INDIAN COUNCIL OF MEDICAL RESEARCH

&

ACADEMY OF SCIENTIFIC AND INNOVATIVE RESEARCH

(Faculty of Medical Research)

संवाद (SANVAD) - 2026

Scholar's Assembly for Next-gen Ventures to Advance their Development

From Ideas to Impact: PhD Research in Action

(19th Feb - 21st Feb 2026)

SOUVENIR

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METHODOLOGY
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CAPACITY-BUILDING
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SANVAD 2026 Souvenir
ISBN:978-93-5737-992-2

ICMR - National Institute of Malaria Research, Sector 8 Dwarka, New Delhi -110077

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MEMBER

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February 16, 2026

MESSAGE

It gives me immense pleasure to address the participants of SANVAD 2026 – Scholar's Assembly for Next-gen Ventures to Advance their Development – being held from 19-21 February 2026 at ICMR-National Institute of Malaria Research, New Delhi.

The theme "From Idea to Impact: PhD Research in Action" perfectly encapsulates the transformative journey that defines doctoral research. In today's rapidly evolving scientific landscape, the ability to translate innovative ideas into meaningful impact is what distinguishes exceptional research from routine academic exercise.

SANVAD represents a pioneering initiative that places the PhD scholars, at the center – not merely as participants, but as organizers, presenters, and thought leaders. This peer-led platform is a testament to ICMR's commitment to nurturing the next generation of scientific leaders who will shape India's health research ecosystem.

As you engage in this conclave, I encourage you to:

- Challenge conventional thinking and explore bold, innovative solutions to pressing health challenges
- Build collaborative networks that transcend institutional boundaries
- Develop the leadership skills essential for translating research into policy and practice
- Embrace interdisciplinary approaches that can unlock new avenues of discovery

India's journey toward Viksit Bharat 2047 depends significantly on the quality and relevance of our research outputs. Your work today in areas such as communicable and non-communicable diseases, health systems strengthening, and emerging health threats will define our nation's health security tomorrow.

Remember, the true measure of research excellence lies not just in publications or citations, but in its ability to improve lives and transform communities. As you present your work and learn from your peers, keep this larger purpose in mind.

I commend ICMR for conceptualizing this unique platform and congratulate all participating scholars. May SANVAD 2026 ignite new collaborations, inspire breakthrough innovations, and strengthen your resolve to contribute meaningfully to India's scientific advancement.

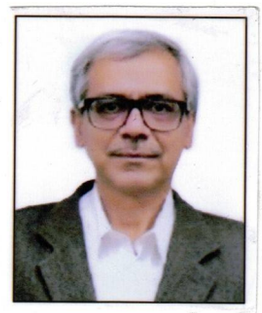
My best wishes for a productive and enriching conclave.

(Vinod Paul)

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

सत्यमेव जयते

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



MESSAGE

Dear PhD Scholars,

Welcome to SANVAD 2026.

Three days. One venue. Hundreds of brilliant minds converging at ICMR-National Institute of Malaria Research, New Delhi. This is your conclave – conceived by scholars, led by scholars, designed for scholars.

What makes SANVAD extraordinary is not just that it exists, but how it exists. You are not attending someone else's conference. You are creating the discourse. You are setting the agenda. You are defining what matters in health research today.

"From Idea to Impact: PhD Research in Action" – this theme asks a fundamental question: What happens between the moment of insight in your laboratory and the moment of change in someone's life? That gap, that critical space where science meets society, is where your generation of researchers must excel.

Your doctoral research is rigorous, detailed, methodical. But it is also deeply human. Behind every data point is a patient waiting. Behind every statistical model is a community hoping. Behind every molecular pathway you decode is the possibility of healing.

Over the next three days, you will present your findings. More importantly, you will listen, debate, question, and reimagine. You will discover that the scholar working on vector biology may hold insights relevant to your immunology research. You will realize that methodology matters as much as results. You will understand that peer learning is not a supplement to your education – it is central to it.

The Department of Health Research and ICMR have always believed that investing in young researchers is investing in India's health future. SANVAD is that belief made manifest. We trust you to lead. We trust you to innovate. We trust you to challenge even us, your mentors and institutions, to think differently.

As you navigate these sessions, remember: the research ecosystem you inherit is not the one you must preserve. It is the one you must transform. Question assumptions. Forge new partnerships. Demand better tools, better funding, better support systems. Your voice matters.

Make these three days count. Build friendships that will sustain your research career. Ask the questions no one else is asking. Share your failures as openly as your successes – they are often more instructive.

SANVAD 2026 belongs to you. Make it unforgettable.

Rajiv Bahl

(Dr Rajiv Bahl)
Secretary, Department of Health Research &
Director General, Indian Council of Medical Research

AcSIR

वैज्ञानिक और नवीकृत अनुसंधान अकादमी

ACADEMY OF SCIENTIFIC AND INNOVATIVE RESEARCH

(An Institution of National Importance Established by an Act of Parliament)

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Dated: February 13, 2026



MESSAGE

I extend my warmest greetings to all participants of SANVAD 2026 – Scholar's Assembly for Next-gen Ventures to Advance their Development – convening from 19th to 21st February at ICMR-National Institute of Malaria Research, New Delhi.

AcSIR was founded on a simple but powerful premise: that India's premier research institutions should not only conduct world-class science but also nurture world-class scientists. As an institution of national importance that promotes interdisciplinary research, AcSIR exemplifies this philosophy in action through SANVAD.

AcSIR's partnership with ICMR has always been driven by a shared commitment to excellence in health research education. Together, we have built a robust doctoral program that balances foundational coursework with cutting-edge research, that values both disciplinary depth and interdisciplinary breadth. Our PhD scholars work on questions that matter – questions with real implications for disease prevention, health equity, and medical innovation.

What distinguishes SANVAD from conventional academic conferences is its recognition that learning flows in multiple directions. Yes, you learn from faculty and experts. But you also learn from the doctoral candidate whose failed experiment led to an unexpected discovery, from the peer who developed an elegant solution to a data analysis problem, from the colleague whose interdisciplinary background offers fresh perspectives on your research question.

