2nd International Conference on Translational Research in Biomedical Sciences

(TRIBS 2.0)

February 19-21, 2025

BOOK OF ABSTRACTS

Organized by

Centre for Drug Discovery and Development

Sathyabama Institute of Science and Technology

India

In association with

Genome Engineering Laboratory
University of Westminster
London, United Kingdom

Translational Immunogenomics Unit
Vivagen Dx Labs
Chennai, India

ISBN: 978-93-83409-98-3

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Patrons

Sathyabama Institute of Science and Technology, India

Dr. Mariazeena Johnson
Chancellor

Dr. Marie Johnson
President

Mr. J. Arulselvan
Vice President

Ms. Maria Bernedette Arulselvan
Vice President

Ms. Maria Catherine Johnson
Vice President

Dr. T. Sasipraba
Vice Chancellor

University of Westminster London, United Kingdom

Prof. Peter Bonfield
Vice Chancellor and President

Prof. Dibyesh Anand
Deputy Vice-Chancellor,
Global Engagement and Employability

Prof. Andrew Linn
Deputy Vice-Chancellor for Research and Knowledge Exchange.

TRIBS 2.0 - Organizing Team

Convenors

Dr. Krupakar Parthasarathy
Professor (Research)
Centre for Drug Discovery and Development
Sathyabama Institute of Science and Technology, Chennai, India.

Dr. Kalpana Surendranath
Director, Gene Editors of the Future,
University of Westminster, London.

Dr. Kanagaraj Radhakrishnan
Senior Lecturer, IMBAE
St George's, University of London, UK.

Organizing Secretaries

Dr. M. Radhakrishnan
Professor (Research)
Centre for Drug Discovery and Development
Sathyabama Institute of Science and Technology, Chennai, India.

Dr. V. Hari Balaji
Founder Director
Chief Scientific Officer
Vivagen Dx Lab, Chennai, India.

About Sathyabama Institute of Science and Technology:

Sathyabama is a prestigious institution which excels in the fields of Engineering, Science and Technology for more than three successful decades. It offers multi-disciplinary academic programmes in various fields of Engineering, Science, Technology, law, Dental Science, Pharmacy, Nursing, Management, Arts and Science and Allied Health Sciences. It is established under Sec.3 of UGC Act, 1956 and is been Accredited with 'A++' Grade by the National Accreditation and Assessment Council. The Institution has been graded as Category I University by UGC under the UGC (Categorization of Universities (only) for Grant of Graded Autonomy) Regulations, 2018. The Institution persistently seeks and adopts innovative methods to improve the quality of higher education and is responsive to the changes taking place in the field of education on a global scale. The Institution has a team of dynamic and outstanding faculty, innovative pedagogical practices, state of the art infrastructure and world class Research Facilities.

Sathyabama has a good presence in rankings and ratings at National and International level. The Institution has been ranked in 51st position by the National Institutional Ranking Framework (NIRF), Government of India among the Universities in India for the year 2023 and ranked one among the top 100 Universities for eight consecutive years. Sathyabama is ranked among the Top 5 Institutions in the Country for Innovation by ATAL ranking of Institution for Innovation Achievements, Govt. of India. Times Higher Education and QS has ranked Sathyabama among the top Institutions worldwide. Sathyabama Institute of Science & Technology has alliances with leading Universities and research establishments at National and International Level. It is a research intensive University with world class laboratories and research facilities and is involved in research in the emerging areas of Science and Technology. Sathyabama has undertaken various sponsored and collaborative R&D projects funded by National and International Organizations. Sathyabama has written a special page in the history of space research on 22nd June 2016 with the launch of "SATHYABAMASAT" in association with ISRO.

About Centre for Drug Discovery and Development, Sathyabama:

The Centre for Drug Discovery and Development (CDDD) was established in 2013 at the university in Col Dr. Jeppiaar Research Park with the goal to discover novel drugs to fight against life-threatening infectious diseases. The centre revolves around microbial bioprospecting, Natural product drug discovery, research on Tuberculosis and Virology, Biofilm biology, Genomics and Proteomics, Translational immunology and vaccine research, marine bioprospecting, Bio-nanomolecular research, Vector-borne disease laboratory and CMOAR lab. The centre has received research grants from esteemed organizations including DST, DBT, NCPOR, ICMR, SERB, MHRD-SPARC, and MoES.

About the University of Westminster, UK:

The University of Westminster started out 180 years ago as the first polytechnic in London and one of the first in the UK, established to educate the working people of London. Our people stand out as significant contributors to their communities - through their innovation, enterprise, and problem-solving skills - seeking to make the world a more sustainable, healthier, and better place. With nearly 20,000 students from 169 different nationalities, the university fosters a global outlook through its inclusive curriculum and co-curricular opportunities. Rated Silver in the 2023 Teaching Excellence Framework UK (TEF, UK) for very high quality teaching and outcomes, it excels in life sciences, art, media, law, tourism, English, and architecture. Recognised in the top 15% globally for contributing to the UN's Sustainable Development Goals (The Impact Rankings 2024), it ranks second in London for research quality and among the top 50 worldwide for international outlook (The Young University Rankings 2024).

The School of Life Sciences at the university occupies modern laboratories in the heart of London with excellent facilities supporting cutting edge research in a number of disciplines including: molecular and cellular biology, fermentation and biotechnology, and human health and performance. Notable examples of internationally recognised research within the school include, but are not limited to, research on genome editing, cancer, obesity, inflammation, human exercise performance and ageing, nutrition and global public health, social prescribing and resilience. MSc and PhD students on postgraduate research degree programs, post-doctoral research assistants, technical services staff and academic members of staff support the research efforts of the school. Research is funded by grants from national and international funding bodies and also by industrial partnerships.

About Gene Editors of the Future:

Gene editing allows the introduction of desirable changes in the genome of living cells using CRISPR/Cas and has fundamentally transformed research and development in biomedical sciences and biotechnology. Termed the largest and longest-running extracurricular initiative in CRISPR, the Gene Editors of the Future program of the School of Life Sciences at the University of Westminster vertically integrates researchers of all levels interested in gene editing, enabling them to develop essential skills through experiential and authentic learning experiences. It equips researchers of all levels with the theoretical knowledge and practical expertise necessary to investigate molecular and cellular puzzles using CRISPR/Cas technology. Since 2020, the program has co-created and collaborated with over 700 participants of all levels through co-curricular and extracurricular activities. The program has seen a surprising majority of women participants across all courses and levels at the University of Westminster, who not only engage actively in training but also gain access to a

wide range of opportunities, equipping them with the skills necessary to take on various leadership roles within the scientific community and the broader society. Funded by the Quintin Hogg Trust, the program is expanding rapidly and actively collaborating with reputed institutions, including Welcome Connecting Science, Queen Mary University London, and Royal Holloway University of London.

About Conference – TRIBS 2.0:

Translational research in Life science aims to understand and refine the process of turning observations in the laboratory, clinic and community into interventions that improve health of individuals and communities. Scientific translational research happens along a spectrum: from bench to bedside and on to populations. But this spectrum is not linear or unidirectional; each stage builds upon and informs the others. In the past decades, there have been an enormous number of proof-of-concept studies in regenerative medicine.

This conclave establishes a platform for accelerating the translational research among the academicians, scientists and industrialists working in several aspects of medicine and healthcare to come closer and share their ideas. Young research scholars and students can present their ideas and innovations as presentations.

Conference Themes:

1. Gene Editing Technologies
2. Genome Integrity & Repair
3. Translational Immunology & Vaccine Research
4. Microbial Technologies
5. Multi-omics, Bioinformatics & Computational Biology
6. Maternal Health & One Health
7. Bioeconomy & Sustainable Healthcare
8. MedTech, Biopharma & Biomanufacturing

SATHYABAMA
INSTITUTE OF SCIENCE AND TECHNOLOGY
(DEEMED TO BE UNIVERSITY)
CATEGORY - 1 UNIVERSITY BY UGC

MESSAGE FROM THE CHANCELLOR

Dr. Mariazeena Johnson

I am glad and happy that the Centre for Drug Discovery and Development at Sathyabama Institute of Science and Technology is organizing the 2nd International Conference on Translational Research in Biomedical Sciences (TRIBS 2.0) from the 19th of February to the 21st of February 2025. The conference will serve as an excellent platform to address some of the most pressing challenges in the field of healthcare and biomedical sciences.

Sathyabama believes in the power of interdisciplinary research and its potential to create meaningful impact, and translational research, which is the need of the hour, helps to bridge the gap between laboratory discoveries and real-world applications. TRIBS 2.0 is designed to bring together academicians, scientists, clinicians, industry experts, and students to share their insights, exchange ideas, and forge collaborations that will drive advancements in healthcare and improve the quality of life for individuals and communities worldwide. At this juncture, I appreciate and thank the association of University of Westminster, London, UK and Vivagen Dx Labs, Chennai, India for their active collaboration.

At Sathyabama, we are deeply committed to research excellence and fostering an ecosystem that nurtures innovation. The participation of esteemed experts and enthusiastic young researchers in TRIBS 2.0 is a testament to our mission of contributing to meaningful scientific advancements that benefit society.

Sathyabama Institute of Science and Technology has always been at the forefront of innovation and excellence. With our 'A++' NAAC accreditation, Category I University status, and consistent good rankings among the top institutions in India and globally, we are committed to fostering a culture of research and innovation. Our Centre for Drug Discovery and Development (CDDD), established in 2013, has been instrumental in advancing research in infectious diseases, natural product drug discovery, and translational immunology. This conference is a testament to our dedication to pushing the boundaries of science and technology.

To all the participants, I encourage you to engage actively, share your insights, and forge meaningful connections. Together, let us harness the power of translational research to create a healthier, more sustainable, and equitable world.

Wishing you all a productive, inspiring, and memorable conference!

Warm regards,

Dr. Mariazeena Johnson M.B.A., M.Phil., Ph.D.,

Chancellor

Sathyabama Institute of Science and Technology

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MESSAGE FROM THE PRESIDENT

Dr. Marie Johnson

It gives me immense pleasure to know that the Centre for Drug Discovery and Development at Sathyabama Institute of Science and Technology is organizing the 2nd International Conference on Translational Research in Biomedical Sciences (TRIBS 2.0). This prestigious gathering of esteemed scientists, clinicians, and industry experts reflects our unwavering commitment to fostering research that translates into meaningful innovations in healthcare and biomedical sciences.

Translational research holds immense potential to bridge the gap between fundamental discoveries and real-world applications, ultimately improving human health and quality of life. At Sathyabama, we strongly believe in the power of interdisciplinary collaborations, and this conference will be a catalyst for nurturing groundbreaking ideas, fostering global partnerships, and empowering young researchers.

I extend my wishes to the organizing team, distinguished speakers, and all participants for their dedication and contributions. May this event be an inspiring and productive experience for all.

Best wishes for a successful conference!
Dr. Marie Johnson, M.B.A., M.Phil., Ph.D.,
President
Sathyabama Institute of Science and Technology

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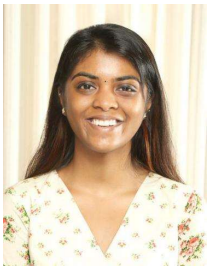
MESSAGE FROM VICE PRESIDENTS

Mr. J. Arul Selvan

Ms. Maria Bernadette Arulselvan



Ms. Maria Catherine Johnson

We are happy to welcome you to the 2nd International Conference on Translational Research in Biomedical Sciences (TRIBS 2.0). This conference is a significant milestone in advancing biomedical research, bringing together leading minds from academia, industry, and healthcare sectors to discuss innovations that can drive scientific and medical breakthroughs.

At Sathyabama Institute of Science and Technology, we are deeply committed to fostering a culture of research and innovation that addresses real-world challenges. The themes of this conference, spanning gene editing, vaccine research, microbial technologies, and sustainable healthcare, emphasize the need for collaborative efforts in tackling global health issues.

We extend our wishes to the esteemed speakers, researchers, and students participating in this conference. Your dedication to scientific excellence and knowledge-sharing will undoubtedly make this event successful.

Wishing you an insightful and productive conference!

Mr. J. Arul Selvan **Ms. Maria Bernadette Arul Selvan** **Ms. Maria Catherine Johnson**

Vice Presidents

Sathyabama Institute of Science and Technology

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MESSAGE FROM THE VICE CHANCELLOR

Dr. T. Sasipraba

It gives me pleasure to invite you all to be a part of the 2nd International Conference on Translational Research in Biomedical Sciences (TRIBS 2.0), hosted by Sathyabama Institute of Science and Technology.

Scientific progress thrives on collaboration, innovation, and the relentless pursuit of knowledge. TRIBS 2.0 serves as an extraordinary platform where eminent researchers, clinicians, industry leaders, and academicians from across the globe come together to discuss the latest advancements in biomedical sciences. This year, we are honored to have eight distinguished international speakers and 21 eminent national speakers who bring invaluable insights from various disciplines, including genomics, immunotherapy, bioinformatics, personalized medicine, microbial biotechnology, and sustainable healthcare solutions. Around 210 participants from across the country have registered to participate in this conference. Totally 110 abstracts received from participants for oral and poster presentations.

The scope of translational research is expanding rapidly, bridging the gap between fundamental discoveries and their real-world applications. With cutting-edge advancements in gene editing, vaccine development, biomaterials, and computational biology, the knowledge shared at this conference will undoubtedly foster interdisciplinary collaborations and inspire future breakthroughs.

This year's conference features an impressive lineup of eminent national and international speakers from USA, UK, Singapore, Chile, and Malaysia. Their expertise and contributions in the fields of gene editing, translational immunology, vaccine research, and sustainable healthcare will undoubtedly inspire and enlighten all participants.

The conference themes, ranging from Gene Editing Technologies and Translational Immunology to Bioeconomy & Sustainable Healthcare, are thoughtfully curated to address the most pressing challenges and opportunities in biomedical sciences. I am particularly excited about the Vertically Integrated Projects (VIPs) session, a pioneering initiative that brings together students, researchers, and industry experts to collaborate on long-term, real-world research projects. This session will reflect our commitment to empowering the next generation of scientists and fostering a culture of innovation and problem-solving.

I would also like to highlight the pre-conference workshop on CRISPR Gene Editing Workflows, led by Dr. Kalpana Surendranath and the Gene Editors of the Future team from the University of Westminster, London, UK. This workshop offers a unique opportunity for researchers to gain hands-on experience with CRISPR/Cas technology, which has transformed biomedical research and holds immense potential for curing diseases, developing sustainable solutions, and advancing healthcare.

I extend my heartfelt gratitude to our esteemed partners, the University of Westminster, UK and Vivagen Dx Labs, Chennai, India and all the sponsors, and speakers for their invaluable contributions to this event. Your expertise and dedication are instrumental in making TRIBS 2.0 a resounding success.

I extend my sincere appreciation to all our keynote speakers, session chairs, panelists, researchers, and students participating in this conference. Special thanks to the organizing committee for their dedication to bringing together such a remarkable assembly of scientific minds. I am confident that this conference will catalyze new ideas, collaborations, and discoveries that will shape the future of biomedical research.

Wishing you all an insightful and productive experience at TRIBS 2.0!

Dr. T. Sasipraba
Vice Chancellor
Sathyabama Institute of Science and Technology

Prof. Andrew Linn

Deputy Vice-Chancellor for Research and Knowledge Exchange.
University of Westminster, London, United Kingdom

Message

The University of Westminster is a 'Global University with London Energy' and is proud to welcome students from over 160 countries to our campuses in London. Working in close collaboration with our international partners, TNE is simply part of our identity, as is the inclusion of our students within our research community. The Gene Editors of the Future project at the University of Westminster is one of our flagship projects to engage students as researchers, and we are thrilled to be working with the Centre for Drug Discovery and Development, Sathyabama Institute of Science and Technology as we commit together to breaking down boundaries and hierarchies to find solutions to our world's biggest challenges.

Prof. Dr. T. Ramani Devi, MD; DGO, PhD

President – TNFOG, National Vice-President, FOGSI 2020, Chairperson Endometriosis Committee of FOGSI 2014-2016, Director – Ramakrishna Medical Centre, Janani Fertility Centre, Trichy, India.

Message

It is my immense pleasure to participate in and invite you to the 2nd International Conference on Translational Biomedical Research Conference TRIBS 2.0, organized as an Indo-UK edition in partnership with Sathyabama Institute of Science and Technology (SIST), India, University of Westminster, UK, and VivagenDx Labs, India. As a speaker and participant in the TRIBS 1.0 conference that was organized as an Indo-Singapore edition in 2023, it is with awe and admiration that I see the trajectory of immense growth the TRIBS conference series has achieved. I congratulate the organizers on this outstanding achievement.

In an era marked by unprecedented scientific discovery and technological advancement, we find ourselves at the frontier of transforming healthcare through translational biomedical research. This conference brings together visionary scientists, healthcare professionals, and industry innovators from around the world, united by a common goal: to bridge the gap between laboratory discoveries and clinical applications.

As a Clinician, I view Translational biomedical research as the interface where cutting-edge science meets the pressing needs of patients. It is where the promise of biotechnology, genomics, Artificial Intelligence (AI)and bioinformatics is translated into tangible benefits for human health through inter-disciplinary collaborations. As we gather here, we celebrate not only the strides made in understanding the intricacies of disease mechanisms but also the relentless pursuit of novel therapies, diagnostics, and preventive measures.

The journey from bench to bedside has its own challenges, yet it is a journey we embark upon with optimism and determination. Our collective efforts are geared towards accelerating the translation of research findings into real-world solutions that enhance the quality of life for individuals and communities globally. In this regard I would like to highlight the pioneering Clinician-Academia-Industry Focus Group Discussion meetings that we have been organizing along with SIST and VivagenDx Labs. The Clinician Panel Talks scheduled on Days 1 and 2 is

an outcome of these focus group meetings and is a testament to the power of collaboration and the spirit of innovation. It is a platform where ideas are exchanged, partnerships are forged, and breakthroughs are realized. We are privileged to host a diverse array of speakers and participants who bring their unique perspectives and expertise to the table.

As you engage in discussions, presentations, and networking sessions, I encourage you to think beyond traditional boundaries and embrace the multidisciplinary nature of translational biomedical research. Let us inspire one another, challenge conventional wisdom, and pave the way for the next generation of medical breakthroughs.

Thank you for being a part of this exciting journey. Together, we can make a profound impact on the future of sustainable healthcare.

Sincerely,

Prof. Dr. T. Ramani Devi, MD; DGO, Ph.D.,

2nd International Conference on Translational Research in Biomedical Sciences (TRIBS 2.0)

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Technical Committee – TRIBS 2.0

Registration committee

Dr. T. Rajasekar
Dr. R. Sam Ebenezer
Ms. T. Thangam
Ms. Sudhanarayani Rao
Ms. S. Ranjani
Mr. J. Sakthivel
Ms. AU. Hemamalani
Ms. A. Anandhi
Ms. K. Akila

Abstract & Publications

Dr. R. Sam Ebenezer
Dr. P. Krupakar
Dr. R Kanagaraj
Dr. Kalpana Surendranath
Dr. S. Vignesh

Scientific Committee

Dr. M. Radhakrishnan
Dr. P. Krupakar
Dr. V. Hari Balaji
Dr. R. Kanagaraj
Dr. Kalpana Surendranath
Dr. V. Gopikrishnan
Dr. S. Vignesh

Accommodation & Transport

Dr. S. Vignesh
Mr. MP. Karthik Prakash

Mr. A. Kishorekumar
Mr. Saimahesh Kumar
Mr. J. Sakthivel
Mr. D. Sakthi
Ms. AU Hemamalani
Ms. S. Ranjani
Ms. T. Vaishnavi

Finance & Purchase Committee

Dr. P. Krupakar
Dr. V. Hari Balaji
Dr. R. Sam Ebenezer
Dr. M. Radhakrishnan
Ms. Sudhanarayani Rao

Reception

Ms. Sudhanarayani Rao
Ms. T. Thangam
Ms. G. Soumiya
Ms. Benitta
Mr. Ashok
Ms. Alna

Food & Refreshment

Dr. T. Rajasekar
Mr. A. Kishorekumar
Ms. T. Vaishnavi
Mr. MP Karthikprakash
Mr. D. Sakthi
Mr. S. Sai Maheshkumar
Mr. Aswin

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Inauguration Agenda

Venue: Tmt. Soundrabai Auditorium, Sathyabama Centre for Advanced Studies (III Floor) Sathyabama Institute of Science and Technology, India

Time: 10.00 – 11.15 AM

9.00 – 10.00 AM	Registration & Guest Arrival
10.00 AM	Welcoming of Guests with Chancellor, President and Vice Presidents
10.00 – 11.15 AM	
Inauguration	Thamizh Thai Vaazhthu
Welcome address:	Dr. T. Sasipraba**,** Vice Chancellor, Sathyabama
About TRIBS 2.0	Prof. Dr. Krupakar Parthasarathy, Convener – TRIBS 2.0
Message (Video)	Prof Dibyesh Anand, Deputy VC - Global Engagement & Employability, University of Westminster, UK
Address by UK Conveners	Dr. Kalpana Surendranath Director, Gene Editors of the Future, University of Westminster, London, UK Dr. Kanagaraj Radhakrishnan, Senior Lecturer, St George's University of London, UK
Honouring of Guests:	Dr. T. Sasipraba**,** Vice Chancellor, Sathyabama
Presidential Address:	Dr. Mariazeena Johnson, Honourable Chancellor, Sathyabama
Inaugural address	Ms. Halima Holland British Deputy High Commissioner to Tamil Nadu and Pondicherry New Delhi, India
Special address	Dr. Siddappa Byrareddy Vice Chair for Research, Nebraska Medical Centre, Nebraska, USA.
Release of Souvenir:	Dr. Siddappa Byrareddy Vice Chair for Research, Nebraska Medical Centre, Nebraska, USA.
Received by :	Dr. Mariazeena Johnson, Hon. Chancellor, Sathyabama Dr. Kanagaraj Radhakrishnan, St George's University of London, UK Dr. T. Sasipraba, Vice Chancellor, Sathyabama & other dignitaries on the dais
Product Launch:	MATHE.AI – India's 1st AI enabled solution for Endometrial Health
About the product:	Dr. V. Hari Balaji, CEO, Vivagen Dx labs, Chennai, India
Released by:	Dr. T. Ramani Devi, President, TNFOG, Tamil Nadu
Received by:	Ms. Halima Holland, British Deputy High Commissioner to Tamil Nadu and Pondicherry Dr E. Babu, Senior Consultant, Kauvery Hospitals, Chennai Dr. Prabhu Kanchi, Senior Consultant, Kauvery Hospitals, Chennai
Felicitation	Mr. K.T. Rajan, Cluster Head, Technology, Innovation, Education & Skills – South Asia, British Deputy High Commission, Bengaluru Dr. T. Ramani Devi, President, TNFOG, Tamil Nadu Dr. Maria Johnson, President, Sathyabama Mr. J. Arul Selvan, Vice President Ms. Maria Bernadette Arulselvan, Vice President Ms. Maria Catherine Johnson, Vice President
MoU Signing:	Stratificare, Singapore Vivekanandha Educational Institutions, Tamil Nadu, India Women Christian College, Chennai, India Vivagen Dx Labs, Chennai, India Biosint Nutraceuticals, Bangalore, India Hindusthan College of Arts & Science, Coimbatore, Tamil Nadu
Vote of Thanks	Prof. Dr. M. Radhakrishnan, Organizing Secretary, TRIBS 2.0

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Sathyabama Institute of Science and Technology, India

List of Plenary Speakers

Plenary Talk (PT) - 1	**Prof. Dr. Siddappa Byrareddy** Vice Chair for Research Nebraska Medical Centre Omaha, Nebraska, USA
PT – 2	**Dr. Uma Kanga** Assistant Professor, Transplantation Immunology and Immunogenetics, AIIMS, New Delhi, India
PT – 3	**Dr. Kanagaraj Radhakrishnan** Senior Lecturer St George's, University of London, London, UK
PT – 4	**Prof. Dr. Sujatha Sunil** Group Leader – Vector Borne Disease Group ICGEB, New Delhi, India
PT – 5	**Dr. Antony Chua** CEO, Stratificare, Singapore
PT – 6	**Dr. Saravanan Matheshwaran** Associate Professor IIT-Kanpur, India
PT – 7 (Online)	**Dr. Amit Awasti** Senior Professor THSTI, Faridabad, India
PT – 8	**Dr. V. Thillai Sekar** Associate Professor Department of Microbiology, Pondicherry University, India
PT – 9 (Online)	**Dr. Pragyan Acharya** Assistant Professor, AIIMS, New Delhi, India
PT – 10	**Dr. Anita Shete-Aich** Scientist E ICMR - NIV Pune, India
PT – 11	**Prof. Dr. Sujatha N** Professor, Department of Applied Mechanics and Biomedical Engineering, IITM, Tamil Nadu, India
PT – 12	**Dr. V. Hari Balaji** CEO, Translational Immunogenomics Unit, Vivagen Dx Labs, Chennai, India
PT – 13	**Dr. Viswanadham Duppatla** Vice President – Biopharma Innovations & Biomanufacturing IKP Knowledge Park, Hyderabad, India
PT – 14	**Dr. Vaibhav Bhatia** Chief Executive Officer Lamark Biotech Pvt. Ltd., Pune, India
PT – 15	**Dr. Kalpana Surendranath** Director – Gene Editors of the Future Leader of the Genome Engineering Laboratory University of Westminster, London, UK

PT – 16 (Online)	**Ms. Munuse C Savash Ishanzadeh** University of Oxford/Life Research Oxford, UK
PT – 17 (Online)	**Dr. Taruna Madan** Scientist G & Head Development Research Division, ICMR, New Delhi, India
PT – 18 (Online)	**Dr. Prashanth Bajpe** Senior Lecturer University of Bedfordshire, Luton, UK
PT – 19	**Dr. Luke Elizabeth Hanna** Scientist F & Head Department of Virology and Biotechnology ICMR-National Institute for Research in Tuberculosis (NIRT), Chennai, India
PT – 20	**Dr. Neelagandan Kamariah** Team Lead and Scientist E Centre for Chemical Biology and Therapeutics InStem, Bengaluru, India
PT – 21	**Dr. Sergio Leiva** Associate Professor Austral University of Chile, Valdivia, Chile
PT – 22	**Dr. Giuseppe Viola** Director Queen Mary Centre for Undergraduate Research Queen Mary University of London, UK
PT – 23 (Online)	**Prof. Dr. J. Joshua Thomas** Department of Computing, UOW Malaysia KDU Penang University College, Malaysia
PT – 24	**Dr. Vasanth Thamodaran** Senior Scientist Tata Institute for Genetics and Society, Bengaluru, India
PT – 25	**Dr. Bala Yeshwanth R. Vummidi** Managing Director & Founder Inger Therapeutics, Chennai, India
PT – 26	**Mr. Shrish Kumar S.** Manager - Applications Qiagen, Hyderabad, Telangana, India
PT – 27 (Online)	**Dr. Anusha Seneviratne** Lecturer, Royal Holloway University of London, UK
PT – 28 (Online)	**Prof. Dr. John Murphy** University of Westminster, London, UK
Clinical Talk (CT) – 1	**Prof. Dr. T. Ramani Devi** President – TNFOG, National, Vice-President, FOGSI 2020, Chairperson Endometriosis Committee of FOGSI 2014-2016, Director – Ramakrishna Medical Centre, Janani Fertility Centre, Trichy, India
CT – 2	**Prof. Dr. Sampathkumari** Secretary – TNFOG, India, National, Vice-President, FOGSI 2023. OGSSI President Elect 2025, HOD ObGyn, Sri Muthukumaran Medical College& Research Institute
CT – 3	**Prof. Dr. N. Hepsibah Kirubamani**

	Consultant, CSI Kalyani Hospital, India, Visiting Prof. Madha Medical College, Chennai, Immediate President, chennai Menopause Society, Treasurer, Indian Menopause Society
CT – 4	**Dr. S. Chitra** Secretary – Indian fertility Society, South Tamil Nadu Chapter Janani Fertility Centre, Laitha Nursing Home and Diagnostics Trichy, India
CT – 5	**Prof. Dr. Vijayalakshmi Kandaswamy** HOD, Dept of ObGyn, Chettinad Hospital and Research Institute, Chennai, India
CT – 6	**Dr. S. Vyjayanthi** Subspecialist in Reproductive Medicine & Surgery (RCOG, UK) Head of Department & Consultant Fertility Specialist KIMS Fertility Centre, Hyderabad, India
CT – 7	**Dr. Runa Acharya** Senior Consultant-Fertility Solutions, Medicover Fertility, Hyderabad
CT – 8	**Dr. Veerendra Gadekar** Senior Project Scientist, IBSE, IITM, Tamil Nadu, India
CT – 9	**Dr. Babu Elangovan** Senior Consultant, Department of HPB and Liver Transplant, Kauvery Hospital, Alwarpet Chennai, India
CT - 10	**Dr. Prabhu Kanchi** Senior Consultant, Kauvery Kidney Institute, Kauvery Hospital, Vadapalani, Chennai, India
VIP Lecture 1	**Ms. Harshana Chaurasia** Research Associate, Gene Editors of the Future & Genome Engineering Lab University of Westminster, London, UK
VIP Lecture 2	**Ms. Julia Karolina Gorczynska** Research Scholar, Gene Editors of the Future & Genome Engineering Lab University of Westminster, London, UK
VIP Lecture 3	**Ms. Jolina Pauline Viessmann** Research Scholar, Gene Editors of the Future & Genome Engineering Lab University of Westminster, London, UK

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Sathyabama Institute of Science and Technology, India

Plenary Session – Chairpersons

Session No	Theme	Chairpersons & Affiliation
Session I	Infection & Immunology and Genome Integrity	**Prof. Dr. Sujatha Sunil** Group Leader – Vector Borne Disease Group ICGEB, New Delhi, India **Dr. V. Hari Balaji,** CEO, Vivagen Dx Labs, Chennai, India
Session II	Transplantation Immunology	**Prof. Dr. H. Shakila,** Madurai Kamaraj University, India **Dr. Prabhu Kanchi** Interventional Nephrology and Renal Transplantation Kauvery Hospitals, Chennai, India **Dr. Babu Elangovan** Department of HPB and Liver Transplant, Kauvery Hospital, Alwarpet Chennai, India
Session III	Maternal Health	**Prof. Dr. T. Ramani Devi** President – TNFOG, India **Prof. Dr. Sampathkumari** Secretary – TNFOG, India
Session IV	Maternal Health & One Health – Panel Discussion	**Dr. S. Kannan** Dean Sathyabama General Hospital, Chennai, India **Dr. K. Supraja** Senior Consultant - Pulmonology & Pulmonary Rehabilitation Medway Hospital, Chennai, India **Dr. C. Anchana Devi** Associate Professor Women's Christian College, Chennai, India
Session V	Vertically Integrated Programme (VIP) for Sustainable Healthcare, Biopharma Innovation and Students as Researchers	**Ms. Harshana Chaurasia** Research Associate University of Westminster, UK **Ms. Julia Karolina Gorczynska** Research Scholar Gene Editors of the Future & Genome Engineering Lab, University of Westminster, UK **Ms. Jolina Pauline Viessmann** Research Scholar Gene Editors of the Future & Genome Engineering Lab, University of Westminster, UK
Sssion VI	Vertically Integrated Programme (VIP) for	**Dr. V. Thillai Sekar** Associate Professor, Dept of Microbiology Pondicherry University, India

	Biomedical Research and Students as Researchers	**Dr. Kanagaraj Radhakrishnan** Senior Lecturer St George's, University of London, UK **Ms. Sneha Latha Rangan** Gene Editors of the Future & Genome Engineering Lab, University of Westminster, London, UK
Session VII	Diagnostics and Structural Biology	**Dr. V. Hari Balaji** CEO, Vivagen Dx Labs, India **Prof. Dr. M. Radhakrishnan** Centre for Drug Discovery and Development Sathyabama Institute of Science and Technology, India
Session VIII	Vertically Integrated Programme (VIP) for Student-to-Researcher Transition and MedTech	**Dr. Kanagaraj Radhakrishnan** Senior Lecturer St. George's, University of London, UK **Dr. Anthony Chua** CEO, Stratificare, Singapore
Session IX	Concluding Keynote Session	**Dr. Kalpana Surendranath** Director – Gene Editors of the Future University of Westminster, London, UK **Prof. Dr. Krupakar Parthasarathy** Centre for Drug Discovery and Development Sathyabama Institute of Science and Technology, India

Oral Presentation – Session Chairpersons

Session No	Date & Time	Chairpersons & Affiliation
Session I	**19.02.2025** **(2.00 PM – 5.00 PM)**	**Prof. Dr. R. Balagurunathan,** Director Research Vivekanandha Educations Institutions, Tamil Nadu, India **Prof. Dr. S. Venkatesan,** Department of Environmental Science Periyar University, Salem, India
Session II	**20.02.2025** **(10.00 AM – 1.00 PM)**	**Dr. C. Pravda** Professor & Head Department Of Oral Medicine and Radiology Sathyabama Dental College and Hospital, Chennai **Dr. S. Sanjeevi Prasath** Assistant Professor (Research) Centre for Nanoscience and Nanotechnology Sathyabama Institute of Science and Technology, India
Session III	**20.02.2025** **(2.00 PM – 5.00 PM)**	**Prof. Dr. Vasantha Kumari Neela,** Department of Medical Microbiology, Universiti Putra Malaysia **Dr. S. Nachiappan** Professor & Head Department of Oral and Maxillofacial Surgery Sathyabama Dental College and Hospital, Chennai, India

Poster Presentation – Session Chairpersons

Session No	Date & Time	Chairpersons & Affiliation
Session I	**19.02.2025** **(2.00 – 5.00 PM)**	**Dr. S. Balaji** Technical Officer, ICMR-National Institute for Research in Tuberculosis (NIRT), Chennai, India **Dr. Amudhan** Theni Govt Medical College, Tamil Nadu, India **Dr. Sam Ebenezer**, Assistant Professor (Research), CDDD-Sathyabama, India
Session II	**20.02.2025** **(10.00 – 1.00 AM)**	**Dr. A. Suresh** Scientist, Meenakshi Academy of Higher Education and Research (MAHER), Kanchipuram, India **Dr. T. Rajasekar** Assistant Professor (Research), Centre for Drug Discovery and Development, Sathyabama Institute of Science and Technology, India
Session III	**20.02.2025** **(2.00 – 5.00 PM)**	**Dr. Amit Kumar** Associate Professor (Research), Centre for Climate Change Studies, Sathyabama Institute of Science and Technology, India **Dr. S. Prakash** Associate Professor (Research), Centre for Climate Change Studies, Sathyabama, Chennai, India **Dr. S. Vignesh**, ICMR- Post Doctoral Researcher, Centre for Drug Discovery and Development, Sathyabama Institute of Science and Technology, India

2nd International Conference on
Translational Research in Biomedical Sciences (TRIBS 2.0)
February 19-21, 2025

Venue: Tmt. Soundrabai Auditorium, Sathyabama Centre for Advanced Studies (III Floor)
Sathyabama Institute of Science and Technology, India

Programme Agenda

Time	Main Sessions	Speakers
	Day I: Wednesday, February 19, 2025	
10.00 – 11.15	Inauguration	
11.15 – 11.30	Tea Break	
Session I:	**Infection & Immunology and Genome Integrity**	**Chairpersons:** **Prof. Dr. Sujatha Sunil,** ICGEB, New Delhi **Dr. V. Hari Balaji,** Vivagen Dx Labs, Chennai, India
11.30 – 12.00	Plenary Talk (PT) - 1	**Prof. Dr. Siddappa Byrareddy** Nebraska Medical Centre Omaha, Nebraska, USA
12.00 – 12.30	PT – 2	**Dr. Uma Kanga,** AIIMS, New Delhi, India
12.30 – 13.00	PT – 3	**Dr. Kanagaraj Radhakrishnan** St George's, University of London, Tooting, London, UK
13.00 – 14.00	Lunch Break	
Session II:	**Transplantation Immunology**	**Chairpersons:** **Prof. Dr. Shakila H,** Madurai Kamaraj University, India **Dr. Prabhu Kanchi,** Kauvery Hospitals, Chennai, India **Dr. Babu Elangovan,** Kauvery Hospitals, Chennai, India
14.00 – 14.30	PT – 4	**Prof. Dr. Sujatha Sunil,** ICGEB, New Delhi
14.30 -15.00	PT – 5	**Dr. Anthony Chua,** Singapore
15.00 - 15.30	PT – 6	**Dr. Saravanan Matheswaran**, IIT Kanpur, India
15.30 – 16.00	PT – 7 (Online)	**Dr. Amit Awasthi, THSTI, Gurugram, India**
16.00 – 16.15	Tea Break	
16.15 – 16.45	PT – 8	**Dr. V. Thillai Sekar** Dept of Microbiology, Pondicherry University, India
16.45 – 17.15	PT – 9 (Online)	**Dr. Pragyan Acharya,** AIIMS, New Delhi, India
14.00 – 15.00	**Parallel Session**	**Oral Paper presentation – Session I** **(Senate Hall, Centre for Advanced Studies – 1 Floor)** **&** **Poster Presentation – Session I** **(Seminar Hall, Centre for Drug Discovery and Development – III Floor)**
	Day 2: Thursday, February 20, 2025	
Session III	**Maternal health**	**Chairpersons:** **Prof. Dr. T. Ramani Devi,** Ramakrishna Medical Centre President – TNFOG, India **Prof. Dr. Sampathkumari**, Secretary – TNFOG, India
9.30 – 10.00	PT – 10	**Dr. Anita Shete-Aich,** ICMR - NIV Pune
10.00 – 10.30	PT – 11	**Prof. Dr. Sujatha N,** IITM, Tamil Nadu, India
10.30 - 11.00	PT – 12	**Dr. V. Hari Balaji,** Vivagen Dx, India
11.00 – 11.15	Tea Break	

