCR transgenic lymphocytes as therapeutic agents for mitigating whole-body irradiation (WBI) induced mortality and cytokine storms in mice. We utilized an injectable scaffold carrying lentiviral vectors to convert xenogeneic lymphocytes into mis-targeted T cells that do not recognize any specific cognate ligand in the host. Strikingly, the administration of unmodified allogeneic and xenogeneic lymphocytes 4 to 24 hours post-irradiation severely exacerbated radiation-induced pathology, precipitating heightened inflammatory cytokine surges, profound proteomic disruption, and systemic inflammation. Conversely, in situ reprogramming via the lentiviral scaffold completely reversed this detrimental trajectory. Mice receiving the scaffold and xenogeneic lymphocytes exhibited robust rescue from lethal 8.5 Gy whole-body irradiation toxicity, marked by normalized inflammation scores, restoration of the serum proteome, and a resurgence of key regenerative cytokines (IL-22 and IL-12). Together, these findings establish the unprecedented utility of mis-targeted chimeric antigen receptor T cells (mis-CAR T cells) as a transformative *in vivo* strategy for therapeutic radioprotection and tissue regeneration. While these findings establish the proof-of-concept for *in situ*–engineered mis-targeted CAR T cells in mitigating acute radiation syndrome, future studies will be required to evaluate long-term biosafety, vector biodistribution, and efficacy across diverse preclinical models prior to clinical translation.

PP-138

Unveiling the bioremediation potential and molecular insights of biofilm-forming marine bacterium *Stutzerimonas stutzeri* BCG2406 for phenanthrene degradation and Pb(II) removal

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Marine biofilms serve as important reservoirs of stress-resilient bacteria and provide dynamic microenvironments that foster microbial adaptation to environmental stress, offering a sustainable approach to bioremediation of contaminated coastal environments. The present study explores bacterial community diversity within marine biofilms at the seawater-substratum interface along the coastal region of Odisha, India. Among 145 bacterial isolates, *Stutzerimonas stutzeri* BCG2406 emerged as a potent biofilm-forming strain with phenanthrene-degrading and Pb(II)-resistant capabilities. SEM, CLSM, and AFM analyses revealed heterogeneous biofilm development of *S. stutzeri* BCG2406 on different substrata, with ceramic substratum exhibiting the maximum biofilm thickness (53.12 ± 6.45 µm), along with the highest surface roughness (172.31 ± 24.57 nm) and peak height (724.58 ± 19.67 nm). These findings indicated that the substratum properties influence bacterial attachment and biofilm development. The stress-responsive potential of *S. stutzeri* BCG2406 was supported by significant upregulation of genes such as *bcsC* and *algZ* for biofilm formation, *catA* and *pcaG* for phenanthrene degradation, and *czc* for Pb(II) efflux. Further, the biofilm mode achieved 87.85 ± 1.68% phenanthrene degradation and 94.57 ± 7.3% Pb(II) removal within 3 days, confirming efficient pollutant removal under environmental stress conditions. This study highlights the stress resilience and bioremediation potential of *S. stutzeri* BCG2406 for efficient phenanthrene degradation and Pb(II) removal in contaminated coastal environments, and establishes marine biofilms as effective biological approaches for the simultaneous remediation of organic and heavy-metal pollutants.

PP-139

PchR-like transcription regulators in *Nostoc* sp. PCC 7120: Integrative genomic, transcriptional, and regulatory analysis