This conclave, conceptualized and led by you, represents a maturation of India's research training ecosystem. We are moving beyond hierarchical models of knowledge transmission toward collaborative models of knowledge creation. This is as it should be. The complex health challenges facing our nation – and our world – demand researchers who can work across boundaries, communicate across disciplines, and lead across sectors.

When we speak of "From Idea to Impact: PhD Research in Action," we are really speaking about the essence of doctoral education itself. A PhD is not merely a degree to be earned; it is a transformative process that reshapes how you think, question, and create knowledge. It is apprenticeship and mastery combined. It is learning to stand at the frontier of human understanding and push that frontier forward, even if only by inches.

As you engage over these three days, I urge you to think expansively about your role as researchers. You are not just generating data for your thesis. You are contributing to a body of knowledge that will inform treatment protocols, shape public health interventions, and influence policy decisions. The rigor with which you conduct your research today determines the reliability of the evidence base tomorrow.

Let SANVAD be a space where you test not just your research findings but your ideas about what research should be and what researchers should do. Challenge assumptions about methodology. Debate the ethical dimensions of your work. Explore how your research can be made more inclusive, more translational, more impactful.

AcSIR is proud to be part of your doctoral journey. We see in you not just the researchers you are today but the research leaders you will become – the principal investigators who will mentor the next generation, the innovators who will launch biotechnology ventures, the policy advisors who will translate evidence into action.

May SANVAD 2026 strengthen your scholarship, expand your networks, and deepen your commitment to research excellence.

With best wishes,

(Manoj Kumar Dhar)

आई सी एम आर–राष्ट्रीय मलेरिया अनुसंधान संस्थान
स्वास्थ्य अनुसंधान विभाग, स्वास्थ्य एवं
परिवार कल्याण मंत्रालय, भारत सरकार
ICMR–National Institute of Malaria Research
Department of Health Research, Ministry of Health &
Family Welfare, Government of India

Date: 16th February 2026



MESSAGE

As Dean of the Faculty of Medical Research at AcSIR, I am delighted to welcome you to SANVAD 2026, taking place from February 19 till 21 at the ICMR-National Institute of Malaria Research, New Delhi.

The doctoral journey is often described as solitary; but it need not be isolating. SANVAD – Scholar's Assembly for Next-gen Ventures to Advance their Development – recognizes a powerful truth: your peers are your greatest resource. The scholar grappling with similar methodological challenges, the researcher who has navigated the same statistical complexities, the colleague who understands the unique pressures of balancing coursework with laboratory work – these connections are invaluable.

What excites me most about this conclave is its architecture. By placing you as organizers, presenters, and contributors, SANVAD creates something rare in academic spaces: genuine peer-to-peer knowledge exchange. This is not about senior faculty lecturing from podiums. This is about you learning from each other's triumphs and setbacks, sharing protocols that work and approaches that do not, building the collaborative networks that will define your research careers.

"From Ideas to Impact: PhD Research in Action" speaks to the core of what we cultivate at the Faculty of Medical Research of AcSIR. We train you not only to be excellent researchers, but also to be translational thinkers who understand the pathway from bench to bedside, from hypothesis to health policy, and from discovery to deployment.

Your research spans the entire spectrum of health challenges – from understanding disease mechanisms at the molecular level to strengthening health systems at the community level. What unites your work is rigor, curiosity, and relevance. These three days offer you a unique opportunity to see your specific research within the broader tapestry of India's health research landscape.

I encourage you to approach SANVAD with openness. Present your work with confidence, but also with honesty about the obstacles you face. Ask difficult questions. Offer constructive critique. Form study groups. Exchange literature. Discuss failures as readily as successes – they are often your best teachers.

The academic rigor you demonstrate in your research must be matched by the leadership and innovation you show in how you collaborate, communicate, and contribute to the scientific community. SANVAD is your training ground for these essential skills.

AcSIR takes immense pride in each one of you. Your commitment to advancing medical research, often under challenging circumstances, reflects the resilience and dedication that will define India's next generation of scientists.

I wish you enriching discussions, meaningful collaborations, and insights that will strengthen your doctoral work and shape your future contributions to medical science.

Warm regards,

Dr Anup Anvikar
Director, ICMR-National Institute of Malaria Research
Dean, Faculty of Medical Research
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MESSAGE FROM THE ORGANIZING TEAM

It is with great pleasure and pride that we welcome you to SANVAD 2026 – Scholar's Assembly for Next-gen Ventures to Advance their Development.

As researchers ourselves, we understand the unique challenges and rewards of the PhD journey. SANVAD was conceived from a simple recognition: while our research questions may differ, our experiences as scholars are deeply shared. The rigors of experimental work, the pursuit of meaningful publications, and the aspiration to create impactful research unite us all.

This conclave exists to address a vital need – a platform where PhD scholars across ICMR can connect, collaborate, and learn from one another. SANVAD embodies our belief that peer-led learning is invaluable, that scholarly dialogue enriches our research perspectives, and that leadership development begins with creating opportunities to lead.

Bringing SANVAD into reality has been a transformative journey marked by diverse experiences—from moments of exhilarating enthusiasm to periods of intense dedication as we balanced our research commitments with the responsibility of materializing this vision. Through collaborative teamwork and unwavering commitment, we navigated every challenge with purpose and determination.

As you immerse yourself in SANVAD, exploring new perspectives and building bridges across disciplines, know that every element has been designed with your intellectual growth and collaborative success in mind. May this conclave become a catalyst for discoveries yet to unfold and partnerships that will shape the future of our collective endeavours.

We have been particularly mindful in ensuring that SANVAD is inclusive, respectful, and welcoming to all. Every aspect – from session design to logistical arrangements – has been planned with careful consideration for diverse backgrounds, varying research stages, and the collective well-being of our scholarly community. We remain open to your valuable suggestions for continuous improvement.

We extend our sincere gratitude to all participants for making SANVAD 2026 possible.