Session IV: Panel Discussion – Maternal Health		
11.15 – 13.00	**Panel Discussion on Maternal and One-Health**	**Moderators** **Dr. S. Kannan,** Sathyabama General Hospital **Dr. K. Supraja**, Medway Hospital **Dr. C. Anchana Devi,** Women's Christian College, Chennai **Speakers** **Prof. Dr. T. Ramani Devi,** Ramakrishna Medical Centre **Prof. Dr. Sampathkumari**, Secretary – TNFOG, India **Prof. Dr. N. Hepsibah,** CSI Kalyani Hospital, India **Dr. S. Chitra,** Janani Fertility Centre, Trichy, India **Prof. Dr. Vijayalakshmi Kandaswamy,** Chettinad Academy of Research and Education, Chennai, India **Dr. S. Vyjayanthi** KIMS Fertility Centre, Hyderabad, India **Dr. Runa Acharya**, Medicover Fertility, Hyderabad, India **Dr. Babu Elangovan,** Kauvery Hospital, Chennai, India **Dr. Prabhu Kanchi**, Kauvery Hospitals, Chennai, India **Dr. Veerendra Gadekar**, IBSE, IITM, India (online)
10.00 – 13.00		**Parallel Session** **Oral Paper presentation – Session II** **(Senate Hall, Centre for Advanced Studies – 1 Floor)** **&** **Poster Presentation – Session II** **(Seminar Hall, Centre for Drug Discovery and Development – III Floor)**
13.00 – 14.00	Lunch Break	
Session V: Vertically Integrated Programme (VIP) for Sustainable Healthcare, Biopharma Innovation and Students as Researchers		**Chairpersons:** **Ms. Harshana Chaurasia,** University of Westminster, UK **Ms. Julia Karolina Gorczynska,** University of Westminster, UK **Ms. Jolina Pauline Viessmann,** University of Westminster, UK
14.00 – 14.30	PT – 13	**Dr. Viswanadham Duppatla,** IKP Knowledge Park, Hyderabad, India
14.30 – 15.00	PT – 14	**Dr. Vaibhav Bhatia,** Lamark Biotech Pvt. Ltd., Pune
15.00 – 15.30	PT – 15	**Dr. Kalpana Surendranath,** University of Westminster, London, UK
15.30 – 16.00	PT – 16 (Online)	**Munuse C Savash Ishanzadeh,** University of Oxford / Life Research Oxford, UK
16.00 – 16.15	Tea Break	
Session VI: Vertically Integrated Programme (VIP) for Students as Researchers and Biomedical Research		**Chairpersons:** **Dr. V. Thillai Sekar,** Pondicherry University, India **Dr. Kanagaraj Radhakrishnan**, St George's, University of London, UK **Sneha Latha Rangan**, University of Westminster, London, UK
16.15 – 16.45	PT – 17 (Online)	**Dr. Taruna Madan,** ICMR, New Delhi, India
16.45 – 17.15	PT – 18 (Online)	**Dr. Prashanth Bajpe,** University of Bedfordshire, Luton, UK
17.15 – 17.30	VIPL – 1	**Ms. Harshana Chaurasia,** University of Westminster, London, UK

17.30 – 17.45	VIPL – 2	**Ms. Julia Karolina Gorczynska,** University of Westminster, London, UK
17.45 – 18.00	VIPL – 3	**Ms. Jolina Pauline Viessmann**, University of Westminster, London, UK
14.00 – 15.00	**Parallel Session**	**Oral Paper presentation – Session III (Senate Hall, Centre for Advanced Studies – 1 Floor) & Poster Presentation – Session III (Seminar Hall, Centre for Drug Discovery and Development – III Floor)**
	Day 3: Friday, February 21, 2025	
Session VII	**Diagnostics and Structural Biology**	**Chairpersons:** **Dr. V. Hari Balaji,** Vivagen Dx Labs, India **Prof. Dr. M. Radhakrishnan,** Sathyabama, India
9.30 – 10.00	PT – 19	**Dr. Luke Elizabeth Hanna,** ICMR-NIRT, Chennai, India
10.00 – 10.30	PT – 20	**Dr. Neelagandan Kamariah,** DBT-InStem, Bengaluru, India
10.30 – 11.00	PT – 21	**Dr. Sergio Leiva,** Austral University of Chile, Valdivia, Chile
11.00 – 11.15	**Tea Break**	
Session VIII: Vertically Integrated Programme (VIP) for Student-to-Researcher Transition and MedTech		**Chairpersons:** **Dr. Kanagaraj Radhakrishnan**, St. George's, University of London, UK **Dr. Anthony Chua,** Stratificare, Singapore
11.15 – 11.45	PT – 22	**Dr. Giuseppe Viola,** Queen Mary University of London, UK
11.45 – 12.15	PT – 23 (Online)	**Prof. Dr. J. Joshua Thomas,** Department of Computing, UOW Malaysia KDU Penang University College, Malaysia
12.15 – 12.45	PT – 24	**Dr. Vasanth Thamodaran,** Senior Scientist, TIGS, Bengaluru, India
12.45 – 13.05	PT – 25	**Dr. Bala Yeshwanth Ram Vummidi,** Inger Therapeutics, Chennai
13.05 – 13.20	PT – 26	**Shrish Kumar S**. Qiagen, Hyderabad, Telangana, India
13.20 – 14.00	**Lunch Break**	
Session IX	**Concluding Keynote Session**	**Chairperson**: **Dr Kalpana Surendranath,** University of Westminster, UK **Prof. Dr. Krupakar Parthasarathy,** Sathyabama, India
14.00 – 14.30	PT – 27 (Online)	**Dr. Anusha Seneviratne,** Royal Holloway University of London, UK
14.30 – 15.00	PT – 28 (Online)	**Prof. Dr. John Murphy,** University of Westminster, London, UK
15.00 – 16.00	**Valedictory Function**	

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Oral Presentation – Session I

Venue : Senate Hall, Sathyabama Centre for Advanced Studies (I Floor)
Date : 19.02.2025
Time : 2.00 PM – 5.00 PM

Chair persons:

Prof. Dr. R. Balagurunathan
Director Research
Vivekanandha Educations Institutions,
Tamil Nadu, India

Prof. Dr. S. Venkatesan,
Department of Environmental Science
Periyar University, Salem, India

S. No	Abstract Number	Title of the Abstract	Authors and Affiliation
1.	S1-OP1	Computational insights into anti-microbial peptides as potential therapeutics for breast cancer	**Raashika K** Central University of Tamil Nadu
2.	S1-OP2	Excitation Emission Matrix Characterization of oral tissue biopsy and blood plasma for effective delineation of oral potentially malignant disorders	**Dr. Pravda Chidambaranathan** Sathyabama Dental College and Hospital, Chennai.
3.	S1-OP3	Cardio-protective effect of nevirapine (NNRTI) against isoproterenol induced pathological hypertrophy in H9C2 Cells.	**Matte Sairam Kalyan** Andhra University
4.	S1-OP4	Studies on formulation and characterization *Piper Nigrum* of HPMC (Hydroxy Propyl Methyl Cellulose) based "Peel Off Gel" for diabetic wound ulcer applications	**Livin S** Bannari Amman Institute of Technology
5.	S1-OP5	Characterization and analysis of a novel endodontic irrigant	**Dr K Sathya Narayanan** Sathyabama Dental College and Hospital, Chennai.
6.	S1-OP6	Reverse genetic bioinformatics approach for cystic fibrosis vaccine development	**Sriyashwanth. A** Saveetha Institute of Medical And Technical Science, Chennai.
7.	S1-OP7	Molecular cloning and functional analysis of the arginine deiminase gene (Arca) from *Limosilactobacillus Reuteri* DSM 20016	**Darshali P. Thakker** SRM Institute of Science & Technology
8.	S1-OP8	Facile plant-mediated biosynthesis of silver nanoparticles and investigation of their antibacterial activity	**Hassan Mahmoodi Esfanddarani** Vellore Institute of Technology- Chennai
9.	S1-OP9	Biosynthesis of silver nanoparticles using *Hedyotis sp.,*: Optimization, characterization, antibacterial activity against multi-drug-	**Miss. Monika.D** Madras Christian College

		resistant bacteria, cytotoxicity, and wound healing in NIH/3T3 cell lines.	
10.	S1-OP10	Licochalcone a promotes neural differentiation and amyloid-β reduction through autophagy in Alzheimer's disease models	**Abhay Kumar Singh** Central University of Tamil Nadu
11.	S1-OP11	Complement components as baseline predictors of poor treatment outcomes in pulmonary tuberculosis	**P. Arul Nancy** National Institute for Research in Tuberculosis (NIRT)
12.	S1-OP12	Utilization of functional genomics in exploring the pathway of tuberculosis	**V Senthilnathan** Thaigarajar College
13.	S1-OP13	Integrative Network Pharmacology and Cell-Based Studies Unveil the Multi-Target Anti-Cancer Potential of Solanum xanthocarpum	**Kirthika S** Anna University
14.	S1-OP14	Development of Moringa leaf gummies for anaemia	**Ms. S. Ilavarasi** **Mr.S.Kabilan** **Ms. M. Sathya Sri** Paavai Engineering College, Namakkal
15	S1-OP15	Antioxidant-Rich Face Cream Using Orange Peel	**Mr. R. Saravanakanth** **Mr.V.Naveen Kumar** **Mr.K.Velmurugan** Paavai Engineering College, Namakkal
16	S1-OP16	Polyherbal mixture for relieving leg cramps during mensuration	**R.Nechika** **Mr.S.Kabilan** Paavai Engineering College, Namakkal
17	S1-OP17	Rational design of phytochemical modulators targeting psa active sites: A dual-stage strategy for prostate cancer therapy	**Keerthi V** Hindustan Institute of Science and Technology, Chennai.
18	S1-OP18	The Potential of CRISPR-Cas9 in Treating Genetic Disorders: Advances and Ethical Considerations	**Ranjith** Saveetha Institute for Medical and Technical Sciences
19	S1-OP19	*Invitro* cytotoxicity, metabolites profiling and *in silico* dengue envelope and capsid protein inhibition of Nilavembu Kudineer components – *Zingiber officinale, Vettiveria zizanioides* and *Piper nigru*	**D. Lavanya** Sathyabama Institute of Science and Technology
20	S1-OP20	Antiviral activity of compounds obtained from *Carica papaya* and *Ocimum sanctum* against Dengue-2 viral protein by in silico analysis	**D. Lavany** Sathyabama Institute of Science and Technology

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Oral Presentation – Session II

Venue : Senate Hall, Sathyabama Centre for Advanced Studies (I Floor)
Date : 20.02.2025
Time : 10.00 AM – 1.00 PM

Chair persons:

Dr. C. Pravda
Professor & Head
Department Of Oral Medicine and Radiology
Sathyabama Dental College and Hospital,
Chennai, India

Dr. S. Sanjeevi Prasath
Assistant Professor (Research)
Centre for Nanoscience and Nanotechnology
Sathyabama Institute of Science and Technology, Chennai, India

S. No	Abstract Number	Title of the Abstract	Authors and Affiliation
1.	S2-OP1	Genomeguard: Detecting Genetic Defects	**Divyaa Shree Lakshmipathy** Saveetha Institute of Medical And Technical Science
2.	S2-OP2	Enhancing ovarian cancer diagnosis using machine learning and deep learning	**Angeline. J** Sathyabama Institute of Science and Technology,
3.	S2-OP3	Automated detection of kidney stones using coronal CT images with deep learning in the field of artificial intelligence	**Riyuktha Suresh** Sathyabama Institute of Science and Technology
4.	S2-OP4	Exploring coordination variability: structural tuning of zinc–carbohydrazone complexes for biological applications	**Lathika P** Bannari Amman Institute of Technology
5.	S2-OP5	Network pharmacology-based insights into *Cissus quadrangularis* l. for osteoporosis management	**Sahil Raman Tanti** Central University Of Tamil Nadu, Thiruvarur
6.	S2-OP6	Exploring Interferon-stimulated Genes (ISGs) modulation as an antiviral strategy against chikungunya virus	**Guhan KS** Rajiv Gandhi Centre for Biotechnology
7.	S2-OP7	Evaluation of anticonvulsant role in acute organophosphorus toxicity	**Dr. Ramarao Golime** Central University of Tamil Nadu, TIRUVARUR
8.	S2-OP8	Anti-Biofilm activity of bioactive compound from marine *Streptomyces* species	**Ms. Rahavi AR** Dr NGP Arts and Science College

9.	S2-OP9	An Empirical Study On Public Opinion About Mediwaste And Their Consequences In Polluting The Environment	**Shreya. M** Saveetha School of law
10.	S2-OP10	Reprogramming the tumor microenvironment: Car-macrophages as immunotherapeutic pioneers	**Lakshmi C** Saveetha Institute for Medical and Technical Sciences
11.	S2-OP11	Evaluating the anticancer activity of *Kappaphycus alvarezii* and *Spirulina Spp*	**R. Amirtha Varshini** **T.Saiakashaya** **Hemalatha S** St.Joseph's College Of Engineering
12	S2-OP12	In vitro studies on the protective effect of Ambrex on acetaminophen induced hepatotoxicity	**Ms Shreya Srinivasan** Rajalakshmi Engineering College
13	S2-OP13	Optimizing Cyanobacterial exopolysaccharides for edible nano-coatings in meat preservation.	**Ms. Vaishnavi Rishikaa** Kamaraj College of Engineering and Technology
14	S2-OP14	Formulation of *Syzygium cumini* tea powder to prevent diabetes mellitus.	**Mr.S.Chandru** **Mr.S.Prasanth** **Mr.A.Naren** Paavai Engineering College, Namakkal
15	S2-OP15	Fabrication of biopolymer with incorporation of bioactive compounds from *Bruguiera Cylindrica*: wound healing application	**Karthih M G** **Adaikala Selvan G** Paavai Engineering College, Namakkal
16	S2-OP16	Preparation and optimization of nutrient enriched papads by using *Ulva lactuca*	**Pragathi S** Paavai Engineering College, Namakkal
17	S2-OP17	Evaluation of actinobacteria for plant growth promotion and biocontrol properties	**Ameeru Nisha** Sathyabama Institute of Science and Technology
18	S2-OP18	Computational Analysis to compare the structural and compositional aspects of the envelope protein of the Omicron and XBB variant aims to investigate the stability and transmissibility characteristics of the SARS CoV-2	**Prisho Mariam Paul** CMS College Kottayam
19	S2-OP19	Isolation and Characterization of Bacterial Cellulose And Its Applications	**Akila K** Sathyabama Institute of Science and Technology
20	S2-OP20	Isolation of bacteriocin-like antimicrobial peptides from *Bacillus*. sp isolated from fish gut	**Karthik Prakash M P**, **Gopikrishnan V,** **Radhakrishnan M** Sathyabama Institute of Science and Technology

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Oral Presentation – Session III

Venue : Senate Hall, Sathyabama Centre for Advanced Studies (I Floor)
Date : 20.02.2025
Time : 2.00 PM – 5.00 PM

Chair persons:

Prof. Dr. Vasantha Kumari Neela,
Department of Medical Microbiology,
Universiti Putra Malaysia

Dr. S. Nachiappan
Professor & Head
Department of Oral and Maxillofacial Surgery
Sathyabama Dental College and Hospital,
Chennai, India

S. No	Abstract Number	Title of the Abstract	Authors and Affiliation
1	S3-OP1	Targeting Kinesin-1 heavy chain in tauopathy promotes autophagy-driven degradation of phosphorylated Tau aggregates and mitigates neurodegeneration in Alzheimer's disease models	**Dr. D.Siva Sundara Kumar** Central University of Tamil Nadu, Thiruvarur.
2	S3-OP2	Comparative study between different artificial intelligence-based prediction methods for dementia	**Vinanthi Gnanasekar Aswini** Saveetha Institute of Medical And Technical Science, Chennai.
3	S3-OP3	Synthesis and characterization of metal-organic framework-based artificial enzyme mimics	**Monishha S** Bannari Amman Institute Of Technology
4	S3-OP4	Eutectic mixture based two phase fermentation of laccase and its studies	**Paripoorani R** Bannari Amman Institute Of Technology
5	S3-OP5	Reverse genetic bioinformatics approach for cystic fibrosis vaccine development	**Sriyashwanth. A** Saveetha Institute of Medical And Technical Science
6	S3-OP6	Unveiling the microbiome of ethnic fermented foods from Manipur and Nagaland through 16s rRNA sequencing	**Ms Sochanphy Keishing** Central University Of Tamil Nadu, Thiruvarur.
7	S3-OP7	A Personalized Scaffold: Bioconjugated Chitosan-Luteolin Complex Incorporated In Alginate Scaffold For Bone Regeneration Under Diabetic Condition	**Mr. Kabilan P** Bannari Amman Institute Of Technology, Chennai.
8	S3-OP8	Loss of trans-translation sensitizes bacterial cells to fluoroquinolone antibiotic – Nalidixic acid	**Dr. T. Nagarajan** Saveetha Institute for Medical and Technical Sciences

9	S3-OP9	Reusable Pesticide Test Slip	**Romanshia Celes G A** Saveetha Institute for Medical and Technical Sciences
10	S3-OP10	Formulation Of Biofertilizer Using Calcium Chloride Extracted From Eggshells	**Ms. Monisha Govindasamy** Dr.N.G.P Arts And Science College, Coimbatore.
11	S3-OP11	Social Impact of Genetic Abnormalities in Prenatal Testing among Maternal Women & their Partners - An Indian Perspective	**Sujithra Appavu** LifeCell International Pvt. Ltd, Chennai
12	S3-OP12	Nanotechnology based approach to combat macrolide-resistant Mycoplasma pneumoniae	**Mr. AJMAL. M.T** Sathyabama Institute of Science and Technology
13	S3-OP13	Evaluation of actinobacteria for Plant growth promotion and biocontrol properties	**Ameeru nisha** **Viveka.S** Sathyabama Institute of Science and Technology
14	S3-OP14	Exploring Cryosphere bacteria for Plant growth promotion and Disease Control	**Mr. Jayakrishnan. M** Sathyabama Institute of Science and Technology
15	S3-OP15	High prevalence of Human Papillomavirus (HPV) Co-infection in cervical biopsy samples from Indian women.	**Ganesh kumar Sarvesan** LifeCell International Pvt. Ltd, Chennai
16	S3-OP16	In Vivo and Ex Vivo characterization of recombinant Mycobacterial strains for its vaccine potential	**Vignesh Sounderrajan** Sathyabama Institute of Science and Technology
17	S3-OP17	Development of VLP-based vaccines to generate broadly neutralizing antibodies against SARS-CoV-2 variants	**Vignesh Sounderrajan** Sathyabama Institute of Science and Technology
18	S3-OP18	Exploring Nucleocapsid Protein Mutations in SARS-CoV-2 and its Variants and Their Interaction with Potential Drugs Through Docking Analysis	**Sudhanarayani S Rao** Sathyabama Institute of Science and Technology
19	S3-OP19	Establishment of a Three-Dimensional Cervical Cancer Spheroid Model for Cytotoxicity and Drug Testing	**Thangam. T** Sathyabama Institute of Science and Technology
20	S3-OP20	Mosquito Surveillance and Simultaneous detection of Vector-Borne Viruses using Multiplex PCR	**Hemamalani. AU** Sathyabama Institute of Science and Technology
21	S3-OP21	*In Silico* Design of a Multi-Epitope Vaccine Targeting PE/PPE Proteins of *Mycobacterium Tuberculosis* for Enhanced Immunogenicity	**Sakthivel Jayaraj** Sathyabama Institute of Science and Technology

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Poster Presentation - Session I

Venue : Seminar Hall, Centre for Drug Discovery and Development
Sathyabama Research Park (III Floor)
Date : 19.02.2025
Time : 2.00 PM – 5.00 PM
Chair persons:

Dr. S. Balaji,
Technical Officer
ICMR-National Institute for Research in Tuberculosis (NIRT), Chennai, India

Dr. Amudhan,
Theni Govt Medical College, Tamil Nadu, India

Dr. Sam Ebenezer,
Assistant Professor (Research),
Centre for Drug Discovery and Development, Sathyabama Institute of Science and Technology, India

S. No	Poster Number	Title of the Abstract	Authors and Affiliation
15.	S1-PP1	Harnessing MicroRNAs for targeted regulation of cell proliferation in biomanufacturing	**Hasmeet Kaur** Manav Rachna International Institute of Research and Studies
16.	S1-PP2	Novel isolation, structural characterization, and therapeutic assessment of mannose-targeted chitosan nanoparticles encapsulating Piperine for drug-resistant tuberculosis therapy	**Abdullah Mohammed Ayedh Al Adhreai** Sathyabama Institute of Science and Technology
17.	S1-PP3	Codon optimization for enhanced expression of HIV-1 transcripts in CRISPR-Cas13-based therapeutics	**Pavithra N** Bharathiar University
18.	S1-PP4	Screening of marine animal toxin-derived peptides and its biological effects for the suppression of inflammation in LPS-induced fibroblast cells	**Akshad Balde** SRM Institute of Science and Technology
19.	S1-PP5	Effects of a marine-derived oligopeptide on suppression of inflammation in an inflammatory model	**Irine Kevina, Ragul Sakthivel, Aashritha Kandala, Kristen Cyril, Sneha Sreeram** SRM Institute of Science and Technology

20.	S1-PP6	Exploring LNAA-enriched protein as a potential PKU supplement: Expression, cytotoxicity in mammalian cells, and insights from Pah Enu2 Mice	**Mithuna K M** CSIR- CFTRI
21.	S1-PP7	Anticancer potential of *Tinospora Cordifolia* (Wild) Miers by *In Silico* ADMET analysis	**D. Varshini** Saveetha Institute of Medical And Technical Science
22.	S1-PP8	PROTACs In neurodegeneration: unlocking therapeutic potential via protein degradation	**Ms. Shirin.V**. Saveetha Institute of Medical And Technical Science
23.	S1-PP9	Analysis Of Protein Ligand Interaction: PYRX docking of g-protein coupled receptor 1 protein causing ovarian cancer	**Gollapudi Maadhvi** Saveetha Institute of Medical And Technical Science
24.	S1-PP10	Bioactive components loaded biopolymeric materials for managing dental caries	**Akshara S** Chettinad Academy of Research and Education
25.	S1-PP11	Structure-based docking and molecular dynamics simulation of small molecules targeting DHCR7 to treat Smith-Lemli-Opitz Syndrome	**Jeevarathanam R** Saveetha Institute of Medical And Technical Science
26.	S1-PP12	Investigation of computational method for the treatment of Alzheimer's by targeting β-amyloid through comparative docking approach	**Ajay Sekaran. A** Saveetha Institute of Medical and Technical Sciences
27.	S1-PP13	Deciphering HTT protein mutations for structural and functional insights into Huntington's disease	**Dasari Akshitha** Saveetha Institute of Medical And Technical Sciences
28.	S1-PP14	Computational Analysis of Structural, Functional, and Evolutionary Variations in Human Peroxiredoxin Variants Using Molecular Modelling and Docking Approaches	**Rajasri A** **Jethasree Sravya Sravani Kandula** Saveetha Institute of Medical And Technical Sciences
29.	S1-PP15	Unraveling the Secondary Metabolite Arsenal of Bdellovibrio: Insights from Comparative BGC Analysis	**Steven Malla** Saveetha Institute of Medical and Technical Sciences
30.	S1-PP16	Potential Therapeutic Role of Phenolic Antioxidants in Targeting Alpha-Synuclein Aggregation in Neurodegeneration with Brain Iron Accumulation	**Konukuru Hemasree** **Jahnavi Damodara** Saveetha Institute of Medical And Technical Science
31.	S1-PP17	Molecular Docking Study of Curcumin Interaction with Collagen and Keratin: Insights into Anti-Aging Protein-Ligand	**Ms. Jalapati Nandini** **Ms Cheerla Praneetha**

		Binding Using Docking and STRING Database Analysis	Saveetha Institute of Medical And Technical Science
32.	S1-PP18	Development of Anti-Freezing Peptide-Enhanced Biofertilizers for Improved Crop Yields and Frost Protection	**Ms.Sanna reddy Poojitha** **Ms.Edapa Gnyaana Abhinaya** Saveetha Institute of Medical And Technical Science
33.	S1-PP19	Unravelling cardiovascular disease in Systemic Lupus Erythematosus (SLE) : Exploring the Influence of autoantibodies and immunosuppressants	**Ms Rachana Kamath** Kasturba Medical College, MAHE
34.	S1-PP20	Folate-decorated, albumin-conjugated BNNTs for targeted Paclitaxel delivery in A549 lung cancer: Antimicrobial activity, hemocompatibility, and cytotoxicity evaluation	**Shanmuga priya R** Anna University
35.	S1-PP21	Investigating The Role of M6A Reader - YTHDC1 In Renal Cellular Pathophysiology	**Aishwarya Ganesan** Bharathidasan University
36.	S1-PP22	Facile and Bioinspired Gelatin Hydrogel for Enhanced Antimicrobial and Wound Healing Applications.	**Ms. Gurupurnima ST** **Shreshta Nair** **Bharath Raj J R** Hindustan Institute of Technology and Science , Chennai

2nd International Conference on

Translational Research in Biomedical Sciences (TRIBS 2.0)
February, 19-21, 2025
Venue: Tmt. Soundrabai Auditorium, Sathyabama Centre for Advanced Studies (III Floor)
Sathyabama Institute of Science and Technology, India

Poster Presentation - Session II

Venue : Seminar Hall, Centre for Drug Discovery and Development
Sathyabama Centre for Advanced Studies (I Floor)
Date : 20.02.2025
Time : 10.00 AM – 1.00 PM
Chair persons:

Dr. A. Suresh,
Scientist,
Meenakshi Academy of Higher Education and Research (MAHER), Kanchipuram, India

Dr. T. Rajasekar,
Assistant Professor (Research),
Centre for Drug Discovery and Development,
Sathyabama Institute of Science and Technology, India

S. No	Poser Number	Title of the Abstract	Authors And Affiliation
1.	S2 – PP1	Enzymatic extraction and purification of marine fish-derived bioactive peptide and its anti-inflammatory effects through suppression of cytokines	**Thilothamai Jegani K** SRM Institute Of Science And Technology, Chennai
2.	S2 – PP2	Systematic approach to biofilm formation and its inhibition on menstrual cups using phyto-extracts.	**Sayli Kulkarni and Aaditi. Dalvi** Priyadarshini College of Engineering
3.	S2 – PP3	Synthesis, spectral characterization and antibacterial activity of some Benzyl derivatives - in silico molecular docking and ADMET Studies	**Satheeshkumar N** Annamalai University
4.	S2 – PP4	Isolation of soil-borne fungi as biological agents and their inhibitory study against *Phytophthora* species.	**Ms. Bhargavi R. Ambatkar** **Ms. Apurva Dohale** Priyadarshini College of Engineering
5.	S2 – PP5	Human Genome Resources Updated Database - A Future Key on Aging Research	**Muthuselvi Gopal** Sathyabama Institute of science and technology
6.	S2 – PP6	Unraveling Novel Lead Compounds Against Autism Susceptibility Gene 2 (AUTS2) Using Comparative Docking of Various Ligands	**B. Reshini Priya** Saveetha Institute of Medical and Technical Science
7.	S2 – PP7	Characterization of surface morphology and pocket analysis of Verona Integron-Encoded Metallo-beta-lactamase(VIM) protein for drug analysis	**Ms. Deveena** Saveetha Institute of Medical and Technical Science
8.	S2 – PP8	Structural analysis of Klebsiella	**Ms. Racharla Mythili**

		pneumonia Carbapenemase (kpc) protein for drug analysis	Saveetha Institute of Medical and Technical Science
9.	S2 – PP9	Harnessing virtual screening for lung cancer drug discovery: A natural product-based approach.	**Nithishkumaran. M** Saveetha Institute of Medical and Technical Science
10.	S2 – PP10	Machine Learning-Based Identification of Binding Pockets in Multidrug Efflux Pumps for Ligand Targeting	**Jishitha Kondapalli** Saveetha Institute of Medical and Technical Science
11.	S2 – PP11	Computational drug discovery for zoonotic diseases using molecular docking approaches for identifying novel therapeutics	**S. Praveen Kumar** Saveetha Institute of Medical and Technical Science
12.	S2 – PP12	Creation of medications using molecular docking to target Alzheimer's	**R. Alekhya** Saveetha Institute of Medical and Technical Sciences
13.	S2 – PP13	Unravelling key molecular drivers of glioblastoma through transcriptomic and network analysis	**Vishal Sai B.J** Saveetha Institute of Medical and Technical Sciences
14.	S2 – PP14	Virtual and in vitro screening of spiroazacyclic compounds for novel TMPRSS2 inhibitors as SARS-CoV-2 therapeutic entry-blockers.	**Moorthi Radhakrishnan** Central University of Tamil Nadu
15.	S2 – PP15	The biosynthetic capacity of *Myxococcus*: A Comprehensive BGC Analysis	**Yaswitha.G** Saveetha Institute of Medical and Technical Science
16.	S2 – PP16	Comparative genomic and biosynthetic gene cluster analysis of *Lysobacter* species for antimicrobial potential	**Poojitha. R and K. Lakshmi Manasa** Saveetha Institute of Medical and Technical Sciences
17.	S2 – PP17	Machine learning enhanced scrutiny of Extended spectrum beta lactamases (CTX-M) for Drug development	**T. Vyshno babu** Saveetha Institute of Medical and Technical Sciences
18.	S2 – PP18	Structure-based approach of binding pocket analysis in crystal structure of New Delhi Metallo-beta-lactamase (NDM-1) for ligand screening	**P. Thanooj kumar reddy** Saveetha Institute of Medical and Technical Sciences
19.	S2 – PP19	Rhodotorula Redefined': Tackling Mitochondrial ROS-induced Leaky-gut Syndrome through *R. glutinis* Probiotic Revitalization.	**V. Sri Sai Amruthaa** **E. Rethika raj** Sri Ramachandra Institute of Higher Education and Research
20.	S2 – PP20	Epitope-based vaccine design against Zika virus	**Shunmughi K V** **S Varshini** Kamaraj College of Engineering & Technology
21.	S2 – PP21	AI- Based DNA Repair Efficiency Predictor for Recombinant DNA Technology	**Sahana. F** Saveetha Institute of Medical and Technical Sciences

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Poster Presentation - Session III

Venue : Seminar Hall, Centre for Drug Discovery and Development
Sathyabama Centre for Advanced Studies (I Floor)
Date : 20.02.2025
Time : 2.00 PM – 5.00 PM
Chair persons:

Dr. Amit Kumar
Associate Professor (Research),
Centre for Climate Change Studies,
Sathyabama Institute of Science and Technology, India

Dr. S. Prakash,
Associate Professor (Research),
Centre for Climate Change Studies,
Sathyabama Institute of Science and Technology, India

Dr. S. Vignesh,
ICMR- Post Doctoral Researcher,
Centre for Drug Discovery and Development
Sathyabama Institute of Science and Technology, India

S. No	Poster Number	Title Of The Abstract	Authors And Affiliation
1.	S3-PP1	In Silico analysis of animal venom-derived matrix metalloproteinase-9 modulators and their therapeutic Implications	**Ansumaan Sharma** SRM Institute Of Science And Technology
2.	S3-PP2	Pharmacological therapy :Selection and designing of lead molecules using molecular docking approach for the cure of cystic fibrosis disease	**Keerthana Sri.S** **Jeevitha.P** Saveetha Institute of Medical and Technical Sciences
3.	S3-PP3	In-Silico Structural and Functional Annotation of Hypothetical Proteins from Nocardia asteroides NCTC11293: A Computational Approach for Novel Drug Target Identification and Therapeutic Development	**Maharaja M. S** Alagappa University
4.	S3-PP4	An efficient framework model for Liver tumor detection and segmentation using Novel Recurrent Neural Network in comparison with Support Vector Machine	**Kethineni Revathi** Saveetha Institute of Medical and Technical Sciences
5.	S3-PP5	Structural insights and Binding pocket analysis of OXA-23 β-lactamase: A computational approach for Inhibitor design	**K. Deepak** Saveetha Institute of Medical and Technical Sciences

6.	S3-PP6	Exploring the complexities of human physiology	**Bharath P** Saveetha Institute of Medical and Technical Sciences
7.	S3-PP7	*In silico* screening of nucleocapsid protein with different ligands for the treatment of Measles	**Akshaya B.,** **Akshaya L.carba,** **Beena Kanimozhi** Saveetha Institute of Medical and Technical Sciences
8.	S3-PP8	Functionalized polymeric nanoparticle as a drug delivery system for anticancer drug	**Harini A** Vellore Institute of Technology Chennai Campus
9.	S3-PP9	Antibacterial potential of Eugenol against methicillin-resistant *Staphylococcus aureus*	**Adithya Shree G** **Jinu Harini R C** PSGR Krishnammal College for Women
10.	S3-PP10	Fabrication and evaluation of herbal nanofillers-based hydrogel for wound dressing application	**Advaith G Prabhu** Hindustan Institute of Technology and Science
11.	S3-PP11	Comparative Molecular Docking on polyprotein P1234 factor with novel ligands for chikungunya	**Otra.Shamitha** Saveetha Institute of Medical and Technical Sciences
12.	S3-PP12	Computational study and molecular docking of ANTXR2 protein involved in anthrax and identification of potential ligand interactions for therapeutic applications.	**Abaya.S** Saveetha Institute of Medical and Technical Sciences
13.	S3-PP13	Computational Study, Molecular Docking, and Toxicity Analysis of Proto-Oncogene 2 Protein and Identification of Ligand for Cervical Cancer Therapy	**Kanishka.S** Saveetha Institute of Medical and Technical Sciences
14.	S3-PP14	An effective approach to detect chronic kidney disease using fine tree algorithm and boosted tree algorithm using MATLAB	**Celine Mary** Saveetha Institute of Medical and Technical Sciences
15.	S3-PP15	Breaking The Clot: Probiotic-Engineered Yeast To Revolutionize APS Treatment	**Susan Jesse Agnes. M** **Harshavardhni Murugesan** Sri Ramachandra Institute of Higher Education and Research
16.	S3-PP16	Bridging evolution and structure homology modelling in phylogenetic studies of moonlight protein	**Raaga Hasini** Saveetha Institute of Medical and Technical Sciences
17.	S3-PP17	Evaluation of actinobacteria From Kashmir Region for anti-mycobacterial activities	**R. Hari Baskar and Akash** Sathyabama Institute of Science and Technology
18.	S3-PP18	Comparison of extraction methods for the isolation of isoflavanoids from soybean-characterization and chemometric analysis	**Rukmani Kanchana Ramanathan** **Tanushree Kannayiram** **and Rohan Rajendran** Hindustan Institute of Technology and Science, Chennai.

19.	S3-PP19	Development of CRISPR-Cas13 Molecular Diagnostic Tool for Detecting Mycobacterium tuberculosis	**P. Venkatesan** National Institute for Research in tuberculosis
20.	S3-PP20	Biosurfactants: Sustainable Solutions for Environmental and Agricultural Applications	**Eswarnath** Sathyabama Institute of Science and Technology
21.	S3-PP21	Adaptations of Cryosphere Microbes: Functional Roles of Siderophores, Antifreeze Proteins, and Cold-Active Enzymes in Extreme Environments	**Sai Mahesh Kumar. S** Sathyabama Institute of Science and Technology
22.	S3-PP-23	Inactivation of BCL11A Using CRISPR-Cas9 for the treatment of sickle cell Anaemia	Ranjanaa V.P, Saveetha School of Engineering (Deemed)

 ISBN: ISBN: 978-93-83409-98-3

ABSTRACTS FROM PLENARY SPEAKERS

PT – 1

Immunotherapeutic Approaches: Implications for Prevention, Treatment, and HIV Cure

Siddappa Byrareddy,
University of Nebraska Medical Center, Omaha, NE, USA

While antiretroviral therapy (ART) effectively suppresses HIV replication, it does not eradicate the virus or fully restore immune function. Immunotherapeutic strategies aim to enhance the immune system's ability to control HIV, reduce viral reservoirs, and potentially achieve long-term remission without ART. Several approaches, including checkpoint inhibitors, cytokine-based therapies, and adoptive T-cell therapy, are being explored to improve treatment outcomes.

In this presentation, I will discuss our ongoing strategies utilizing anti-α4β7 therapy, as well as a combination approach with Interleukin-21 (IL-21) and anti-α4β7 dual therapy, alongside Chimeric Antigen Receptor (CAR)-engineered T cells. Additionally, I will present data aimed at refining these strategies, optimizing their safety profiles, and developing combination therapies that effectively target both actively replicating and latent HIV reservoirs.