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PchR is an AraC-family transcription regulator in *Pseudomonas aeruginosa* that positively regulates pyochelin siderophore biosynthesis and transport under iron limitation[1]. Of the 22 AraC-family regulators previously identified in *Nostoc* sp. PCC 7120[2], a few were reported to show similarities to PchR[3-5], but the number of PchR-like regulators, their transcriptional responses and regulation remain largely unknown. Here, we investigated all 22 AraC-family regulators through genomic analysis to identify PchR-like regulators, followed by transcriptional and regulatory analyses of representative regulators. Phylogenetic analysis of the 22 regulators, together with PchR from *P. aeruginosa* and AraC from *E. coli*, placed 17 regulators closer to PchR, whereas the remaining five were more closely associated with AraC. Sequence, motif, and domain analyses further supported this grouping. Neighbouring-gene analysis showed that all 17 PchR-like regulators were close to siderophore transport genes, while only one of the remaining five was near putative siderophore biosynthesis genes. Transcript analysis of representative PchR-like regulators under siderophore-inducing conditions such as iron-, nitrogen-, and copper-limitation, cadmium, and oxidative stress revealed differential, condition-specific transcriptional responses, with mostly upregulated expression. Promoter analysis identified putative FurA-, NtcA-, and LexA-binding sites in their upstream regions, and the regulations were further assessed by EMSA and qRT-PCR using FurA-, NtcA-, and LexA-overexpressing strain. The results showed NtcA regulated only few PchR-like genes, whereas broader regulation was observed for FurA and LexA. Together, these findings provide insights into the diversity, transcriptional responses, and regulation of PchR-like regulators in *Nostoc* and a basis for future studies to elucidate their condition-specific roles in siderophore regulation.

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PP-140

Molecular signatures of interaction between multimetals and extracellular polymeric substances (EPS) in *Pseudomonas aeruginosa* CSA06P for heavy metal remediation

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The bacterial biofilm associated extracellular polymeric substances (EPS) matrix serves as a chemically reactive interface for heavy metal interactions through its diverse biochemical constituents and functional groups[1]. The present study investigated the structural, physicochemical, and molecular interactions of EPS from the marine biofilm-forming bacterium *Pseudomonas aeruginosa* CSA06P with Pb(II), Cr(VI), and Hg(II). Upon multimetal exposure, the EPS exhibited altered biochemical composition and surface compaction, accompanied by metal-specific elemental signatures detected through FESEM-EDS analysis. Moreover, it transitioned from an amorphous to semi-crystalline structure (CI_{XRD} – 0.576) with reduced thermal stability (weight loss of 65.49%), while shift in zeta potential (-20.37 to -6.46 mV) and increased mean particle (384.53 to 903.83 nm), indicated reduced surface electronegativity and enhanced aggregation of EPS macromolecule. Further, ATR-FTIR and ^{1}H NMR analyses revealed the involvement of EPS-associated hydroxyl, carboxyl, amide, and carbohydrate groups in multimetal interactions, while protein conformational rearrangements were evident from reduced α-helical content and increased random coil content. XPS analysis confirmed the presence of Pb(II), Cr(III)/Cr(VI), and Hg(0)/Hg(II) on the EPS surface, suggesting partial reduction during metal binding. The 3D-EEM analysis revealed concentration-dependent fluorescence quenching of tryptophan-like fluorophores, predominantly through static quenching[2]. These molecular interactions were corroborated by EPS-mediated removal of Pb(II) [88.21%], Cr(VI) [45.39%], and Hg(II) [55.38%], with adsorption fitting the Langmuir isotherm ($R^2 \geq 0.997$) and pseudo-second-order kinetic ($R^2 \geq 0.998$) models. Collectively, these findings elucidate the structural and molecular interactions underlying EPS-mediated multimetal binding and sequestration, highlighting its potential as a biosorbent for environmental bioremediation.

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PP-141

Decoding the molecular machinery involved in Carbaryl pesticide uptake and metabolism in *Pseudomonas* sp. C5pp