Wishing you enriching discussions and memorable experiences.

with warm regards,

The SANVAD 2026 Organizing Team

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Organizing Committee
SANVAD 2026

INDEX

S.No	Abstract No	Name	Abstract Title	Page No.
1	SA-001	Naveen Chandrahas Khargekar	Grey-Zone Hepatitis B In The Real World: Implementation Barriers And Short-Term Effectiveness Of Antiviral Therapy In A Public Hospital.	1
2	SA-002	Vivek Kumar	Understanding Recovery Variability In Hepatitis C Patients Through Mitochondrial Markers In An Indian Cohort	2
3	SA-003	Priyanka Panale	Tenofovir-Associated Renal Toxicity And Mitochondrial DNA Alterations In HIV Patients	3
4	SA-004	Anna Maria Mathews	Vitamin D Receptor Targeted Modulation By Plant-Derived Bioactive Compounds: A Host-Directed Strategy Against Hepatitis B Virus	4
5	SA-005	Pallavi Rushil Thaker	Utility Of Droplet Digital PCR For Non-Invasive Prenatal Diagnosis Of Sickle Cell Disease: A Protocol Standardization Study	5
6	SA-006	Prachi Sunil Kamble	Beyond Variant Detection: Integrating Functional Genomics To Improve Variant Interpretation In Diamond–Blackfan Anemia	6
7	SA-007	Pradnya Prasanna Dehadrai	Title Of The Study: Ion Homeostasis And Oxidative Injury Underlie Erythrocyte Fragility In Sitosterolemia: Evidence From An Indian Cohort	7
8	SA-008	Ridi Arvindbhai Khatri	Unsupervised Machine Learning For Immune Signature-Based Stratification Of Systemic Lupus Erythematosus (SLE) Patients From Western India	8-9
9	SA-009	Karishma Vyas	Bridging The Diagnostic Gap In Hemophilia A Patients Using Targeted Long-Read Sequencing	10
10	SA-010	Somprakash Dhangar	Comprehensive Analysis Of Tyrosine Kinase Domain Mutations And Imatinib Resistance In Chronic Myeloid Leukemia Patients	11
11	SA-011	Pooja Jaiswal	Matrix Metalloproteinase (MMP)- Based Clustering For Unravelling Heterogeneity Among Indian Interstitial Lung Disease (ILD) Patients	12
12	SA-012	Shreyasi Athalye	Viral Determinants Of Occult Hepatitis B Infection Among Household Contacts: Insights From S Gene And Precore/Core Region Analysis	13
13	SA-013	Shreyasi Chakrabarti	Study Of Molecular Mechanisms And Mirna Expressions In Association Of Mitochondrial Dysfunction In Aplastic Anemia	14

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S.No	Abstract No	Name	Abstract Title	Page No.
14	SA-014	Sayali Tiwari	Providing Optimum Care To Pregnant Women With Sickle Cell Disease: Exiting Programme Services, Challenges, & A Way Forward	15
15	SA-015	Monali Lokhande	Prevalence Of Clinically Significant Blood Group Antigens And Rate Of Alloimmunization In Sickle Cell Disease Patients And Blood Donors In Chandrapur, Maharashtra.	16
16	SA-016	Maithili Dalvi	A Systematic In-Silico And In-Vitro Approach For The Characterisation Of RASGRP2 Variants In Inherited Platelet Disorders.	17
17	SA-017	Sayali Shinde	Unravelling Early-Onset Myocardial Infarction And Coronary Artery Disease (<40 Years): A Multi-Pathway Genetic And Functional Analysis.	18
18	SA-018	Nidhi Nitin Desai	Integrating Genomics And Transcriptomics To Resolve Variant Consequences In Monogenic Autoinflammatory Disorder	19
19	SA-019	Gratial Theres Joseph	Validation Of Diagnostic Screening Test For Pharmacogenomic Targets For Thiopurine Drugs In Indian Pediatric Acute Lymphoblastic Leukemia Patients	20
20	SA-020	Aalaap Anand Naigaonkar	The PCOS Follicle At A Crossroads: Imbalance In The Glucose Metabolism Pathways	21
21	SA-021	Noreen Grace George	An Ultra-Sensitive And Cost-Effective Method For Cell-Free Dna Isolation From Blood Sample	22
22	SA-022	Sunena Bamoriya	Dissecting Molecular Mechanisms Of Viral Replication In Trophoblast Cells: Implications For Transplacental Transfer During Pregnancy	23
23	SA-023	Vishakha Thanwar	DNA Break Mapping In Placental Cells Reveals Vulnerability Of Repetitive Sequences In Pregnancy Complication	24
24	SA-024	Situl Mahanta	Insights From Transcriptomic Profiling Into Cellular Homeostasis In Aicardi–Goutières Syndrome	25
25	SA-025	Rushigandha Salunke-Rane	Dynamic Regulation Of TLR9 During Progression Of Triple-Negative Breast Cancer	26

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S.No	Abstract No	Name	Abstract Title	Page No.
26	SA-026	Nisha Bilkhiwal	The Moonlighting Face Of HMGB1 In Endometrial Regeneration	27
27	SA-027	Durva Ashok Panchal	Understanding The Molecular Crosstalk Guiding Sperm Towards The Egg	28
28	SA-028	Kshitija Sachin Rahate	Decoding Host-Candida Albicans Interactions In Vaginal Infection: A Systems-Level Perspective	29
29	SA-029	Sharad Bhagat	Immune And Drug Resistance Mutation Profiling Of Putative HIV-1C Reservoirs In An Indian Cohort	30
30	SA-030	Pratik Dayanand Rasal	Development And Characterization Of 3D Human Placentoids And Their Application In Drug Testing	31
31	SA-031	Ponsankaran R	Non-Coding RNA-Mediated Regulatory Networks In The Maternal Endometrium In Recurrent Implantation Failure And Pregnancy Loss	32
32	SA-032	Sapna Yadav	Maternal Cellular Immune Determinants Associated With Ccmv And Adverse Pregnancy Outcome	33
33	SA-033	Nikita Sharma	Pancreatic B Cell Functions And Heterogeneity Of Gestational Diabetes Mellitus In Indian Women	34
34	SA-034	Shilpa Dinesh Bhowmick	Systemic And Antigen-Specific Immune Signatures Associated With Latent Tuberculosis Infection In PLHIV	35
35	SA-035	Rishikesh Kumar	Deciphering Role Of Novel Salmonella Typhi Effector In Controlling Host Cell Death And Intracellular Bacterial Survival	36
36	SA-036	Puja Kumari	Evaluation Of Circulating Micrornas For Early Detection Of Breast Cancer	37
37	SA-037	Pratik Guru Devadiga	ART Driven Immune Reconstitution Is Linked To Heterogeneous Longitudinal Gut Microbiome Remodelling And TB Associated Dysbiosis Risk In HIV+LTBI+ Individuals	38
38	SA-038	Ananda Pal	Isolation, Characterization, And Therapeutic Potential Of Lytic Bacteriophage Targeting MDR Pseudomonas Aeruginosa	39