PT – 2

Solid Organ Transplantation: Acceptable Mismatches and Anti-HLA Antibodies

Dr Uma Kanga
Clinical Immunogenetics Laboratory
Department of Transplant Immunology and Immunogenetics
All India Institute of Medical Sciences, New Delhi

Renal Replacement therapy is routinely offered to patients diagnosed with end stage renal disease. Overwhelming evidence indicates the benefits of HLA matching in organ transplantation, including superior graft function, longer patient and graft survival, lower risk of sensitization, fewer rejection episodes and possibility of reduced immunosuppression. Mismatches in HLA lead to rejection episodes, higher immunosuppression requirement, which in turn, leads to malignancy as well as risk of infections. Risk of sensitization increases with mismatches, which complicates and delays subsequent transplantation, if required. All recipients may not find a well matched donor, therefore strategies to optimize transplantation should take into account immunological barriers due to mismatches: acceptable and unacceptable mismatches, sensitization to particular HLA types, strength and nature of anti-HLA antibodies. HLA antibodies are the primary cause of transplant rejection. HLA antibodies recognize epitopes, which can be structurally defined as eplets that are small configurations of polymorphic amino acid configuration on the surface of HLA molecules and play important role in reactivity with antibodies. It is well recognized that antibodies are specific for epitopes rather than antigens. These epitopes could be structural or functional and therefore play a dominant role in determining antibody specificity. Several transplant programs select donors based on epitope mismatch. Eplets are considered to be equivalent to functional epitopes. Appearance of donor specific antibodies (DSA) is associated with allograft rejection and failure. However, some transplants continue to function quite well in presence of DSA. Therefore it is important to understand which antibodies are clinically relevant in transplantation. Significant correlations are observed between eplet loads of HLA mismatches and development of DSA as well as rejection incidence and allograft outcome.

This is clinically relevant, as mismatched eplet load can be a risk factor during post transplant monitoring for antibody-mediated rejection. Additionally, eplet loads can be used to develop new donor selection strategies for non-sensitized recipients. Understanding the acceptable mismatches and mechanism of antibody development, strength and nature of antibodies helps to minimize the rejections and improve graft survival.

PT – 3

RNA-DNA Damage Response: From Mechanisms to Models to Medicines

Kanagaraj Radhakrishnan[1,2,3]

[1] Section of Molecular Biology, Institute of Medical, Biomedical and Allied Health Education, St George's, University of London, Tooting, London, UK; [2] Genome Engineering Laboratory, School of Life Sciences, University of Westminster, London, UK; [3] Centre for Drug Discovery and Development, Sathyabama Institute of Science and Technology, Chennai, India.

Genome integrity must be carefully maintained to guarantee cell survival and prevent the onset of disease. RNA-DNA damage response (RDDR) pathways counteract endogenous and exogenous stressors that pose threats to genomic stability by forming co-transcriptional RNA-DNA hybrids (R-loops). Intriguingly, R-loops form across the entire genome, and if left unresolved they can impede the transcription, replication and DNA repair processes, which can cause genomic instability through different mechanisms that are still not fully understood. Accumulating evidence suggests that R-loops are avoided by cells either preventing or removing RNA-DNA hybrids directly or by DNA repair-related mechanisms. In human cells, R-loops are mainly resolved by either RNA-DNA helicase Senataxin (SETX) or RNaseH1 ribonuclease. Our recent large-scale proteomic analysis identified numerous RNA- and R-loop-binding proteins, which may be essential for the resolution of R-loops and maintenance of genome stability. Notably, mutations in the genes that encode several of these proteins have been linked to cancer, neurological diseases and autoimmune disorders. Using a combination of multi-omics and molecular/cell biology approaches, our ongoing research aims to discover different cellular pathways that are involved in regulating R-loops genome-wide. Importantly, our most recent findings suggest that a few RNA helicases collaborate with SETX in preventing R-loop-induced genomic instability via different mechanisms. Furthermore, our findings show that R-loop accumulation is linked to cell death via the innate immune response in *SETX*-mutated cells derived from patients with AOA2 neurodegenerative disease. Our future research directions will involve identifying potential therapeutic strategies for diseases that are caused due to dysregulation of R-loops.

PT – 5

Predicting sustained response to radioembolization with high accuracy in hepatocellular carcinoma patients

Dr Anthony Chua

Stratificare, Singapore

Yttrium-90 radioembolization (Y90-RE) is an effective locoregional therapy for hepatocellular carcinoma (HCC), inducing tumour regression and delaying progression. This study investigates the immune-modulatory effects of Y90-RE and explores biomarkers predictive of long-term treatment response. To characterize immune alterations following Y90-RE, we performed high-dimensional analyses using time-of-flight mass cytometry, next-generation

sequencing (NGS), and flow cytometry on tumour-infiltrating lymphocytes, tumour tissues, and peripheral blood mononuclear cells (PBMCs) collected before and after treatment. Post-treatment tumour samples displayed an enriched immune environment, with increased infiltration of cytotoxic CD8+ T cells, CD56+ NK cells, and CD8+CD56+ NKT cells, alongside elevated granzyme B expression, indicative of enhanced immune activation. NGS data revealed significant innate and adaptive immune response-related gene upregulations. Chemokine pathways, particularly those involving CCL5 and CXCL16, were linked to the recruitment of activated GB+CD8+ T cells into treated tumours. In PBMCs, Y90-RE induced systemic immune changes, including an upsurge in tumour necrosis factor-α expression in CD8+ and CD4+ T cells and an increase in antigen-presenting cells. Notably, a subset of PD-1+/Tim-3+CD8+ T cells co-expressing CCR5 and CXCR6 emerged as a marker of sustained response. Leveraging these findings, we developed a predictive test that accurately identifies sustained responders before treatment with 100% accuracy. Y90-RE triggers both localized and systemic immune activation, with distinct immune signatures correlating with therapeutic success. Our predictive test offers a reliable, pre-treatment method for identifying patients who will derive long-term benefits, facilitating personalized treatment strategies.

PT – 6

Targeting Mycobacterial "SOS" Response- a strategy to toggle Antimicrobial Resistance (AMR)

Saravanan Matheshwaran, PhD
Associate Professor
Microbial Adaptation and Chromatin Dynamics Laboratory
Department of Biological Sciences and Bio-engineering,
Environmental Microbiology Laboratory, Centre for Environmental Sciences and Engineering,
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The "SOS" response is an essential systematic mechanism against DNA damage in bacteria. It is indispensable for its regulatory role in maintaining genome integrity and in gaining fitness advantage by developing useful mutations to tolerate genotoxic stress, leading to the development of antimicrobial resistance. LexA and RecA are the key players regulating the global network of stress-responsive and damage-repair genes involved in this pathway. In an era of expanding drug resistance, targeting such non-traditional yet non-compromising pathways can provide useful answers in tackling global health hazards such as Tuberculosis (TB). The potential of targeting the "SOS" response is gathering increasing support to strengthen therapeutic efficacy. RecA inhibitors have been reported from chemical screening assays conducted in *E.coli* and *Mycobacterium tuberculosis* (Mtb), the latter being the causative agent of TB. However, RecA bears homologs not only across prokaryotic but also eukaryotic organisms, posing a challenge for specific action. Consequently, a shift in gears has taken place with scientists switching to the other master regulator, LexA, which does not possess any eukaryotic counterpart. An academic-industry partnership successfully delivered the first-of-its-kind inhibitors targeting *E.coli* LexA autoproteolysis. Such efforts have not yet been extended to Mtb and addressing this gap forms a major objective of our study. Here, we report potential inhibitors of Mtb LexA. We have elucidated the kinetic parameters of

interaction and generated a homology model to obtain an idea of possible drug-binding sites in Mtb LexA. Our studies involve characterizing such compounds with the broader aim of improving the existing arsenal of anti-TB therapeutics. Characterizing such inhibitors of Mtb LexA autoproteolysis can be effective in stalling "SOS" induced mutagenesis and AMR in mycobacteria.

PT – 8

Tumor Immune Cell Specific Antibody Mimetics

Dr. V. Thillai Sekar
Department of Microbiology, Pondicherry University, India

Monoclonal antibodies are promising therapeutic molecules in immune checkpoint targeting cancer immunotherapy. Many antibodies are already approved by Food and Drug Administration (FDA), and in clinical practice. However, it is not affordable to cancer patients in many parts of the world due to the cost of production involved. Any alternative biologics that are cheap to produce and highly efficient in binding with the target would revolutionize the field of medicine. We used antibody mimetic such as nanobody and affibody displayed in M13 bacteriophage (Phage library) to identify nanobodies highly specific to various immune cell subtypes in the tumor microenvironment.

Antibody, lacking light chain, was identified from (Heavy chain only antibody) from camelid species. Single variable domain of heavy chain only antibody is called as nanobody, which retains the paratope property of a complete antibody by having all three complementary determining regions (CDR). They are highly resistant to thermal and chemical denaturation, and the smaller size of nanobodies makes it accessible to any part of biomolecules, and easy to express and mass-produce for various applications. Affibody is the protein sequence isolated from the Z domain of protein A originally isolated from *S. aureus,* and created as a library by introducing random mutations in the C-terminal region of affibody. Diversity in nanobody and affibody was confirmed by sequencing 20 different clones in each library.

We induced two tumor types (Py8119, and Py117) in C57BL/6 mice and screened nanobodies and affibodies selectively targeting five different subtypes (Dendritic cells, Macrophages, T-Helper cells, Cytotoxic T cells and Regulatory T cells) of tumor immune cells 3 weeks post-implantation. Selected nanobody clones were subcloned and expressed in *E. coli* to make Venus-Nanobody, and IgGFc-Nanobody fusion proteins. Nanobody protein binding was evaluated by flowcytometry-based assays by using splenocytes isolated from C57BL/6, and Venus tagged nanobodies. MiSeq NGS method was followed to sequence all nanobody samples after every biopanning. Enrichment of specific nanobodies monitored following NGS and traditional clone selection of all four biopanning steps. Overall, we have identified group of nanobodies specifically binding to each subtype of immune cell selected, and the binding ability of few nanobodies validated for further studies.

PT – 9

Understanding the molecular pathogenesis of Acute-on-Chronic Liver Failure with a combined OMICS approach

Pragyan Acharya

Department of Biochemistry, All India Institute of Medical Sciences, New Delhi

Acute-on-chronic liver failure (ACLF) is an innate immune-driven liver disease characterized by multiple organ failure (MOF) and high short-term mortality. While it is known that the extensive damage of the liver and release of damage and pathogen associated molecular patterns (DAMPs and PAMPs) trigger the dysfunctional activation of innate immunity, the molecular interactions that render innate immunity dysfunctional and lead to mortality, are not yet fully understood. In the present study, we aimed at understanding the molecular factors, specifically lipids, that are associated with MOF and mortality in ACLF since they have been shown to cause immune-modulation in other systems. Plasma derived lipids from 60 ACLF patients and 30 healthy individuals were subjected to HILIC-based separation and identification using LC-MS/MS coupled to triple Q-TOF (SciEx 6500). ACLF patients were stratified as 28-day survivors (n=30) and non-survivors (n=30). Peak mapping and method creation was done using MultiQuant software, followed by data analysis in MetaboAnalyst software. Differential lipids were identified area under receiver operating curve (AUROC) were generated in order to identify lipids associated with mortality. The ability of these lipids to cause immunomodulation were investigated with the help of *ex vivo* neutrophil The transcriptomic profiles of ACLF derived neutrophils were compared to healthy controls. A total of 110 lipid species were altered in ACLF patient derived plasma as compared to healthy controls. PLS-DA showed distinct separate clustering of ACLF vs healthy samples, whereas among ACLF 28-day non-survivors and survivors, partial overlap of lipid species was observed. The ex vivo assays revealed the ability of ACLF derived lipids in causing modulation of gene expression including genes that were found to be altered in the differential transcriptomic analyses of neutrophils derived from ACLF vs HC. ACLF patients harbor lipid signatures that are associated with MOF and short-term mortality. These lipids have prognostic potential for the prediction of mortality in ACLF and may also have a causative role in ACLF.

PT – 11

Intelligent biophotonic tools and optical biopsy

Dr. N. Sujatha

Professor

IIT Madras, Tamil Nadu, India

Applications of light-based technologies are highly appreciated in devising non-invasive diagnostic tools based on light-tissue interactions. Alternatively known as optical biopsy, biophotonic technologies reveal the structural and functional details of the biological sample in real-time, thus speeding up the entire diagnostic process. Integrating artificial intelligence in biophotonics has revolutionized the application of such techniques for accurate quantitative tissue analysis. This talk will elaborate on the research in the biophotonics lab, IITM, in this vertical, focusing on current and future prospects for cancer diagnostics

PT – 12

Deep Tech Innovations Enabling Sustainable Cervical Cancer Screening and Therapy

V. Hari Balaji

CEO&CSO, Translational Immunogenomics Unit, VivagenDx Labs, Chennai, India

Cervical Cancer (CaCx), cancer of the uterine cervix is the second most common cancer in India and fourth most common in the world. However, CaCx is also one of the most easily preventable cancers with regular screening. Therefore, sustainable screening, diagnostics and therapeutics interventions are urgently needed to combat this disease. In the first part of the talk a novel Tumor-Infiltrating Lymphocyte (TIL) therapeutic approach would be discussed. TIL is an innovative form of immunotherapy that uses a patient's own T cells, extracted from their tumor, to fight cancer. These T cells are expanded in the lab and then reintroduced into the patient's body, where they target and destroy cancer cells. TIL therapy has shown promise in treating various cancers, including cervical cancer, and has received breakthrough therapy designation from the FDA for its potential to significantly improve outcomes for patients with advanced cervical cancer. This personalized treatment leverages the body's immune system to offer a new hope for those with recurrent or metastatic cervical cancer. In this context, this talk will present recent data regarding the generation and characterization of TILs from both primary and metastatic cervical cancer lesions. In the second part of the talk, a novel deep tech innovation aiming to make cervical cancer screening sustainable using Artificial intelligence (AI) enabled portable point-of-care digital cytology would be discussed.

PT – 13

Research to Reality: Innovations for Equitable Healthcare

Viswanadham Duppatla

IKP Knowledge Park, Genome Valley, Hyderabad, India.

Email: viswanadham@ikpknowledgepark.com

Translating scientific discoveries into tangible healthcare solutions is a complex yet crucial effort being coordinated by funding agencies and entrepreneurial support organisations. This talk will explore the journey of supporting biopharmaceutical and healthcare innovations from the laboratory to the marketplace, with a focus on achieving equitable access and affordability. Drawing on extensive experience in biopharmaceutical development, grant management, and mentoring, the talk will cover insights gained from empowering 390+ scientists, clinicians, engineers, and early-stage startups. This support has facilitated the follow-on funding of INR 950 crores, enabling the transition of numerous technologies from research to real-world application. The talk will highlight successful case studies of researchers establishing enterprises, like Parisodhana NeoWarm and Bycus Therapeutics PEGloticase. This talk will also discuss the critical role of mentorship, funding programs (such as BIG, AGC, JanCare, CAWACH, and I-CO Fund), and collaborative ecosystems (including incubators and foundations) in driving innovation. Q&A session will be open to discuss the challenges and opportunities in bridging the gap between research and reality, emphasizing the importance of fostering partnerships between clinicians, academia, and industry to improve global healthcare access and affordability, particularly within the Indian context.

PT – 14

A journey towards advancing sustainable and accessible biopharmaceuticals at Lamark biotech

Vaibhav Bhatia

Lamark Biotech Private Limited, NCL Innovation Park, Pune, India.

Lamark is driven by a bold vision: to revolutionize molecular medicine and make life-saving treatments more accessible and sustainable. In a world where millions lack access to essential medicines, we believe that equity in healthcare is as crucial as innovation itself. Supported by BIRAC, National Biopharma Mission, and some prestigious European grants; we are developing high-concentration, extra-stable biopharmaceuticals. We are working to eliminate cold chain dependencies and reduce dosage frequency, paving the way for wider global accessibility and patient-centric solutions.

I will be sharing our journey that begins with InStrong, an extra stable insulin formulation. Currently, over 450 million people worldwide live with diabetes, with 110 million of them dependent on insulin. However, due to issues with cold chain logistics and high costs, more than 40% of diabetes patients globally cannot reliably access this life-saving medicine, especially in low-resource regions. InStrong is engineered to overcome these barriers, offering unmatched stability and ensuring its availability where it is needed the most. But our mission doesn't stop here. We are also addressing diabetic retinopathy (DR), the leading cause of vision loss among diabetes patients, which affects over 60% of this population. Despite the widespread use of anti-VEGF therapies, up to 50% of DR patients develop resistance to treatment. Our leading candidate, LCT, shows promise in overcoming this resistance and enhancing treatment outcomes, aiming to redefine the future of DR treatment. Through our commitment to developing novel, patient-centric biologics, LAMARK is dedicated to ensuring equitable access to life-saving treatments worldwide.

PT – 15

Advancing Research-Integrated Education: The Gene Editors Network of Excellence for Multidisciplinary Student Innovations and Global Impact

Kalpana Surendranath

Gene Editors of the Future & Genome Engineering Laboratory, School of Life Sciences, University of Westminster, London, UK.

The United Nations Educational, Scientific and Cultural Organisation (UNESCO) highlights higher education as an invaluable resource that "equips students with the skills to meet ever-changing labour markets" and serves as a "passport to economic security and a stable future" for vulnerable students. The Gene Editors of the Future (GEOTF) program at the University of Westminster (www.geneeditorsofthefuture.uk) exemplifies an innovative approach to integrating higher education with lifelong learning and professional development. GEOTF complements academic learning while equipping participants with laboratory and interpersonal skills for career advancement in the life sciences sector. Divided into 3 phases (basic, advanced, and research internships) over 8 months the program offers students an immersive learning experience in Nobel Prize-winning CRISPR gene editing technology on an entirely free and extracurricular platform. Through authentic learning experiences, GEOTF

stands as a first-of-its-kind initiative in the United Kingdom in CRISPR-based learning. Launched during the COVID-19 pandemic, it overcame challenges to showcase institutional preparedness and student resilience. Since 2020, GEOTF has grown annually by 22.96%, engaging over 700 students and researchers across undergraduate, postgraduate, and PhD levels. Participants survey from four iterations indicate that 61.7% of participants seek research internships, 25% aspire to advanced training, and 13.3% aim for basic certification in gene editing, with a focus on disease modelling, drug discovery, and diagnostics. As the UK life sciences industry employs over 250,000 professionals and is projected to create more than 130,000 new jobs over the next decade, there is a growing demand for biotechnologists skilled in CRISPR and related technologies. GEOTF addresses this gap by enhancing employability, bridging CV gaps, and fostering professional networks. Importantly, the program has cultivated a networked and unified scientific community, where students engage actively and authentically with nuances of cutting-edge research. By offering opportunities to participate in academic conferences, publishing, and public speaking, GEOTF fosters a culture of inquiry, innovation, and intellectual growth. Furthermore, students act as ambassadors for the University's values, promoting social responsibility and a global perspective, preparing them to lead positive change in their careers and communities.

Recent data shows that women represent only 35% of STEM graduates and remain underrepresented in leadership roles. However, across the four iterations of the program, the number of female participants has steadily increased at all levels, culminating in 83% in 2024. These students actively train and gain diverse opportunities, equipping them with the skills to pursue leadership roles within the scientific community and beyond. Gene editing is often perceived as a highly complex science; GEOTF challenges this notion by breaking stereotypes and expanding training opportunities across national and international institutions, while also increasing access to remote parts of the world through hands-on workshops. Looking ahead, GEOTF is set to lead the vertically integrated global CRISPR initiative, collaborating with leading institutions worldwide.

Taken together, this talk will focus on sharing best practices to redefine how cutting-edge science is explored, taught, and communicated within the higher education landscape.

PT- 16

Cross-Level Student Collaboration – The Key to Shaping the Success of the Future

Munuse C Savash Ishanzadeh

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Collaboration among students at varying levels is a powerful tool and crucial for personal and academic growth. This talk will explore how engaging with peers at different stages in their educational journey can provide unique opportunities for learning, skill development, and future success. Providing direct examples of collaborations within my own academic journey which allowed me to pursue an MSc and PhD at Oxford University and join a start-up company as a Senior Research Scientist. Collaborating with others who have diverse perspectives and experiences, not only provide new insights but also enhance other skills such as communication, leadership, and personal skills such as confidence and drive. This session will highlight the long-term benefits of cross-level student collaboration, emphasizing its role

in the future success of individuals. It will also detail the importance of grasping any opportunity to inspire, motivate and guide young individuals on their journey to greatness.

PT – 18

CRISPR screen to identify novel factors in the cellular response to UV-induced DNA damage and heat shock

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Maintenance of genome integrity is vital for the very survival of an organism. Mistakes in this process can have serious consequences on the ability of cells to perform cellular processes like replication, transcription and translation. When bulky DNA lesions, such as those induced by UV, block the path of faithfully transcribing RNA Polymerase II, a cascade of complex molecular events is triggered, collectively referred to as transcription-coupled DNA damage response. Intriguingly, bulky DNA lesions like those generated by UV also trigger a temporary global shut down of transcription, even of genes that are not damaged. In a similar way, in response to heat shock, the heat shock factor binds to target gene promoters, leading to increased expression of heat shock proteins that help maintains protein homeostasis and cell survival. We performed a CRISPR screen to identify novel factors in UV-induced DNA damage and heat shock pathways. These results will be presented in the talk.

PT – 19

Multiplex detection of circulating cell-free *Mycobacterium tuberculosis* DNA in non-sputum-based samples for early diagnosis of tuberculosis

Dr. Luke Elizabeth Hanna
Scientist F and Head
Department of Virology and Biotechnology
ICMR – National Institute for Research in Tuberculosis, Chennai, India

Tuberculosis (TB) is an important infectious disease and a persistent public health challenge. India accounts for a quarter of the global TB burden, with an estimated 2.7 million new infections and 323,200 deaths equivalent to about 37 deaths per hour in 2023. TB control is still significantly hampered due to the limitations of traditional diagnostic methods in early and rapid diagnosis of the disease in many cases. Recent advances in molecular diagnostics have provided us with highly sensitive technologies and platforms that can be beneficially exploited for the accurate diagnosis of tuberculosis in diagnostically challenging cases, and possibly even early identification of individuals with high risk of progression from latent TB infection to active infectious disease so that they can be targeted for early intervention.
Our team has been engaged in research aimed at identifying host and pathogen-derived biomarkers for early and accurate identification of individuals with high risk for progression to active TB disease. In this line we optimized a multiplexed digital PCR-based approach to detect circulating cell-free DNA of *Mycobacterium tuberculosis* in plasma, as it can be used to detect both pulmonary and extrapulmonary forms of TB (EPTB) as against sputum which may not be useful for EPTB detection. Our study generated compelling evidence to support the diagnostic utility of the assay for early identification of individual at high risk for developing

TB, as well as in cases of EPTB and subclinical TB where establishing an accurate diagnosis is often a challenge.

PT – 20

Characterization and enablement of molecular targets of SARS-CoV-2 for therapeutic development

Dr Neelagandan K

InStem, Bengaluru, India

The coronavirus disease 2019 (COVID-19) has significantly impacted personal health, healthcare systems, and economies around the globe. The pandemic has stimulated tremendous efforts to develop therapeutic strategies for the prevention and treatment of COVID-19 disease. Developing successful intervention strategies relies on the knowledge of the molecular targets critical for viral and host determinants for disease development. SASR-CoV-2 research focuses on key viral life cycle stages such as viral entry, polyprotein processing, viral RNA replication, and viral assembly, which aids in vaccine and drug development. In my talk, I will describe current findings on how the SARS-CoV-2 N protein domains and inherently disorder regions (IDRs) region participate in RNA binding, oligomerization, and liquid-liquid phase separation (LLPS) with viral genome RNA, potentially facilitating virus assembly. In addition, current efforts to develop inhibitors of molecular target implicated in viral maturation will be described.

PT – 21

Culturable bacteria associated with marine macroalgae in antarctica

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The Antarctic continent is of exceptional biological interest, possessing a rich diversity of marine macroalgae and a high endemism. However, the natural distribution, biodiversity and possible biotechnological uses of the microbial community associated to Antarctic macroalgae remains largely uncharted. Our studies shed light on the diversity and biotechnological potentials of epiphytic bacteria associated with marine macroalgae inhabiting King George Island, Antarctica. How diverse is the epiphytic bacterial community on Antarctic macroalgae? How host-specific the epiphytic microbiota is among macroalgae species? Are Antarctic macroalgae a source of novel bacterial species? What is the biotechnological relevance of Antarctic epiphytic bacteria? Our research is addressing these questions using a combination of cultivation-based methods, 16S rRNA gene sequencing and enzymatic studies. In addition, a polyphasic taxonomic characterization was performed on isolates suspected to be novel species. An unprecedented diversity of pigmented, Gram-positive epiphytic bacteria was isolated from different macroalgae species. 18 different bacterial phylotypes were recorded, which were clustered into 11 genera of Actinobacteria and one genus of the Firmicutes. Analysis of the Gram-positive epibionts of the co-occurring intertidal macroalgae *Adenocystis utricularis*, *Iridaea cordata* and *Monostroma hariotii* showed a dominance of Microbacteriaceae and Micrococcaceae. Seventeen genera of Actinobacteria and two of Firmicutes were cultured from the three macroalgae, containing 29 phylotypes.

The bacterial phylotype composition was distinct among the three macroalgae species, suggesting that these macroalgae host species-specific Gram-positive associates. Three subtidal red macroalgae (*Georgiella confluens, Pantoneura plocamioides* and *Plocamium cartilagineum*), two of them endemic of Antarctica, were also investigated as a source for isolation of bacterial epibionts. Representatives of nineteen bacterial families were isolated from these three macroalgae, with a dominance of Pseudoalteromonadaceae and Flavobacteriaceae, mostly isolates belonging to the Gram-negative genus *Pseudoalteromonas*. In this communication, two novel bacterial species isolated from intertidal macroalgae belonging to the genera *Amycolatopsis* and *Radiobacillus* are described. Together, this research highlights the importance of Antarctic macroalgae as a source of a unique bacterial diversity with potentially important biotechnological applications.

PT – 22

Promoting the Student-to-Researcher Transition at the Queen Mary Centre for Undergraduate Research

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The present contribution explores the development and impact of the Queen Mary Centre for Undergraduate Research (QMCUR), established to integrate research-based learning into undergraduate education and support students in transitioning from learners to independent researchers. QMCUR was designed by integrating established models of undergraduate research, while introducing innovative elements and procedures. Through faculty-guided investigations, student-led research, and interactive symposia, QMCUR provides a structured yet flexible environment where students engage in real-world research challenges, developing academic independence. Its pedagogical framework combines inquiry-driven learning with hands-on projects, structured mentorship, interdisciplinary collaboration and strategies to promote heutagogy and student emancipation. These strategies include approaches to promote self-efficacy, elements of democracy in learning, and principles of progressive education. The achievements of QMCUR students highlight how early exposure to research strengthens academic skills, builds confidence, and supports a seamless transition from undergraduate study to professional research environments.

PT – 25

Revolutionising ligand discovery with Suprabodies

Bala Yeshwanth Ram Vummidi

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At Inger Therapeutics, we are passionate about discovering high affinity peptide-based ligands called Suprabodies for therapeutic and diagnostic applications. Suprabodies are ligands that are synthetic and low molecular weight discovered using a stringent and robust Suprabody selection methodology. Suprabody and its generation methodology addresses the limitations of the existing technologies and still retains its strengths. The innovative elements in the Suprabody scaffold include: (i) completely synthetic scaffold with a possibility to include

unnatural moieties (ii) multiple loops aids in cooperativity (iii) introduce recombination in the selection process that helps in delivering the best binders via multiple rounds of selection. Eventually, these advantages reflect in smaller synthetic products that are scalable and favourable in tissue penetration.

PT – 26

Use of Digital PCR in Translational Research

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Digital PCR is a highly precise approach to sensitive and reproducible nucleic acid detection and quantification. Measurements are performed by dividing the sample into partitions, such that there are either zero or one or more target molecules present in any individual reaction. Each partition is analyzed after end-point PCR cycling for the presence (positive reaction) or absence (negative reaction) of a fluorescent signal, and the absolute number of molecules present in the sample is calculated. It does not rely on a standard curve for sample target quantification. Eliminating the reliance on standard curves reduces error and improves precision. Contrary to real-time qPCR, digital PCR does not rely on every amplification cycle to determine the relative amount of target molecule; rather, it relies on Poisson statistics to determine the absolute target quantity following an end-point amplification. As the target molecule is distributed randomly across all available partitions, Poisson distribution estimates the average number of molecules per partition (zero, one or more) and calculates the copies of the target molecule per positive partition. Poisson statistical analysis of the number of positive and negative reactions yields precise, absolute quantitation of the target sequence. Absolute quantification with digital PCR offers significant advantages over qPCR when quantifying rare targets in complex backgrounds and detecting small-fold change differences. By partitioning the sample into thousands of individual reactions and cycling to end point, dPCR eliminates amplification bias and increases tolerance to PCR inhibitors. Moreover, non-reliance on standard curves or references makes dPCR a simple and affordable next-gen technology. Applications requiring superior precision, high accuracy, better reproducibility, high sensitivity and multiplexing can benefit from dPCR.

Digital PCR allows for increased sensitivity in the detection and absolute quantification of rare events/sequence variants because target quantification is independent of the number of amplification cycles. Besides, partitioning increases the signal-to-noise ratio and decreases false-positive rates when detecting low-frequency targets (allelic variants, SNPs) in a pool of High frequency Non- specific targets or background

PT – 27

Intersection of Planetary Health and Cardiovascular Disease Prevention - From Research to Empowering Youth

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This presentation will explore the critical intersection of planetary health and cardiovascular disease (CVD) prevention. Environmental factors, including air and chemical pollution, significantly contribute to CVD risk, with over half of deaths linked to air pollution, being

caused by CVD deaths. While epidemiological associations are unequivocal, the biological mechanisms are unclear. The presentation will discuss recent research findings on the impact of environmental exposures on the development and severity of atherosclerotic vascular disease, emphasizing the need for mechanistic studies to develop evidence-based strategies to mitigate these risks. Finally, it will highlight the "Girawa" Project's achievements in planetary health education, which has successfully launched an international Planetary Health Youth Club network for secondary school students in Global South countries. This initiative has been recognised by the Planetary Health Alliance as one of few programmes globally that empower youth to address the interconnected challenges of environmental sustainability and human health.

PT – 28

The RNA binding protein ZFP36L1 suppresses replication stress-induced DNA damage and genomic instability

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ZFP36L1, a well-studied RNA binding protein (RBP), plays a pivotal role in post-transcriptional regulation of gene expression and cell fate determination underlying normal physiological processes and disease. Recent evidence has shown frequent alterations in both intronic and exonic regions of *ZFP36L1* that are consistent with its role as a driver gene in certain cancers. Replication stress is a common feature of cancer cells that compromises the efficiency and accuracy of DNA replication and in turn, cell fate. Here, by using human U2OS cells as an *in vitro* model, we provide evidence that ZFP36L1 is required for maintaining genomic stability under conditions of DNA replication stress. Loss of functional ZFP36L1 resulted in reduced U2OS cell proliferation and increased levels of hallmarks of genomic instability including incidence of micronuclei, 53BP1, γH2AX and RPA foci, and chromosomal mis-segregation during cell division. RNA-Seq analysis revealed a differential gene expression signature consistent with deregulated oncogenic signalling, most notably for KRAS in ZFP36L1-deficient cells. Our data provide evidence that loss of ZFP36L1 in cancer cells increases DNA replication stress that likely contributes to tumorigenesis. These studies highlight the involvement of ZFP36L1 in the prevention of replication stress-induced genome instability in cancer cells.

CT – 1

The Role of Microbiome in Infertility

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ABSTRACT

The human microbiome plays a pivotal role in reproductive health, influencing natural conception and assisted reproductive technologies (ART). This review delves into the interplay between microbiome alterations and infertility, focusing on the vaginal, endometrial, ovarian, and tubal microbiomes. A balanced microbiome, dominated by Lactobacillus species, supports gametogenesis, fertilization, and early embryonic development by preventing infections, maintaining an optimal pH, and modulating immune responses. Dysbiosis, however, can lead to pathological conditions such as bacterial vaginosis, pelvic inflammatory disease, endometriosis, and polycystic ovarian syndrome, all of which impair fertility.

Emerging studies highlight the significance of the follicular fluid microbiome and its impact on ART outcomes. For example, a Lactobacillus-dominated endometrial microbiome is associated with higher implantation and live birth rates, while a diverse vaginal microbiota may reduce pregnancy success. Similarly, microbiome alterations in the male reproductive tract, particularly within the gut-testes axis, can affect sperm quality and fertility.

The review underscores the potential of next-generation sequencing to uncover microbial influences and explores therapeutic interventions, including probiotics and prebiotics, which aim to restore microbial balance. Lifestyle modifications, such as a diet rich in fibre and reduced sugar intake, are also recommended to enhance reproductive outcomes. Future directions emphasize longitudinal studies and the development of personalized microbiome-targeted therapies to address infertility.

KEY WORDS: Infertility; Assisted Reproductive Technologies (ART); Dysbiosis; Lactobacillus; Microbiome-targeted therapies;

CT – 3

To compare the new smart and handy device developed with standard colposcope for cancer cervix screening

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Introduction: Cervical cancer annually in India, accounting for nearly one-fifth of the global cervical cancer burden[1]It is estimated that cervical cancer will occur in Indian women approximately 1 in 53 during their lifetime compared with 1 in 100 women in developed countries.[2] Several screening options are available. Patients with abnormal screening tests are evaluated by colposcopy and detection of high-risk Human papillomavirus DNA [3,4]. Visual methods are the low-cost alternatives for low- and middle-income countries like India.[5]

Though various methods/devices are available in the state of art for detecting cervical abnormalities, .still there is a need for a more accurate and affordable device for detecting and screening abnormalities in the cervix (6).

The existing Colposcope instrument for cancer cervix has an LED light source and it requires a power supply, and to display images captured and requires a separate monitor. It is may not portable in most centers. This needs to have a working distance of 300 mm. The New Smart and Handy device found to be easy to handle for cancer cervix screening and also cost-effective. The USB camera attached to android phone captures pictures and video from a distance of 3cm to 4cm with good quality and clarity and with MScopes Application, both image and Video can be saved in the phone

Aim objectives of the research project: To compare the images of a standard Colposcope with those of images of a Smart and handy device to detect precancerous and cancer cervix.

Objectives of the research project:

1. To determine whether smart and handy device can be utilized in low-resource centers to detect cancer cervix

2. To determine whether the quality of images captured is comparable with standard Colposcope

3. To determine the sensitivity & specificity of the smart and handy device diagnosis with that of standard Colposcope

Methodology & Research design: After informed, after ethical clearance 154 Women attending the Gynaec outpatient department were screened for detection of precancerous and cancerous lesions of the cervix using a standard Colposcope and with a Smart& Handy device. Inclusion criteria were women for routine cancer cervix screening, women with abnormal Pap Test, women with white discharge, and women with postcoital bleeding and exclusion criteria were women with cervical growth.

Results: Focus of the image at 91%, Sharpness of the image at 92% and zoom at 94% with a Smart & handy instrument and by colposcope Focus -at 94%, sharpness at 98% and Zoom at 100%

In Smart & hand device evaluation done with Swede score without vessels

Based on Aceto-white uptake, Margins, Lesion size, and Iodine uptake. Each was given two. score. Among -0 -3 score - 53.3%, 4-5 score -33.3%, 5-8 score - 13.3%

In Colposcopy evaluation done with Swede score based on Aceto-white uptake, Margins, Lesion size, Iodine uptake,5. Vessels, Among 0-3 score -60% 4-7 score- 26.6 %.8-10score - 13.4%

Biopsy reports results in SMART AND HANDY DEVICE when score 0 -3 -Normal -72%, Score of 4-5 – LSIL - 15.8%, Score of 5-8- - HSIL-6.2%

COLPOSCOPY biopsy results when score of 0-4 –Normal-78% , Score of 5-7 – LSIL- 14.8%, Score of 8-10-HSIL -7.2%. The sensitivity, Specificity, Positive likelihood Ratio, and Negative Likelihood Ratio of Smart and hand Device are as follows 93.10%,90.32%,9.62, 0.08.

The sensitivity, Specificity, Positive likelihood Ratio, and Negative Likelihood Ratio of colposcopy are as follows 96.55 % 93.33%, 14.48, 0.04

Conclusion: SMART AND HANDY DEVICE gives high-quality images and video and an efficient method to store data,handy and portable ,cost effective . This can be incorporated into cervical screening methods in low-setting resources.

Keywords: Cancer cervical Screening, Low resources settings, Smart and handy devices, colposcopy

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CT – 5

Assessing the burden of anemia among pregnant women

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Anemia is the condition where there is a decreased oxygen carrying capacity of blood due to low haemoglobin levels. It is one of the major medical problems that is very much prevalent among pregnant women in our country. The National Family Health Survey 5 2019-21, has found a prevalence of 52.5% anemia among pregnant women. It has several implications, being one of the major causes of maternal and perinatal mortality and morbidity. Anemia has been the focus of the Government of India , and the nation-wide Anemia Mukt Bharat scheme has been rolled out to down its incidence. Anemia is identified by the estimation of haemoglobin by drawing 2 ml blood to perform Complete Blood Count by calorimetric methods on the auto analyser. Doing this on a large scale in the field settings can be tedious and expensive. The Eze-check is a simple non- invasive portable point of care screening device, developed by EzeRx Health Tech Pvt Ltd, Bhubaneswar, India, which works on the principle of LED capture of reflection from the skin of the finger- tip and absorbance spectroscopy in the range of 300- 750nm. The result is generated using Artificial Intelligence (AI) and Machine Learning (ML) based on a specific algorithm and displayed on the application. This device promises to be a valuable, non-invasive point of care tool well suited for mass screening in the community , and thus help in early initiation of treatment.