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Carbaryl is a widely used carbamate pesticide that poses environmental risks due to its persistence and toxicity. *Pseudomonas* sp. C5pp, a soil bacterium can metabolise Carbaryl as sole source of carbon as well as nitrogen. Carbaryl is hydrophobic (water solubility 40 $mg.L^{-1}$) and cannot cross the outer-membrane barrier *via* partitioning due to lipid asymmetry or *via* water filled porins. We identified McbT, a COG4313 family outer membrane protein to be involved in Carbaryl uptake, the first essential step in Carbaryl metabolism[1]. In the periplasm, Carbaryl hydrolase converts Carbaryl to 1-naphthol, a toxic intermediate which diffuses into the cytoplasm where a key enzyme 1-naphthol-2-hydroxylase (1NH) detoxifies 1-naphthol to 1,2-dihydroxynaphthalene. Homology model guided site-directed mutagenesis of 1NH revealed key residues involved in FAD binding, substrate entry tunnel, active site and dimerization[2]. During Carbaryl degradation in strain C5pp, metabolic pathway intermediates like salicylate and gentisate are transiently effluxed out and re-uptaken. We identified McbM, an AAHS type MFS transporter in the inner membrane to be involved in uptake of gentisate. Understanding of transporters involved in uptake of Carbaryl and metabolic intermediates, and reaction mechanism of key enzyme 1NH in strain C5pp advances our understanding of bacterial adaptation to toxic xenobiotics and has implications in devising strategies for sustainable bioremediation.

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PP-142

A highly active phosphate-irrepressible alkaline phosphatase PafA from *Chryseobacterium* sp. strain PMSZPI facilitates efficient uranium bioprecipitation

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Bacteria require phosphate (P) for survival and growth and the preferred source of exogenous P is inorganic phosphate (Pi). They overcome environmental Pi scarcity through expression of Pi-dependent phosphatases, which cleave the Pi moiety from various organophosphorus compounds (1). Unlike other alkaline phosphatases in bacteria, PafA, a phosphate-insensitive phosphatase is fully functional in the presence of excess phosphate. In this study, PafA phosphatase from a Bacteroidota bacterium, *Chryseobacterium* sp. PMSZPI, isolated from uranium (U) enriched environment was purified to homogeneity and biochemically characterized. PafA was cloned in *E. coli*, expressed and purified as a ~60 kDa recombinant protein. The phosphatase activity of PafA in recombinant *E. coli* cells was phenotypically detected on phenolphthalein diphosphate (PDP)-methyl green (MG) agar plates. Size-exclusion chromatography of PafA revealed two protein species with molecular masses of 332.52 kDa and 165.95 kDa, corresponding to the pentameric and trimeric forms of PafA, respectively. The zymogram analysis exhibited PafA to be catalytically active as a multimer. The activity of PafA was evaluated at pH, ranging from 3-10 using p-nitrophenyl phosphate as a substrate and maximum activity was found at pH 9. Complete loss of enzymatic activity was observed after treatment with 25 μM EDTA. The supplementation with 100 μM Zn^{2+}or Ca^{2+}or Mg^{2+}or Co^{2+}, partially restored the activity. PafA overexpressing *E. coli* cells demonstrated efficient uranium precipitation (~93%) from 1 mM U solution in presence of 5 mM β-glycerophosphate in 20 mM MOPS buffer (pH 8.0) within 5 h. SEM analysis revealed the formation of cell-bound uranyl phosphate precipitates with the EDX spectroscopy confirming the association of U, as indicated by the characteristic U Mα peak at 3.14 keV. This study shows that PafA is a metal-dependent phosphatase having optimal activity at alkaline pH that is a potential biocatalyst for phosphate-mediated uranium biomineralization.

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PP-143

Structural basis of Griffithsin–gp120 engagement- integrating structural, energetic, and functional analyses