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S.No	Abstract No	Name	Abstract Title	Page No.
39	SA-039	Ragini G	Comparative Microbiome Analysis In Field-Caught Aedes Aegypti Populations From Puducherry, India	40
40	SA-040	Jibi Lukose	Nanofiber-Encapsulated Bacillus Thuringiensis Israelensis VCRC B668 For Eco- Friendly Mosquito Control	41
41	SA-041	Hajra Akil Gupta	Evaluating The Immunotherapeutic Potential Of Rfhsp-D In LPS-Induced In Vitro And In Vivo Models Of Pre-Eclampsia	42
42	SA-042	Snehal Suresh Bhingardeve	An Integrative Epigenetic-Epitranscriptomic Landscape Of PCOS: Micrornas At The Regulatory Crossroads	43
43	SA-043	Rithika Rajendran	Effects Of Altered Levels Of Extracellular High Mobility Group Box – 1 (HMGB1) On Embryo Implantation	44
44	SA-044	Debolina Saha	Integrated Buccal Swab Based Biochemical And Genetic Analyses Revealed 18 Novel Variants In Indian Paediatric Mitochondrial Cases	45
45	SA-045	Samina Rahman	Development Of A Low-Cost, Rapid And Ultrasensitive CRISPR-Cas12a Based Diagnostic Kit For Tuberculosis	46
46	SA-046	Apoorva Subhash Pawar	Distinct Temporal Regulation Of Trop2 And Epcam Expression In Rat And Human Placenta	47
47	SA-047	Komal Ranjan	Trypanothione Synthetase Mediated Antileishmanial Drug Resistance And Redox Balance In Leishmania Donovani	48
48	SA-048	Abhishek Kumar Rai	Identified Secreted Leishmanial Protein As A Novel Biomarker For The Diagnosis Of VL, PKDL And VL Co-Infected Cases In Bihar	49
49	SA-049	Shakshi Dahiya	From Stigma To Suffering: Impact Of Stigma On Health-Related Quality Of Life And Healthcare Access In Sickle Cell Disease	50
50	SA-050	Karishma Sharma	Epidemiological And Molecular Surveillance Of Dengue Virus Circulating In Jodhpur District, Rajasthan, India	51
51	SA-051	Akash Ashok Dhotre	Proteomic And Genetic Characterization Of A Potent Mosquitocidal Bacillus Thuringiensis Isolated From Spoiled Fruit For Sustainable Mosquito Control	52

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S.No	Abstract No	Name	Abstract Title	Page No.
52	SA-052	Ngangbam Pushparani Devi	CRISPR-Cas Based Detection Of Pseudomonas Aeruginosa And Associated Antibiotic Resistance.	53
53	SA-053	Shubham Bhatt	In Silico Drug Discovery Approach To Target Isocitrate Lyase In Dormant Mycobacterium Tuberculosis	54
54	SA-054	Priya Priydarshni	Exploring The Role Of Iron As A Critical Determinant In Leishmania Donovani For Survival, Oxidative Stress Tolerance And Infectivity	55
55	SA-055	Sapna Yadav	Evaluation Of Natural Coumarins For Anti-Biofilm Activity Against Mycobacterium Smegmatis: A Dual-Mechanism Approach	56
56	SA-056	Vishal Rajendra Koligudde	Cervical Cytology Abnormalities And High-Risk HPV Genotype Distribution Among Women From North East India	57
57	SA-057	Vennela Gande	Comparative Analysis Of Body Composition, Metabolism, Diet, And Gut Microbial Characteristics Of Elite Indian Endurance And Resistance Athletes	58
58	SA-058	Tammireddy Sai Pragathi	Reduced Oral Bacterial Nitrate Reductase Activity In Hypertension : A Case Control Study	59
59	SA-059	Raghavendra Rao Chowdavarapu	Unveiling The Path To Nutrition: Factors Influencing Nutritional Resilience In Low-Birth-Weight Under-Five Children	60
60	SA-060	Prerna Jyoti	Preconceptional Paternal Calorie Restriction Dysregulates The AMPK/SIRT Pathways In Diet-Induced Obese Wistar Rats Offsprings	61
61	SA-061	Suneesh NS	Multiepitope Mrna Vaccine Design Targeting Structural And Regulatory Proteins Of HSV-2 To Induce Robust T-Cell Immunity	62
62	SA-062	Shivangi Singh Chauhan	Seasonal Variation In Dietary Intake And Nutritional Parameters Among Children Aged 6-23 Months: Evidence From NFHS-5 Data	63
63	SA-063	Pratisthita Baruah	Melioglowpcr: A Rapid, Low-Cost, Ultra-Sensitive CRISPR-Cas-Based Molecular Diagnostic System For Detecting Melioidosis In Hospital Settings	64