CT – 6

Improved outcomes in women with poor ovarian reserve by using autologous bone marrow-derived stem cells and platelet- rich plasma therapy

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Introduction : Autologous bone marrow-derived stem cells (ABMDSCs) represent a specific type of stem cell and Platelet-rich plasma (PRP) on the other hand is blood plasma that has been enriched with platelets and various growth factors. These components can stimulate cellular processes promoting the regeneration of new healthier tissue and the formation of new blood vessels. This process is particularly relevant for ovarian rejuvenation and potentially improving outcomes in individuals with Poor Ovarian Reserve (POR) and Premature Ovarian Failure (POF).

Aim and Objective: The objective of the study is to evaluate the therapeutic role of Autologous Bone marrow derived Stem cells and Platelet rich plasma Therapy in women with Poor Ovarian Reserve and Premature Ovarian Failure desiring pregnancy.

Materials and Methods: In this case series, out of ten women, eight were diagnosed with POR and two with POF respectively. The study group received a combined treatment of ABMDSCs and PRP through either laparoscopic or transvaginal intraovarian instillation.

Results: In the group of women with POR, 7 of them showed a marginal increase in antral follicles and embryo numbers in subsequent ART cycles. Three of the 7 women with POR achieved successful pregnancies. One has significant increase in antral follicles and is awaiting IVF. The two women with POF did not show any evidence of response, however one of them had spontaneous conception 3 months later resulting in a term live birth.

Conclusion: In women with POR and POF, the application of ABMDSCs combined with PRP was associated with an increase in the number of antral follicles and additionally, there was an observed trend toward increased embryo formation and improved clinical pregnancy and live birth rates. This research could pave the way for a potential treatment strategy for patients with POR.

CT – 7

Reprogenetics

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Infertility is increasing day by day. The cause may be multifactorial, from environmental influence to genetics and so on and so forth. But approximately 50% of the causes of infertility are of genetic origin. At the same time the development and introduction of new technologies in reproductive and genetic medicine is constantly evolving. Genetic tests also have becoming increasingly relevant in reproductive medicine. The unprecedented complexity of generated research data and the fast (and often hurried) implementation of new technologies into the fields of assisted reproduction as well as of reproductive genetics render the translation of

research results into clinical practice challenging. The need of the hour is understanding the causation and association of genetics and infertility which would help early intervention, especially in the field of recurrent implantation failure and pregnancy loss. It also serves to be a important counselling tool in terms of inheritance to off-springs. I would be putting forth some evidence-based data in this presentation.

CT – 9

Robust and Scalable Generation of Donor-reactive Regulatory T-Cells Relevant in Kidney Transplantation

Prabhu Kanchi[1], Savithri Vemulavada[2,3], Shriya Karthikvatsan[2,4], Naveen Vigneswaran[2], Babu Elangovan[5], Swaminathan Sambandam[6], Krupakar Parthasarathy[6], Hari Balaji[2]

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Regulatory T cells (Tregs) play a crucial role in maintaining immune homeostasis and regulating immune responses, making them ideal candidates for immune-related therapies. In Solid Organ Transplantation (SOT), especially Kidney transplantation - Treg-based therapies have shown promise in mediating transplant tolerance and prolonging graft survival, both in preclinical and human clinical trials. Various factors determine the clinical success of Treg therapy in kidney transplantation, such as an optimal Treg phenotype, donor reactivity and dosage. Therefore, a robust and scalable generation of donor-reactive Tregs would greatly aid the rapid adoption of this novel immunotherapy into clinical practice. In this context, this talk would describe an optimized protocol for generating donor B cell antigens-reactive Tregs generated using multimeric CD40L. In addition, spatiotemporal characterization of these Tregs within an *in vitro* immunosuppressant culture system would also be discussed.

CT – 10

Indian population-specific Garbhini-GA2 model for estimating gestational age in second and third trimesters"

Veerendra Gadekar,

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In India, a large proportion of pregnant women begin antenatal care only in the second trimester, making early and accurate gestational age (GA) determination challenging. Most commonly used GA estimation formulas, developed from Western populations, often lack precision in low- and middle-income countries (LMICs), including India. To bridge this gap, we developed the Garbhini-GA2 model, which significantly outperforms existing formulas. Trained on ultrasound data from the extensive GARBH-Ini cohort and externally validated on participants at CMC Vellore, Tamil Nadu, this model highlights the need for region-specific GA estimation. By enabling more precise pregnancy dating, Garbhini-GA2 can help optimize maternal care and improve clinical outcomes.

VIP – 1

The silent and global threat of PFAS and genetic vulnerability in breast cancer

Harshana Chaurasia & Kalpana Surendranath

Gene Editors of the Future & Genome Engineering Laboratory, School of Life Sciences, University of Westminster, London, UK

Gene editing allows precise manipulation of cellular pathways to uncover mechanisms of disease. Using CRISPR-engineered breast cancer cells, this study investigates how PFAS exposure alters cellular behaviour, shedding light on gene-environment interactions in cancer development. PFAS are ubiquitous, persistent chemicals implicated in diseases, including reproductive disorders and cancer. Understanding PFAS toxicity in humans is limited and requires disease modelling to replicate the body's vulnerability to exposure-induced diseases. This study explores the molecular effects of PFAS exposure in MCF7 wild-type breast cancer cell lines and a CRISPR-engineered version lacking ZFP36L1. Two PFAS-PFOA and PFDA-at 30 µM were used to analyse colony-forming capacity, migration, morphology, cell cycle disruption, and RNA/protein expression. Additional functional analysis assessed cell redox potential, viability, and proliferation through double dilutions of both drugs ranging from 0 to 500 µM. Our investigation showed that cells lacking ZFP36L1 protein are more susceptible to PFAS, particularly from PFDA. These findings highlight concerns about short-chain PFAS like PFDA, which might lead to endocrine disruption and cancer. Further research on the impact of mixed PFAS at varying concentration levels in healthy and diseased cells on gene expression and cell fate might offer insights into cellular disruptions and disease-related interactions.

VIP - 2

Developing students into researchers: The bioinformatics of CRISPR/Cas9 gene editing

Julia Karolina Gorczynska & Kalpana Surendranath

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All undergraduate students, regardless of institution, must have opportunities to engage in research-based learning. Curricula and timetabled learning have long supported employability and civic engagement, but the evolving landscape of higher education necessitates a renewed emphasis on research at the core of undergraduate study. Notably, in many systems, funding priorities have marginalised teaching and distanced undergraduates and academic staff from research. This presentation explores the impact of engaging in a bioinformatics workflow in developing students as researchers. The design of sgRNA and genomic PCR primers is essential for plasmid-mediated CRISPR-Cas9 gene knockout, facilitated by various online tools. Embedded within these algorithms are numerous skills that integrate closely with laboratory work. However, students must develop the ability to critically assess and refine computer-generated outputs, which requires a strong foundation in manual oligonucleotide design. The Gene Editors of the Future program, founded by Dr Kalpana Surendranath at the University of Westminster, equips students with the analytical skills necessary to maximise the potential of bioinformatics tools while recognising their limitations. This presentation outlines the bioinformatics workflow for CRISPR-Cas9 knockout of the ATP7B gene, guiding optimising design and key variables for novice gene editors.

VIP - 3

Students at the forefront of driving CRISPR for sustainable development

Jolina Pauline Viessmann & Kalpana Surendranath

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Young researchers are integral to global progress in achieving the Sustainable Development Goals (SDGs) through scientific innovation, policy influence, and technological advancements. Data from Innovate UK indicates that only 29% of funding applicants identify as female, highlighting the need for targeted initiatives. Addressing this gap, the Gene Editors of the Future programme has, since 2020, trained over 700 students-predominantly women-through hands-on experience in CRISPR/Cas9 gene-editing technology. By providing free access to participants across all educational levels, from Level 2 to PhD, as well as academic staff and international candidates, the initiative actively promotes gender equality and reduced inequalities (SDGs 5 and 10). In collaboration with leading academics and industry partners, the programme fosters innovation and infrastructure development (SDG 9) by offering access to state-of-the-art laboratories and cutting-edge equipment. Beyond research training, the programme equips students with career-enhancing opportunities, strengthening their prospects in both academia and the job market. As emerging CRISPR experts, graduates contribute to advancements in healthcare, climate resilience, clean water solutions, food security, and biodiversity conservation (SDGs 3, 6, 13, 15). By integrating education, research, and industry collaboration, the initiative embodies Partnerships for the Goals (SDG 17), positioning students as leaders in genomic innovation and sustainable development.

ABSTRACTS FOR ORAL PRESENTATION

S1-OP1

Computational Insights into Antimicrobial Peptides as Potential Therapeutics for Breast Cancer

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ABSTRACT

Breast cancer is the most frequent cancer worldwide, accounting for 12.5% of all new cancer cases. Projections estimate over 3 million new cases and 1 million deaths by 2040. Triple-negative breast cancer (TNBC), a particularly aggressive subtype, makes up 10-20% of global breast cancer cases and 31% of cases in India. TNBC is defined by the absence of estrogen, progesterone, and HER2 receptors, which makes it resistant to conventional chemotherapeutic therapies. In AR-positive TNBC, androgen receptors (AR) promote apoptosis and inhibit cell proliferation; however, AR-negative TNBC lacks this therapeutic approach. This study explores the potential of antimicrobial peptides (AMPs) as a treatment option for AR-negative TNBC. AMPs derived from *Lactobacillus* species were identified for their ability to induce cancer cell cytotoxicity, activate immune responses, and inhibit tumor growth. The study analysed upregulated genes in AR-negative TNBC and identified three genes as therapeutical targets, using various bioinformatics databases. In silico molecular docking and dynamics simulations were conducted to evaluate interactions between AMPs and the therapeutical target proteins. The conclusion of the study is identifying novel AMPs which could potentially target receptors thereby capable of silencing the other upregulated genes in AR-negative TNBC to combat tumor progression.

Keywords: Tumor, Therapeutical, TNBC, Cytotoxicity.

S1-OP2

Excitation Emission Matrix characterization of oral tissue biopsy and blood plasma for effective Delineation of Oral Potentially Malignant Disorders

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ABSTRACT:

Clinical evaluation of oral Potentially Malignant Disorders may be misleading during their early stage of malignant transformation. Native fluorescence spectroscopy has been extensively used to characterise the normal tissues and biofluids from that of oral cancer patients. In this study, it is aimed to compare the Excitation Emission Matrix characteristics of tissue and blood plasma of normal subjects and PMD patients, to know whether native fluorescence spectroscopic characterization of biofluids can be considered as an alternative analyte to tissue biopsies. For the present study, biopsy specimens and blood samples were collected from 10 patients who were clinically diagnosed with oral potentially malignant disorders (Oral submucous fibrosis and Leukoplakia), Similarly, biopsy specimens and blood samples were collected from 10 healthy individuals with no history of use of tobacco or betel nut and with clinically normal oral mucosa. The samples were subjected to Fluorescence spectroscopic analysis and excitation emission matrix was obtained. From EEM measurements of blood plasma, it is observed that there is a maximum emission around 340±5nm at 307±3nm

excitation for normal subjects and around 337±5nm emission at 300 ± 3nm excitation for PMD patients. Linear Discriminant Analysis is carried out for blood plasma and tissues of normal group and PMD group. As sensitivity of blood plasma is higher than tissues for original group and is the same for cross validated group, blood plasma may be considered as an alternate analyte in the mass screening of oral cancer.

Keywords: Biopsy, PMD patients, Blood plasma, Biofluids.

S1-OP3

Cardio-protective effect of Nevirapine (NNRTI) against Isoproterenol induced pathological hypertrophy in H9C2 cells.

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ABSTRACT

Nevirapine (NVP) is a non-nucleoside reverse transcriptase inhibitor often utilized alongside other antiretroviral drugs in highly active antiretroviral therapy (HAART) for patients with human immunodeficiency virus type 1 (HIV-1). Research indicates that this drug can stimulate the production of high-density lipoprotein in HIV patients, which is beneficial for heart health. This study aims to reveal the positive effects of Nevirapine on the H9c2 Cells which is a cardiac cell line and it's capability to attenuate the hypertrophy which is induced by Isoproterenol. The present study the anti-hypertrophic effect of Nevirapine was evaluated using various assays such as protein carbonylation, cell size measurement and ROS production with florescence imaging to check the metabolism of the drug while reverting the pathological hypertrophy. Further molecular evidences in support of hypothesis will be collected by Immunoblotting.

Key words: H9C2 Cells, Nevirapine, Isoproterenol, NNRTI, ROS

S1-OP4

Studies on Formulation and Characterization Piper Nigrum of HPMC (Hydroxy Propyl Methyl Cellulose) Based "Peel off Gel" For Diabetic Wound Ulcer Applications

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ABSTRACT

Diabetic foot ulcers (DFUs), in particular, are prone to infections and slow healing, necessitating innovative treatments. This study focuses on the formulation and characterization of a "peel-off gel" containing saponins extract from Piper nigrum, incorporated into a Hydroxy Propyl Methyl Cellulose (HPMC) base, aimed at treating diabetic wound ulcers. Diabetic wounds are a significant concern due to their chronic nature and slow healing process. The need for effective, convenient, and patient-friendly treatment options is paramount. Piper nigrum, commonly known as black pepper, is renowned for its medicinal properties. Saponins extracted from Piper nigrum exhibit antimicrobial, anti-inflammatory, and wound healing activities, making them suitable candidates for enhancing wound care. The HPMC-based gel acts as an effective delivery system, providing sustained release of the active ingredients, thereby promoting prolonged interaction with the wound site. The study

involves meticulous formulation techniques to ensure optimal consistency, adhesion, and bioavailability of the peel-off gel. Various parameters, such as gel strength, peel ability, and release profile, are assessed to determine the gel's efficacy and user acceptability. In vitro and in vivo evaluations are conducted to gauge the gel's performance in terms of wound contraction, microbial load reduction, and overall healing time. The findings suggest that the formulated saponin-enriched HPMC peel-off gel demonstrates significant potential in accelerating the healing of diabetic wound ulcers.

Keywords: Peel off Gel, Diabetic foot ulcer (DFUs), HPMC, Piper Nigrum, saponin

S1-OP5

Characterization and Analysis of a Novel Endodontic Irrigant

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ABSTRACT

This study investigated the characterization and analysis of a novel combination of sodium hypochlorite and hyaluronic acid as an endodontic irrigant. 3% sodium hypochlorite solution was mixed with 1% Hyaluronic acid gel (Sigma-Aldrich, Co, USA) in a 3:1 ratio. Different characterization tests like Thin layer chromatography (TLC), H1 NMR Spectroscopy, Fourier Transform Infrared Spectroscopy (FTIR) analysis, UV Spectrophotometry test were performed to confirm the stability and structural modifications of hyaluronic acid in the novel endodontic irrigant mixture. The chromatographic graphs obtained from the above tests correlated with the previous studies in the identification of the hyaluronic acid biopolymer. Chemical characterization and different analytic tests confirmed the presence of hyaluronic acid when combined with sodium hypochlorite solutions. Further long-term antimicrobial studies, mechanical and structural properties of root dentin need to be conducted to evaluate the effectiveness of this novel endodontic irrigant.

Keywords: Thin layer chromatography, structural properties, mechanical properties.

S1-OP6

Reverse Genetic Bioinformatics Approach for Cystic Fibrosis Vaccine Development

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ABSTRACT:

This study explores the use of reverse genetic bioinformatics in order to develop vaccines for cystic fibrosis, accelerate and find antigen targets as well as optimize vaccine candidates. Sequencing was conducted through the help of next-generation sequencing platforms and was analysed in the light of comparative genomics by the means of bioinformatics tools such as blast, AlphaFold and Swiss-Model and also the codon optimization for designing mRNA candidates for vaccines with the encapsulation of Lipid Nanoparticles (lnps). Immunogenicity and efficacy were tested by *in vitro* and *in vivo* studies. The primary candidate for antigenic targets was the spike protein, and modelling of the protein showed structural stability. Immunogenicity assays also revealed strong antibody and t-cell responses. High vaccine efficacy was predicted by the computational models. Discussion:

This study demonstrates the efficiency of reverse genetic bioinformatics in vaccine design. Different types of challenges were surmounted, including immune complexity and genomic variability, using ai-driven analysis and structural validation. This study shows that reverse genetic bioinformatics can rapidly produce vaccines against emerging diseases and offers a framework for the future preparedness for pandemics.

Keywords: Cystic Fibrosis, Antigenic Targets, Next Generation Sequencing, Lipid Nanoparticles.

S1-OP7

Molecular Cloning and Functional Analysis of the Arginine deiminase gene (*arcA*) from *Limosilactobacillus reuteri* DSM 20016

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ABSTRACT

The guanidino group modifying enzymes (GME) super family include the arginine deiminase (ADI), an arc degrading enzyme that hydrolyzes L-arginine to L-citrulline and ammonia by guanidine deamination. It is among the essential enzymes of the microbial ADI pathway. In this study, the ADI- encoding gene *arcA* from *Limosilactobacillus reuteri* DSM 20016 was cloned and expressed. The open reading frame ORF for nucleotide sequence is 1233 base pairs long encoding a protein of 417 amino acids. The recombinant prokaryotic expression vector, pET28b-*arcA* was constructed and then transformed into *Escherichia coli* BL21 (DE3) for heterologous expression. Protein expression was induced using IPTG, and the recombinant protein ADI (LrADI), was purified via Ni – NTA histidine tagged affinity chromatography. The biochemical characterization revealed an optimal reaction temperature 40 ℃ and the pH optimum of 6 respectively. Kinetic parameters determined the Michaelis constant Km and Vmax of the recombinant ADI (LrADI) were calculated as 1.08mM and 1.63 (mM/min) respectively. The molecular mass of ~46 kDa was confirmed by SDS – PAGE analysis. These findings provide insights into the enzymatic properties and potential applications of LrADI in biotechnological and industrial processes.

Keywords: Arginine deiminase, *Limosilactobacillus reuteri* DSM 20016, Ni-NTA chromatography.

S1-OP8

Facile plant-mediated biosynthesis of silver nanoparticles and investigation of their antibacterial activity

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Abstract

In this study, biosynthesis of silver nanoparticles (AgNPs) using Malva Sylvestris flower extract was performed as an eco-friendly approach. In this method, phytochemicals in the extract play a key role as both reducing and stabilizing agents in synthesis of AgNPs. This method offers a sustainable alternative to traditional chemical methods, eliminating the need for toxic reagents and reducing environmental impact. The biosynthesized AgNPs were confirmed through different characterization techniques, including UV-Vis spectroscopy, which showed the characteristic surface plasmon resonance peak and X-ray diffraction (XRD)

and transmission electron microscopy (TEM), which revealed spherical AgNPs with an average size of 70nm. The green synthesis of AgNPs using Malva Sylvestris provides a cost-effective and environmentally friendly method for nanoparticle production. The antibacterial activity of the biosynthesized AgNPs was evaluated against pathogenic bacterial strains, including both Gram-positive and Gram-negative bacteria. The results demonstrated significant antibacterial activity with AgNPs exhibiting broad-spectrum inhibitory effects, as evidenced by zone of inhibition tests. The study highlights the potential of Malva Sylvestris-mediated biosynthesis of AgNPs as an effective antimicrobial agent, which could serve as a promising alternative to conventional antibiotics. This work demonstrates the benefits of green synthesis in the manufacturing of nanoparticles, providing a bioinspired and sustainable approach to the creation of antimicrobial agents. The green synthesis approach offers a sustainable alternative to traditional chemical methods by eliminating toxic reagents and minimizing environmental impact.

Key Words: Nanotechnology; Green Synthesis; Silver Nanoparticles; Antibacterial Activity

S1-OP9

Biosynthesis of silver nanoparticles using *Hedyotis sp.,*: Optimization, characterization, antibacterial activity against multi-drug-resistant bacteria, cytotoxicity, and wound healing in NIH/3T3 cell lines.

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Abstract:

The distinct physical and chemical characteristics of green synthesized silver nanoparticles (Ag NPs) have drawn much interest in the scientific community. Including phytochemicals in a nano-formulation may increase its usefulness in medical applications. The current work is the first report on green Ag NPs synthesized using the leaf of *Hedyotis sp.,* (*Hs*- AgNP), and the evaluation of their antibacterial activity against Multi-Drug Resistant (MDR) bacteria, and wound-healing capabilities in 3T3 cell lines. The analyses of nanoparticles are performed with UV-visible spectrophotometer (UV-Vis), Scanning Electron Microscopy (SEM), and Zeta potential. Energy-dispersive X-ray diffraction and Fourier transform infrared have been used to determine other significant characteristics, such as elemental composition and constituent capping agent. The production of *Hs*-AgNPs was confirmed by UV-vis absorption of the Surface Plasmon Resonance center at 413 nm, SEM analysis revealed the range of size from about 50 to 80nm, the face-centered cubic shape was confirmed in X-ray diffraction, and Zeta potential analysis showed a very stable colloidal solution with a surface charge of -9.49 mV. The synthesized *Hs*-AgNP has surpassed MDR bacteria isolated from patients with Diabetic Foot Ulcer (DFU) infections. As a research result, *Hs*-AgNP had potent antibacterial activity against MDR bacteria showing improved wound healing in ulcers, and can be used as therapeutic substances for wound treatment in DFU patients with negligible cytotoxicity.

Keywords: Green synthesis, Antibiotic resistance, Leaf extract, Diabetic Foot Ulcer.

S1-OP10

Licochalcone A promotes Neural Differentiation and Amyloid-β reduction through Autophagy in Alzheimer's disease Models

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Abstract

Neurodegenerative disorders, such as Alzheimer's disease (AD), are characterized by the pathological accumulation of amyloid-beta (Aβ) and neuronal loss, which lead to memory impairment. An effective therapeutic strategy should address both the regeneration of neurons through stem cell differentiation and the modulation of disease pathology by clearing accumulated Aβ from neurons. Drug therapy represents a promising non-invasive approach to achieve these goals. Licochalcone A (LA), a polyphenol derived from Glycyrrhiza inflata (liquorice), has demonstrated significant therapeutic potential due to its diverse biological activities, including anti-oxidative, neuroprotective, antibacterial, anti-stroke, osteogenic, anti-inflammatory, and antidepressant properties. Our findings reveal that LA (1.25–5 μM) promotes neuronal differentiation in P19 embryonic stem cells in a dose- and time-dependent manner, evidenced by increased expression of βIII-tubulin (TuJ1) and synaptic vesicle formation (FM1-43-labeled) over a 7-day period. Mechanistically, LA triggers neuronal differentiation by activating the ERK signaling pathway, resulting in a twofold increase in phosphorylated ERK (p-ERK) within 12 hours, which subsequently drives downstream differentiation processes. In APP-overexpressing SH-SY5Y and 7AP2 cell models, LA treatment significantly reduced APP levels by 50% ($p < 0.05$) and decreased Aβ40/42 peptide levels by 30–60% ($p < 0.05$). Moreover, LA enhanced autophagy, as evidenced by a 1.5-fold increase in LC3-II accumulation and a 40% reduction in p-mTOR levels, facilitating toxic protein clearance and improving neuronal survival. The in vivo effects of LA were evaluated using 5xFAD transgenic mouse models of AD. LA administration (5 and 15 mg/kg) led to notable improvements in spatial memory, as shown by a 56% reduction in escape latency during the Morris water maze test ($p < 0.01$) and an 80% higher novel object discrimination index ($p < 0.05$). Behavioral assessments revealed enhanced exploratory activity without anxiety-like effects in the open field test. Importantly, LA (5 mg/kg) reduced Aβ plaque levels by 55% ($p < 0.01$) in the cortical and amygdalar regions of the mouse brain. These findings underscore LA's potential as a dual-action therapeutic agent, promoting neuronal differentiation while enhancing neuroprotection through Aβ clearance and autophagy induction. This study highlights LA's unique approach in addressing AD pathology, offering advantages over conventional therapies that primarily target Aβ clearance or cholinergic pathways.

Keywords: stem cell, neuroprotective, signaling pathway, osteogenic, anti-inflammatory.

S1-OP11

Complement Components as Baseline Predictors of Poor Treatment Outcomes in Pulmonary Tuberculosis

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Abstract:

Complement proteins play a crucial role in the immune system's defence against infections, including tuberculosis (TB). Understanding the balance between complement activation and regulation is critical in the TB patients with unfavourable TB treatment outcome.This study aims to examine the levels of complement components and its regulators along with complement activation products in the unfavourable TB treatment outcome (cases) in comparison to cured controls (Controls). All participants were from Chennai, South India, and enrolled in the prospective Effect of Diabetes on Tuberculosis Severity (EDOT) study conducted between 2014 and 2019.It is a clinically well- characterized cohort with newly diagnosed patients with drug sensitive pulmonary TB, confirmed through smear and culture positivity. The plasma levels of complement proteins like C2, C3, C3b/iC3b, C4, C4b, C5, C5a, mannose-binding lectin (MBL), and complement regulatory proteins such as factor B, factor D, factor H, and factor I, were measured in pulmonary TB patients with unfavourable TB treatment outcome (cases, n=68) and cured controls (Controls, n=108) at pre (Baseline) and post TB treatment (at month 2) using the Luminex Technology platform. At baseline (pre-treatment), plasma levels of C1q, C3, C3b, C4b, C5 and C5a were significantly higher in the cases compared to the controls. Similarly, at month 2 of anti-TB treatment, the plasma levels of C3, C3b, C4b, C5, C5a, and C1q remained significantly elevated in the case group, while the levels of regulatory proteins like Factor B and Factor H were lower compared to the controls. Principal component analysis (PCA, in Figure 1a, 1b) revealed clear differentiation in the complement factors between the cases and controls at both baseline and month 2.This also reveals the complement factors of classical and lytic pathway plays a crucial role in differentiating cases from cured controls. This study concludes that the complement components such as C1q, C3, C3b, C5 And C5a can be used as a novel inflammatory immune marker for predicting adverse treatment outcomes in PTB patients.

Keywords: Novel, Inflammatory, Immune, Marker, TB.

S1-OP12

Utilization of Functional Genomics in exploring the pathway of Tuberculosis

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ABSTRACT:

Tuberculosis (TB) remains a significant global health threat, claiming millions of lives each year. The causative agent, *Mycobacterium tuberculosis*, exhibits remarkable adaptability by altering its metabolic pathways in response to drug exposure, thereby ensuring its survival in diverse microenvironments. Functional genomics plays a crucial role in understanding these adaptive mechanisms by analyzing gene expression patterns and protein functions. Through *in silico* analysis of experimental data, researchers can identify significant genes involved in key metabolic pathways by assessing their upregulation and downregulation. This gene expression analysis aids in mapping crucial biological functions and pathways, which are categorized into five major databases: KEGG (Kyoto Encyclopedia of Genes and Genomes), REACTOME, and Gene Ontology, which includes Molecular Functions, Biological Processes, and Cellular Components. These databases provide a comprehensive repository of genes associated with various pathways, offering insights into TB pathogenesis and potential therapeutic targets. Understanding these molecular interactions is essential for developing effective strategies to combat TB and improve global health outcomes.

Keywords: Gene Expression, metabolic pathway, databases, significant genes

S1-OP13

Integrative Network Pharmacology and Cell-Based Studies Unveil the Multi-Target Anti-Cancer Potential of *Solanum xanthocarpum*

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ABSTRACT

Solanum xanthocarpum (SX) has been used in traditional medicine since time immemorial. This study integrates network pharmacology and cell-based approaches to elucidate its unexplicit multi-target mechanisms against malignancy. Bioactive phytochemicals from SX were identified and retrieved from IMPPAT and HERB databases, and screened based on drug-likeliness score and oral bioavailability. The protein targets of SX, cancer-related targets and overlapping targets were identified using SWISS TARGET prediction, GeneCards database and Venn diagram visualization respectively. Top 10 hub genes identified using Protein-Protein Interaction (PPI) network from STRING and core PPI target analysis using Cytoscape revealed NCOA1, 2, STAT3, GRB2, PTPN11, and CBL as the primary targets. Pathway enrichment analysis acquired using KEGG and Gene Ontology demonstrated the involvement of SX in protein kinase, phosphotransferase activity and programmed cell death. Molecular docking simulations (MDS) revealed high binding affinity between key SX phytochemicals and the identified cancer-related targets. To validate these computational findings, MTT-based cytotoxicity assays performed on HeLa cells treated with SX extract demonstrated a dose-dependent reduction in cell viability. Thus, network pharmacology, MDS and cytotoxicity assay concordantly, demonstrated the multi-targeting action of SX against tumorigenesis, highlighting its potential as a promising therapeutic

candidate against malignancy while providing a scientific basis for further in-vivo studies and clinical trials.

Keywords: Solanum xanthocarpum, Network pharmacology, Molecular docking simulations, Malignancy, MTT cytotoxicity assay, Tumorigenesis inhibition.

S1-OP14

Development of Moringa Leaf Gummies for Anemia

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ABSTRACT

Moringa gummies for Anaemia is a dietary supplement designed to help individuals with Anemia increase their iron levels and alleviate symptoms such as fatigue, weakness, and shortness of breath. The product utilizes the nutrient-dense properties of moringa, a plant rich in iron, vitamins, and antioxidants, in a convenient and delicious gummy form. Our target audience includes individuals with iron-deficiency anemia, pregnant women and those with dietary restrictions. We promote healthy blood cell production and function, contributing to overall health and wellness. Moringa gummies is a game changer solution for Anemia. Our product offers a convenient iron boost bioavailable iron and a tasty and enjoyable experience. Moringa gummies provide a natural energy boost and support healthy red blood cells. It is natural product, it has no side effects and also cost effective.

Keywords: Moringa Oleifera, Anemia, Antioxidants, Nutraceuticals, iron-deficiency.

S1-OP15

Antioxidant Rich Face Cream Using Orange Peel

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ABSTRACT:

The pursuit for better skin health, driven by collective and individual perceptions, has led to the demand for sustainable skincare products. Environmental factors and lifestyle choices can accelerate skin aging, causing issues like inflammation, wrinkles, elasticity loss, hyperpigmentation, and dryness. Actual problem faced by teenager related to facial skin issues are acne, oily skin, dry skin, Eczema, sunburn and cold soresImprove skin texture and tone.Reduce appearance of fine lines and wrinkles.Enhance skin brightness and radiance.Provide hydration and moisturization and Soothe and calm irritated skin.

Keywords: Orange peel, Face Cream, Antioxidants, skin care.

S1-OP16

Polyherbal mixture for relieving leg cramps during mensuration

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ABSTRACT

Most of the women are facing leg cramps during their menstrual period every month. For that, our herbal product act as an effective analgesia to alleviate discomfort from cramps. Upon consuming our herbal product it ensures the availability of the electrolytes like magnesium and potassium which will help to reduce cramp pain. Our main ingredients are Gotu cola (*Centella asiatica*), Spinach (*Spinacia oleracea*) leaves, Peanuts(Arachis hypogaea), Prunes (*Prunes domestica*) and Cola nuts (*Cola acuminata*) which are used in these product to get relief from leg pain, depression, fatigue and efficiently promotes vitamin D and E. This product works effectively to get relief from leg cramps by enhancing the vitamins B1, C, D and E, promotes calcium, potassium and flavonoids level in our body and also acts as anti-inflammatory agents. Our product will be in Legiyam based texture, the preparation involves heating the sesame oil along with above mentioned ingredients. Currently available tablets are of high cost with some side effects but our product is very cost efficient with side effects. It can be consumed by women of all age groups. This product can be used in Pharmaceutical industries, Ayurvedic industries and women healthcare.

Keywords : Gotu cola- vitamin B1, Spinach leaves- VitaminD, E, Peanuts Vitamin C, cola nuts- Relief from headache and act as Flavouring agent.

S1-OP17

Rational design of phytochemical modulators targeting psa active sites: A dual-stage strategy for prostate cancer therapy

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ABSTRACT:

Prostate-Specific Antigen (PSA) is a serine protease that exists in two forms: free PSA (fPSA), which is active, and complex PSA (cPSA), which is inactive due to binding with

inhibitors like Alpha-1 Chymotrypsin (ACT). In prostate cancer, malignant cells produce excess ACT, which irreversibly inactivates PSA through a suicidal substrate mechanism. This prevents PSA from performing its natural tumor-suppressive functions, such as degrading cancer cells, cleaving growth factors, and activating immune responses. Cancer cells moderately regulate PSA activity, allowing it to contribute to extracellular matrix (ECM) remodeling, which facilitates metastasis. However, excessive ACT production can lead to further PSA inactivation, promoting tumor progression. Current treatments, including androgen deprivation therapy (ADT) and chemotherapy (docetaxel, cabazitaxel), have severe side effects and limited long-term efficacy, highlighting the need for alternative strategies.This study proposes a novel *in silico* approach to design a phytochemical that binds near PSA's active site, preventing ACT from interacting while preserving PSA's activity. Two potential therapeutic outcomes are envisioned: (i) in early-stage prostate cancer, the phytochemical would block ACT binding, keeping PSA active to degrade cancer cells and suppress tumor growth; (ii) in advanced metastatic castration-resistant prostate cancer (mCRPC), the phytochemical could induce structural changes that fully disrupt PSA function, preventing ECM degradation and metastasis. Molecular docking (AutoDock), molecular dynamics simulations, and ADMET profiling will be used to identify and optimize candidate phytochemicals. This dual-stage strategy aims to leverage PSA's tumor-suppressing properties in early stages while neutralizing its metastasis-promoting effects in advanced cancer, providing a targeted and less toxic alternative to existing therapies.

Keywords: complex PSA, ECM degradation, structural changes, therapeutic.

S1-OP19

Invitro cytotoxicity, metabolites profiling and *in silico* dengue envelope and capsid protein inhibition of Nilavembu Kudineer components – *Zingiber officinale, Vettiveria zizanioides* and *Piper nigrum*.

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ABSTRACT:

Nilavembu kudineer, a siddha poly-herbal formulation, widely used for the treatment of dengue viral fever in the state of Tamil Nadu, India. It is very effective and found to prevent and provide protection against dengue virus in vitro. However, studies on phytochemical constituents of major plant ingredient of Nilavembu kudineer are limited. Hence the present study is attempted to determine the phytocompounds present in the major three components of *Nilavembu kudineer* such as *Zingiber officinale, Vettiveria zizanioides* and *Piper nigrum* and to evaluate their potential inhibition of dengue envelope and capsid protein by *in-silico* analysis. The ethanolic and aqueous extract of the *Z. officinale, V. zizanioides* and *P. nigrum* were studied, off these ethanolic extracts showed less toxicity in Vero cell line and higher inhibition of Dengue virus at lower concentration in *in-vitro* study. GC MS analysis revealed the presence of forty four, fourteen and eight phytocompounds in ethanolic extract of *Z. officinale, V. zizanioides* and *P. nigrum,* respectively. Based on Lipinski rule, 16 out of 66 compounds were selected as less toxic and best fit compounds. The selected 16 compounds were docked with capsid and envelope proteins of dengue virus and results were interpreted based on docking

score. Based on this analysis and leveraging their properties, the selected 16 compounds can be explored for the therapeutic molecules against dengue infections through *in vitro* and *in vivo* studies.

Keywords: Nilavembu kudineer, Dengue, *Zingiber officinale, Vettiveria zizanioides, Piper nigrum*.

S1-OP20

Antiviral activity of compounds obtained from *Carica papaya* and *Ocimum sanctum* against Dengue-2 viral protein by insilico analysis

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ABSTRACT

Background: Dengue, arthropod borne disease is present major threat leading to millions of affected people and thousands of deaths around the world. In recent times dengue cases have been increasing since there is no vaccine and proper drug available. The presently available DenVax and yellow fever vaccine is no efficient for India. So, there is increase for need of drug and vaccine development for dengue in India. As there are lots of medicinal properties in commonly occurring medicinal plants in India, we have selected few medicinal plant seeds to study their antiviral properties against Dengue-2 virus. To identify the antiviral activity of compounds obtained from *Carica papaya* and *Ocimum sanctum* seeds against Dengue-2 viral protein by insilico method. Tulsi and papaya seeds showed less toxicity in Vero cells and proceeded with antiviral activity. The antiviral activity of medicinal plants showed promising results in vero cells. Hence proceeded with phytochemical, antioxidant and other analysis. The phytochemical analysis of Tulsi and papaya seeds showed positive for many bioactive compounds. When the sample extract proceeded with TLC, GC-MS and UV-vis spectrophotometer analysis bioactive 34 and 51 compounds were identified in Papaya and Tulsi respectively. These compounds were further analyzed for inhibiting Dengue viral proteins insilico. Docking of the bioactive compounds were done using Autodock software and the site of activity were identified.