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GRFT (griffithsin), a mannose-binding lectin isolated from *Griffithsia*, is known to recognize the high-mannose glycans present on the HIV gp120 surface glycoprotein and block virus entry. However, the role played by specific GRFT residues in this process and the effect of altering such residues on binding properties is not clear. In this study, a combination of structural docking, molecular dynamics (MD) simulation, MM/GBSA free energy calculation, physicochemical and ADMET profiling, and lectin ELISA was employed to investigate the recognition between GRFT and gp120 and the effects caused by the substitutions at D30, D70, and D112 positions. According to GRAMM docking, all mutants kept the same global binding conformation with slight changes in docking score from 576 in WT to 563-571 in single mutants and 565 in triple mutant. MD simulations further supported persistent stable complex formation, characterized by RMSD, RMSF, and sustained H-bonding interactions. Further MM/GBSA analysis yielded favorable predicted binding free energies across the variants, ranging from -49.96 kcal/mol for WT and Mut30 to -45.24, -42.03, and -34.22 kcal/mol for Mut70, Mut112, and the triple mutant, respectively. WT GRFT (chain A) comprised 121 residues, with a molecular mass of 12.69 kDa, pI of 5.4 ± 0.1, and net charge of -3.1 ± 0.3 at pH 7.4; mutation progressively shifted the predicted electrostatic state toward neutrality, reaching pI 7.4 ± 0.4 in the triple mutant. Lectin-ELISA established quantitative gp120 recognition and showed an approximately 39.5% reduction following Endo Hf treatment, supporting a substantial contribution of N-glycans to GRFT recognition. Taken together, these studies have characterized structural, energy-based, and glycan-specific components of GRFT-gp120 interaction specificity, thereby providing a rational basis for designing GRFT derivatives with antiviral or diagnostic properties.

PP-144

Integrated transcriptomic and *in silico* identification of novel small secreted cysteine-rich proteins (SSCPs) in *Trichoderma virens*

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Trichoderma virens, a well characterized biocontrol agent, secrets a diverse repertoire of small secreted cysteine-rich proteins (SSCPs) during its interaction with plant and pathogens. However, this group of proteins remains poorly studied and largely functionally uncharacterized. Here, we developed an integrated *in-silico* pipeline combining experimental transcriptomic data with bioinformatics-based functional characterization for identification of novel SSCPs in *T. virens*. RNA-seq datasets from *T. virens* challenged with the three ecologically important phytopathogens, *Rhizoctonia solani*, *Pythium spp.* and *Sclerotium rolfsii* were analyzed for differential gene expression. Bioinformatics analysis of *Trichoderma virens Gv*29-8 proteome generated a curated SSCP dataset comprising 324 proteins, filtered using the criteria: length ≤400 amino acids, ≥4 cysteine residues, presence of signal peptide and absence of transmembrane domains. This dataset compared with the RNA-seq results to identify SSCPs that were consistently upregulated or downregulated across the three pathogen-challenge conditions using thresholds of adjusted $p<0.05$ and $log2FC| \geq 1$ or ≥ -1. Candidate SSCPs were further characterized based on their expression patterns, functional novelty using BLAST P homology searches, conserved domain prediction using Inter Pro, structural prediction using AlphaFold and analysis of cysteine-rich scaffolds. The resulting candidate set provides a focused group of SSCPs for further experimental validation. More broadly, this integrated R-based bioinformatics pipeline can serve as a useful screening framework for prioritizing candidate secreted proteins from other genomic and transcriptomic datasets and may be adapted for secretome studies in other organisms.

PP-145

Development of a hyper-sporulating mutants from commercial composting strain *Trichoderma koningiopsis* Trombay 1 through gamma ray mutagenesis

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Trichoderma spp. are prolific producers of hydrolytic enzymes and are widely used in agricultural and environmental biotechnology. We previously isolated and commercialized *Trichoderma koningiopsis* Trombay 1 for accelerated composting of dry leaves, floral residues, and kitchen waste. However, conidiation in Trichoderma is strongly influenced by light, which can constrain conidial production during large-scale biomass production and formulation. In this study, gamma-radiation-induced mutagenesis was used to generate improved strain of commercial *T. koningiopsis*. Two mutants with enhanced sporulation were isolated and characterized. One mutant exhibited profuse sporulation under dark conditions but lost cellulolytic activity, whereas the second showed hyper-sporulation under light while retaining cellulose-degrading ability and composting potential. Transcriptome analysis revealed that conidiation involves coordinated regulation of environmental sensing, signal transduction, transcriptional regulation, secondary metabolism, stress responses, and cellular energy metabolism. These findings indicate that enhanced sporulation is governed by multiple interacting regulatory pathways. Overall, gamma-ray-induced mutagenesis offers an effective approach for developing hyper-sporulating Trichoderma strains while retaining desirable biotechnological traits. The high-sporulating, cellulolytic mutant has potential for improving conidial production and formulation efficiency of *T. koningiopsis*-based composting technologies.