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S.No	Abstract No	Name	Abstract Title	Page No.
64	SA-064	Souma Raj Das	Development Of 5-FU Resistant Gallbladder Cancer Cell Line And Identification Of Predictive Biomarkers Associated With Chemoresistance	65
65	SA-065	Neeraj Saklani	Stage-Specific Mirna Profiling Reveals Key Regulators Of EMT And EGFR-TKI Resistance In Gallbladder Cancer	66
66	SA-066	Pratiksha Sudhakar Pansambal	Microglial Senescence Triggered By Dolutegravir: Potential Links To Neurodegenerative Pathology	67
67	SA-067	Nikhita Ramesh Boda	Effect Of Finger Millet-Based Supplementation On Anthropometry And Body Composition Among Moderately Acute Malnourished Under 5 Children In Telangana, India: A Randomized, Community-Based Trial	68
68	SA-068	Jyoti Jayvant Sawant	Distinct Fcγiia-Mediated Entry Of SARS-Cov-2 Induces SYK–MAPK–AP-1–Biased Inflammatory Signalling With Delayed Innate Antiviral Responses	69
69	SA-069	Tapu Barman	Formulation, Characterization And Antimicrobial Investigation Of Nobel Natural Antibiotics On Clinically Isolated Enteric Bacterial Strains.	70
70	SA-070	Parishmita Boruah	Lyme Borreliosis In Assam: A Study Among Acute Febrile Illness Cases And Animal Farm Workers	71
71	SA-071	Aman Akhilesh Chaurasia	Clinical Relevance Of Differentially Methylated Sperm Long-Noncoding RNA Genes In Male Partners Of Couple Experiencing Idiopathic Recurrent Pregnancy Loss	72
72	SA-072	Pratik Kumar Rath	Genomic Landscape Of Gastric Cancer Patients From North East India	73
73	SA-073	Parth Sarin	Gut Microbial Dysbiosis And Elevated Mucosal Inflammation In Severe Acute Malnutrition: A Case-Control Study From India	74
74	SA-074	Sayli Raghunath Rasal	Impact Of Different Emicizumab Doses On Clinical Outcomes And Global Coagulation Profiles	75

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S.No	Abstract No	Name	Abstract Title	Page No.
75	SA-075	Precious Lyngdoh	Role Of Climate On Dengue And Malaria In Thane, India	76
76	SA-076	Kota Sri Naga Hridayanka	Intra-Articular Delivery Of Nanoemulsified Curcumin Ameliorates Joint Degeneration In A Chemically Induced Model Of Osteoarthritis	77
77	SA-077	Pritha Ghosh	Impact Of Lead And Amyloid-B Co-Exposure On ER Stress And ER Stress-Associated Cell Death In Human Neuronal Cells	78
78	SA-078	Gopal Vishwas	Prevalence Of Malnutrition In Visceral Leishmaniasis And Its Association With Relapse Frequency And LD Body Positivity: A Retrospective Cohort Study	79
79	SA-079	Anil Kumar	Topic: Phytochemical Warfare: Exploring Catharanthus Roseus Leaf Extract As A Natural Insecticide For Sandfly Management.	80
80	SA-080	Madhukar	Prevalence Of TB Among The Inmates Of A Prison In Patna District	81
81	SA-081	Roshan Kamal Topno	PKDL- Challenges To Early Diagnosis	82
82	SA-082	Tannu Joshi	A Pipeline For Analysis Of Therapeutic Potential Of Phytomedicines: In-Silico Analysis	83
83	SA-083	Manvi Naugain	An Impediment To Breast Carcinogenesis: Bioinformatic Analysis With Molecular Characterization Of A Long Unappreciated Factor SALL2 In Breast Carcinogenesis	84
84	SA-084	Navya Sree Boga	Prevalence Of Leptin-Specific Epigenetic Modulation In Preterm Cord Blood And Its Correlation With Neonatal Adiposity	85
85	SA-085	Priyanka Bai	Malaria Vector Bionomics In Highly Endemic District Dantewada, Chhattisgarh	86
86	SA-086	Chirantan Maity	Sero-Epidemiological Landscape And Clinico-Demographic Determinants Of HAV And HEV Infections In Jabalpur, Madhya Pradesh: A 2024–2025 Study	87

© ICMR 2026

S.No	Abstract No	Name	Abstract Title	Page No.
87	SA-087	Shivam Gupta	Harnessing Structural Biology And Computational Tools For The Screening Of Broad-Spectrum Antimalarials	88
88	SA-088	Dilkash Ara	Aflatoxin B1 Exposure Decreases Hepatic Iron Intake: Potential Cause For Global Anaemia Prevalence	89
89	SA-089	Soumam Dutta	Vitamin D3 Outperforms Vitamin D2 In Regulating Specific Classical Functions In A Rat Model	90
90	SA-090	Sonali Vedika	Metabolomics-Driven Discovery Of Metabolite Biomarkers In PKDL	91
91	SA-091	Anjusha Bhasker	"Unraveling The Impact Of Maternal Deficiencies Of Protein And Folic Acid In Critical Windows Of Embryonic Development In Mice "	92
92	SA-092	Ravi Ranjan	Exploring The Molecular Architecture And Function Of 3-MST In Leishmania Donovani For Drug Target	93
93	SA-093	Kundan Kunal	Bioactive Compounds Of Azadirachta Indica As Promising Antileishmanial Agents With Defined Molecular Targets And Immunoregulatory Effects.	94
94	SA-094	Anisha Shah	Molecular Surveillance Of Rickettsia Felis In Ticks From Tripura: Insights From India's Northeast Border	95
95	SA-095	Sritama Sarkar	Development And Evaluation Of Peptide-Based Vaccine Candidate Targeting Immunodominant Regions Of The Envelope Protein Of Kyasanur Forest Disease Virus	96
96	SA-096	Gajendra Ravindra Shahapure	Development Of CAR NK Cells To Target Latent HIV-1 Reservoirs	97
97	SA-097	Nitya Bansal	Relative Validation Of Telephonic Versus In-Person 24-Hour Dietary Recalls Among Primary School Children: A Pilot Study	98
98	SA-098	Urvashi Yadav	Potential Of Secondary Malaria Vector In Malaria Transmission Dynamics In Northeastern States Of India	99
99	SA-099	Bharti Goyal	Unraveling The Symphony Of HSP 70 In Indian Malarial Vector- A Molecular Ballet Shaping Mosquito Development And Influencing Plasmodium Transmission	100