Keywords: Dengue-2, *Ocimum sanctum, Carica papaya*, Flavivirus, Oleic acid, Eugenol

S2-OP1

Genomeguard: Detecting Genetic Defects

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ABSTRACT

This study aims to enhance the detection of gene defects by comparing the predictive accuracy of K-Nearest Neighbors (KNN) and Decision Tree algorithms to improve diagnostic accuracy in genetic testing. Accurate gene defect detection is crucial for identifying hereditary diseases and enabling personalized treatment strategies. Machine learning techniques, such as KNN and Decision Trees, have emerged as powerful tools in analyzing genomic data to identify genetic abnormalities. KNN classifies samples based on proximity to neighboring data points, while Decision Trees offer an interpretable framework by outlining decision rules that guide classification. This study evaluates the performance of both algorithms in gene defect detection, focusing on accuracy, sensitivity, specificity, and computational efficiency.

The findings highlight that both algorithms show promising performance, with notable differences. KNN offers an intuitive approach, while Decision Trees provide better interpretability and can identify critical features related to gene defects. The choice between these models depends on data complexity and the need for accuracy versus interpretability. In conclusion, this study demonstrates the potential of KNN and Decision Tree models to improve diagnostic accuracy in genetic testing. These insights can guide the selection of optimal machine learning approaches for detecting gene defects. Future research is needed to validate these findings in diverse clinical settings to further enhance the management of genetic disorders.

Keywords: K-Nearest Neighbors (KNN), genetic disorders, Machine learning

S2-OP2

Enhancing Ovarian Cancer Diagnosis Using Machine Learning and Deep Learning

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ABSTRACT

Ovarian cancer is a leading cause of gynecological malignancies, requiring accurate and early detection for improved patient outcomes. This study explores the classification of ovarian cancer as benign or malignant using machine learning and deep learning approaches. A biomarker-based dataset is utilized, and feature selection techniques are applied to extract the top 10 most relevant features based on a predefined threshold. Principal Component Analysis (PCA) was performed before and after outlier removal to analyze its impact on data distribution and model performance. Machine learning classifiers, including Logistic Regression, Decision Tree, ensemble classifiers include AdaBoost, Gradient Boosting, XGBoost, and a Voting Classifier, is employed for classification. Additionally, a Convolutional Neural Network (CNN) was implemented to enhance predictive accuracy. The models were evaluated based on key performance metrics, demonstrating that feature selection, outlier removal, and PCA contribute to improved classification accuracy. As a result CNN has shown better performance when compared to machine learning and ensemble classifiers.

Keywords – Principal Component Analysis, Machine learning, Ensemble, Convolutional Neural Networks, Feature selection, Threshold.

S2-OP3

Automated Detection of Kidney Stones using Coronal CT Images with Deep Learning in the Field of Artificial Intelligence

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ABSTRACT

Various imaging technique are used for the diagnosis of kidney stone disease. Specialists are needed for the interpretation and full diagnosis of these images. Computer-Aided Diagnosis (CAD) systems are the practical approaches that can be used as auxiliary

tools to assist the clinicians in their diagnosis. In this work, an automated detection of kidney stones using coronal Computed Tomography (CT) images was proposed with Deep Learning (DL) technique which has made significant progress in the field of artificial intelligence. So, to detect the stone and that too precisely paves the way to image processing because through image processing there is a tendency to get the precise results and it's an automatic method of detecting the stone. Doctor generally uses the manual method to detect the stone from the Computed Tomography image but our technique is fully automated so it is advantageous as the time reduced and with the chances of error also reduces.

Keywords - Kidney stone, medical image, Deep Learning, Computed Tomography.

S2-OP4

Exploring Coordination Variability: Structural Tuning of Zinc–Carbohydrazone Complexes for Biological Applications

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ABSTRACT

The design and development of metal-based complexes have gained significant attention in medicinal chemistry, particularly in cancer treatment. This study focuses on synthesizing, characterization, and biological evaluation of zinc-carbohydrazone complexes, exploring their coordination variability and structural tuning for enhanced therapeutic applications. Four carbohydrazone ligands were synthesized using Schiff-base condensation of carbohydrazide with various aldehydes. The resulting ligands and their zinc complexes were characterized using spectroscopic techniques such as FTIR, ^{1}H NMR, ^{13}C NMR, UV-Vis, and mass spectrometry to confirm their structural integrity. The biological relevance of these complexes was evaluated by investigating their interaction with biomolecules such as glutathione (GSH), a crucial regulator of redox balance in cancer cells. Various *in vitro* assays were conducted to assess their anticancer potential, including cytotoxicity (MTT assay), ROS generation, apoptosis induction, and DNA interaction studies. Additionally, molecular docking and computational analyses were performed to understand binding mechanisms with target proteins. The results suggest that zinc–carbohydrazone complexes can effectively disrupt cellular redox homeostasis, induce oxidative stress, and promote apoptosis in cancer cells, making them promising candidates for further therapeutic development. This study highlights the significance of structural tuning in metal coordination complexes for targeted cancer therapy.

Keywords: DNA interaction, regulator, DNA interaction, ROS generation.

S2-OP5

Network Pharmacology-Based Insights into *Cissus quadrangularis* L. for Osteoporosis Management

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ABSTRACT

Osteoporosis is a progressive bone disorder characterised by reduced bone density and strength, increasing fracture risk. It is often asymptomatic until fractures occur, resulting from an imbalance between bone resorption and formation. A significant public health

concern, it primarily affects older adults, especially postmenopausal women. Early diagnosis and treatment are crucial for fracture prevention and disease management. *Cissus quadrangularis* L. (CQ), a medicinal plant from the Vitaceae family, has been traditionally used in Ayurveda for its bone-healing properties. Pharmacological studies suggest that CQ exhibits antioxidant effects and supports bone regeneration. This study utilises a Network Pharmacology approach to investigate the therapeutic mechanisms of CQ phytochemicals in osteoporosis. Bioinformatics analyses, including target gene identification, Gene Ontology, pathway enrichment, molecular docking, and visualisation, were conducted using Cytoscape, PyRx, and BIOVIA Discovery Studio. The analysis identified 11 phytochemicals, 885 predicted target genes, 33,356 osteoporosis-related genes, and 595 shared genes. The top ten Hub genes were identified with different centrality measurements by the Cytoscape-CytoHubba plugin. Further, molecular docking highlighted top bioactive compounds with a binding affinity of >7 kcal/mol that show strong therapeutic potential. These findings provide insights into CQ's role in osteoporosis management and warrant further experimental validation.

Keywords: Bone disorder, therapeutic potential, phytochemicals, and Pharmacological studies.

S2-OP6

Exploring Interferon-stimulated Genes (ISGs) modulation as an antiviral strategy against chikungunya virus

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ABSTRACT:

Host-Directed Antivirals (HDA) such as Interferons and Interferon-stimulated Genes (ISGs) are actively studied for their potential application in antiviral therapy. Interferons are the family of cytokines which play an important role in restricting viral infection. Upon induction these cytokines induce ISGs through JAK-STAT pathway which will restrict viruses at different stages of its lifecycle. There is a greater interest in identifying and developing a small molecule drug that can activate ISGs and restrict viral infection at early stages. In our study, we have developed cell-based reporter assay to identify the small molecules that can directly activate these ISGs. Initially we screened a small panel of flavonoid molecules for ISG modulation. We found that isoflavones, a subclass of flavonoids had good ISRE-luc reporter activity and minimal IRF1-luc activity. One of the isoflavones had potent anti-CHIKV activity in HEK293 and HepG2 cell lines (from 40μM to 10μM). Further experiments with the isoflavone through luciferase assay and western blot confirmed the moderate ISG modulation in wide range of concentrations. We yet to confirm the role of ISG modulation and PTK inhibitor property of the isoflavone in its invitro antiviral activity. We have also developed a lethal animal model for CHIKV infection (5 days old Balb/c is used) and currently testing the efficacy of the isoflavone in vivo.

Keywords: JAK-STAT pathway, PTK inhibitor, Interferons.

S2-OP7

Evaluation of effective anticonvulsant role in acute organophosphosphate toxicity treatment

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ABSTRACT:

Organophosphorus (OP) chemicals are tailor-made to use for several purposes such as pesticides and OP nerve agents are used in terrorist attacks, and civilian conflicts due to their high toxicity and mortality. OP pesticides can cause acute and chronic toxic effects due to acute or chronic exposures through occupational or accidental exposures. OP chemicals inhibit the acetylcholinesterase function at neuronal synapses resulting an acute cholinergic crisis due to excess accumulation of acetylcholine at muscarinic and nicotinic receptors leading to excessive secretions, muscle fasciculation's, seizures, convulsions and death due to hypoxia. OP exposure can also lead to long-term neurotoxic effects through multiple mechanisms involved in neuronal impairments as observed in case of Japanese civilian victims of terrorist attacks with nerve agent sarin and Gulf-War victims. Currently used post-exposure medical countermeasures against OP agents (atropine, oximes, and diazepam) requires improvement as they are not effectively protecting against chronic and long-term toxic effects. Immunoreactivity levels of glial fibrillary acidic protein (GFAP) showed significant increase in the rat brain after acute subcutaneous DFP (di isopropyl fluorophosphate) exposure. DFP exposure increased the fluorojade-C-stained neurons in the rat brain indicating the neurodegenerative neurons. Treatment with atropine, 2-PAM and midazolam has reduced the OP induced neurodegeneration indicating the role of midazolam in the OP treatment.

Keywords: Organophosphorus (OP) chemicals, neurodegeneration, glial fibrillary acidic protein, diisopropyl fluorophosphate, midazolam.

S2-OP8

Anti-Biofilm activity of bioactive compound from Marine *Streptomyces* species

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ABSTRACT:

Biofilm was defined as the growth and interaction of different species of microbes within the matrix that was mainly composed of extra polymeric substance and attached to the abiotic or biotic surfaces. The formation of biofilm was found to be a complicated issue greater than ever. It was escalating as a serious threat to humans all around the world. Biofilm was the main cause of bacterial infections. Approximately 80% of the nosocomial infections were mainly due to biofilm-associated infections. The pathogenicity of the bacteria in the microbial infection was increased by the biofilm formation. The main cause of infections is due to the matrix that protects and acts as a layer for the bacterial species present inside them from the antibiotic compound. So, in order to overcome the biofilm associated infections, the biofilm matrix should be dispersed. In order to disperse the biofilm matrix, new and effective methods have to be discovered. The compound isolated from the marine

Streptomyces species, can be effective treatment to control the biofilm formation. The biofilm disruption using bioactive compound from marine *Streptomyces* species is studied using Scanning electron microscope and High content screening microscope.
Keywords: Biofilm, Marine Streptomyces, Bioactive compound, SEM.

S2-OP10

Reprogramming the Tumor Microenvironment: Car-Macrophages as Immunotherapeutic Pioneers

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Abstract:

A paradigm shift in cancer immunotherapy is emerging with macrophages as engineered warriors against solid tumors. While Chimeric Antigen Receptor (CAR) T cell therapy has revolutionized hematologic cancer treatment, its success in solid tumors remains limited. One key challenge is the CD47-SIRPα interaction, a "don't eat me" signal that shields cancer cells from macrophage-mediated clearance.To address this, I propose a novel CAR-Macrophage (CAR-M) design integrating the Hu5F9-G4 scFv with CD247, CD137, and CD40 signaling domains to enhance phagocytosis and tumor destruction. This theoretical model aims to overcome macrophage suppression within the tumor microenvironment (TME), ensuring a sustained M1 proinflammatory phenotype while resisting conversion to the immunosuppressive M2 state.Beyond direct tumor clearance, CAR-M could reshape the TME by inducing a proinflammatory signature and recruiting T cells, potentially priming adaptive immune responses against tumor neoantigens. This concept underscores the potential of CAR-M as a multifaceted immunotherapeutic strategy, bridging innate and adaptive immunity for solid tumor treatment. Further research and experimental validation are needed to explore its feasibility and translational impact in cancer therapy.
Keywords: CAR-M, macrophages, Cancer, solid tumors

S2-OP11

Evaluating the Anticancer Activity of *Kappaphycus Alvarezii* and *Spirulina Spp*

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ABSTRACT

Colon cancer is one of the most prevalent malignancies worldwide, with oxidative stress and chronic inflammation playing a central role in its onset and progression. Reactive oxygen species (ROS)-induced damage and pro-inflammatory responses contribute to DNA mutations, tumor initiation, and metastasis. Natural bioactive compounds with antioxidant and anti-inflammatory properties have gained significant attention for their potential in cancer prevention and functional food applications. This study investigates the therapeutic potential of phycoerythrin extracted from *Kappaphycus alvarezii* and phycocyanin derived from *Spirulina Spp*. The antioxidant activity of these phycobiliproteins was evaluated using invitro DPPH and ABTS radical scavenging assays, confirming their strong free radical neutralization capacity. Additionally, their anti-inflammatory potential was assessed through invitro assays,

demonstrating their ability to regulate inflammatory pathways. To explore their functional food applications, phycoerythrin and phycocyanin were separately incorporated into yogurt, jelly, and Badam Pisin, alongside a composite extract formulation. Furthermore, the composite extract was tested for its anticancer potential against colon cancer cells, revealing significant cytoprotective effects, oxidative stress reduction, and anti-inflammatory benefits. These findings underscore thepotential of *K.alvarezii*-derived phycoerythrin and *Spirulina*-derived phycocyanin as natural functional food ingredients with promising health benefits, particularly in colorectal cancer prevention, oxidative stress management, and inflammation control. This research emphasizes the importance of marine-derived nutraceuticals in creating functional foods for health promotion and disease prevention.

Keywords: Colon Cancer, Kappaphycus alvarezii; Spirulina spp; Phycoerythrin; Antioxidant; Antiinflammatory; Functional Foods

S2-OP12

In Vitro Studies on the Protective Effect of Ambrex on Acetaminophen Induced Hepatotoxicity

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ABSTRACT:

Liver is the main organ that is involved in metabolizing xenobiotics. Drug induced liver damage is a prospective complication of most prescribed medications. The present study was designed to develop efficacy of Ambrex, a polyherbal formulation in the management of hepatocellular damage induced by acetaminophen in Chang liver cell lines. The effect of Ambrex on cell proliferation was analysed using MTT assay in Chang liver cells and IC50 value of Ambrex was found out. *In vitro* studies were carried out to analyse the role of Ambrex in offering protection against oxidative damage induced by acetaminophen (100 µg/ml) in Chang liver cells. The mRNA expression of Cytochrome P2E1, UGT, and Albumin were analysed in Ambrex-treated and untreated Chang liver cells exposed to acetaminophen. Chang liver cells challenged with acetaminophen exhibited increase in expression of CYP2E1 and down regulation of UGT1A1. This induces oxidative stress, leading to decreased expression of gene coding for albumin and certain other proteins. Decrease in albumin gene expression, a marker for hepatic dysfunction, was observed in this study. Ambrex exposure at 5, 50 and 500 ng/ml dose dependently protected the cell lines from oxidative damage by maintaining near normal levels of mRNA expressions. These results gave an insight into the molecular mechanism of acetaminophen hepatotoxicity and the efficacy of Ambrex to combat this damage.

Keywords: hepatotoxicity, mRNA expressions, acetaminophen.

S2-OP13

Optimizing Cyanobacterial Exopolysaccharides for Edible Nano-Coatings in Meat Preservation

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ABSTRACT:

Global meat consumption is projected to exceed 350 million tonnes in 2024, driven by poultry (41%), pork (34%), beef (20%), and lamb (5%). The processed meat market is expected to reach $353.40 billion by 2025, with an annual growth rate of 5.04%, fuelled by strong demand from Asian markets. Major exporters like the United States and Brazil benefit from this trend, while importers such as China and Japan rely heavily on these supplies.

However, meat spoilage caused by microorganisms like *Pseudomonas*, *Acinetobacter*, and *Streptococcus* results in annual losses of about 20%. Addressing just 5% of this waste could provide a day's nutrition for 320,000 individuals. Effective preservation methods, such as refrigeration and Modified Atmosphere Packaging (MAP), are essential to extend shelf life. While chemical preservatives like sodium nitrite are effective, their health risks, including carcinogenic effects and antibiotic resistance, have driven demand for natural alternatives.

Polysaccharides from cyanobacteria such as *Spirulina platensis* and *Nostoc commune* offer eco-friendly, antimicrobial coatings that extend shelf life by 30% while maintaining quality without harmful residues. These coatings meet clean-label demands, but further research on antimicrobial properties is needed. This study explores replacing harmful chemicals with eco-friendly solutions to extend meat shelf life and prevent spoilage.

Keywords: cyanobacterial polysaccharides, nano-edible coatings, natural alternatives, symbiotic relationships, food preservation, extending shelf life.

S2-OP14

Formulation of syzygium cumini tea powder to prevent diabetes mellitus.

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ABSTRACT:

The syzygium cumini is traditionally used as alternative medicine to prevent diabetes mellitus. It contains antidiabetic compounds the mixture of five herbal plants to prepare syzygium cumini tea this product is used for the diabetic patients to maintain blood sugar level. Most of the peoples are suffered from diabetes effect of improper diet this tea powder has diet concentrated the product contains antidiabetic compounds like gallic acid, umbelliferone.ellagic acid, chlorogenic acid and rutin. The diabetes mellitus is causes by improper working of pacreas, effect of maintaining diet. invluding children's also affected by diabetes. It helps to improve the volume of pancreatic islets of langerhans. And free from the harmful side effects. The tea powder is easy to consume day to day life like normal tea. Our research focuses on the development of antidiabetic-herbal tea powder, utilizing the potent properties of herbal plants. This natural approach make healthier diet and blood sugar levels. Antidiabetic compounds suppressed the high blood sugar level, there is no medication for diabetes mellitus this product is prevent and maintain blood sugar levels. This innovative work aligns with the growing global demand for prevent diabetes and eco-friendly.

Keywords: syzygium cumini,herbal plants, antidiabetic compounds, eco-friendly.

S2-OP15

Fabrication of Biopolymer with Incorporation of Bioactive Compounds from *Bruguiera Cylindrica*: Wound Healing Application

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ABSTRACT:

Bandage is a piece of material used to support a medical device such as dressing, on its own and it provide support to the movement of a part of the body. Bandages are essential tool for treating external wound with wound healing properties. But some commercially available bandages cause moisture retention, skin irritation, impaired oxygen exchange, adherence problems and lead damages to human skin and delayed wound assessment. *Burgueria cylindrica* is a remarkable natural source from the Mangrove plant species. Mangroves, specifically *Brugueria cylindrica* contain bioactive compounds like tannin, alkaloid, saponin, phenols, flavonoid and they were extracted by using the aqueous extraction method. The presence of phytochemicals was confirmed by using standard chemical tests both qualitatively and quantitatively. The liquid-chromatography mass spectroscopy (LC-MS) was performed to determine the presence of individual phytochemicals. Extraction of gelatin from the Octopus species *Cistopus indicus* are used for the formation of film and incorporation of bioactive compounds from *Brugueria cylindrica*. The final formulation was checked for its anti-inflammatory, anti-oxidant activity and anti-bacterial activity. The film parameters were also evaluated. Thus, the bandage prepared in this study can overcome the adherence problems associated with the commercial films, easily degradable and improves wound healing activity.

Keywords: *Brugueria cylindrica*, Mangrove Plant, Phytochemical Analysis, LC-MS Analysis, Gelatin, *Cistopus indicus,* Anti-Inflammatory, Anti-Oxidant and Anti-Bacterial Activity.

S2-OP16

Preparation and Optimization of Nutrient Enriched Papads by Using *Ulva lactuca*

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ABSTRACT:

This study focuses on creating nutritious and sustainable seaweed-infused papads, a traditional first-generation snack. By incorporating nutrient-rich green seaweed, also known as sea lettuce, the project aims to develop vegan papads fortified with bioactive compounds. Using the Papadification technique, the papads are formulated with seaweed, Urad flour, and locally sourced ingredients. The inclusion of green seaweed in the diet can improve blood sugar levels and promote digestive health. Urad flour enhance the texture and appearance of the papads. Replacing regular salt with Moringa Salt helps to combat oxidative stress and supports overall health. The ingredient quantities are optimized by using design expert software, with a maximum of 20 runs to determine the best formulation. Sensory analysis was done to assess the taste, smell, appearance, texture, and physical properties like weight, diameter, and thickness of the prepared papads. Nutritional profiles, including total

carbohydrate, protein, and fat content are evaluated. This project aims to develop innovative, nutrient-dense food products that promote public health and sustainable resource utilization.

Keywords: Seaweed, Papadification, taste, smell, appearance, texture, Sensory analysis.

S2-OP16

Evaluation of Actinobacteria for Plant Growth Promoting and Biocontrol Properties

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ABSTRACT

Actinobacteria, renowned for their bioactive potential, were isolated from soil samples collected in Kodaikanal (KS) and the Indian Himalayan Region (IHR) to evaluate their plant growth-promoting and biocontrol properties. A total of 24 isolates were obtained from the two samples using serial dilution and spread plate methods, followed by subculturing on streak plates. These isolates were screened for enzymatic activities, revealing positive results for amylase (18 isolates), protease (22 isolates), lipase (14 isolates), and cellulase (11 isolates). Additionally, they were assessed for plant growth-promoting traits, including ammonia production (17 isolates), phosphate solubilization (21 isolates), siderophore production (16 isolates), indole acetic acid (IAA) production (14 isolates), acetoin production (5 isolates), and nitrogen fixation (17 isolates). Among these, five isolates—KS 13, HS 2, KS 14, HS 13, and KS 23—showed consistent positive results across all assays. Further these cultures tested for paper towel and pot method for root and shoot measurement. Heavy metal tolerance tests at 1000 ppm further demonstrated robust growth for KS 13, KS 14, HS 2, and HS 13, highlighting their adaptability to extreme conditions. This study emphasizes the potential of actinobacteria, particularly KS 13 and HS 2, as effective biofertilizers and biocontrol agents. Their application could significantly contribute to sustainable agriculture by reducing reliance on chemical inputs.

Keywords: Actinobacteria, Kodaikanal Soil, Himalayan Soil, Plant Growth Promotion, Biocontrol, *Ralstonia solanacearum*

S2-OP18

Computational Analysis to compare the structural and compositional aspects of the envelope protein of the Omicron and XBB variant aims to investigate the stability and transmissibility characteristics of the SARS CoV-2

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ABSTRACT

Over the course of the last five years, the COVID-19 pandemic has been a global health concern, driven by the continued evolution and mutation of the SARS-CoV-2 virus. Of its four structural components—spike (S), membrane (M), nucleocapsid (N), and envelope (E)—the envelope protein plays a key role in assembly, replication, and release of the virus. In this study, the hydrophobic envelope (E) protein is explored in terms of how its unique structural properties impact viral stability and transmission efficacy. In particular, a comparative analysis of the original SARS-CoV-2 strain, the Omicron variant, and the XBB variant reveals key mutations that impact envelope protein stability and function. A detailed breakdown of its amino acid composition shows a high ratio of polar and aromatic residues that help in making the protein hydrophobic in combination with reinforcing stability through higher polarity. Intra-protein interactions, including cyclic salt bridges and aromatic-aromatic interactions, also help in ensuring that the structure of the protein is maintained and that it is functionally active. An understanding of these interactions, particularly in molecular binding pockets, is of immense significance in identifying potential areas of drug binding and in enhancing therapeutic interventions. The findings underscore the importance of specific mutations in the envelope protein, pointing to how such mutations have facilitated the heightened stability and flexibility of SARS-CoV-2. By offering new insights to the structure and function of the envelope protein, this work establishes a foundation for designing targeted antiviral drugs and vaccines to restrict the ongoing threat of SARS-CoV-2.

Keywords: SARS CoV-2, Omicron, XBB, Envelope protein, Mutation

S2-OP19

Isolation and Characterization of Bacterial Cellulose and its Applications

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ABSTRACT

Cellulose is a naturally available biopolymer produced by different biological sources such as plants, fungi, bacteria, marine algae, and waste substances like so many. Cellulose is a larger group of carbohydrates present in the world. which has a linear polymeric chain of β (1-4) D-glucose bonds it gives a unique form of structural properties to cellulose like high-temperature tolerance, high tensile strength, water retention, and flexibility with high water holding capacity these are some characteristics that make the cellulose as a unique form of biomaterial. The biocompatibility of Bacterial cellulose makes it a promising biomaterial for diverse applications. This research study focuses on isolating and characterizing bacterial cellulose from novel bacterial strains and exploring its potential applications in different fields. This bacterial strain was isolated from a wine sample in an open environment The subculture process was done for that particular bacterial strain and identified with 16S rRNA and some biochemical tests that can help to identify the cellulose presence. Sequencing method. Gram staining was then inoculated in Hestrin-Schramm (HS) synthetic growth media, which contains glucose, peptone, yeast, citric acid, and disodium hydrogen phosphate. The cultured flasks were incubated in static conditions at room temperature 27 to 35˚C for 15 to 20 days, and purified with NaOH solution, and distilled water to remove the impurities, the yield was measured. The isolated BC was characterized using various analysis processes to study the structural and physiochemical properties which are SEM, FT-IR, XRD, PSA, TGA, tensile, water

absorbance test, and HPLC analysis. Based on the characterized properties the isolated BC demonstrated potential for biomedical applications like wound healing, and food packaging material dye absorption application.

Keywords: Biopolymer, HPLC, Hestrin-Schramm, SEM, FT-IR, XRD

S2-OP20

Isolation of bacteriocin-like antimicrobial peptides from *Bacillus. sp* isolated from fish gut

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ABSTRACT

This study investigates the isolation, solvent extraction, and purification of bacteriocin derived from Bacillus species obtained from the gut microbiota of Oil Sardine, emphasising its potential as a natural antibacterial agent for aquaculture use. Bacillus strains were extracted from the digestive tracts of healthy fish and evaluated for antibacterial efficacy against prevalent fish infections. A bacterium (OS40) that produces bacteriocin like antimicrobial peptides was chosen and cultured in optimised media. The bioactive molecule was extracted from the cell-free supernatant utilising ethyl acetate as the solvent, subsequently concentrated under reduced pressure. The purified Bacteriocin antimicrobial peptides demonstrated broad-spectrum antibacterial efficacy against both Gram-positive and Gram-negative pathogens such as *E. coli* and *Staphylococcus aureus*, maintaining stability across various pH and temperature settings. Mass spectrometry indicated that the molecule's size is 23-25 kDa, categorising it as a class III Large bacteriocin. Ethyl acetate served as an excellent solvent for the initial extraction, yielding a substantial amount of bioactive chemicals. The results indicate that Bacillus strains obtained from fish guts possess promise as natural antimicrobials, emphasising their use in aquaculture for disease control and as alternative for antibiotics. This study presents a systematic methodology for the extraction and purification of bacteriocin through solvent-based techniques, aiding in the development of sustainable ways to promote fish health and aquaculture productivity.

Keywords: Bacteriocin, Antimicrobial activity, Aquaculture

S3-OP1

Targeting Kinesin-1 Heavy Chain in Tauopathy Promotes Autophagy-Driven Degradation of Phosphorylated Tau Aggregates and Mitigates Neurodegeneration in Alzheimer's Disease Models

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ABSTRACT:

Many neurodegenerative diseases, such as Alzheimer’s disease (AD) and frontotemporal dementia with Parkinsonism linked to chromosome 17, are characterized by tau pathology. Numerous motor proteins, many of which are involved in synaptic transmission, mediate transport in neurons. Dysfunction in motor protein-mediated neuronal transport mechanisms occurs in several neurodegenerative disorders but remains understudied in AD. Kinesins are

the most important molecular motor proteins required for microtubule-dependent transport in neurons, and kinesin-1 is crucial for neuronal transport among all kinesins. Although kinesin-1 is required for normal neuronal functions, the dysfunction of these motor domains leading to neurodegenerative diseases is not fully understood. Here, we reported that the kinesin-I heavy chain (KIF5B), a key molecular motor protein, is involved in tau homeostasis in AD cells and animal models. We found that the levels of KIF5B in transgenic P301S tau mice are high. Kinesin 1 proteins cannot progress along MTs due to an accumulation of tau on their surfaces. We found that tau interacts with the motor domain of KIF5B, possibly through its N-terminal projection domain. This interaction leads to the inhibition of the ATPase activity of the motor domain. We also found that the knockdown and knockout (KO) of KIF5B significantly decreased the tau stability, and overexpression of KIF5B in KIF5B-KO cells significantly increased the expression of phosphorylated and total tau levels. In addition, the KIF5B KO results in autophagy initiation, which subsequently assists in tau degradation. The mechanisms behind KIF5B KO-mediated tau degradation seem to involve its interaction with tau, promoting the trafficking of tau through retrograde transport into autophagosomes for subsequent lysosomal degradation of tau. Our results suggest how kinesin-1 removal facilitates the movement of autophagosomes towards lysosomes for efficient tau degradation. This mechanism can be facilitated by suppressing the production kinesin-1 or interrupting the interaction between kinesin-1 and tau, especially when neurons detect disruptions in intercellular axonal transport. By conducting experiments on P301S tau mice, we showed that partially reducing KIF5B levels can reduce the hyperphosphorylation of tau, formation of insoluble tau aggregates, and memory impairment. Our results collectively indicate that reducing KIF5B levels is sufficient to prevent or slow down abnormal tau-induced Alzheimer's disease and other tauopathies.

Keywords: Alzheimer’s disease, Tau pathology, Kinesin 1 heavy chain, KIF5B motor, ATPase, Autophagy, P301S Tau mice, KIF5B KO Mice.

S3-OP2

Comparative study between different Artificial intelligence-based prediction methods for Dementia

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ABSTRACT

This study aims to enhance the detection of gene defects by comparing the predictive accuracy of K-Nearest Neighbors (KNN) and Decision Tree algorithms to improve diagnostic accuracy in genetic testing. Accurate gene defect detection is crucial for identifying hereditary diseases and enabling personalized treatment strategies. Machine learning techniques, such as KNN and Decision Trees, have emerged as powerful tools in analyzing genomic data to identify genetic abnormalities. KNN classifies samples based on proximity to neighbouring data points, while Decision Trees offer an interpretable framework by outlining decision rules that guide classification. This study evaluates the performance of both algorithms in gene defect detection, focusing on accuracy, sensitivity, specificity, and computational efficiency. The findings highlight that both algorithms show promising performance, with notable differences. KNN offers an intuitive approach, while Decision Trees provide better interpretability and can identify critical features related to gene defects. The choice between

these models depends on data complexity and the need for accuracy versus interpretability. In conclusion, this study demonstrates the potential of KNN and Decision Tree models to improve diagnostic accuracy in genetic testing. These insights can guide the selection of optimal machine-learning approaches for detecting gene defects. Future research is needed to validate these findings in diverse clinical settings to further enhance the management of genetic disorders.

Keywords: K-Nearest Neighbors, machine learning, AI, genetic disorders.

S3-OP3

Synthesis and characterization of metal-organic framework-based artificial enzyme mimics

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ABSTRACT

Enzymes are nature's elite proteins that catalyze many biological and physiological processes. They are precise and versatile. Enzymes have found diverse roles in several industrial and biomedical applications. However, natural enzymes pose several limitations including the cost and procedures involved in the extraction process. Moreover, being sensitive to several factors such as temperature, pH, etc., further makes it difficult to store and utilize them under a wide range of experimental parameters. In this regard, artificial enzyme mimics have found immense interest over the years as an alternative to natural enzymes finding application in biomedical and biotechnology fields. Several artificial enzymes have been reported including inorganic metal complexes, metal-oxides, and carbon-based materials showing impressive stability and high catalytic efficiency. This project aims to utilize metal-organic frameworks (MOFs) based nanoparticles to mimic the enzyme-like activity with improved features and high catalytic efficiency. MOFs are three-dimensional porous structures made up of metal ion clusters and organic linkers. MOFs have gained immense interest in catalysis owing to their unique structural properties such as large surface area, chemical functionality, improved stability, tunability adjustable pore size and volume, etc. Their composition and structural features can be evaluated using various spectroscopic and analytic techniques such as X-ray diffraction, Scanning electron microscopy, etc. This study can assist in designing artificial enzyme mimics with their potential use in biomedical applications.

Keywords: metal-organic frameworks, enzyme-like activity, natural enzymes, artificial enzymes

S3-OP4

Eutectic Mixture Based Two Phase Fermentation of Laccase and Its Studies

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ABSTRACT

Laccases are multicopper oxidases known to catalyse the transformation of a wide range of phenolic and non-phenolic substrates using oxygen as an electron acceptor and

forming water as the only by-product of concomitant four-electron reduction. This property makes it a valuable biocatalyst in environmentally sustainable processes, with wide industrial applications, including bioremediation, bio-bleaching, biofuels, biopolymer synthesis and dye degradation. Nonetheless, the application of laccase on a commercial level is limited by issues such as the high enzyme cost, as well as its lower activity and stability under specific conditions. This study focuses on the production and purification of laccase using a green solvent-based aqueous two-phase system (ATPS), a sustainable alternative to conventional purification methods. Laccase was produced using *Bacillus sp.* and parameters such as pH, temperature, C/N source and incubation time are to be optimized using resonance surface methodology. Moreover, the effect of the addition of inducers such as copper sulphate, guaiacol and phosphate on laccase production is to be investigated. Further, the enzyme is purified using green solvent-based ATPS, a novel approach that is biocompatible with environmental benefits. Unlike traditional methods, this ATPS uses non-toxic, recyclable solvents to create a two-phase system, enabling selective partitioning of laccase.

Keywords: Aqueous two-phase system, Green solvents, Selective partitioning

S3-OP5

Reverse Genetic Bioinformatics Approach for Cystic Fibrosis Vaccine Development

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ABSTRACT:

This study explores the use of reverse genetic bioinformatics to develop vaccines for cystic fibrosis, accelerate and find antigen targets as well as optimize vaccine candidates. Materials and Methods: Sequencing was conducted through the help of next-generation sequencing platforms and was analysed in the light of comparative genomics by the means of bioinformatics tools such as blast, AlphaFold and Swiss-Model and also the codon optimization for designing mRNA candidates for vaccines with the encapsulation of Lipid Nanoparticles (lnps). Immunogenicity and efficacy were tested by in vitro and in vivo studies. Results: The primary candidate for antigenic targets was the spike protein, and modelling of the protein showed structural stability. Immunogenicity assays also revealed strong antibody and t-cell responses. High vaccine efficacy was predicted by the computational models. Discussion: This study demonstrates the efficiency of reverse genetic bioinformatics in vaccine design. Different types of challenges were surmounted, including immune complexity and genomic variability, using ai-driven analysis and structural validation. Conclusion: This study shows that reverse genetic bioinformatics can rapidly produce vaccines against emerging diseases and offers a framework for the future preparedness for pandemics.

Keyword: Cystic Fibrosis, Antigenic Targets, Next Generation Sequencing, Lipid Nanoparticles.

S3-OP6

Unveiling the Microbiome of Ethnic Fermented Foods from Manipur and Nagaland through 16s rRNA Sequencing

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ABSTRACT

Fermented foods are rich sources of probiotics and are integral to the cuisine of Northeast India, with traditional preparation methods varying across ethnic groups. These variations influence the microbial composition, affecting both the nutritional profile and health benefits of the foods. This study aims to characterize the microbial diversity and functional potential of traditionally fermented soybean bamboo shoots, fish, and vegetable leaves collected from local markets in Manipur and Nagaland. 16S rRNA sequencing using the Illumina-MiSeq platform was employed to identify and classify bacterial communities. Taxonomic analysis was performed using QIIME2 software with the Greengenes database, revealing a diverse microbial community. Functional profiling was predicted using PICRUSt2 and subsequently mapped to the KEGG database for pathway prediction. The major probiotic genera detected across our samples were Lactobacillus, Streptococcus, Paenibacillus, Levilactobacillus, Leuconostoc, Weissella and Enterococcus. The findings highlight the health-promoting potential of traditional fermented foods and provide insights into their microbial ecology, supporting future probiotic applications and the preservation of traditional fermentation practices.

Keywords: Fermented Foods, Probiotics, 16S rRNA Sequencing, Microbial Diversity, Gut Health

S3-OP7

A Personalized Scaffold: Bioconjugated Chitosan-Luteolin Complex Incorporated In Alginate Scaffold for Bone Regeneration under Diabetic Condition

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ABSTRACT

Bone regeneration is a critical challenge in orthopaedics, especially in the presence of inflammatory conditions that can impair the healing process. This project aims to develop a chitosan-based scaffold loaded with the natural compound luteolin to promote bone regeneration in an inflammatory environment. Chitosan, a natural polysaccharide, has been widely investigated for its biocompatibility, biodegradability, and ability to promote bone formation. To achieve optimal properties suitable for bone tissue engineering, CS-based scaffolds are developed by the addition of copolymers due to their fast degradation rate, reduced mechanical strength and diminished bioactivity. The scaffold is formed using a matrix of chitosan and sodium alginate, which is then crosslinked with luteolin. Luteolin, a flavonoid compound, has demonstrated antioxidant, anti-inflammatory and bone regeneration properties. Luteolin is known to activate the Wnt/β-catenin, TGF-β and p38 MAPK signalling pathway and also suppresses the NF-κB signaling pathway, essential for the proliferation and differentiation of osteoprogenitor cells in the various stages of bone regeneration. To achieve

the effective composition of the chitosan-luteolin scaffold, the structural and compound analysis was performed using various characterization techniques, including FTIR, SEM-EDX and XRD. The efficacy of this chitosan-luteolin scaffold will be evaluated through in vitro and in vivo studies, including an angiogenesis assessment using a chick embryo model and bone regeneration studies using zebrafish models with causal fin amputation/fracture, skull fracture, and scale regeneration. This project work may assist and open up to an effective targeted drug delivery system for the treatment of osteolytic and osteoblastic metastatic bone diseases.