PP-146

Molecular, structural, and immunoinformatic characterization of the *Mycobacterium tuberculosis* ESX-1 secretory protein EspE (Rv3864): Implications for host-directed interventions in tuberculosis

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Tuberculosis remains a major global health threat, requiring novel host-directed strategies. The ESX-1 type VII secretion system secretes virulence factors critical for phagosomal rupture and immune evasion. Among them, EspE (Rv3864) plays a dual role in transcriptional regulation and membranolytic activity. We evaluated EspE's structural stability, immunogenicity, and capacity to modulate macrophage inflammatory pathways. EspE was computationally evaluated for 3D physicochemical stability, virulence, and immunogenic epitopes (B-cell and T-cell/MHC-I/MHC-II). Codon-optimized espE was cloned into pET28a (+), expressed in *E. coli* BL21(DE3) and Rosetta strains, and purified via Ni-NTA chromatography. Recombinant EspE (rEspE) was evaluated for membranolytic activity via an *in vitro* hemolysis assay and used to stimulate THP-1 macrophages to quantify cytokine profiles and nitric oxide production via Griess nitrite assay. *In silico* structural analyses confirmed EspE's structural stability, high antigenicity, and strong binding affinity to HLA alleles (HLA-B*53:01, HLA-DRB1*15:01, HLA-DRB5*01:01). Recombinant expression was optimized at 37°C with 0.1 mM IPTG. Functional assays revealed dose-dependent hemolytic activity, confirming membrane disruption. Additionally, espE significantly altered THP-1 macrophage cytokine secretion and modulated extracellular nitrite levels, proving its active role in host immune regulation. EspE was successfully characterized, cloned, and purified. Structural, immunoinformatic, and functional immunology results highlighted by hemolytic activity and nitric oxide modulation, positioning espE as a promising target for structural biology-guided host-directed tuberculosis interventions.

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Characterization of polysaccharide utilization loci (PUL) of a macroalgae-associated *Bacillus stercoris* RS73_I1 using a whole genome sequencing approach

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We isolated a bacterial strain, *Bacillus stercoris* RS73_I1, from the surface of the marine red algae *Gracilaria multifurcata* from the Visakhapatnam coast of the Bengal coast, capable of degrading various polysaccharides, including those in red algal biomass. In the present study, we characterized the polysaccharide utilization loci (PUL) present in the genome of *B. stercoris* RS73_I1 using a next-generation sequencing approach. The draft genome was analyzed using the dbCAN3 web server to identify CAZymes and Carbohydrate-active Gene Clusters (CGCs) responsible for polysaccharide degradation. A total of 94 CAZymes were identified in the genome, including five different classes, i.e., 40 glycoside hydrolases (20 families), 35 glycosyl transferases (11 families), seven polysaccharide lyases (5 families), six carbohydrate binding modules (4 families), and six carbohydrate esterases (3 families). Further analysis of PUL in dbCAN3 identified 73 CGCs in the genome that are capable of degrading pectin, starch, xylan, cellulose, chitin, peptidoglycan, lignin, and sulfoquinovoside. In addition, SulfAtlas, InterProScan, and signalP analyses identified five specialized sulfatases, indicating the capacity to degrade complex algal sulfated polysaccharides. Experimentally, we confirmed the strain's capability for various types of polysaccharide degradation using qualitative and quantitative analyses. The strain RS73_I1 showed activities (U/ml) for agarase (18.11 ± 2.65), amylase (19.88 ± 1.00), carrageenase (14.78 ± 1.10), cellulase (70.90 ± 8.47), pectinase (84.32 ± 13.55), and xylanase (80.39 ± 9.99). Altogether, our results highlighted the potential of *B. stercoris* RS73_I1 as a multi-enzyme-encoding bacterial strain for the bioconversion of complex marine macroalgal biomass into various products for the future industrial application.