© ICMR 2026

S.No	Abstract No	Name	Abstract Title	Page No.
100	SA-100	Shankar G	Burden And Distribution Of Pfhrp2 And Pfhrp3 Gene Deletions In Plasmodium Falciparum In India: A Systematic Review And Meta-Analysis Protocol	101
101	SA-101	Vinita Mamnani	Assessment Of Antibody Responses To Plasmodium Falciparum Antigens For Malaria Serosurveillance In India	102
102	SA-102	Jayakrushna Kumbhar	Assessment Of Pathogenicity Of 2.3.4.4b HPAI H5N1 Virus And Evaluation Of Inactivated Virus As A Vaccine Candidate	103
103	SA-103	Sapna Choudhary	Isolation And Virological Characterisation Of Respiratory Syncytial Virus From Clinical Samples	104
104	SA-104	Pooja Umare	Isolation Of Coxsackievirus B4 From A Case Of Acute Gastroenteritis: A Rare Occurrence	105
105	SA-105	Sneha Rani	Towards Exploring Novel Inhibitors Against Leishmania Donovani	106
106	SA-106	Shrabani Das	Co-Exposure To Lead And Aβ Peptides Disrupt Autophagy And Synaptic Protein Homeostasis Via CDK5 And CRMP1 Dysregulation In SH-SY5Y Cells	107
107	SA-107	Komal Shrivastav	Integrative Network Analysis Of Metabolic Syndrome	108
108	SA-108	Kashung Shangamla	Somatic Mutation Profiling Of Esophageal Cancer In Northeast India: An Ongoing Phd Study	109
109	SA-109	Sudipta Mondal	Epitope Centric Mutational Profiling Of Dengue Virus Serotype 3 Envelope Protein With Relevance To Vaccine Design	110
110	SA-110	Amrita Kumari	Exploration Of Epitope Ensembled Chimera To Boost Immunity To Leishmaniasis	111
111	SA-111	Pooja Yadav	Iron Homeostasis And Reproduction: Unveiling The Microbiome-Gut-Brain-Axis Connection In The Mosquito Anopheles Culicifacies	112
112	SA-112	Dipti Yadav`	Addressing Antimicrobial Resistance: Challenges And Opportunities In Nursing Practice	113

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S.No	Abstract No	Name	Abstract Title	Page No.
113	SA-113	Kanniganti Bharathi	Artificial Intelligence In Infectious Disease Research: An Analysis Of Global Trends And Applications	114
114	SA-114	Dilip Kumar	Prevalence Of Linezolid Resistance Among Multidrug-Resistant Mycobacterium Tuberculosis Isolates Recovered From Pulmonary Tuberculosis Patients In Uttar Pradesh, North India	115
115	SA-115	Nishanth Kumar S	Development And Validation Of High-Throughput Taqman Probe-Based Multiplex Qpcr Assays For Pathogen Monitoring In Laboratory Rodent Colonies	116
116	SA-116	Aruna Mishra	Uncovering Inhibitory Mechanisms Of HIF-1α Signaling To Enhance Mesenchymal Stem Cell Efficacy In Myocardial Ischemia–Reperfusion Injury	117
117	SA-117	Neetu Bhargav	Antiviral Activity Of Bacteriocins Against The Dengue Virus In Different Cell Lines	118
118	SA-118	Supratim Ghosh	Coinfection Dynamics And Pathogenic Interplay Between Parasitic Microorganisms And Helicobacter Pylori For Unravelling The Complex Microbial Interrelationship	119
119	SA-119	Vinaya Thorat	Antiviral Activity Of Anti-Psychotic Drugs Against Dengue And Chikungunya Viruses	120
120	SA-120	Aarti Patel	Detection Of High-Risk Human Papillomavirus Using Molecular Assays.	121
121	SA-121	Pallavi Indwar	An AI-Driven Voice Assistance System To Improve Medication Safety In Visually Impaired	122
122	SA-122	Rashmi G Shinde	Utility Of Mathematical Models Of Dengue Vaccination For Public Health Decision-Making: Critical Elements And Evidence Gaps	123
123	SA-123	Megholi Roy	Antimicrobial Resistance Patterns Of Enteric Bacterial Pathogens Isolated From Acute Diarrhoeal Cases: Evidence From A Hospital-Based Surveillance System	124
124	SA-124	Ankita Mourya	Determination Of Host Preference In Malaria Vector An Anopheles Culicifacies In Madhya Pradesh	125
125	SA-125	Pramit Ghosh	Exploring Strategic Interventions Targeting Antibiotic Resistance From One-Health Perspective	126

© ICMR 2026

S.No	Abstract No	Name	Abstract Title	Page No.
126	SA-126	Suyesh Shrivastava	Metabolic Syndrome In A Particularly Vulnerable Tribal Group: A Study Among The Bharia Tribe Of Chhindwara	127
127	SA-127	Deepak Kumar	Tempo-Spatial Pattern And Risk Factors Of Gender Disparity In Infant And Child Mortality In India	128
128	SA-128	Sudipta Kumar Sahu	Access And Utilization Of Maternal And Child Health Services During Covid19 Pandemic: Findings From Odisha, India	129
129	SA-129	Jyotirmayee Turuk	Developing An Integrated Tiered Molecular Diagnostic And DST Framework For Nontuberculous Mycobacteria	130
130	SA-130	Satyendra Kumar Shukla	Dietary Influence On Oral Microbial Taxa: Vegetarian Vs. Omnivorous	131
131	SA-131	Khyati Shukla	Meta-Analysis Of Oral Microbiome Dysbiosis In Oral Potentially Malignant Disorders	132
132	SA-132	Gayathri K	Developing A Respectful Maternity Care Tool: A Delphi Based Consensus Approach	133
133	SA-133	Diksha Saini	Analyses Of The Oral Microbiome In OSCC Patients Using Metaproteomics And Metagenomics Reveal Enrichment Of Pathobionts And Abundance Of Immunosuppressive Proteins	134-135
134	SA-134	Priyanka Verma	Prevalence Of Substance Abuse Among Tribal Population Of Asia: A Systematic Review And Meta-Analysis	136
135	SA-135	Shreya Singh	Emerging Resistance In Colistin And Mcr Gene Distribution In Gram-Negative Bacteria From A Tertiary Care Hospital In Odisha, India	137
136	SA-136	Alisha Sinha	ISSR-PCR Based Molecular Surveillance Of Multidrug-Resistant Bacteria From Street-Vended Foods And Evaluation Of Costus Igneus As A Natural Antibacterial Alternative	138
137	SA-137	Utkalika Mallick	Molecular Identification And Antifungal Susceptibility Profiling Of Candida Species From Vaginal Infections With PCR-Based Detection Of Resistance Genes	139
138	SA-138	Aditi Pal	Integrated Molecular Surveillance And Eco-Friendly Control Of Aedes Mosquitoes: Detection Of Dengue Virus Serotypes And Evaluation Of Plant-Based Biopesticides In Bhubaneswar, India	140