Keywords: Chitosan, biocompatibility, Luteolin, Wnt pathway, osteoprogenitor, chick embryo, causal fin, osteolytic, osteoblastic metastatic

S3-OP8

Loss of *trans*-translation sensitizes bacterial cells to fluoroquinolone antibiotic Nalidixic acid

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ABSTRACT:

Antibiotic resistance is increasing worldwide in an alarming rate. This poses a serious threat to public health. Bacteria responsible for commonly occurring infections are increasingly developing resistance to multiple antibiotics rendering standard treatments ineffective. Therefore, it is essential to develop alternative strategies to counteract this emerging threat. Recent studies suggest that apart from resistance factors certain intrinsic cellular factors are also crucial for bacterial survival during antibiotic stress. They enable bacteria to tolerate antibiotic stress and enhance the fitness of bacteria during the situation. Identification and characterization of those factors helps in development of novel therapeutics that disrupt bacterial resilience. In this study, we identified that the ribosome rescue pathway, *trans*-translation is essential for cellular survival up on exposure to fluoroquinolone antibiotic nalidixic acid. We found that *trans*-translation alleviates DNA damage up on antibiotic treatment by influencing transcription and translation. Cells without tmRNA and SmpB (key players of trans-translation) experience enhanced mutation rate which depict the enhanced intracellular DNA damage. These results suggest a *trans*-translation pathway to be a novel candidate for drug targeting against various fluoroquinolone resistance.

Keywords: fluoroquinolone, nalidixic acid, tmRNA, antibiotic resistance, *trans*-translation

S3-OP09

Reusable Pesticide Test Kit

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ABSTRACT

The detection of presence of pesticides, typically requires long, complex procedures involving enzymatic and thermal applications. These procedures are time-consuming and often result in delayed results, which can be problematic in real-time analysis. Moreover, the testing slip used in these processes is designed for single use, contributing to additional

waste and inefficiency. This study proposes the design of a reusable pesticide testing slip, which can be rinsed and used multiple times. The solution utilizes a chemical reaction with ninhydrin and acetone to quickly identify pesticide contamination, specifically glyphosate and monocrotophos. Upon exposure to these pesticides, the slip undergoes a colour change, turning violet in the presence of these compounds. This colour change occurs within just 10 minutes of the reaction, providing rapid results compared to traditional methods. The proposed design aims to significantly reduce testing time, minimize waste and enhance the efficiency of pesticide detection. By integrating a reusable testing slip with a simple and quick chemical reaction, this solution provides a more sustainable and faster approach to pesticide analysis, benefiting industries and ensuring more effective environmental monitoring. Additionally, the simplicity of the method allows for easy implementation, making it accessible for widespread use in various settings, from agricultural to environmental testing.
Keywords: Reusable pesticides, Kit, environmental monitoring, agricultural monitoring

S3-OP10

Formulation of Biofertilizer Using Calcium Chloride Extracted From Eggshells

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ABSTRACT:
The formulation of biofertilizers from sustainable, waste-derived materials has gained significant attention for its potential to promote environmentally friendly agricultural practices. This study investigates the use of eggshells, as a rich source of calcium chloride ($CaCl_2$), to formulate a biofertilizer and evaluate its effect on seed germination. Green gram (*Vigna radiata*) was used to test the efficacy of formulated biofertilizer. Eggshells were processed to extract calcium, which was then incorporated into a biofertilizer formulation. *In vitro* experiments involved applying the biofertilizer to seeds and assess the impact on germination, root and shoot growth, and seedling vigour. The results showed that seeds treated with eggshell-derived biofertilizer exhibited enhanced germination rates, improved root and shoot development, and increased seedling vigour. The efficacy of eggshell derived Calcium was checked in Plant Tissue Culture by supplementing the MS media with eggshell derived Calcium. The plants raised in MS media supplemented with eggshell Calcium showed better seedling emergence, enhanced root and shoot growth, and greater biomass accumulation than control plants grown in MS media. The findings suggest that the biofertilizer derived from eggshell calcium promotes better seed germination and improves plant growth in both controlled and natural environments. Molecular profiling using RAPD markers and Phytochemical analysis further confirmed that Plants retain its natural identity. The increased calcium content in the soil helps to strengthen plant cell walls, boosting overall plant health and resistance. This study highlights the potential of eggshell-derived biofertilizer as an eco-friendly alternative to chemical fertilizers, contributing to sustainable farming practices. Future research explores the potential of eggshell derived Calcium as nanocomposites and further evaluating the long-term impacts of eggshell-based nano fertilizers on soil health and crop yield.
Keywords: Eggshells, Calcium Chloride, biofertilizer, green gram (Vigna radiata)

S3-OP11

Social Impact of Genetic Abnormalities in Prenatal Testing among Maternal Women & their Partners - An Indian Perspective

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ABSTRACT

In the realm of prenatal care, amniocentesis has emerged as a crucial technique for the accurate detection of genetic abnormalities. This research study delves into the social impact of genetic abnormalities in prenatal testing within the Indian context, specifically focusing on the perspectives of expectant parents. This study contributes valuable insights to the ongoing discourse, contemplating the preference for invasive prenatal screening procedures to ensure a comprehensive and ethically sound approach to prenatal care in the unique socio-cultural landscape of India. The study utilized a cross-sectional design conducted over 12 months at a prominent tertiary care hospital in India. A total of 190 pregnant women who underwent invasive prenatal testing via amniocentesis alongside 95 partners who participated in the research were selected through convenience sampling. To ensure a representative sample, participants were recruited from diverse demographic backgrounds. Data collection was executed via a structured questionnaire, covering key aspects such as demographics, awareness of genetic testing, decision-making factors, and societal impact concerns associated with prenatal genetic testing. Pregnant women and their partners were categorized into distinct groups based on factors such as age, socio-economic status, and educational background, facilitating a comprehensive analysis of diverse perspectives.

In this study, conducted among pregnant women and their partners in India, we observed a substantial level of awareness and knowledge regarding prenatal genetic testing. Of the participants, 80% of pregnant women and 75% of partners were aware of genetic testing options. Amniotic Fluid (AF) test emerged as the most recognized method, with 70% of pregnant women and 65% of partners familiar with the procedure. Notably, a significant portion believed these tests to be highly accurate, with 45% of pregnant women and 50% of partners were certain with the precision. Moreover, our findings revealed that a majority of both pregnant women (85%) and partners (80%) expressed their intention to undergo genetic testing during pregnancy. Healthcare provider advice played a crucial role in influencing this decision, as 60% of pregnant women and 55% of partners considered it a pivotal factor.

Personal beliefs and access to comprehensive test information also played significant roles in the decision-making process.
This study highlights the need to consider both personal and societal viewpoints in the implementation of invasive prenatal screening with special emphasis to utilization of amniocentesis procedure in India. The substantial awareness and positive perception of test and its accuracy holds as promising indicators for the effective implementation of genetic testing programs in the region.

Keywords: Amniocentesis; Genetic Abnormalities, Social Impact, Expectant Parents, India.

S3-OP12

Nanotechnology-Based Approach to Combat Macrolide-Resistant *Mycoplasma pneumoniae*

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ABSTRACT

Mycoplasma pneumoniae is a leading cause of atypical pneumonia, with rising macrolide resistance (MR) posing significant treatment challenges, particularly in paediatric and immunocompromised patients. The resistance rate, exceeding 90% in Asia, necessitates novel therapeutic approaches. This study aims to evaluate the prevalence and clinical impact of MR *M. pneumoniae*, analyse molecular mechanisms of resistance and assess the efficacy of gold nanoparticle (GNP)-impregnated antibiotics as an alternative treatment. A total of 200 respiratory specimens are being analysed for MR *M. pneumoniae* using real-time PCR and sequencing of the 23S rRNA gene. Resistance patterns are being correlated with demographic factors. GNPs impregnated with antibiotics are synthesized and tested for cytotoxicity, stability, and antimicrobial efficacy both in vitro and in a rat model. Preliminary results confirm macrolide resistance (A2058G mutation). Standardized GNP formulations exhibit reduced cytotoxicity on A549 lung cells, suggesting biocompatibility. This study seeks to advance nanotechnology-based strategies to counteract antibiotic resistance, potentially offering a more effective treatment for MR *M. pneumoniae*.

Keywords: *Mycoplasma pneumoniae*, macrolide resistance, gold nanoparticles, antibiotic resistance, nanomedicine, genotoxicity.

S3-OP13

Evaluation of Actinobacteria for Plant Growth Promoting and Biocontrol Properties

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ABSTRACT

Actinobacteria, renowned for their bioactive potential, were isolated from soil samples collected in Kodaikanal (KS) and the Indian Himalayan Region (IHR) to evaluate their plant growth-promoting and biocontrol properties. A total of 24 isolates were obtained from the two samples using serial dilution and spread plate methods, followed by subculturing on streak plates. These isolates were screened for enzymatic activities, revealing positive results for amylase (18 isolates), protease (22 isolates), lipase (14 isolates), and cellulase (11 isolates). Additionally, they were assessed for plant growth-promoting traits, including ammonia production (17 isolates), phosphate solubilization (21 isolates), siderophore production (16 isolates), indole acetic acid (IAA) production (14 isolates), acetoin production (5 isolates), and nitrogen fixation (17 isolates). Among these, five isolates—KS 13, HS 2, KS 14, HS 13, and KS 23—showed consistent positive results across all assays. Further these cultures tested for paper towel and pot method for root and shoot measurement. Heavy metal tolerance tests at 1000 ppm further demonstrated robust growth for KS 13, KS 14, HS 2, and HS 13, highlighting their adaptability to extreme conditions. This study emphasizes the potential of actinobacteria, particularly KS 13 and HS 2, as effective biofertilizers and biocontrol agents. Their application could significantly contribute to sustainable agriculture by reducing reliance on chemical inputs.

Keywords: Actinobacteria, Kodaikanal Soil, Himalayan Soil, Plant Growth Promotion, Biocontrol, *Ralstonia solanacearum*

S3-OP14

Exploring Cryosphere bacteria for Plant growth promotion and Disease Control

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ABSTRACT:

This study explores the potential of cryosphere bacteria for plant growth promotion and disease control. Samples were collected from Ny-Ålesund and later procured from the Centre for Drug Discovery and Development, Sathyabama Institute of Science and Technology. A total of 100 morphologically distinct bacterial isolates were initially selected, which were narrowed down to 66 isolates using the KOH test. These isolates were screened for plant growth-promoting traits and enzymatic activities. The results revealed 12 isolates with siderophore production, 32 with nitrogen fixation, 9 with phosphate solubilization, 58 with ammonia

production, 27 with indole acetic acid (IAA) production, and 66 with acetoin production. Enzymatic activities included 10 isolates with cellulase, 38 with lipase, 33 with protease, and 31 with amylase. Based on these screenings, two bacterial isolates were selected for further biocontrol assays. These isolates exhibited a 25 mm zone of inhibition against *Ralstonia solanacearum,* the causative agent of wilt disease. In vitro plant growth promotion assays using the paper towel method demonstrated an average shoot length of 20.3 cm and root length of 2.5 cm. Further studies will include pot experiments and characterization of the bacterial cultures.

Keywords: Cryosphere Bacteria, Plant Growth Promotion, Disease Control, Plant Growth Properties, *Ralstonia solanacearum*

S3-OP15

High prevalence of Human Papillomavirus (HPV) Co-infection in cervical biopsy samples from Indian women.

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ABSTRACT:

Human Papillomavirus infection primarily transmitted through direct contact of infected person. It is the leading cause of cause of cancer and the most common cancer among women in India. Co-infection with HPV strains can influence disease progression and severity. This study aims to assess the prevalence of HPV co-infection in cervical biopsy samples from women across different regions of India. Cervical biopsy samples were collected from women. HPV detection, genotyping, Tissue Culture were performed using Polymerase chain Reaction, Genotyping and Microbiological plate culture method respectively. The prevalence of HPV positive strains and bacterial infection was analysed. A high prevalence of the HPV infection was observed with a significant proportion of cases involving in co-infection was associated with higher incidence of cervical lesions. The findings highlight the widespread occurrence of HPV co-infection among Indian women emphasizing the need for enhanced screening programs, HPV vaccination and early intervention strategies to reduce the burden of cervical cancer.

Keywords: Human papillomavirus, HPV Co-infection, Cervical cancer, Indian women, Cervical Biopsy, HPV genotypes

S3-OP16

In Vivo and *Ex Vivo* characterization of recombinant Mycobacterial strains for its vaccine potential

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ABSTRACT

Tuberculosis is one of the most prevalent diseases in developing countries. In general, many individuals get infected with *Mycobacterium tuberculosis* but fails to develop active tuberculosis. In certain cases, there will be an onset of active disease progression, after several years of infection due to various risk factors like immunosuppression. This phenomenon is generally called latent TB. Moreover, the only available vaccine *Mycobacterium bovis* Bacilli Calmette Guerin (BCG) fails to stop adult TB cases and successful in the pediatric population only. In this current study two immunogenic proteins namely HspX and Mpt51 of M.tb were cloned and overexpressed in *M.smegmatis* which are nonpathogenic and are a closer counterpart to *M. tuberculosis*. The HspX is a latency associated highly immunodominant antigen produced during the latent stage of infection. Mpt51 has been reported to be overexpressed during the re-activation of tuberculosis in HIV positive individuals. The HspX and Mpt51 antigens were cloned into Mycobacterium expression vector containing a mycobacterial promoter for developing recombinant *M. smegmatis* and *M.bovis* as a vaccine preparation. Characterization of recombinant strains were done and results depicts that recombinant strain containing HspX played a vital role in the survival of bacterium under stress conditions like acidic and limited air conditions and also changed the morphology of bacterium when compared with the strain containing Mpt51. The *M. smegmatis* strain containing HspX and HspX protein alone differentiated monocytes into macrophages efficiently than the recombinant strains containing Mpt51. Among the recombinant strains of *M. smegmatis,* the strain having *the HspX was* able to stimulate a better Th1 cytokines response than the strain containing the Mpt51.

Keywords: *Mycobacterium tuberculosis*, Th1 cytokines, Mpt51, *HspX*

S3-OP17

Development of VLP-based vaccines to generate broadly neutralizing antibodies against SARS-CoV-2 variants

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ABSTRACT:

Virus-like particles (VLPs) represent a highly safe and immunogenic vaccine platform with versatile applications in vaccine development. Recently, VLP-based vaccines have been explored for targeting SARS-CoV-2, the virus responsible for the global COVID-19 pandemic,

which has caused immense human and financial losses worldwide. As the pandemic continues, new variants of concern (VOCs) are emerging, raising concerns about the efficacy of current vaccines against these evolving strains. VLP-based vaccines, unlike traditional vaccines, do not contain viral genomes, making them replication-incompetent while retaining key characteristics of conventional vaccines. These vaccines can incorporate variations in the structural proteins of SARS-CoV-2, enabling the presentation of multiple antigens. The morphology and size of VLPs further enhance their ability to display a range of antigens, facilitating broader immune responses. A significant advantage of VLP-based vaccine technology is the simplicity of the conjugation process compared to the complex chemical methods often required for other conjugated vaccines. In our study, we developed a VLP-based vaccine for the wild-type SARS-CoV-2 and characterized it using transmission electron microscopy (TEM). The morphological features of the developed VLPs closely mimic those of the virus, offering a promising approach for vaccine development. This technology provides an opportunity to create vaccines capable of targeting emerging SARS-CoV-2 variants, potentially enhancing vaccine effectiveness across evolving strains and contributing to global efforts in pandemic control.

Keywords: Virus-like particles, SARS-CoV-2, TEM, vaccines.

S3-OP18

Exploring Nucleocapsid Protein Mutations in SARS-CoV-2 and its Variants and Their Interaction with Potential Drugs through Docking Analysis

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ABSTRACT

The severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) that caused the COVID-19 pandemic has spread rapidly to both humans and animals in nearly every nation. Since the pandemic started, an enormous amount of research has been done to acquire an extensive knowledge of the biology of viral infection. There are several challenges in understanding the molecular basis of the function of several SARS-CoV-2 proteins, which has accelerated the development of therapies and vaccines. The nucleocapsid (N) protein is one of the four structural proteins of SARS CoV-2 is a multifunctional RNA binding protein required for transcription and viral RNA replication. It serves numerous vital functions throughout the viral life cycle, making it a possible target for several antiviral drugs. This study investigates the impact of mutations in the nucleocapsid (N) protein of SARS-CoV-2 across all the variants, such as Alpha, Beta, Delta, and Omicron, on viral replication, immune evasion, and host interactions. This comprehensive analysis offers insights into how N protein mutations influence viral fitness, transmission, and immune resistance, providing valuable information for therapeutic and vaccine strategies. We have identified the potential inhibitors targeting the RNA binding domain including repurposed drugs, small molecules identified from natural

products and small peptides. This study will shed insights on the potential inhibitors for COVID-19 therapeutics.

Keywords: SARS-CoV-2, Variants, Nucleocapsid protein and Mutations

S3-OP19

Establishment of a Three-Dimensional Cervical Cancer Spheroid Model for Cytotoxicity and Drug Testing

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ABSTRACT

Traditionally, the two-dimensional (2D) cell culture has been employed for *in vitro* testing of cell viability, proliferation, cytotoxicity and drug efficacy. Over the last decade, there has been a tremendous increase in the number of research focused on establishing a suitable three-dimensional (3D) culture model as an advanced technique over the traditional method, since they are physiologically more relevant model systems. Spheroids are the most common and simplest 3D model and are best for performing cytotoxicity and drug screening assays. In this study, we have developed a 3D cervical cancer spheroid model using HeLa cell lines (Henrietta Lacks' cervical cancer cells) to study the cytotoxicity and drug efficacy of cervical cancer. The spheroids were developed using simple liquid overlay and hanging drop methods. The development of the spheroids using HeLa cell lines was optimized for different seeding densities. The spheroid characterization was performed by immunofluorescent staining for cell viability using inverted fluorescent phase contrast microscopic analysis. The cytotoxicity and drug efficacy of the anti-cancer drugs Camptothecin and Olaparib were performed using XTT and flow cytometry analysis. The spheroids formed effectively using the Hanging drop method when compared to the liquid overlay method. The viability of the spheroid was observed using co-staining of acridine orange (live cells) and Propidium iodide (Dead cells). The cytotoxicity and drug efficacy were tested in spheroids using MTT/XTT assays and apoptosis analysis in flow cytometry. This model can be employed as an efficient method for examining drug penetration and their efficacy.

Keywords: 3D Organoid model, flow cytometry, cervical cancer, MTT/XTT assays

S3-OP20

Mosquito Surveillance and Simultaneous detection of Vector-Borne Viruses using Multiplex PCR

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ABSTRACT

Notable arthropod-borne viral diseases such as Dengue, Japanese Encephalitis, Chikungunya, and Zika belong to the genus *Flavivirus* of the *Flaviviridae* family. It is extremely concerning when pathogenic viruses that are not particular disease-transmitting vectors are found in

mosquitoes. The mosquitoes and larvae were collected during field surveys from different areas of Chennai and reared under a controlled laboratory setup to identify the presence of disease-causing viruses in these mosquitoes. The mosquitoes were collected over a period of three months and classified according to the collection region, and segregated based on sex after species identification using a Nikon SMZ25 stereomicroscope. The mosquitoes were pooled in Trizol reagent and stored at -20 degrees Celsius for future analysis. For processing, the mosquitoes were homogenized in pools using BioRad Trizol reagent, and RNA was extracted using both the Trizol procedure and the Qiagen spin column procedure as per respective protocols. The extracted RNA was quantified using a Qubit 4 fluorometer, following which it was converted into complementary DNA (cDNA) using a BioRad cDNA conversion kit. Viral presence was ascertained with the help of multiplex polymerase chain reaction (PCR), which needs to be standardized in combination with the primers. This test plays a crucial role in the identification of pathogenic viruses in mosquitoes obtained from the field, thus allowing for the estimation of disease-bearing mosquito populations within a given area.

Keywords: *Flaviviridae*, stereomicroscope, Vector-Borne Viruses**,** Multiplex PCR.

S3-OP21

In Silico Design of a Multi-Epitope Vaccine Targeting PE/PPE Proteins of *Mycobacterium Tuberculosis* for Enhanced Immunogenicity

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ABSTRACT:

Mycobacterium tuberculosis (MTB), the causative agent of tuberculosis (TB), possesses a unique class of Proline-Proline-Glutamate (PPE) proteins, which play crucial roles in immune evasion and virulence. Given their antigenic nature and involvement in host-pathogen interactions, PPE proteins serve as promising targets for vaccine development. In this study, an in-silico multi-epitope vaccine was designed to target conserved and immunogenic PPE proteins of MTB using a computational immune-informatics approach. The methodology involved the selection of conserved PPE proteins from MTB reference strains using genomic databases, followed by epitope prediction of highly antigenic B-cell, CD4+ and CD8+ T-cell epitopes based on MHC binding affinity, immunogenicity, and population coverage. The selected epitopes were linked using appropriate linkers (e.g., AAY, GPGPG) and adjuvants (e.g., TLR-4 agonists) to enhance immunogenicity. The designed vaccine construct was modeled and docked with TLR-2 and TLR-4 receptors to evaluate its potential for immune activation, and molecular dynamics simulations were performed to validate its stability and interactions. Additionally, codon optimization and in-silico cloning were conducted to ensure optimal expression in *E.coli* for future experimental studies. The designed multi-epitope vaccine exhibited high immunogenic potential, capable of stimulating both cellular (Th1, Th17) and humoral immunity, while ensuring minimal allergenicity and toxicity. This computational approach provides a cost-effective and time-efficient strategy for TB vaccine development, warranting further in-vitro and in-vivo validation for clinical translation.

Keywords: *Mycobacterium tuberculosis,* Virulent PE/PPE proteins, *in-silico* cloning, Epitope-based vaccine candidates.

 ISBN: ISBN: 978-93-83409-98-3

ABSTRACTS FOR POSTER PRESENTATION

S1-PP1

Harnessing microRNAs for targeted regulation of cell proliferation in biomanufacturing

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Abstract:

Cell proliferation is fundamental to tissue growth, maintenance, and regeneration, is a cornerstone for physiological processes and industrial applications. Biomanufacturing industries spanning pharmaceuticals, vaccines, synthetic hormones, and cultivated meat rely heavily on efficient cell proliferation. However, optimizing proliferation remains challenging for reasons like density-dependent inhibition, environmental stressors, and metabolic constraints in widely used mammalian cell lines, including CHO and HEK293. Unregulated or suboptimal proliferation can compromise product quality, lead to inconsistent yields, and escalate production costs, emphasizing the need for precise regulation. Current strategies to control proliferation often lack precision and adaptability, limiting their application across diverse cell lines.

MicroRNAs (miRNAs), small non-coding RNA molecules, present a promising approach to address these challenges through their regulatory roles in gene expression. miR-101 is known to influence proliferation pathways in cancers, while miR-760, often downregulated in tumors, impacts cellular growth and metabolism. miR-145 exhibits dual roles, with its expression downregulated in various cancers, including cervical, hepatic, and breast, and upregulated in conditions like pancreatic adenocarcinoma and vascular stress.

Keywords: MicroRNAs, miR-145 exhibits, Cancers, HEK293

S1-PP2

Novel Isolation, Structural Characterization, and Therapeutic Assessment of Mannose-Targeted Chitosan Nanoparticles Encapsulating *Piperine* for Drug-Resistant Tuberculosis Therapy

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Abstract

Drug-resistant tuberculosis (TB) remains a critical global health challenge, necessitating innovative therapeutic strategies. This study focuses on the isolation of piperine (PIP) from *Piper nigrum* and the development of mannose receptor-targeted bioadhesive chitosan nanoparticles for enhanced treatment efficacy. A novel extraction method was employed to isolate PIP from black pepper fruits, and its purity was validated using advanced analytical techniques, including TLC, UV-visible spectrophotometry, SEM, EDX, FT-IR, HPLC, Raman spectroscopy, XRD, HPTLC, and NMR spectroscopy. The isolated PIP exhibited high yield and purity, comparable to standard PIP. Chitosan nanoparticles loaded with PIP were synthesized, characterized for size (133–184 nm), surface charge, polydispersity index (PDI), entrapment efficiency (81.71–90.95%), and in vitro release kinetics. Mannose functionalization was confirmed via FTIR, enhancing targeted delivery to macrophages.

Cellular uptake studies on Raw 264.7 cell lines demonstrated superior internalization of mannosylated nanoparticles compared to non-targeted counterparts. Anti-mycobacterial efficacy was evaluated against *Mycobacterium tuberculosis* H37Rv using a luciferase reporter phage (LRP) assay. PIP-loaded nanoparticles exhibited significantly enhanced activity, with non-targeted and targeted formulations achieving 93% and 98% inhibition, respectively, compared to only 2% with free PIP. This marked improvement is attributed to the bioadhesive properties and targeted delivery facilitated by chitosan nanoparticles. In conclusion, this study presents a promising approach for combating drug-resistant TB by leveraging the synergistic effects of PIP and chitosan-based nanocarriers. The developed formulation demonstrates enhanced drug delivery, cellular uptake, and anti-mycobacterial activity, offering a potential therapeutic advancement for TB treatment.

Keywords: *P. nigrum, Piperine (PIP); Chitosan, Mannose, Antimicrobial Activity, Mycobacterium* Tuberculosis

S1-PP3

Codon Optimization for Enhanced Expression of HIV-1 Transcripts in CRISPR-Cas13-Based Therapeutics

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Abstract:

Clustered Regularly Inter-Spaced Repeats (CRISPR)-cas13 shows a promising growth that specifically edit viral RNAs. Nevertheless, antiviral therapy is delayed in response to infection because of higher replication rate. Human immunodeficiency virus (HIV-1) is a virus that attacks the body's immune system which leads to Acquired Immunodeficiency Syndrome (AIDS) if left untreated and remained as a significant problem in humans. HIV-1 genome made up of ss-RNA, with 9750bp. Based on evidence from previous studies, 5 mRNA transcripts playing critical roles to enhance translational efficiency within host cells. This study attempted to optimize the transcripts for possible improvement in CRISPR-Cas13 system that will lead to effective guide RNA synthesis to remove mutation rate in human cells. By utilizing the GenScript algorithm, we optimized the transcript sequences and achieved an average codon adaptation index (CAI) of 0.93 and increased GC content, thereby enhancing expression efficiency in human cells while preserving the native structure and function of the mRNA transcripts. Our findings suggest that optimized mRNA transcripts will enhance CRISPR-Cas13 efficiency in targeting HIV-1 RNA. This breakthrough facilitates the development of HIV-1 therapies and advances gene-editing technologies against viral infections through optimized codon and RNA-targeting protocols.

Keywords: CRISPR, HIV-1, Codon optimization, RNA virus

S1-PP4

Screening of marine animal toxin-derived peptides and its biological effects for the suppression of inflammation in LPS-induced fibroblast cells

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Abstract

Marine animal toxins have emerged as a promising source of bioactive peptides with therapeutic potential. Although, currently only limited venom-derived peptides are used having therapeutic approaches in pain management, cardiovascular diseases, and other conditions. This study focuses on screening toxin-derived peptides from marine animals for their ability to suppress inflammation in lipopolysaccharide (LPS)-induced fibroblast cells. The marine animal toxin database was used for screening and peptides were studied for pharmacokinetic and physicochemical properties. A total of four toxins generated 342 peptides consisting of dipeptide to 23 residue peptides. Through machine learning based bioactivity screening, 30 peptides were selected and the binding affinity for the same was checked against various inflammatory receptors such as NLRP3, xanthine oxidoreductase, and interleukin 1 beta. The results revealed that the 4 peptides showed improved binding ability compared to inhibitory control. Further, the viability assay on fibroblast cells showed non-toxicity of the peptide till 125 µM. Further, the peptide treatment reduced the LPS-induced inflammation by suppressing nitrite levels (14.05±1.02 µM) and reactive oxygen species (23.51±2.58%). Further, the protein expression studies revealed suppressing of pP65 and NLRP3 signalling. Computational approach can be used to screen toxins for the generation of novel peptide sequences with unique biological activities.

Keywords: Venom, Peptides, *in silico* studies, inflammation, fibroblasts, cell culture, NLRP3

S1-PP5

Effects of a marine-derived oligopeptide on suppression of inflammation in an inflammatory model

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Abstract

Bioactive peptides have been attracting attention because of their potential as therapeutic agents in the treatment of several inflammatory illnesses and as a substitute for commercially available non-steroidal therapies that have adverse effects. Bioactive peptides have shown suppression of inflammation through the inhibition of key inflammatory signaling molecules like COX-2, INOS, and MMP9 as well as a decrease in oxidative stress. This project aims to explore the potential anti-inflammatory properties of a marine-derived bioactive peptide through an integrated *in silico* and *in vitro* approach. Our preliminary *in silico* molecular docking simulations, for the peptide of interest, demonstrated a strong binding affinity to the inhibitory sites of key inflammatory mediators, including COX-2 (- 6.7 kcal/mol),

iNOS (-6.6 kcal/mol), and MMP9 (-7.1 kcal/mol) receptors. These mediators are crucial signaling molecules that are involved in the controlling of oxidative stress and inflammatory pathways. Further, the peptide was studied for the cytotoxic effects on L929 fibroblast cells. To check the peptide's inflammation-suppressing activity and anti-oxidant effects, fibroblast cells were induced with lipopolysaccharide, and treated with peptide concentrations ranging from (25-150 µM). The peptide could potentially be used as an alternative to commercially available anti-inflammatory drugs having various adverse effects.

Keywords: Marine animals, bioactive peptide, Molecular docking, Inflammation, Cytokines

S1-PP6

Exploring LNAA-Enriched Protein as a Potential PKU Supplement: Expression, Cytotoxicity in Mammalian Cells, and Insights from *Pah enu2* Mice

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Abstract

Phenylketonuria (PKU) is a genetic metabolic disorder caused by mutations in the phenylalanine hydroxylase (PAH) gene, resulting in elevated phenylalanine (Phe) levels in the brain. A key therapeutic challenge is the lack of natural proteins enriched in large neutral amino acids (LNAA) and devoid of Phe. Previously, we designed a 100-amino-acid peptide rich in LNAAs using in silico methods and expressed it in *Pichia pastoris* but the yield was low. In this study, we performed codon optimization exclusively for *P. pastoris*, resulting in successful cloning and expression of the LNAA66c gene. Colony PCR confirmed the successful transformation of the gene into *P. pastoris*. Protein expression was assessed in four different media: BMMY, MMY, MM, and BMM. Optimal expression occurred in BMMY medium at pH 6 and 30°C. SDS-PAGE and western blot analyses confirmed the successful expression of the recombinant protein. Using His-tag nickel affinity chromatography, we achieved a protein yield of 174.59 mg/L. In vitro, digestibility was evaluated using simulated gastric and intestinal fluids, and cytotoxicity was assessed in RAW 264.7 macrophage-like cells showed favorable results. Additionally, the purified protein was incorporated into the diet of *Pah enu2* PKU mice, revealing significant behavioral improvements and a reduction in blood phenylalanine level after four weeks of treatment. These findings highlight the potential of LNAA-enriched recombinant proteins as a therapeutic strategy for PKU.

Keywords: Phenylketonuria, SDS-PAGE, *Pah enu2* Mice, RAW 264.7

S1-PP7

Anticancer Potential of *Tinospora cordifolia* (Wild) Miers by In Silico ADMET Analysis

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ABSTRACT

A total of over 180 unique kinds of cancer, and each one requires a specific method to diagnosis and treatment. Most prevalent of these are colon, lung, and breast cancers, together pose a grave risk to global wellness. Despite the advances in cancer treatment, it

has been shown that natural products can be useful in the search for safer and more effective treatment options. Since several anticancer medications, such as vincristine and paclitaxel are derived from plants, medicinal plants are advantageous research subjects for cancer. The purpose of the following study was to evaluate the anticancer potential of Tinospora cordifolia (Wild) Miers, a plant used in traditional medicine to strengthen the immune system and to treat certain disorders. To forecast its pharmacokinetic characteristics, an ADME analysis was performed utilising the SwissADME server. The findings support the prospect of using Tinospora cordifolia as a cancer treatment by demonstrating that its phytochemicals have potential anticancer effects. Its effectiveness and the mechanisms of action in the therapy of cancer, however, require more research both in vitro and in vivo.
Keywords: Cancers, ADME analysis, Tinospora cordifolia, Traditional medicine.

S1-PP8

PROTACs in Neurodegeneration: Unlocking Therapeutic Potential in Protein Degradation

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Abstract

In order to facilitate the preservation of cellular homeostasis, protein degradation mechanisms are essential, as they regulate the quality and turnover of proteins. Disruptions in these processes are linked to the accumulation of misfolded and aggregated proteins, which is a characteristic of neurodegenerative disorders such as Parkinson's, Alzheimer's, and Huntington's diseases. Neurodegenerative diseases (NDs) are distinguished by the progressive degeneration of neurones, which has an impact on movement and cognitive functioning. The buildup of proteins in the brain and other peripheral organs that have altered their physicochemical properties is the cause of neurodegenerative disorders, which are characterized by a progressive loss of neurons. The most often occurring proteins in the pathophysiology of neurodegenerative illnesses include tau, α-synuclein, prion protein, and amyloid-β. Traditional therapy approaches have not been very successful in targeting these aberrant proteins because they are unable to eradicate the proteins that cause sickness specifically. A novel method for eliminating harmful proteins from the ubiquitin-proteasome system (UPS) is provided by proteolysis-targeting chimaeras (PROTACs), which have become a potential tool for targeted protein degradation. PROTACs aid in the ubiquitination and removal of the disease-relevant protein by binding to the target protein with an E3 ligase.
Keywords: PROTACs, Protein degradation, Neurodegenerative disorders

S1-PP9

Analysis of Protein-Ligand Interaction: Pyrx Docking of G-protein coupled receptor 1 protein causing ovarian cancer

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Abstract

Disorders affecting receptors linked to G-proteins (GPCRs), that are crucial for cell signaling, are linked associated ovarian cancer. The creation of drugs is aided by molecular docking studies, which show that potential ligands bond to proteins of interest. In this research, PyRx, a free virtual screening software, is employed to screen the docking of chosen ligands with GPCR1, a protein implicated in ovarian cancer development. The docking process involves energy minimization, ligand preparation, and receptor optimization to identify potential binding affinities. PyRx employs the AutoDock Vina algorithm to predict binding free energies, which reveal information on ligand-receptor interaction. The results indicate that some ligands exhibit strong binding affinity with GPCR1, which renders them potential therapeutic agents. Docking scores, hydrogen bonding interaction, and molecular conformations are compared to identify the most promising ligand.This research demonstrates the utility of PyRx in computational drug discovery, offering a cost-effective approach for screening potential inhibitors of GPCR1. Results can aid in the development of adapted therapies for ovarian cancer while offering insight into GPCR-mediated carcinogenesis pathways. The beneficial effects of the discovered drugs must be verified through empirical validation, involving both in vitro and in vivo experment.

Keyword: G-proteins, AutoDock Vina, PyRx, ovarian cancer

S1-PP10

Bioactive Components Loaded Biopolymeric Materials for Managing Dental Caries

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Abstract

Dental caries is a disease which results in demineralization of teeth enamel. Managing dental caries requires materials that not only restores the teeth structure but also exhibit anti-microbial and tissue regenerating properties. In this study, multiple components with their unique properties were combined together in a nano-scale as a composite material. The biopolymers selected are known for their anti-microbial properties and also helps in strong adhesion and binding of the materials to the enamel surface. They also penetrate the biofilm and helps in disruption of bacterial structure. These components tend to form a gel-like matrix when crosslinked with a crosslinker that supports both structural integrity and functional activity. The incorporation of bioactive components has potent anti-oxidant activity and further, inhibits bacterial growth, plaque formation, and tends to tissue regeneration. These materials are synthesized, characterized, and evaluated for their antibacterial properties against common oral pathogens. These multifunctional

nanocomposite materials offer a promising approach in dental caries prevention and treatment, combining restorative and antimicrobial properties as a single formulation.
Keywords: anti-microbial, biopolymers, Bioactive Components**,** Dental caries.