PP-148

Integrated phytoremediation and post-harvest biomass management for cesium and strontium: For sustainable secondary waste management

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Contamination with the long-lived radionuclides ^{137}Cs and ^{90}Sr poses persistent environmental and radiological risks, while conventional remediation methods may be costly, disruptive, and generate substantial secondary waste. This study evaluated an integrated phytoremediation strategy combining phytoextraction, radionuclide uptake under irradiation, and post-harvest biomass conversion into biochar. Four fast-growing, non-edible terrestrial plant species were screened under hydroponic conditions for 21 days using cesium (Cs; 0–5 mM) and strontium (Sr; 0–3 mM). Among the tested species, *Abutilon indicum*, *Catharanthus roseus*, *Ricinus communis*, and *Alstonia scholaris* demonstrated comparatively high Cs and Sr accumulation. *A. scholaris* exhibited the greatest accumulation capacity, with Cs concentrations ranging from 5,452.8 to 24,771.4 mg kg^{-1} dry weight and translocation factors (TFs) of 85.2–57.6. Sr accumulation in this species ranged from 1,307.4 to 8,705.7 mg kg^{-1} dry weight, with TFs of 85.3–1.46. Selected species were subsequently assessed for tolerance to ^{137}Cs irradiation at 5R and 50R and for uptake of ^{137}Cs, ^{90}Sr, and low-level radioactive waste. *C. roseus* demonstrated the highest ^{137}Cs reduction following exposure to 5R (0.23%) and 50R (0.13%), whereas *A. indicum* showed the greatest ^{90}Sr reduction under non-irradiated conditions (0.50%). Pot experiments further demonstrated species-specific responses to potassium supplementation and K-enriched biochar. Pyrolysis of phytoremediated biomass reduced biomass volume by 86.5% for Cs and 85.02% for Sr in *A. scholaris*, and by 84.23% and 87.95%, respectively, in *C. roseus*. The integrated approach offers a low-disturbance strategy for radionuclide removal and secondary waste minimization. The work aligns with UN Sustainable Development Goals; SDGs- 12 (Responsible Consumption and Production), 15 (Life on Land).

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PP-149

Development and evaluation of a novel symbiotic consortium for protection against intestinal inflammation and radiation-induced intestinal injury

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Inflammatory bowel disease (IBD) is a chronic gastrointestinal disease marked by persistent inflammation, oxidative stress, immune dysregulation, epithelial barrier disruption and gut microbiota dysbiosis. Plant-derived prebiotic-probiotic combinations offer a promising strategy for restoring intestinal homeostasis and reducing inflammation. In this study, the potential of corn silk (*Zea mays L.*) extract (CSE) was evaluated as a prebiotic component to formulate a novel synbiotic consortium combined with *Lactobacillus plantarum, Lactobacillus rhamnosus* and *Streptococcus thermophilus*. Preliminary result of our study showed a significant increase in the proliferation and metabolic activity of CSE treated bacteria compared to control and Fructooligosaccharide (FOS) treatment groups. The formulated synbiotic exhibited higher DPPH and ABTS radical-scavenging activities, suggesting improved antioxidant potential of CSE. Our FT-IR analysis confirmed carbohydrate/ polysaccharide- associated functional group in the con silk extract. Based on this finding, the optimized synbiotic is being further evaluated for anti-inflammatory and intestinal barrier protective effect, including the assessment of inflammatory cytokines, intracellular reactive oxygen species, transepithelial electric resistance, and tight-junction markers in in-vitro and in-vivo model of IBD. Beyond IBD the synbiotic consortium`s potential is also being explored in radiation induced intestinal injury (RIII), where similar pathological features, including inflammation, oxidative stress, barrier disruptions, and microbial dysbiosis are prominent. This work is in progress in our laboratory to assess probiotic viability, antioxidant activity, inflammatory response, ROS level, and barrier integrity under radiation-induced stress. Overall, this study supports the development of our synbiotic as a promising therapeutic strategy for protecting intestinal damage under both inflammatory and radiation-associated gastrointestinal conditions.