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S.No	Abstract No	Name	Abstract Title	Page No.
139	SA-139	Arpita Panda	The Gendered Burden Of Care: Experiences Of Female Family Caregivers In Sickle Cell Disease And Thalassemia	141
140	SA-140	Swatismita Priyadarsini	Whole Genome Sequencing And Genomic Characterization Of Dengue Virus Circulating In Odisha During 2024–2025	142
141	SA-141	Rojalin Priyadarshini	Evaluating The Gut-Brain Axis In Parkinson's Disease: Integrating Clinical Non-Motor Symptoms With Microbiota	143
142	SA-142	Stuti Tripathi	Childhood Immunisation In India During COVID-19: An Interrupted Time Series Analysis Of Health Management Information System (HMIS) Data	144
143	SA-143	Kratika Pandiya	Identifying Latent Groups Within Rural Populations And Exploring Their Phenotypic Differences In Relation To Infant Mortality Rate	145
144	SA-144	Rajalakshmi Elumalai	Infertility Care Pathways And Lived Experiences Of Care Seekers In Tamil Nadu: A Rapid Qualitative Analysis	146
145	SA-145	Shaina Beg Mirza	Development Of A Novel Direct Drug Susceptibilitytesting Protocol For M. Tuberculosis Using Phage Lysin: A Pilot Study	147
146	SA-146	Pallavi Kanade Shidhaye	Advanced HIV Disease And Associated Factors Among HIV Infected Individuals Registered In A Programme Clinic At Pune: A Retrospective Study	148
147	SA-147	Kaustubh Bora	Are Hemoglobinopathies Important Contributors to Anemia During Pregnancy In Assam? Insights From An Observational Study In A Population-Based Cohort	149
148	SA-148	T Nithu	Seasonal Patterns & Risk Factors Of Respiratory Syncytial Virus Among Nicobarese Tribal Populations Of Andaman & Nicobar Islands	150
149	SA-149	Suneetha H	Evidence Of Leptospira Spp. In The Soil Of Andaman Islands	151
150	SA-150	Sarath K S	Structural, Biochemical, And Functional Insights Into The Periplasmic Serine Protease Mucd (LIC_12812) Of Leptospira Interrogans	152

© ICMR 2026

S.No	Abstract No	Name	Abstract Title	Page No.
151	SA-151	S Fatima Firdaus	Emergence And Re-Emergence Of The Chikungunya In The Andaman And Nicobar Islands	153
152	SA-152	Sunanda Sahoo	Designing A Multi-Stage Malaria Vaccine Against Plasmodium Falciparum	154
153	SA-153	Sushmita Kerketta	Healthcare Accessibility And Utilization Of Facility- And Community-Based Health Services Among Tribal Populations In Odisha: A Cross-Sectional Study	155-156
154	SA-154	Pratikshya Pati	Targeting Regulatory T Cells To Improve Cancer Immunotherapy	157
155	SA-155	Shanparvish E	High Burden Of Bacterial Childhood Diarrhoea And Emerging Antimicrobial Resistance In The Nicobar Group Of Islands	158
156	SA-156	Monalisha Padhiary	Chitosan Nano-Scaffold To Combat MDR Strain For Chronic Wound Healing Applications	159
157	SA-157	Subhashree Mishra	Immunology And Nanotechnology Synergy To Combat Multi-Drug Resistant Pathogens	160
158	SA-158	Sonalisha Bahalia	Epigenetic Regulation Of Chikungunya Virus Replication By Chaetocin-Mediated H3k9me3 Inhibition	161
159	SA-159	Pratibha Singh	In-Silico Design And Validation Of RT-LAMP Primers Targeting The 3′UTR Of Dengue, Japanese Encephalitis, And West Nile Viruses	162
160	SA-160	Saloni Basu	Aetiology Of Enteric Viruses Associated With Childhood Diarrhoea Among Tribal And Non-Tribal Population Of Nicobar Islands	163
161	SA-161	Zeeshan Ahmad	Screening For Potential Inhibitory Molecules Against KIF4A To Target Breast Cancer Stem Cells	164
162	SA-162	A Parveen	Identification Of Vaccine Targets In Leptospira Using Convalescent Serum (CS) And Validation Of Immunoprotection	165
163	SA-163	Abhishek	In Vitro Antiviral Activity Of Extracts Of Medicinal Plant, Euphorbia Hirta, Against Chikungunya	166
164	SA-164	Banshanlang Marboh	Identification Of Diagnostic Target From Leptospiremic Urine Sample And Development Of Point-Of-Care Test (Poct) Based On Lateral Flow Assay (LFA)	167

© ICMR 2026

S.No	Abstract No	Name	Abstract Title	Page No.
165	SA-165	Tsupongsangla Lcr	Study Of Biofilm Formation Of Leptospira And Its Role In The Survival Of Leptospira In The Environment	168
166	SA-166	Chandralakha C	Spatial Distribution And Habitat Preference Of Dengue Vectors Across Tribal And Non-Tribal Settlements In The Andaman And Nicobar Islands	169
167	SA-167	Soumyadeep Moyra	Socio-Epidemiological Burden Of Malaria In Central India: A Biocultural Anthropological Perspective.	170
168	SA-168	Ansari Md. Afzal Md. Idris	Novel Genomic Markers For Accurate Identification Of M. Leprae Genotypes And Drug Resistance Mutations	171
169	SA-169	Swarup Sanjay Gujarathi	Anti-Hepatitis B Virus Activity Of Terminalia Chebula Mediated By Reverse Transcriptase Inhibition And Modulation Of Host Inflammatory Pathways	172
170	SA-170	Surthi Ravedar	Hepatoprotective Potential Of Tamarindus Indica L. Against Isoniazid–Rifampicin-Induced Hepatotoxicity: An Integrated In-Vitro And In-Silico Study	173
171	SA-171	Amritha Das	Triclosan-Induced Activation Of ERK/NF-Kb Signaling Pathways Drives The Inflammatory Responses In Epithelial Cells And Macrophages	174
172	SA-172	Deepanker Das	Machine Learning Driven Spatiotemporal Prediction Of Dengue Vector Dynamics From Landscape And Microclimatic Variables	175
173	SA-173	Namrata Pal	Isolation And Characterization Of Lytic Bacteriophages Against Multi Drug-Resistant Acinetobacter Baumannii	176
174	SA-174	Tarun Patil	In-Silico Analysis Of Genomic Diversity And Mutational Landscape Of Human Astrovirus	177
175	SA-175	Lokendra Rathod	Biomonitoring Of Serum Endocrine-Disrupting Chemicals (Edcs) Exposure And Type 2 Diabetes Risk: A Case-Control Study	178
176	SA-176	Swati Pal	Small Area Estimation Of Cognitive Impairment Among Older Adults In India: A Multilevel Approach	179
177	SA-177	Nitika Monga	Oral Health Inequity In India: Magnitude, Determinants, And Policy Imperatives	180