S1-PP11

Structure-Based Docking and Molecular Dynamics Simulation of Small Molecules Targeting DHCR7 to Treat Smith-Lemli-Opitz Syndrome

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Abstract:
Smith-Lemli-Opitz Syndrome (SLOS) is a rare autosomal recessive disorder caused by mutations in the DHCR7 gene, leading to defective 7-dehydrocholesterol reductase (DHCR7) and impaired cholesterol biosynthesis. This study aims to identify small-molecule stabilizers or activators that enhance DHCR7 function using structure-based molecular docking and molecular dynamics (MD) simulations. The 3D structure of DHCR7 will be obtained through homology modeling. Potential ligands, including cholesterol analogs and drug-like molecules, will be screened from databases (ZINC, PubChem). The Auto Dock and PyRx software will be used for molecular docking to identify high-affinity binders. The top-ranked complexes will undergo MD simulations in GROMACS to evaluate stability, conformational changes, and interaction dynamics over time. This computational approach could provide novel insights into DHCR7-targeted drug design, offering potential therapeutic interventions for SLOS.
Keywords: Smith-Lemli-Opitz Syndrome, DHCR7, Molecular Docking, Molecular Dynamics, Drug Discovery, Cholesterol Biosynthesis

S1-PP12

Investigation of computational method for the treatment of Alzheimer's by targeting β-amyloid through comparative docking approach

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ABSTRACT:
The objectives of managing Alzheimer's disease are to enhance quality of life, decrease the rate at which the disease advances, and make improvements. The Nucleosome-remodelling factor subunit's amino acid sequence was obtained from the UniProt database, while the protein's three-dimensional structure was obtained from the Protein Data Bank. We conducted protein-ligand interactions and molecular docking using free software and databases. ADMET analysis was performed to assess the absorption, distribution, metabolism, excretion, and toxicity of the ligands, confirming their potential as safe and effective therapeutic candidates. Initially, we modeled the structure of the protein to identify appropriate warhead lead ligands for the Nucleosome-remodelling factor subunit protein. This structure is monomeric, consisting of a single chain, and two distinct receptor chains bind to distinct regions of the protein. Results of docking and screening against the

Nucleosome-remodelling factor subunit protein indicate which interacting lead ligands are the best. The Chimera and Pymol software showed good agreement with the projected structure. The recognized ligand molecules exhibit a strong interaction with the protein Nucleosome-remodelling factor subunit. Our results imply that the ligand molecules can bind to and block the Nucleosome-remodelling factor subunit protein, hence preventing the spread of infected cells.

Keywords: Uniprot, PDB, Chembl, PubChem, PyRx, Pymol.

S1-PP13

Deciphering HTT Protein Mutations for Structural and Functional Insights into Huntington's disease

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Abstract:

Huntington's disease is an autosomal-dominant neurodegenerative disorder that is caused by expansions in the CAG repeat within the HTT gene, leading to the expression of the mutant Huntington (mHTT) protein. Ultimately, it causes folding defects, abnormal aggregation, and thus cytotoxicity within the cellular environment interfering with such important biological processes as transcription, protein degradation, and mitochondrial activity. It would be the change of mHTT at both the structural and functional levels and, therefore opens the comprehension of Huntington's disease (HD) pathogenesis and speeds the development of targeted therapy. The paper explores the conformational changes brought about by the polyglutamine expansion based on integration between computational modelling, biophysical analysis, and experimental validation. It detailed the mechanism of misfolding and aggregation in the context of their involvement in the disruption of cellular homeostasis. We also defined the contribution of post-translational modifications and protein-protein interactions toward the modulation of mHTT toxicity. Our results uncover structural bases for HTT dysfunction, which might lead to therapeutic approaches that could slow the disease's progression. It advanced our knowledge of HD pathology by combining the structural and functional analyses, bringing evidence for developing new therapeutic interventions. This thereby opened an avenue for future therapies aimed at reinstituting HTT function as well as halting neurodegeneration in patients with Huntington's disease (HD).

S1-PP14

Computational Analysis of Structural, Functional, and Evolutionary Variations in Human Peroxiredoxin Variants Using Molecular Modelling and Docking Approaches

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Abstract

Peroxiredoxins (Prx) are multifunctional moonlighting proteins involved in redox regulation, stress response, and signalling pathways. In this study, ten human Prx variants were analyzed computationally to understand their structural, functional, and evolutionary differences. The 3D structures of all variants were predicted, and structural deviations were evaluated through comparative analysis. Hydrophobicity assessments provided insights into solubility and stability variations. Potential ligand-binding pockets were identified to explore functional diversity across the variants. Molecular docking was performed to assess binding affinities with key ligands, highlighting differences in interaction strength and specificity. Additionally, evolutionary relationships were determined through phylogenetic analysis, revealing divergence among variants based on sequence conservation. The study offers a comprehensive investigation of how structural variations influence the functional roles of peroxiredoxins in different biological contexts. By integrating structural modelling, binding site analysis, docking, and evolutionary comparisons, this research provides deeper insights into the molecular mechanisms underlying functional divergence. The findings contribute to understanding the moonlighting nature of peroxiredoxins and their role in oxidative stress regulation, with potential implications in drug targeting and protein engineering. The results emphasize the importance of computational approaches in bridging structural bioinformatics with functional genomics to elucidate protein function and interaction mechanisms. Such analyses can further aid in designing therapeutic strategies targeting specific peroxiredoxin variants implicated in disease mechanisms.

Keywords: Peroxiredoxins, moonlighting proteins, 3D structure prediction, evolutionary relationships, drug targeting

S1-PP15

Unraveling the Secondary Metabolite Arsenal of *Bdellovibrio*: Insights from Comparative BGC Analysis

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Abstract:

Predatory bacteria, including Bdellovibrio species, exhibit unique metabolic capabilities that contribute to their ecological role as microbial predators. By producing a set of antibacterial compounds, they can kill other bacteria and acquire nutrition. Biosynthetic gene clusters (BGCs) play a crucial role in producing secondary metabolites that may influence predation, interspecies interactions, and survival strategies. In this study, we systematically analyzed the BGCs of different Bdellovibrio species from NCBI and compared them with other predatory bacteria. Using genome mining tools, we identified and characterized the diversity,

composition, and potential functional roles of these BGCs. Comparative analysis revealed distinct and shared biosynthetic pathways across different predatory taxa, highlighting potential evolutionary adaptations. Notably, Bdellovibrio species exhibited a lower abundance of BGCs compared to other predatory bacteria, with a preference for clusters encoding potential signalling molecules rather than classical antimicrobial compounds. These findings provide insights into the metabolic potential of predatory bacteria and their ecological interactions, paving the way for further exploration of novel bioactive compounds.
Keywords: BGCs, antibacterial activity, predatory bacteria, novel metabolites, Bdellovibrio species

S1-PP16

Potential Therapeutic Role of Phenolic Antioxidants in Targeting Alpha-Synuclein Aggregation in Neurodegeneration with Brain Iron Accumulation

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Abstract
Neurodegenerative diseases often share common molecular mechanisms, particularly protein misfolding and aggregation, leading to neuronal dysfunction and progressive cognitive and motor impairments. Dementia with Lewy Bodies (DLB) and Neurodegeneration with Brain Iron Accumulation (NBIA) are two such disorders associated with alpha-synuclein (P37840) dysfunction. In this study, the structural basis of alpha-synuclein aggregation in DLB was initially examined, followed by a sequence similarity analysis to identify homologous protein structures linked to NBIA. Given the established role of oxidative stress and iron dysregulation in NBIA, natural phenolic antioxidants from green tea—which have shown neuroprotective effects against DLB—were investigated as potential therapeutic agents. The binding interactions between these antioxidants and alpha-synuclein structures were assessed, revealing significant inhibitory potential against protein aggregation. Furthermore, reverse docking demonstrated that these phenolic compounds could also interact with NBIA-associated alpha-synuclein, suggesting their ability to mitigate neurodegeneration beyond DLB. The dual therapeutic action of these antioxidants—reducing oxidative stress, preventing fibril formation, and potentially chelating iron—positions them as promising candidates for targeting multiple neurodegenerative pathways. Given their natural origin and existing evidence of neuroprotection, these compounds could be repurposed as lead molecules for drug development in NBIA. The findings highlight the importance of identifying common pathological targets across neurodegenerative diseases and leveraging bioactive natural compounds for multi-target therapy. Future experimental studies and clinical trials will be essential to validate these computational insights and establish phenolic antioxidants as a viable therapeutic approach for DLB and NBIA.
Keywords: Alpha-synuclein, Dementia with Lewy Bodies (DLB), Neurodegeneration with Brain Iron Accumulation (NBIA), Phenolic antioxidants, Reverse docking

S1-PP17

Molecular Docking Study of Curcumin Interaction with Collagen and Keratin: Insights into Anti-Aging Protein-Ligand Binding Using Docking and STRING Database Analysis

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Abstract:

Aging is an inevitable biological process characterized by a decline in cellular function, skin elasticity, and structural integrity. However, targeted interventions can mitigate its effects. This study explores curcumin as a therapeutic agent combined with collagen and keratin to enhance skin and hair health. Curcumin, a polyphenol from *Curcuma longa*, has gained significant attention for its antioxidant, anti-inflammatory, anti-cancer, and anti-aging properties. It has been shown to prolong lifespan in model organisms such as *C. elegans* and *D. melanogaster* by enhancing superoxide dismutase (SOD) activity and reducing malondialdehyde (MDA) and lipofuscin levels, which contribute to cellular longevity. Curcumin also plays a crucial role in reducing oxidative stress, supporting collagen production, and preventing skin damage from UV exposure and environmental pollutants.

Collagen supplementation enhances skin elasticity, hydration, and structure, while keratin supports skin barrier function, strengthens hair, and protects against environmental stressors. Hydrolysed keratin further boosts collagen production and moisture retention, reinforcing anti-aging benefits.

The synergistic effects of curcumin, collagen, and keratin offer promising applications in cosmeceuticals and nutraceuticals for healthy aging. Future studies will focus on in vivo validation and clinical applications.

Keywords: Curcumin, Collagen, Keratin, Anti-Aging, Skin Elasticity, Oxidative Stress, string database

S1-PP18

Development of Anti-Freezing Peptide-Enhanced Biofertilizers for Improved Crop Yields and Frost Protection

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Abstract:

Frost damage is a significant constraint to crop yields worldwide, resulting in substantial economic losses. While in the other hand AFP's has thermal hysteresis phenomena. AFPs are naturally occurring proteins that inhibit ice crystal growth and protect plants from frost damage. To address this challenge, we propose the development of biofertilizers enhanced with anti-freezing proteins (AFPs). Our project aims to clone and express AFPs in biofertilizer microorganisms, which will be formulated into a biofertilizer product. We will evaluate the efficacy of the AFP-enhanced biofertilizers in promoting plant growth and protecting plants from frost damage in greenhouse and field trials. Our results will contribute to the development of novel, environmentally friendly biofertilizers that improve crop yields and reduce the economic impacts of frost damage. This review presents the potential applications of AFPs from different sources and types. AFPs can be found in diverse sources such as fish, yeast, plants, bacteria, and insects. AFPs into biofertilizers may not only protect plants from frost damage but also enhance nutrient uptake and microbial activity in cold climates. This paper explores the integration.

S1-PP19

Unraveling Cardiovascular Disease in Systemic Lupus Erythematosus (SLE) : Exploring the Influence of Autoantibodies and Immunosuppressants

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Abstract:

To determine the prevalence of cardiovascular disease (CVD) in a cohort of patients with Systemic Lupus Erythematosus (SLE). Stratify SLE patients with CVD based on clinical manifestations, autoantibody profiles, and the use of immunosuppressants and anticoagulants. A retrospective analysis of 200 SLE patients from the Lupus registry was performed in the Department of Medicine, Rheumatology, Cardiology, and Nephrology in KMC, Manipal from January 2019 to November 2024. Thirty-three SLE patients with CVD were evaluated with clinical manifestations, diagnosis, and treatment with immunosuppressants, steroids, and anticoagulants. Out of 33 (16.5%) patients with CVD, 98% were female and 2% were male. The mean patient age was 37.21 years. Libman-Sacks endocarditis and myocarditis were common in our cohort. Autoantibody profiling revealed high dsDNA positivity (63.64%) along with nucleosomes (36.36%), anti-SM (30.30%), lupus anticoagulant (15.15%), and anticardiolipin (18.18%). HCQ (84%) was the drug of choice in the majority of the patients in comparison to MMF (30%) 21%.

Keywords: Systemic Lupus Erythematosus; Cardiovascular Diseases;

S1-PP20

Folate-Decorated, Albumin-Conjugated BNNTs for Targeted Paclitaxel Delivery in A549 Lung Cancer: Antimicrobial Activity, Hemocompatibility, and Cytotoxicity Evaluation

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Abstract

In the rapidly evolving field of biopharmaceuticals, the integration of advanced nanomaterials into drug delivery systems has revolutionized the development and administration of therapeutics. Boron nitride nanotubes (BNNTs) and albumin nanoparticles are two promising nanomaterials being explored for their potential to enhance targeted drug delivery, biocompatibility, stability, and effectiveness as drug carriers. In this study, albumin nanoparticles were synthesized using the desolvation method from BSA and conjugated with amino-functionalized BNNTs to enhance drug encapsulation, solubility, protecting from premature degradation, and circulation time. Folic acid, a targeting ligand, was grafted onto BNNTs to enable selective binding to folate receptors, overexpressed in cancer cells, improving target specificity. Characterization using FE-SEM, XRD, FT-IR, and UV spectroscopy confirmed successful conjugation and paclitaxel encapsulation. On comparison with pure compounds, Drug entrapment and loading efficiencies increased to 97.71 ± 0.4% and 49.16 ± 0.9%, respectively. Drug release kinetics showed 72% release over 78 hours at pH 6.5 and 27% at pH 7.0. Folate conjugation efficiency was quantified to be 8.38 µg/mg of the total nanocomposites. Hemolysis and coagulation assay revealed high

compatibility and safety on RBC cells and in-vitro cytotoxicity studies against A549 lung cancer cells showed an IC50 value of 44 µg/mL, proving the potentiality of the nanocomposites as a targeted drug delivery system.

Keywords: Target Drug delivery, Boron nitride nanotube, biological assay, Albumin nanoparticles, in-*vitro* studies, cytotoxicity analysis.

S1-PP21

Investigating The Role Of m6A Reader - YTHDC1 In Renal Cellular Pathophysiology

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Abstract:

Diabetes, a chronic metabolic disorder that has a higher impact on individuals irrespective of age, has been an important global concern for decades. Diabetic patients have been perturbed by consequences such as hyperglycemia, nephropathy, skin diseases, neuropathy, arterial diseases, retinopathy and other collateral effects. Amongst the various epigenetic causes, it is evident that the N6-methyladenosine (m6A) modifications are closely intertwined with the emergence and prognosis of diabetes. YTHDC1, a prominent m6A reader, localized in the nucleus has been recognized distinctly for its role in modulating the outcome of gene expression. Recent research focuses on the translational intervention of YTHDC1 in modulating the cellular microenvironment of various complications associated with diabetes, like retinopathy, and foot diseases. Our current investigation addresses the role of YTHDC1 and its mechanism of contributing to pathophysiology in the hyperglycemic conditions. We use mouse mesonephric cells, M15 where knockdown of YTHDC1 using CRISPR-Cas9 gene editing technology was created. This genome edited cell lines and their cellular dynamics is being investigated using cellular, molecular and biochemical assays, which will be presented.

Keywords: Diabetic nephropathy, YTHDC1, m6A modifications, epigenetics, CRISPR-Cas9

S1-PP22

Facile and Bioinspired Gelatin Hydrogel for Enhanced Antimicrobial and Wound Healing Applications

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Abstract

Wound healing is a complex and dynamic biological process involving several biological conditions in promoting and accelerating the process. It also remains a significant clinical challenge, with current treatments often plagued by slow healing rates, infection, and scarring. Traditional wound healing processes using bandage, gauze and ointment often fall short in providing necessary biological conditions for healing. In this case hydrogel emerges as a promising alternative for wound healing. Hydrogels are a network of polymer chain that can be made up of synthetic or natural materials. They are capable of holding large amount of water. Due to their unique properties such as water retention, flexibility and bio compatibility they have wide application in medical field. Polymeric hydrogels have garnered

significant attention in the field of biomedical applications due to their unique ability to absorb large amounts of water while maintaining structural integrity. These hydrophilic polymer networks closely mimic the natural extracellular matrix, providing a moist and protective environment conducive to wound healing.The current investigation discusses the preparation and characterization of gelatin–based hydrogels for better wound healing properties. To address the current limitations in wound healing, our study focusses on developing herb infused and metal oxide nanoparticles incorporated gelatin hydrogel that can synergistically combine the benefits of gelatin's biocompatibility, biological properties of herbal extract and nanoparticles' enhanced therapeutic delivery. Our hydrogel system is being studied on the combined effect of incorporation of biosynthesized Copper oxide nanoparticles and zinc oxide nanoparticles within a gelatin hydrogel matrix. The resulting biomaterial exhibits improved mechanical properties, enhanced antimicrobial activity, and sustained release of phytochemicals. In vitro studies demonstrated that the nanoparticle incorporated hydrogel promotes cellular proliferation, migration, and differentiation. The research work involves in-vivo cell line experiments for demonstrating the wound model showing accelerated wound closure, reduced bacterial load, and improved tissue regeneration. Our findings would play a significance role in providing a promising biomaterial for wound healing applications offering a novel approach to enhance tissue repair and regeneration.

Keywords: Polymer; Hydrogel; Antimicrobial; Nanoparticles; Wound healing, Herbal extract.

S2-PP1

Enzymatic extraction and purification of marine fish-derived bioactive peptide and its Anti-inflammatory effects through suppression of cytokines

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Abstract

Aquatic organisms and plants produce a vast array of bioactive chemicals. These bioactive compounds possess antibacterial, anti-inflammatory, antioxidant, and immunomodulatory activities. This study examines the anti-inflammatory properties of a bioactive peptide derived from marine fish hydrolysate, which was enzymatically processed using alcalase, trypsin, and papain, achieving over 70% hydrolysate at the 12th hour, with the highest degree of hydrolysis attained through alcalase treatment. High-performance liquid chromatography examination revealed a significant presence of amino acids. The hydrolysate's functional qualities were assessed, demonstrating significant suppression of protein denaturation between 15-60% and stabilisation of human red blood cell membranes between 20-70%. Furthermore, among the fractions derived from ultrafiltration, the 10-3 kDa fraction exhibited superior anti-inflammatory efficacy, which was then refined using gel filtration chromatography. A hexapeptide with the most anti-inflammatory qualities was obtained by subjecting the purified active peaks to LC-MS/MS. *In vitro* cytotoxicity studies conducted on LPS-stimulated L929 fibroblasts shown negligible toxicity around 200 µM concentration, characterised by reduced levels of nitric oxide and reactive oxygen species, alongside the downregulation of COX-2 and iNOS production through the modulation of inflammation,

particularly influencing MMP9 expression. The peptide's bioactivity encourages future *in vivo* research and demonstrates its potential as a natural anti-inflammatory agent.
Keywords: Enzymes, Hydrolysates, Peptides, Anti-inflammation, *in vitro* studies, Western blot, Molecular docking

S2-PP2

Systematic Approach to Biofilm Formation and Its Inhibition On Menstrual Cups Using Phyto-Extracts

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Abstract:
Menstrual cups are reusable menstrual hygiene products that offer environmental and economic benefits. However, their prolonged use and inconsistent cleaning can lead to microbial biofilm formation on their surfaces, posing potential health risks. Biofilms, composed of bacteria embedded in a self-produced protective layer, are resistant to conventional cleaning methods and antimicrobial agents. Pathogens such as *Staphylococcus aureus, Escherichia coli, Pseudomonas aeruginosa, and Proteus mirabilis* can colonize menstrual cups, leading to infections and, in rare cases, toxic shock syndrome (TSS). While synthetic antimicrobial agents are available, they often cause irritation, allergic reactions, and environmental harm. This study aims to explore plant-based extracts as natural inhibitors of biofilm formation on menstrual cups. Medicinal plants like neem (*Azadirachta indica*), and papaya (*Carica papaya* are known for their antimicrobial and anti-biofilm properties. The research involves isolating plant extracts, testing their antibacterial activity, and evaluating their effectiveness in preventing or reducing biofilm formation. The methodology includes biofilm formation studies on menstrual cup materials, screening of plant extracts for antibacterial properties, and quantitative biofilm inhibition assays using techniques such as crystal violet staining. The findings will provide insights into the potential of plant-based solutions as safe and eco-friendly alternatives to synthetic chemicals. This research contributes to sustainable menstrual hygiene practices by promoting safer, natural antimicrobial strategies, ultimately reducing the health risks associated with menstrual cup biofilm.
Key words: Menstrual cup, Biofilm formation, Microbial contamination, Natural anti-biofilm agents, Eco-friendly hygiene

S2 – PP3

Synthesis, Spectral Characterization and Antibacterial Activity of some benzil Derivatives - In Silico Molecular Docking and Admet Studies

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Abstract
This study investigates the synthesis of 2-oxo-1,2-diphenylethylidene thiosemicarbazide and 2,4-dinitrophenyl hydrazone-1,2-dinitrophenylethanone from benzil. The synthesized compounds are characterized by IR, 1H NMR and 13C NMR spectroscopy. The synthesized compounds were investigated for their potential anti-inflammatory and antibacterial activities. Molecular docking studies were performed using AutoDock software against an anti-inflammatory protein (PDB: 2H24) and an antibacterial protein (PDB: 1JIJ). In-vitro biological activity of these compounds is evaluated against Gram-positive and Gram–negative bacterial strains. *In silico* studies, including drug-likeness prediction using SwissADME and toxicity assessment using the ProTox-3 application were also conducted. These investigations provide insights into the synthesis and characterization of the newly synthesized benzil derivatives and their potential as therapeutic agents.
Keywords: SwissADME, *In silico*, benzyl, therapeutic

S2-PP4

Isolation of Soil-Borne Fungi as Biological Agents and Their Inhibitory Study against Phytophthora Species

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Abstract:
Phytophthora species are among the most devastating plant pathogens, responsible for diseases such as root rot, late blight, and dieback, leading to significant agricultural and economic losses. While chemical fungicides are widely used for disease management, they pose challenges such as environmental contamination, health risks, and the emergence of resistant pathogen strains. As a sustainable alternative, biological control using soil-borne fungi offers a promising eco-friendly solution. Several fungal species exhibit antagonistic activity against *Phytophthora* through mechanisms such as nutrient competition, antimicrobial metabolite production, and mycoparasitism.
This study focuses on the isolation and identification of potential fungal biocontrol agents from various agricultural fields. Soil samples were collected from the rhizosphere of sugarcane, orange, tomato, and brinjal plants. Fungal isolates were obtained through traditional culturing techniques, followed by morphological and microscopical characterization. The identified fungi include *Trichoderma* spp., *Fusarium* spp., and several *Aspergillus* species, all of which are known for their potential antagonistic properties. A systematic evaluation of these fungal isolates provides insights into their diversity and ecological significance. The findings reinforce the role of native soil fungi in integrated disease management and pave the way for their application as sustainable biocontrol agents against *Phytophthora*-induced plant diseases.

Key words: Phytophthora spp., Soil-borne fungi, Biocontrol agents, Dual culture assay, *Trichoderma* spp., *Fusarium* spp., *Aspergillus* spp.

S2-PP5

Human Genome Resources Updated Database -A Future Key to Aging Research

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Abstract

As people age, their metabolic stability gradually deteriorates, impairing their activities and raising their risk of dying. The current work aims to retrieve the genes linked to human aging from the GenAge database and use literature mining to investigate the top gene. Genes associated with lifespan and/or aging in biological models (yeast, mice, flies, worms, etc.) and genes related to aging in humans compose GenAge. Thus, this database was used, and the aging-related genes were acquired from the GenAge section's human datasets option. DAVID was used to extract the KEGG pathways for the aging-related genes. From the GenAge database, 307 genes that relate to aging were extracted together with their gene symbol, name, Entrez gene ID, UniProt ID, and the type of model organism. Nine pathways related to longevity and neurodegenerative illnesses were terminally extracted from the 135 pathways identified in the KEGG data. This identification of aging genes to be used for the researchers and scientists to build a network of protein-to-protein interactions and KEGG annotation pathways will be examined to determine the comorbidity disorders linked to aging neurodegenerative diseases.

Keywords: Genes, Aging, KEGG, Uniprot, DAVID, GenAge

S2-PP6

Unraveling Novel Lead Compounds Against Autism Susceptibility Gene 2 (AUTS2) Using Comparative Docking of Various Ligands

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Aim: To identify potential lead compounds targeting Autism Susceptibility Gene 2 (AUTS2) protein using comparative molecular docking for therapeutic intervention in Autism Spectrum Disorder (ASD). **Materials and Methods:** AUTS2 structure was retrieved and optimized, while bioactive ligands were selected from databases (PubChem, ZINC).AutoDock Vina for ligand docking.and predicted using the swiss ADME and Lipinski rule. stability assesment using GROMACS (MOLECULAR DYNAMICS) **Results:** Several ligands shows high binding affinity (-7.5 to -10.2 kcal/mol) and ADMET analysis revealed three promising compounds. **Conclusion**: This study identified novel lead compounds with potential for ASD therapy targerting AUTS2

Keywords: Leveraging, Omics dataset, Hybrid data fusion, Deep learning, Databases, DTI, prediction, Transcriptomics, Traditional models.

S2-PP7

Characterization of surface morphology and pocket analysis of Verona Integron-Encoded Metallo-beta-lactamase (VIM) protein for drug analysis

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Abstract:
Verona integron-encoded metallo-β-lactamase (VIM) is a clinically significant enzyme that confers resistance to a broad spectrum of β-lactam antibiotics, including carbapenems, through the hydrolysis of their β-lactam ring. As an Ambler Class B metallo-β-lactamase (MBL), VIM exhibits a zinc-dependent catalytic mechanism, rendering traditional β-lactamase inhibitors ineffective. The dissemination of VIM genes is facilitated by mobile genetic elements, particularly class 1 integrons, which enable horizontal gene transfer among diverse Gram-negative pathogens such as Pseudomonas aeruginosa, Klebsiella pneumoniae, and Enterobacter spp. The widespread proliferation of VIM-producing bacteria has precipitated severe nosocomial outbreaks, significantly complicating antimicrobial therapy and infection control. Conventional treatment options are severely limited, with colistin, tigecycline, and fosfomycin often serving as last-resort agents, albeit with variable efficacy and toxicity concerns. The emergence of combination therapies and novel β-lactamase inhibitors targeting metallo-β-lactamases remains an active area of research, yet no clinically approved inhibitors have demonstrated substantial efficacy against VIM to date. The increasing prevalence of VIM necessitates robust surveillance systems, rapid molecular diagnostics, and stringent antimicrobial stewardship. A multifaceted strategy incorporating genomic epidemiology, infection control measures, and innovative therapeutics is paramount in mitigating the global threat posed by VIM-mediated carbapenem resistance.

Keywords: VIM, metallo-β-lactamase, carbapenem resistance, β-lactam hydrolysis, Gram-negative bacteria, horizontal gene transfer, integrons, antimicrobial resistance, nosocomial infections, molecular diagnostics

S2-PP8

Structural analysis of Klebsiella pneumonia Crabapenemase (kpc) protein for drug analysis

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Abstract:
Klebsiella pneumoniae carbapenemase (KPC) represents a formidable challenge in contemporary antimicrobial resistance, conferring extensive drug resistance in *Klebsiella pneumoniae* and other Gram-negative pathogens. As an Ambler Class A β-lactamase, KPC hydrolyzes a broad spectrum of β-lactam antibiotics, including carbapenems, which are often considered the last line of defense against multidrug-resistant infections. The global dissemination of KPC-producing strains is primarily mediated through horizontal gene transfer via plasmids, thereby exacerbating nosocomial outbreaks and limiting therapeutic options. Molecular characterization of KPC variants has elucidated their structural

adaptability, enabling the emergence of novel subtypes with enhanced catalytic efficiency against β-lactams. Conventional treatment regimens, reliant on polymyxins, tigecycline, and fosfomycin, have exhibited diminishing efficacy due to escalating resistance rates. In response, innovative β-lactamase inhibitors such as avibactam, vaborbactam, and sulbactam have been developed, restoring susceptibility to certain β-lactam antibiotics. The clinical burden of KPC-producing pathogens necessitates vigilant surveillance, rapid diagnostic methodologies, and stringent infection control measures to mitigate transmission. Advances in genomic epidemiology and novel antimicrobial strategies hold promise in counteracting the persistence and evolution of these formidable resistance determinants. A multifaceted approach integrating molecular diagnostics, antimicrobial stewardship, and novel therapeutics remains imperative in curbing the global threat posed by KPC-mediated resistance.

Keywords: KPC enzyme, Carbapenemase-producing Enterobacteriaceae (CPE), β-lactamase, Antimicrobial resistance (AMR), Multidrug-resistant (MDR) bacteria, Extended-spectrum β-

S2-PP9

Harnessing Virtual Screening for Lung Cancer Drug Discovery: A Natural Product-Based Approach

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Abstract:

Globally, lung cancer continues to be one of the main causes of cancer-related death, emphasizing the pressing need for innovative treatment approaches. Bioactive substances with anticancer potential have long been found in natural products. In this study, virtual screening techniques to identify potential lung cancer inhibitors from a database of natural compounds are utilized. Molecular docking was performed to predict interactions between natural product candidates and the target (IM17). ADMET (absorption, distribution, metabolism, excretion, and toxicity) predictions were used to further investigate the top-ranked compounds in order to evaluate their pharmacokinetic characteristics and drug-likeness. The results show that a number of interesting natural compounds have good pharmacological profiles and strong binding affinities, which supports their potential as lead agents for lung cancer treatment. The work demonstrates how computational drug discovery can speed up the process of finding new anticancer drugs while cutting down on the expense and time involved in experimental screening. Future research will use in vitro validation and molecular dynamics simulations to verify the chemicals' biological activities.

S2-PP10

Machine Learning-Based Identification of Binding Pockets in Multidrug Efflux Pumps for Ligand Targeting

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Abstract

Multidrug efflux pumps play a crucial role in bacterial resistance by expelling a wide range of antibiotics and toxic compounds. This highly limits the efficacy of antimicrobial therapies. Targeting these pumps through small-molecule inhibitors requires a precise understanding of their structural features, particularly potential binding pockets across the protein surface. In this study, we employ a machine learning-based approach to systematically characterize the surface of those proteins and predict potential binding pockets in multidrug efflux pumps. This enables the identification of potential ligand interaction sites which can be employed for designing small molecules. Our methodology integrates protein structural analysis, binding pocket prediction, and comparative genomics to map key sites across different efflux pump families. We first analyze the three-dimensional structures of efflux pumps using deep-learning-based pocket detection algorithms, which predict druggable sites based on geometric and physicochemical properties. The identified binding pockets are further classified into core and accessory sites, distinguishing conserved functional regions from variables. This study presents a computational framework for ligand-based targeting of multidrug efflux pumps, offering new avenues for rational drug design. By leveraging machine learning and structural bioinformatics, our approach facilitates the discovery of efflux pump inhibitors, contributing to the development of next-generation antimicrobials.

Keywords: efflux pumps, drug binding pockets, ligand interaction, small molecules, antimicrobial interaction

S2-PP11

Computational Drug Discovery for Zoonotic Diseases Using Molecular Docking Approaches for Identifying Novel Therapeutics

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Abstract:

Zoonotic infections are an international problem and there is a great need to find new effective methods to counteract their escalating mode. One of the emerging innovations in drug development is the method of computational drug discovery which regards the task of determining compounds capable of blocking various proteins in pathogens. In our current investigation, the target is arsenate reductase - a causative factor that results in Brucellosis, an infectious zoonotic disease that broadly prevails among animals and humans. This profile candidate inhibitors for arsenate reductase and molecular docking were carried out using Discovery Studio and PyRx. A set of ligands was downloaded from the Protein Data Bank (PDB) and docked to the target protein to determine the binding affinity. Metformin which is one of the drug candidates showed the best binding affinity at -5.0 kcal/mol. Other drug

candidates are Curcumin obtained from natural sources which showed an activity level of docking amounting to -4.9 kcal/mol. Thus are taken as examples, the methods of Computational drug development have been providing new drug forms and have extended the scope of the medicinal use of drugs. Subsequently, the activity of these drugs was confirmed through the in vitro and in vivo methods, showing that our new drug to treat zoonotic infections as well as *Brucella melitensis* infections could work.

S2-PP12

Creation of Medications Using Molecular Docking to Target Alzheimer's

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ABSTRACT:
A serious neurological condition that impacts millions of individuals globally is Alzheimer's disease (AD). It is defined by an endless deterioration in mental capacity. It is defined by an endless deterioration in mental capacity. The urgent need for novel drug development approaches is highlighted by the lack of effective medical products despite years of study. Through the prediction of their interactions with important disease targets, including tau and amyloid-beta (Aβ) proteins, computational methods—in particular, molecular docking—have become effective tools for discovering prospective therapeutic candidates. The stability and binding affinities of certain drugs against AD-related targets are assessed in this work using molecular docking simulations. Furthermore, pharmacokinetic characteristics and drug-like characteristics has been assessed by ADME (Absorption, Distribution, Metabolic Health, and Excretion) studies using Swiss ADME. Several bioactive compounds with good pharmacokinetics and substantial binding potential are highlighted in the data, indicating their therapeutic potential.
Keywords: Alzheimer's disease; Drug Discovery.

S2-PP13

Unravelling Key Molecular Drivers of Glioblastoma through Transcriptomic and Network Analysis

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Abstract:
The most aggressive and common primary brain tumor, glioblastoma multiforme (GBM), is distinguished by its quick growth, widespread infiltration, and strong resistance to conventional therapies. Developing individualized treatment plans requires an understanding of the molecular underpinnings of GBM. Protein-protein interaction (PPI) networks were investigated using STRING and Cytoscape visualization after a comprehensive transcriptome analysis using GEO2R to identify genes with differential expression. Finding important hub genes and pathways linked to the pathophysiology of GBM was made easier by this unified approach. The study identifies novel potential indicators and therapeutic targets in addition to well-known oncogenes like EGFR and PTEN. It enriches our knowledge of the biology of GBM and might eventually result in the creation of more effective diagnostic and treatment

alternatives. Further experimental validation of these putative genes and pathways may improve precision medicine techniques for GBM treatment.

Keywords: Alzheimer's disease; Drug Discovery.

S2-PP14

Virtual and *in vitro* screening of spiroazacyclic compounds for novel TMPRSS2 inhibitors as SARS-CoV-2 therapeutic entry-blockers.

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Abstract

SARS-CoV-2, the highly contagious virus behind the COVID-19 pandemic, has killed over 7.1 million people globally as of January 19, 2025. The FDA has approved three antiviral drugs for COVID-19 treatment; however, their efficacy has shown inconsistent outcomes in clinical settings. Consequently, there is an urgent need for novel antivirals to combat the pandemic. A transmembrane serine protease 2 (TMPRSS2) is crucial for SARS-CoV-2 entry and spread and for SARS-CoV, MERS-CoV and influenza A viruses and is a promising antiviral target. TMPRSS2 cleaves the viral spike protein, enabling viral entry into host cells. Since TMPRSS2 expression is unessential for normal development and homeostasis in mice, TMPRSS2 inhibitors can block viral spread without causing significant side effects. Therefore, inhibiting TMPRSS2 represents a promising strategy for antiviral intervention. Using *in silico* and *in vitro* platforms, we screened 112 spiroazacyclic compounds against human TMPRSS2's activity. The primary screening involved assessing enzyme activity inhibition using a TMPRSS2 assay kit, with IC50 values of the compounds compared against the reference inhibitor, camostat. Compounds 40, 43, 103, 104, and 106 exhibited potent inhibitory activity with IC50 values of 0.29μM, 0.26μM, 0.33μM, 0.58μM, 0.48μM, respectively. Further, spiroazacyclic compounds effectively inhibited spike protein and receptor-mediated cell-cell fusion and demonstrated a dose-dependent inhibition of pseudovirus entry in the Vero-TMPRSS2-ACE2 cell line without influencing cell viability. Our study successfully identified spiroazacycles as TMPRSS2 inhibitors, potentially leading to novel SARS-CoV-2 treatment.

Keywords: COVID-19; SAR-CoV2; TMPRSS2

S2-PP15

The Biosynthetic Capacity of *Myxococcus*: A Comprehensive BGC Analysis

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Abstract:

Myxococcus is a genus of soil-dwelling, predatory bacteria belonging to the order Myxococcales within the class Deltaproteobacteria. They are renowned for their ability to produce diverse secondary metabolites. These bioactive compounds are largely encoded within biosynthetic gene clusters (BGCs), which can be mined for novel natural products. In this study, we employed a genome-wide approach to analyze the biosynthetic potential of multiple *Myxococcus* strains using antiSMASH for BGC identification, followed by core and accessory gene analysis to determine conserved and strain-specific biosynthetic capabilities. Using anti-SMASH, we identified and annotated a variety of BGCs, including polyketide synthases (PKS), non-ribosomal peptide synthetases (NRPS), and hybrid PKS-NRPS clusters, as well as clusters encoding terpenes, bacteriocins, and other specialized metabolites. Notable metabolites include myxovirescin, myxopyronin, corallopyronnin A, and Ambruticin which are potential antibiotic activity. It is interesting to note a high prevalence of metabolic clusters of unknown function. Our results reveal that while a core set of biosynthetic genes is conserved across *Myxococcus* species, there is significant variability in accessory BGCs, suggesting a role in niche adaptation and strain-specific metabolite production. Our findings pave the way for further functional characterization and bioprospecting efforts aimed at harnessing *Myxococcus* for natural product discovery and biotechnological applications.