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PP-150

Two-stage microalgal-bacterial granular sludge (MBGS)-based photobioreactor system for tributyl phosphate biodegradation and phosphate removal

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Microalgal-bacterial granular sludge (MBGS) photo-biofilm system can offer an efficient and sustainable technology for the simultaneous biodegradation of recalcitrant pollutants and biological nutrient removal. An MBGS capable of near-complete biodegradation of 1 mM of tributyl phosphate (TBP) was developed through enrichment. The community also exhibited efficient ammonium removal (91.9%–97.9%). However, accumulation of up to ~7 to 10.5 mg/L PO_4^{3-}-P was observed due to TBP levels and incomplete removal of the released phosphate. To evaluate TBP biodegradation and the removal of released phosphate, a two-stage MBGS photo-sequencing batch reactor (photo-SBR) system was investigated. Photo-SBR1 removed the added 0.5-1 mM TBP within a 10-h cycle, which led to the release and accumulation of 7.5 mg/L PO_4^{3-}-P. The effluent of photo-SBR1 was used as the feed for photo-SBR2 for studying phosphate removal and final polishing under different process conditions. The addition of ammonium to photo-SBR2 did not improve phosphate removal. Supplementation of the effluent of photo-SBR1 with ammonium and acetate resulted in near-complete removal of phosphate in photo-SBR2. The data suggest that decoupling TBP biodegradation and phosphate removal in two distinct bioreactors can avoid the impact of TBP or its degradation products on biological phosphate removal. This study provides a proof of concept for the use of a two-stage photo-bioreactor system with algal-bacterial granules for efficient and sustained biological degradation of TBP and the removal of phosphate released during TBP biodegradation.

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PP-151

Mineralogical and metagenomic profiling reveals microbial resilience and adaptation in monazite-rich soils of Kerala, India

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Naturally occurring radioactive materials (NORM), including thorium and uranium, together with associated heavy metals, represent persistent environmental contaminants that exert chronic radiological and chemical stress on soil ecosystems. The microbial adaptation under long-term exposure was investigated by integrating mineralogical characterization with metagenomic sequencing of monazite-rich soils from the High-Level Natural Radiation Area (HLNRA) of Kerala, India, spanning a natural background radiation gradient of 0.6 to 150 mGy/year. Mineralogical analyses revealed marked enrichment of thorium and uranium alongside elevated titanium, aluminum, and iron concentrations, with X-ray diffraction indicating mild lattice disorder in high-radiation soils. Despite a >1000-fold variation in radionuclide concentrations, microbial alpha diversity remained stable across sampling sites. However, significant community reorganization and species-level turnover were observed, while dominant bacterial phyla remained conserved. Fourteen species, notably *Egicoccus halophilus* and *Woeseia oceani*, were positively correlated with radiation dose, whereas species mediating carbon degradation and nitrogen transformation showed negative associations. Functional profiling demonstrated clear metabolic shifts along the radiological-geochemical gradient, with high-radiation taxa showing enrichment in pathways for aromatic-compound degradation, heavy-metal resistance, and oxidative-stress tolerance. Furthermore, BacMet annotation identified specific resistance determinants against arsenic, copper, and oxidative-stress-inducing agents. These findings demonstrate that chronic radiological and chemical stress drives targeted microbial adaptation and selects for resistant taxa without compromising overall community diversity, highlighting key mechanisms of microbial resilience in NORM-contaminated ecosystems.