Keywords: BGCs, antibacterial activity, predatory bacteria, novel metabolites, myxococcus

S2-PP16

Comparative Genomic and Biosynthetic Gene Cluster Analysis of *Lysobacter* Species for Antimicrobial Potential

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Abstract

Lysobacter species are emerging as prolific producers of antimicrobial compounds, making them valuable for biotechnology and biocontrol applications. These bacteria possess diverse biosynthetic gene clusters (BGCs) responsible for synthesizing secondary metabolites with antibacterial and antifungal activities. However, the genomic diversity and metabolic potential of *Lysobacter* remain underexplored. In this study, we perform a comprehensive genome analysis of *Lysobacter* species to characterize their biosynthetic potential and evolutionary relationships. We utilize antiSMASH to identify and annotate BGCs, revealing the presence of polyketide synthase (PKS), nonribosomal peptide synthetase (NRPS), and hybrid biosynthetic pathways. The identified clusters are compared across multiple *Lysobacter* genomes to determine conserved and strain-specific gene sets. Additionally, comparative genomics is conducted to classify core and accessory genes involved in

secondary metabolism. Phylogenetic analysis provides insights into the evolution of biosynthetic pathways among *Lysobacter* species. This study highlights the metabolic versatility of *Lysobacter* and provides a genomic framework for identifying novel antimicrobial compounds. By integrating biosynthetic pathway analysis and comparative genomics, our findings contribute to the rational discovery of bioactive molecules and potential applications in antibiotic development and biocontrol strategies.

Keywords: Lysobacter, predatory bacteria, novel metabolites, antimicrobial resistance

S2-PP17

Machine Learning Enhanced Scrutiny of Extended-Spectrum Beta-Lactamases (CTX-M) for Drug Development

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Abstract

Extended-spectrum beta-lactamases (ESBLs), particularly the CTX-M family, have emerged as a major public health concern due to their ability to hydrolyze third-generation cephalosporins such as cefotaxime, ceftazidime, and ceftriaxone, contribute to multidrug resistance (MDR) in Gram-negative bacteria. The rapid evolution and diversification of CTX-M variants pose significant challenges for conventional drug discovery. In this study, we employ a machine learning-enhanced approach to systematically analyze the structural and functional characteristics of selected CTX-M enzymes (particularly CTX-M9, CTX-M15, CTX-M14, CTX-M96), facilitating the identification of novel binding pockets for small molecules and inhibitors. Our methodology integrates deep learning models with structural bioinformatics to scrutinize the binding dynamics of CTX-M enzymes. The analysis includes the classification of binding sites based on their physiochemical properties providing a refined understanding of the enzyme's active site dynamics. Our results highlight previously uncharacterized binding pockets and reveal structural adaptations that contribute to CTX-M-mediated resistance. By integrating machine learning with structure-based drug design, this study provides a robust framework for accelerating the development of next-generation β-lactamase inhibitors. This study not only advances our understanding of ESBL resistance mechanisms but also contributes to the global effort to combat antimicrobial resistance through AI-powered drug development.

Keywords: Beta-lactamase, antimicrobial resistance, hydrolases, small molecules

S2-PP18

Structure-Based Approach of Binding Pocket Analysis in Crystal Structure of New Delhi Metallo Beta-Lactamase (NDM-1) For Ligand Screening

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Abstract

New Delhi Metallo-β-lactamase-1 (NDM-1) is a clinically significant enzyme capable of hydrolyzing a broad range of β-lactam antibiotics, including carbapenems. Since its discovery

in 2008, NDM has rapidly spread across Gram-negative pathogens, posing a significant public health threat worldwide. NDM-producing bacteria, including *Klebsiella pneumoniae*, *Escherichia coli*, *Acinetobacter baumannii*, and *Pseudomonas aeruginosa*, resist nearly all β-lactam antibiotics, limiting treatment options. Understanding the structural basis of ligand binding in NDM-1 is crucial for the design of effective inhibitors. In this study, we employ a structure-based approach to analyze potential binding pockets in the crystal structure of NDM-1, facilitating ligand screening and drug discovery. Using high-resolution data available in a protein data bank (PDB), we identify and characterize the key structural features (including the active site and potential allosteric binding pockets) in NDM-1. The study also integrates machine learning-based detection algorithms to classify binding sites based on their physicochemical properties and druggability. Our results provide a detailed view of the NDM-1 binding landscape, revealing crucial interactions between metal cofactors (Zn^{2+} ions) and candidate ligands. The identified binding pockets are further validated through virtual screening of small-molecule libraries, identifying potential inhibitors with strong binding affinity.

Keywords: NDM-1, ligand, inhibitors, substrate, drug designing, antibiotic resistance

S2-PP19

Rhodotorula Redefined: Tackling Mitochondrial ROS-induced Leaky-gut Syndrome through *R. glutinis* Prebiotic Revitalization.

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Abstract:

Mitochondrial reactive oxygen species (mtROS) are key disruptors of gut-barrier integrity, fueling a cascade of debilitating pathologies such as gastritis, inflammatory bowel disease (IBD), leaky-gut syndrome, gastric cancer and colorectal malignancies. Underlying mechanism is due to oxidative stress defined by overproduction of oxidative free radicals and the associated reactive oxygen species (ROS) that disintegrate epithelial tight junctions, alter cell signalling and cell cycle control, impair energy metabolism and cause inflammation. This review unravel the potential of *Rhodotorula glutinis,* an untapped yeast species, as a prebiotic, revitalizing microencapsulated supplement in mitigating mitochondrial ROS-induced leaky-gut syndrome. Chronic exposure to physiological stressors of modern-day lifestyle such as anxiety, unbalanced and unhealthy diet, overconsumption of alcohol, smoking etc., induce increased intestinal permeability to exogenous and endogenous toxins, undigested food particles, and luminal pathogens by disrupting tight junction protein complexes (occludins, claudins and zonula occludens proteins), resulting in systemic inflammation and higher ROS production. *Rhodotorula glutinis*, a carotenoid-rich, antioxidant-producing, non-pathogenic yeast is known for its ability to produce industrially important bioactive compounds such as beta-carotene, catalase, and superoxide dismutase that serve as potent ROS scavengers as well as promote the growth of beneficial gut bacteria, thus making it a promising choice for gut health supplements. A potential use of CRISPR-Cas9 genome editing in strategically modifying the genome of *Rhodotorula glutinis* to overexpress superoxide dismutase, catalase and beta-carotene-producing genes under the influence of a strong transcriptional and translational activity could enhance the overall rate of ROS clearance thereby stabilizing gut health.

Keywords: Mitochondrial ROS; Occuldins; Inflammatory Bowl Disease

S2-PP20

Epitope-based vaccine design against Zika virus

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ABSTRACT
Zika virus (ZIKV) is a mosquito-borne flavivirus that has caused significant public health concerns, particularly due to its association with congenital malformations and neurological complications. The recent outbreak of ZIKV in Rajasthan, India, in 2024 has further highlighted the urgent need for effective preventive measures, including vaccine development. The design of epitope-based vaccines represents a promising strategy for generating specific immune responses against ZIKV without the need for live virus. This approach focuses on identifying and synthesizing short peptide sequences (epitopes) from the virus that can trigger protective immunity. The aim of this study is to design and evaluate potential ZIKV-specific epitopes for vaccine development. By utilizing bioinformatics tools and immunoinformatics, we aim to predict B-cell and T-cell epitopes, which can elicit robust immune responses, paving the way for safe and effective vaccines against ZIKV. The findings will lay the groundwork for experimental validation and a potential vaccine against ZIKV.
Keywords: Zika virus, epitope-based vaccine, immunoinformatics, B-cell epitopes, T-cell epitopes, bioinformatics, flavivirus, vaccine design.

S2-PP21

AI- Based DNA Repair Efficiency Predictor for Recombinant DNA Technology

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ABSTRACT
DNA repair prediction is a highly important area within molecular biology and bioinformatics because of the insights it gives concerning genomic stability and disease prevention, especially for cancer. This paper presents an AI model capable of predicting DNA repair functionality from DNA sequences. A curated dataset is processed to extract essential sequence features like GC content, sequence length, nucleotide composition, and binary encodings. Sophisticated feature preprocessing techniques ensure that the model will have clean data to work with, thereby boosting its probabilities of success. Machine learning algorithms are prescribed for classifying and predicting DNA repair efficiency, making overcrowded use of sequence alignment strategies and statistical methodologies for robust training and testing. The model aims to derive conserved patterns and essential regions relative to the process of repair to improve the understanding of genetic stability. This research lays the groundwork for using artificial intelligence in advanced computational methods to analyze genomics. The estimates will allow pelagic advances in DNA repair evaluation, thus helping in the study of genetic disorders and improving existing therapeutic strategies. This denotes the establishment of artificial intelligence as a potent tool in

demystifying complex biological processes, which further enhances the prospects of computational biology and bioinformatics.

S3-PP01

In silico analysis of animal venom-derived matrix metalloproteinase-9 modulators and Their therapeutic implications

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Abstract

Matrix Metalloproteinase 9 (MMP9) belongs to a family of proteolytic enzymes that degrade extracellular matrix components, such as collagen, elastin, laminin, and fibronectin. They also play a part in tissue remodeling by cleaving and rejoining the tissue proteins. Cancer, neurodegenerative disorders, cardiovascular diseases, arthritis, and chronic inflammatory conditions are just some of the diseases that can start or get worse due to the dysregulation of MMP9. Venomous animals such as honeybees, toads, snakes, spiders, scorpions, jellyfish, and sea anemones contain venom-secreting glands, which help them defend against predators and immobilize their prey. The molecules that come from animal venom are a complicated mix of bioactive molecules, such as peptides, enzymes, proteins, and small organic compounds that do several biological things. Venom-derived molecules have been found to modulate MMP9. These venoms and their components target specific cellular signaling pathways, modifying MMP9 expression levels to either induce inflammation or exhibit anti-inflammatory effects. Different types of molecules derived from marine and land animal venom are used as MMP9 modulators. This study further investigates the role of animal venom-derived MMP9 modulators as novel therapeutics for the suppression of MMP9 activity in vitro.

Keywords: Venom, Animal toxin, Modulation, Matrix metalloproteinase 9, Inflammation

S3-PP02

Pharmacological Therapy: Selection and Designing of Lead Molecules Using Molecular Docking Approach for the Cure of Cystic Fibrosis Disease

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Abstract:

Cystic fibrosis (CF) is a genetic disorder caused by mutations in the cystic fibrosis transmembrane conductance regulator (CFTR) protein, leading to impaired ion transport and severe respiratory and digestive issues. This study aimed to identify potential lead molecules for CF treatment through molecular docking approaches, evaluating their binding affinity, stability, and therapeutic potential. Molecular docking was performed using CB-Dock, and Pymol was used for visualization. PROTAC ligands were retrieved from the PubChem database for screening against the CFTR protein. Among the tested compounds, VX-445 exhibited the highest binding affinity, with a docking score of 10.3, indicating a strong

interaction with the CFTR protein. The results highlight VX-445 as a promising candidate for restoring CFTR function. Additionally, the molecular interactions observed suggest that VX-445 may effectively correct the protein's misfolding, which is a primary cause of CF. The findings underscore the potential of VX-445 as a lead compound for further development. However, additional in vitro and in vivo studies are essential to validate these computational results and establish its therapeutic efficacy. Experimental evaluations, such as cellular assays and clinical trials, will be crucial to confirm its ability to restore CFTR function and improve patient outcomes. This study demonstrates the value of molecular docking in drug discovery and highlights the importance of computational methods in identifying novel therapeutics for cystic fibrosis. VX-445 stands out as a promising candidate, potentially paving the way for more effective CF treatments and improving the quality of life for patients.
Keywords: CFTR, Cystic Fibrosis, Molecular Docking, F508del Mutation, VX-445, pharmacological Therapy.

S3-PP3

In-Silico Structural and Functional Annotation of Hypothetical Proteins from *Nocardia asteroides* NCTC11293: A Computational Approach for Novel Drug Target Identification and Therapeutic Development

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Abstract:

Nocardiosis, caused by the opportunistic pathogen *Nocardia asteroides*, primarily affects immunocompromised individuals, often presenting as a pulmonary infection. Despite extensive research, novel therapeutic targets and effective lead molecules are needed. Whole genome sequencing of *N. asteroides* strain NCTC11293 revealed a high completeness level (98.19%), encoding 6,476 proteins, including 1,130 (17.45%) hypothetical proteins (HPs). Functional annotation identified 59 HPs classified as Binding Proteins (17%), Enzymes (68%), Cell Regulatory Proteins (3%), Transporters (5%), and Other Proteins (7%). Metabolic pathway analysis suggested **Aldolase 1-epimerase (A1-E)** (WP_019046482.1) as a potential therapeutic target. Structure-based virtual screening (SBVS) against the IMPPAT database identified five hit compounds (IMPHY003535.1, IMPHY011540.1, IMPHY010165.1, IMPHY003784.1, IMPHY007341.1) with docking scores of −8.2 to −8.5 kcal/mol and MMGBSA binding energy between −46.82 and −59.93 kcal/mol. Key interactions were observed with residues Gly41, Phe45, Met47, Ala51, Met77, His78, His143, Trp145, Asn169, Asp188, Trp221, Pro237, and Asp238. These molecules adhered to Lipinski's Rule of Five and exhibited favorable pharmacokinetics with stable HOMO-LUMO functional groups. Molecular dynamics simulations (MDS) and principal component analysis (PCA)-based free energy landscape (FEL) analyses confirmed structural stability within A1-E's binding pocket.

Keywords: *Nocardia;* WGS; Molecular Dynamics; Target Prediction

S3-PP5

Structural Insights and Binding Pocket Analysis of OXA-23 β-Lactamase: A Computational Approach for Inhibitor Design

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Abstract

OXA-23 is a critical resistance determinant in *Acinetobacter baumannii*, complicating infection management. They are Ambler Class D β-lactamase (Oxacillinase family) capable of hydrolyzing carbapenems (e.g., imipenem, meropenem), leading to multidrug resistance (MDR). OXA classes of beta-lactamase, lead to serious hospital-acquired infections (HAIs), particularly in intensive care units (ICUs) complicating treatment regimes. OXA-23-mediated resistance limits therapeutic options, making it crucial to understand its structural characteristics and binding pockets for the development of effective inhibitors. This study employs a comprehensive computational approach, integrating molecular modeling, machine learning, and molecular dynamics (MD) simulations, to analyze the structural features of OXA-23 and identify potential druggable sites. We begin with a detailed examination of the crystal structure of OXA-23, focusing on the active site architecture and key catalytic residues involved in β-lactam hydrolysis. Using pocket discovery algorithms, we identify the primary binding pocket and explore secondary sites that could serve as allosteric targets. Additionally, we apply machine learning-based binding site prediction to classify pocket druggability and prioritize potential inhibitor candidates. This study presents a systematic, structure-based approach to characterizing OXA-23 binding pockets, offering valuable insights for inhibitor design. By combining machine learning, structural bioinformatics, and molecular simulations, our findings provide a roadmap for the development of next-generation β-lactamase inhibitors capable of overcoming OXA-23-mediated resistance.

Keywords: Oxacillinase, antimicrobial resistance, hydrolases, small molecules, binding pocket analysis

S3-PP7

In silico screening of nucleocapsid protein with different ligands for the treatment of Measles

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Abstract

This study aims to perform an in silico screening of the Nucleocapsid protein with various ligands for potential measles treatment. The 3D structure of the Nucleocapsid protein was obtained from the Protein Data Bank (PDB). Bioactive compounds were selected from chEMBL and PubChem databases. Molecular docking was carried out using CB-Dock 2, and protein-ligand interactions were analyzed using LigPlot+ software. Ten ligands were identified from plant-derived compounds, and five were selected for docking. The highest binding affinity and interaction were observed in the novel protein-ligand complex. The 3D

structure of the Nucleocapsid protein showed strong interactions with all five ligands, with saponins demonstrating the most significant binding affinity. Our study suggests that the Nucleocapsid protein-saponin complex provides valuable insights for the development of measles treatments.

Keywords: Measles, Morbilivirus, PDB, Chembl, Pubchem, CB Dock2, G binding protein, Ligplot plus

S3-PP8

Functionalized Polymeric Nanoparticle as a Drug Delivery System for Anticancer Drug

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Abstract

Nanoscale drug delivery systems offer various advantages for therapeutic drug delivery, such as good biodegradability, nontoxicity, biocompatibility, and increased therapeutic impact compared with free drugs. alkylating agents is the key medication used to treat a range of solid malignancies; however, many side effects, such as ototoxicity, nephrotoxicity, vomiting, neurotoxicity, and nausea, frequently restrict its therapeutic efficacy. Drug delivery via nanoparticles has demonstrated potential in improving the therapeutic index of several drugs, including alkylating agents, by overcoming several obstacles associated with traditional chemotherapy. Polymeric nanoparticles serve as crucial tools for improving targeted drug delivery at the site of action and enhancing drug bioavailability. Polymers may be an optimal choice because of their versatility in meeting the specific requirements of each drug delivery system. In this study, we will investigate the drug loading efficacy and cytotoxicity of the polymeric nanoparticles for alkylating agents to optimize their formulation and enhance the therapeutic outcomes.

Keywords: Polymeric nanoparticle; Cancer drug delivery

S3-PP9

Antibacterial potential of Eugenol against Methicillin-Resistant *Staphylococcus aureus*

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Abstract:

One major threat to global health is the rise of multi-drug-resistant *Staphylococcus aureus* (MDR *S. aureus*), especially methicillin-resistant *S. aureus* (MRSA). The antibacterial activity of eugenol obtained from clove oil, examined against MRSA in this work. Strong binding interactions between eugenol and important bacterial targets, such as cell wall production and virulence-associated proteins, were found by molecular docking experiments. Eugenol's ability to suppress bacterial growth, biofilm formation, and the oxidative stress response was shown by experimental investigations. Eugenol's strong antibacterial action was validated by minimum inhibitory concentration (MIC) and minimum bactericidal concentration (MBC) tests, which showed total inhibition at particular values. Its bactericidal qualities were confirmed by the time-kill experiment, which showed a notable decrease in germs over time. Tests of biofilm inhibition revealed a 74.95% decrease in biofilm development and haemolysin activity of *S. aureus* decreased in haemolysis assays, indicating a reduction in its

pathogenicity. Assays for hydrophobicity verified alterations in the surface properties of bacteria for adhesion to host surfaces. Eugenol-treated *S.aureus* showed decreased survival under oxidative circumstances, suggesting weakened bacterial defence systems. Cellular damage in treated bacterial populations was verified by fluorescence staining. These results imply that eugenol is a promising natural antibacterial drug that inhibits *S. aureus* growth, biofilm formation, and the oxidative stress response, among other modes of action.

Key Words: MDR, MBC, MRSA, Haemolysin, biofilm

S3-PP10

Fabrication and Evaluation of Herbal Nanofillers-Based Hydrogel for Wound Dressing Application

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Abstract

Herbal nanofillers-based hydrogel has emerged as an emerging option in its application towards the fabrication of novel wound dressing materials. Although herbal extracts have been used traditionally to heal wounds of different kinds and hydrogels and nanomaterials have been studied for their efficiency in wound healing, a study combining all of these is limited. Thus this study aims to develop a hydrogel composed of biopolymers such as sodium alginate and gelatine which would be incorporated with an herbal extract such as raw banana peel as it's less explored in the area of wound healing, and with nanofillers. This hydrogel then would be fabricated with traditional wound dressing material which possibly would aid in the wound healing process by fastening it up along with improved efficiency in wound healing. Here, sodium alginate and gelatine are used to create the hydrogel due to their biocompatibility, biodegradability, and ability to form hydrogels under mild conditions. The amount of collagen present in gelatine further aids in the re-growth of the skin. The dressing of the wound along with the incorporation of herbal components that are known for their antimicrobial, anti-inflammatory, and healing properties, enhances the overall efficacy of the dressings.

Keywords: Hydrogel; Wound Healing; Herbal Nanofillers; Biocompatible

S3-PP11

Comparative Molecular Docking on polyprotein P1234 factor with novel ligands for Chikungunya

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Abstract

Chikungunya virus (CHIKV) is a mosquito-borne alphavirus causing severe arthralgia and fever, with no specific antiviral treatment available. The viral polyprotein P1234 plays a crucial role in CHIKV replication by processing it into non-structural proteins (nsP1–nsP4), which are essential for viral RNA synthesis. In this study, we performed a comparative molecular

docking analysis of P1234 with novel ligands using CB2 Dock to identify potential inhibitors. The three-dimensional structure of P1234 was retrieved, prepared, and subjected to docking simulations. Binding affinities and interaction profiles were analyzed to determine the most promising ligands. To further validate the docking results, LigPlot+ was employed to visualize hydrogen bonding and hydrophobic interactions between the ligands and active site residues. The docking analysis revealed that ligand X exhibited the highest binding affinity, forming stable interactions with key catalytic residues. LigPlot+ analysis confirmed these interactions, highlighting crucial molecular contacts that contribute to ligand stability. The findings suggest that novel ligands could serve as potential inhibitors of CHIKV replication by targeting P1234. Further molecular dynamics simulations, as well as in vitro and in vivo validation, are required to confirm the efficacy of these compounds as antiviral agents against CHIKV.

Keywords: Chikungunya, P1234, viral RNA, LigPlot+

S3-PP12

Computational study and molecular docking of ANTXR2 protein involved in anthrax and identification of Potential Ligand Interactions for therapeutic applications.

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Abstract:

Anthrax is a severe infectious disease, and targeting the ANTXR2 protein offers a promising approach for therapeutic intervention. In this study, the amino acid sequence of ANTXR2 was obtained from the NCBI database, and its three-dimensional structure was modeled using the Swiss Model. Molecular docking techniques were employed to analyze potential protein-ligand interactions using freely available databases and software. The computational analysis identified several promising ligands with strong binding affinities to key residues of the ANTXR2 protein. These findings highlight potential inhibitors that could disrupt anthrax toxin binding and prevent infection progression. The study provides valuable insights into the structural basis of ANTXR2 inhibition and lays a foundation for developing novel therapeutics to combat anthrax, contributing to public health efforts against this deadly disease.

Keywords: Anthrax, ANTXR2 protein, Molecular docking, Protein-ligand interactions

S3-PP13

Computational study and molecular docking of proto-oncogene 2 protein involved in cervical cancer and identification of potential ligand interactions for therapeutic applications.

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Abstract:

To study and investigate the ability of cervical cancer protein of degrading and treating cervical cancer through therapeutic conditions using molecular docking.

Methods and Materials: The NCBI (National Centre for Biotechnology Information) database provided the amino acid sequence for the proto-oncogene 2 protein, and a Swiss model was

used to retrieve the 3D structure of the protein. We used databases and software to perform molecular docking and protein-ligand interaction. In order to find suitable warhead, lead molecules from the novel PROTAC database for proto-oncogene 2 Protein, we first predicted the proto - oncogene 2 protein structure. The best interacting lead compounds are shown by the docking and screening results against the proto-oncogene 2 protein with novel PROTAC molecules. The predicted structure was in good agreement with ERRAT and Ramachandran plot. The identified novel PROTAC molecules show good interaction with LKB1 protein by forming three hydrogen bonds and eleven hydrophobic interactions. Our findings suggest that the novel PROTAC compounds can target the LKB1 protein and inhibit it, which stops the growth of cancerous diseases.

Keywords: cervical cancer, nanotechnology, nanomedicine, therapeutics, risk factors

S3-PP14

An Effective Approach to Detect Chronic kidney Disease using Fine tree Algorithm and Boosted tree Algorithm

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ABSTRACT:

To compare the accuracy of two machine learning algorithms namely fine tree algorithm and boosted tree algorithm by detecting chronic kidney diseases by implementing MATLAB software and SPSS software. A dataset from Kaggle was downloaded which contained patient information like family history related to kidney diseases, patient's BMI,lifestyle factors etc.. The two algorithms used are the Fine tree algorithm and the boosted tree algorithm in both matlab and SPSS software. The sample size taken into consideration is 5. the accuracy while detecting chronic kidney diseases using fine tree algorithm was higher yielding 99.8% accuracy rate. Whereas boosted tree algorithm yielded 87.2% accuracy rate. The study shows that the outcome of both the algorithms vary significantly. With fine tree being more accurate than boosted tree algorithm. Thereby for medical analysis, it should be more preferable to use fine tree algorithm. As fine tree algorithm was proven to be more effective than fine tree algorithm as fine tree algorithm achieved a accuracy of 99.8% and boosted tree algorithm achieved a 62.5% accuracy rate.

Keywords: accuracy results, matlab coding, SPSS graphs, machine learning algorithms, chronic diseases.

S3-PP15

Breaking the Clot: Probiotic-Engineered Yeast to Revolutionize APS Treatment

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Abstract:

Antiphospholipid Syndrome (APS), also known as Hughes Syndrome, is a systemic autoimmune disorder characterized by the presence of antiphospholipid antibodies that increase the risk of blood clots and pregnancy complications. Affecting 1-5% of the global population, APS is particularly prevalent in women and is observed in 30-40% of patients with

systemic lupus erythematosus. Alarmingly, APS accounts for 15-20% of deep vein thrombosis and pulmonary embolism cases. Despite its significant impact on morbidity and mortality, research into effective long-term treatments remains limited, leaving patients reliant on anticoagulants such as warfarin and heparin. While these treatments provide temporary protection against thrombosis, they do not address the underlying causes of APS or fully prevent recurrent thrombotic events. To address this unmet need, we propose an innovative therapeutic strategy that combines the precision of molecular medicine with the safety and accessibility of probiotics. Our approach involves genetically engineering *Saccharomyces boulardii*, a well-known gut-friendly yeast, to secrete extracellular vesicles (EVs) loaded with anti-thrombotic microRNAs (miRNAs). These EVs are absorbed by intestinal epithelial cells via the Clathrin-Mediated Endocytosis pathway and subsequently released into systemic circulation, where the miRNAs counteract APS-induced hypercoagulability. This strategy leverages the natural probiotic properties of *S. boulardii* and the cost-effective production of yeast-derived EVs, offering a novel, non-invasive means of delivering therapeutic agents. Additionally, when compared to bacterial exosome-based therapies, the use of yeast-derived EVs offers a more affordable and scalable solution, providing an accessible treatment option that could have a broader impact in improving patient outcomes and transforming APS management.

Keywords: Yeast-derived EVs, *Saccharomyces boulardii*, miRNAs, APS, Therapeutic delivery.

S3-PP16

Bridging Evolution and Structural Homology Modeling in Phylogenetic Studies of Moonlighting Proteins

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Abstract:

Moonlighting proteins exhibit multiple, often unrelated, functions without gene duplication, challenging traditional sequence-based evolutionary analyses. Standard phylogenetic approaches relying solely on sequence homology may overlook functional divergence driven by structural constraints. This study integrates structural homology modeling with phylogenetic analysis to better understand the evolutionary history and functional adaptations of moonlighting proteins. We employ sequence-structure hybrid phylogenetics, using structural modeling techniques such as homology modeling (Modeller, SWISS-MODEL) and machine learning-based structure prediction (AlphaFold) to reconstruct ancestral conformations. Comparative structural analyses help identify evolutionary constraints and functional hotspots that remain conserved despite sequence divergence. By mapping co-evolving residues and structurally conserved motifs onto phylogenetic trees, we provide deeper insights into the selective pressures shaping moonlighting protein evolution. Our findings demonstrate that structural conservation plays a pivotal role in the functional versatility of moonlighting proteins, suggesting that structure-based phylogenetics offers a more reliable framework for tracing their evolutionary pathways. This interdisciplinary approach enhances our understanding of protein evolution, function, and adaptation, with implications in drug design, synthetic biology, and evolutionary genomics.

Keywords: Moonlighting proteins, phylogenetic analysis, AlphaFold, synthetic biology

S3-PP17

Evaluation of actinobacteria From Kashmir Region for antimycobacterial activities

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Abstract:
Tuberculosis (TB) remains a major global health concern, necessitating the discovery of novel antimycobacterial agents. Actinobacteria, particularly those from unique and unexplored ecosystems, have been a prolific source of bioactive compounds. This study aims to evaluate the antimycobacterial potential of actinobacteria isolated from soil samples of the Kashmir region, a geographically distinct and ecologically rich area. A total of *35* actinobacterial cultures were isolated, followed by selective isolation, morphological and molecular characterization of actinobacterial strains. The isolates were screened for antimycobacterial activity using *M.smegmatis* as surrogate. Bioactive extracts from the potential strains were further analyzed for their antimycobacterial properties against *M.tb H37RA* and chemical composition using chromatographic and spectroscopic techniques was also performed. Preliminary findings indicated two isolates with significant antimycobacterial activity, suggesting the presence of novel bioactive metabolites. This study highlights the potential of Kashmir's actinobacterial diversity in the search for new antimycobacterial compounds and underscores the importance of bioprospecting underexplored environments for drug discovery. Further studies on compound purification and mechanism of action are warranted.

Keywords: Actinobacteria, antimycobacterial activity, *Mycobacterium tuberculosis*, Kashmir, bioactive compounds, drug discovery.

S3-PP18

Comparison of Extraction Methods for the Isolation of Isoflavonoids from Soybean-Characterization and Chemometric Analysis

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ABSTRACT
Daidzein (DAI), also known by its IUPAC designation 4,7-dihydroxyisoflavone, is a naturally occurring phytoestrogen isoflavone that is mostly obtained from leguminous plants, including mung beans and soybeans. This substance has drawn a lot of interest as an unique pharmacophore with exceptional promise for the treatment of a number of illnesses. The effect of extraction methods and solvents on the measurement of soybean isoflavones was examined. The purpose of this systematic investigation was to address significant differences between the methods and solvents employed by various research groups to extract isoflavones from soybeans. In this work, we use three solvents—isopropyl alcohol,

ethanol, and distilled water—to show two extraction techniques: Soxhlet extraction for 5 hours and water bath ultra sonicator for 20 minutes at 40 degree Celsius .When the two extraction techniques were compared using GCMS and FTIR analysis, the Soxhlet extraction method produced preferentially greater quantities of the main isoflavones, and organic solvents (ethanol and IPA) demonstrated superior extraction efficiency over distilled water. In GCMS analysis, the plant-derived sterols like Stigmasterol and gamma-Sitosterol were identified while in FTIR analysis, strong O-H (hydroxylgroups 3200-3500cm^-1), C-O-C(ether bonds,1000-1300^-1),C=O(carbonyl,1600-1660 cm^-1) and aromatic ring vibrations (800-900 cm^-1)confirm the presence of flavonoids.

Keywords: Daidzein, Isoflavone, plant-derived sterols, flavonoids, phytoestrogen

S3-PP19

Development of CRISPR-Cas13 Molecular Diagnostic Tool for Detecting *Mycobacterium tuberculosis*

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Abstract

A rapid, simple, and highly sensitive diagnostic method is essential for tuberculosis (TB) detection. Clustered Regularly Interspaced Short Palindromic Repeats (CRISPR) and associated Cas proteins have emerged as powerful tools for clinical diagnostics due to their high flexibility, sensitivity, and specificity. This study aimed to develop a CRISPR-Cas13a-based assay for the detection of *Mycobacterium tuberculosis* (MTB) and evaluate its diagnostic performance in clinical specimens. The assay was designed using CRISPR-derived RNAs (crRNAs) targeting the conserved *rpoB* gene sequence of MTB. Its performance was assessed using biological samples (n = 60). The CRISPR-Cas13a-based assay demonstrated a low limit of detection of 20 copies/μL and high specificity. When applied to sputum samples, the assay exhibited a sensitivity of 95.5% and a specificity of 93.3%, with culture serving as the gold standard. The CRISPR-Cas13a-based MTB detection assay offers high sensitivity and specificity for MTB identification in sputum samples, highlighting its potential as a promising diagnostic tool for tuberculosis.

Keywords: Tuberculosis*, Mycobacterium tuberculosis*, CRISPRCas13a, crRNA, diagnosis.

S3-PP20

Biosurfactants: Sustainable Solutions for Environmental and Agricultural Applications

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Abstract:

Biosurfactants are surface-active compounds produced by microorganisms that offer eco-friendly alternatives to synthetic surfactants. Their unique properties, including biodegradability, low toxicity, and effectiveness under extreme conditions, make them suitable for various applications in environmental remediation and agriculture. In environmental contexts, biosurfactants enhance the biodegradation of hydrophobic pollutants by increasing their bioavailability. For instance, rhamnolipids produced by

Pseudomonas aeruginosa have been shown to effectively emulsify hydrocarbons, facilitating their breakdown in contaminated soils and water bodies. In agriculture, biosurfactants contribute to sustainable practices by promoting plant growth and offering biocontrol against pathogens. Lipopeptides like surfactin, produced by Bacillus subtilis, exhibit antimicrobial properties that can suppress soil-borne diseases, reducing the need for chemical pesticides. Despite their potential, large-scale production of biosurfactants faces challenges such as high production costs and variability in yield. Recent research focuses on optimizing fermentation processes and utilizing renewable resources to enhance production efficiency. Advancements in biotechnology and a growing emphasis on sustainable development highlight the promise of biosurfactants in addressing environmental and agricultural challenges. Ongoing research aims to overcome current limitations, paving the way for broader industrial applications.

Keywords: Biosurfactants, environmental remediation, sustainable agriculture, rhamnolipids, lipopeptides.

S3-PP21

Adaptations of Cryosphere Microbes: Functional Roles of Siderophores, Antifreeze Proteins, and Cold-Active Enzymes in Extreme Environments

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Abstract:
The cryosphere, which includes glaciers, polar ice caps, sea ice, and permafrost, is home to a diverse array of cold-adapted microorganisms that have evolved specialized survival mechanisms to withstand extremely low temperatures, high salinity, and limited nutrient availability. Among the key adaptations, siderophores, antifreeze proteins (AFPs), and cold-active enzymes play crucial roles in microbial survival and ecological function. Siderophores, which are low-molecular-weight iron-chelating compounds, enable microbes to acquire essential iron in iron-limited cryosphere environments, supporting cellular processes such as respiration and DNA synthesis. The production of siderophores also plays a role in microbial competition and community interactions in cold ecosystems. Antifreeze proteins (AFPs) are another vital adaptation that prevents intracellular and extracellular ice formation, protecting microbial cells from mechanical damage caused by ice crystallization. By binding to ice nuclei and inhibiting their growth, AFPs enhance microbial viability in freezing conditions and stabilize cryosphere microbial communities. Cold-active enzymes exhibit high catalytic efficiency at low temperatures, allowing essential biochemical reactions to proceed in cold environments where conventional enzymes would be inactive. These enzymes maintain functional flexibility and stability under extreme conditions, enabling microbial survival in subzero temperatures. They are involved in various metabolic pathways, including nutrient cycling, organic matter degradation, and symbiotic interactions. This study examines the molecular mechanisms and ecological roles of siderophores, AFPs, and cold-active enzymes in cryosphere microbes, providing a deeper understanding of their survival strategies. Investigating these cold-adaptive mechanisms is essential for elucidating microbial diversity, biogeochemical processes, and the resilience of life in extreme environments.

Keywords: cryosphere, Antifreeze proteins, cryosphere microbes, Siderophores

S3-PP-22

Inactivation of BCL11A Using CRISPR-Cas9 for the treatment of sickle cell Anaemia

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Sickel cell anaemia (SCA) is a hereditary blood disorder caused by a mutation in the HBB gene, leading to the production of sickle-shaped red blood cells. Gene-editing technologies, especially CRISPR-Cas9, have shown tremendous potential in correcting genetic disorder, including SCA. One of the promising strategies for treating sickle cell anaemia is the inactivation of BCL11A, a gene that suppresses fetal hemoglobin (HbF) production. Reactivating HbF can alleviate the symptoms of sickle cell anaemia by preventing hemoglobin from sickling. This paper discuss the advancements in gene-editing technique, specifically the use of CHOPCHOP, an online CRISPR design tool, to target BCL11A for the treatment of sickle cell anaemia. The paper provides a step-by-step outline for using CHOPCHOP to design effective CRISPR guide RNAs (gRNAs) to inactivate BCL11A and explores the potential impact of this approach on clinical therapies for sickle cell anaemia.

Keywords: Sickle cell anaemia, Gene editing, CRISPR-Cas9, BCL11A, CHOPCHOP, Guide RNA and Hemoglobin disorder.

2nd International Conference On
Translational Research in Biomedical Sciences (TRIBS 2.0)
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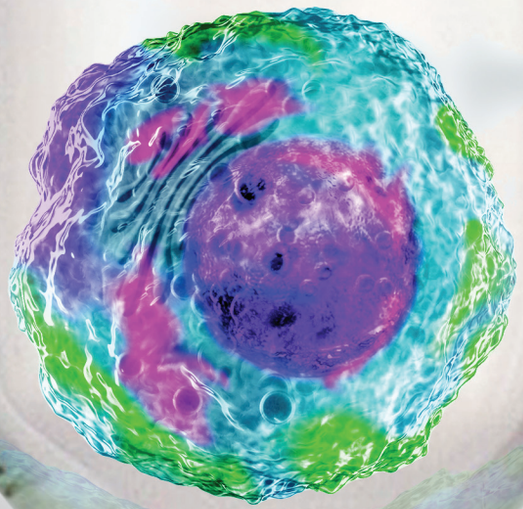

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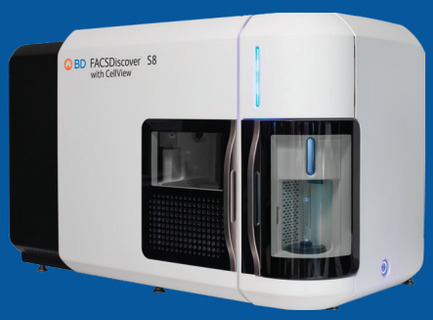

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