PP-152

Intricately regulated guanylate monophosphate kinase modulates cellular homeostasis in *Nostoc* sp. PCC 7120 through dNTP pool management and fine tuning of proteomic profile

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Guanylate monophosphate kinase (Gmk) is a central enzyme in guanine nucleotide metabolism that catalyzes the conversion of GMP to GDP, thereby sustaining nucleotide homeostasis. In plants, Gmk is implicated in regulating growth and chloroplast biogenesis[1], and in bacteria, it contributes to nucleotide pool management and is subject to control by the stress-inducible alarmone (p)ppGpp[2]. However, the mechanisms governing its regulation and physiological role under abiotic stress in unexplored in the photosynthetic cyanobacteria. Using the model system, *Nostoc* PCC 7120, mechanisms regulating expression of *gmk* and the physiological role of the protein was delineated. The global regulator LexA[3] was shown to function as a positive regulator of *gmk* in *Nostoc*, and the gene was found to be differentially regulated both at the transcript and protein level under different abiotic stresses. To understand the physiological role of Gmk, recombinant *Nostoc* strain overexpressing Gmk (An*gmk*$^{+}$) was generated. Though the overexpression of Gmk resulted in 40% lower growth under normal growth conditions, it did not affect the survival under most abiotic stresses tested, with that under gamma irradiation enhanced. Proteomic profiling further revealed altered abundance of proteins associated with transcription, translation, photosynthesis, exopolysaccharide (EPS) biosynthesis, and multiple stress responses, including oxidative stress, DNA damage, and nutrient scarcity, to tune itself to the metabolic shift occurring due to higher production of GDP and GTP. Collectively, these findings established that Gmk plays a significant role as a nucleotide metabolism as well as cellular homeostasis and stress acclimation in *Nostoc* 7120.

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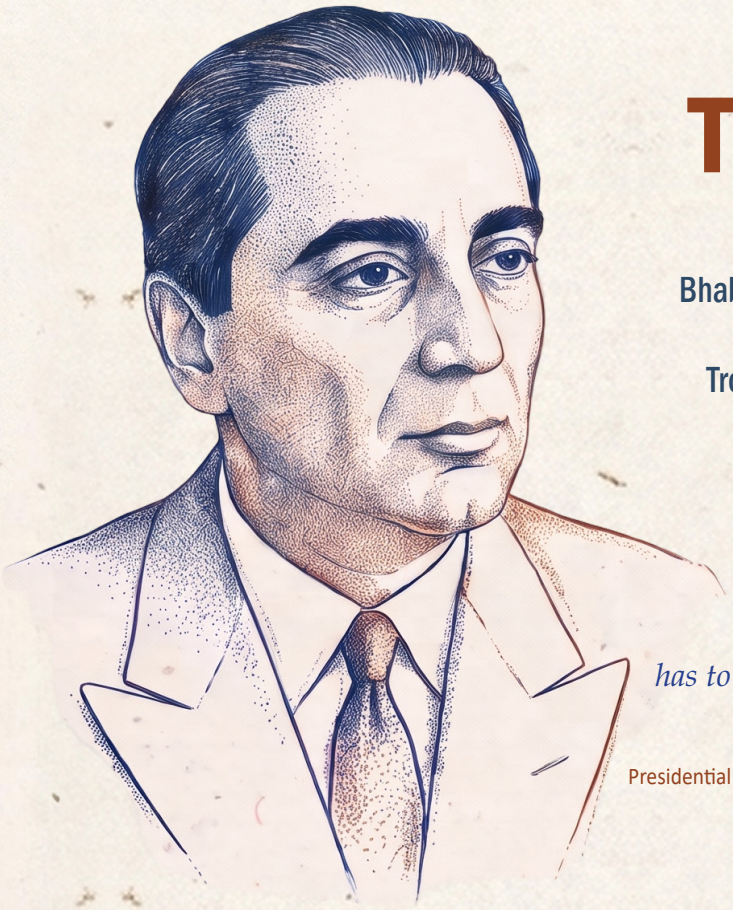
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- Dr. Homi J. Bhabha
Presidential Address, National Institute of Sciences of India, 1963