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S.No	Abstract No	Name	Abstract Title	Page No.
178	SA-178	Josephine Pradhan	Antibiotic-Resistant Enterobacterales Colonization Among Children In A Sub-Urban Community In South India	181
179	SA-179	Gladys Angelin Rachel Durairaj	Isolation, Detection & Characterization Of Exosomes From HIV-1 Infected And Uninfected CD4+ T Cells	182
180	SA-180	Biswajit Swain	Exploring Non-Parenteral Routes For Delivery Of Peptide Therapeutics.	183
181	SA-181	Matrujyoti Pattnaik	Perception And Determinants Leading To Antimicrobial (Mis)Use In The Rural Communities Of Odisha, India	184
182	SA-182	Nandita G	Monocyte TNF-Superfamily Signalling Dysregulation In Tuberculosis–Type 2 Diabetes Mellitus Comorbidity	185
183	SA-183	Sundrakumar K	Hybrid Artificial Intelligence Modelling Of Longitudinal Cough Acoustics For Early Treatment Response In Pulmonary Tuberculosis	186
184	SA-184	Harinisri Gunasekaran	Profiling Of Circulating Inflammatory Biomarkers In Individuals With Latent Tuberculosis Infection Compared With Healthy Controls	187
185	SA-185	Venkatesan P	A CRISPR-Cas13a- Based Molecular Assay For Rapid And Accurate Detection Of Mycobacterium Tuberculosis	188
186	SA-186	Michel Prem Kumar M	Rapid And Cost Effective Detection Of Bedaquiline And Linezolid Drug Resistance In Mycobacterium Tuberculosis By Luciferase Reporter Phage Assay	189
187	SA-187	Sathyamurthi P	Tb-Induced Immunosenescence Contributes To Increased Mortality Among Successfully Treated And Cured Tb Patients	190
188	SA-188	Sandhya Vivekanandan	Design And Characterization Of Peptido-Mimetics Of Broadly Neutralizing Antibodies Targeting Vulnerable Sites On The Hiv-1 Envelope	191
189	SA-189	Arul Nancy P	Plasma And TB Antigen Stimulated Immune Signatures Associated With Treatment Outcomes In Pulmonary Tuberculosis	192

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S.No	Abstract No	Name	Abstract Title	Page No.
190	SA-190	Silambuchelvi K	Structural Insights Into Rifampicin Interaction Altered By Borderline Rpob Mutations: An Insilico Study	193
191	SA-191	Lucia Precilla K	Low-Frequency Of Hiv-1 Protease Resistance Mutations In A Pi-Naïve And Pi-Exposed Hiv-Infected Cohort	194
192	SA-192	Radhika.G	Drug Susceptibility Profiling Of Pulmonary Nontuberculous Mycobacteria (NTM) Isolated From Presumptive Pulmonary Tuberculosis Patients	195
193	SA-193	Dharmesh Lal	Strengthening Continuum Of Care (COC) For Patients Of Hypertension And Diabetes In Dibrugarh District, Assam, Using Hybrid-III Interrupted Time Series Design	196
194	SA-194	Tanu Anand	Morbidity Profile, Patterns And Determinants Of Healthcare Utilization And Out Of Pocket Expenditure On Healthcare Among Elderly In India: A Secondary Analysis Of Longitudinal Ageing Study Of India (LASI) Wave 1	197
195	SA-195	Priya	PMCA4b: The Host Switch Controlling Malaria Parasite Growth And Artemisinin Resistance	198
196	SA-196	Rubal Kumari	Essential Oil Nano-Formulation For Prolonged And Sustainable Mosquito Vector Control	199
197	SA-197	Ravleen Kaur Bakshi	Addressing Multilevel Barriers To Lifestyle Change In Obesity: Development And Validation Of A Behavioural Intervention	200
198	SA-198	Priyanka Kumari	Development Of A Recombinase Polymerase Amplification Assay For Spotted Fever Group Rickettsia	201
199	SA-199	Prashansha Srivastvava	Determination Of Methicillin-Resistant Staphylococcus Aureus From Clinical Samples In A Tertiary Care Hospital Of Eastern Uttar Pradesh By Phenotypic And Molecular Methods.	202
200	SA-200	Jyoti Singh	A Comprehensive Scoping Review Of Biochemical Newborn Screening Landscape In India (1985 - 2025)	203

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Abstract No: SA-001

Grey-Zone Hepatitis B in the Real World: Implementation Barriers and Short-Term Effectiveness of Antiviral Therapy in a Public Hospital



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Introduction: Chronic hepatitis B (CHB) patients with low-level viremia represent a clinical "grey zone" in which treatment is often deferred despite ongoing risk of liver injury.[1] In public-sector settings, care is further shaped by structural constraints, fragmented pathways, and patient perceptions, and real-world evidence integrating biological outcomes with implementation challenges remains limited.

Objectives: To conduct a hybrid Type 2 effectiveness–implementation study among adults with low-viremia CHB in a public-sector hospital, evaluating antiviral treatment.

Methods: An observational effectiveness–implementation study was conducted among 54 adults with CHB and low viremia attending a tertiary public hospital in Mumbai. Baseline demographic and risk profiles were recorded. Barriers to care were mapped using the Consolidated Framework for Implementation Research (CFIR).[2] Patients on antiviral therapy were followed for 6 months with paired analyses.

Results: The cohort (34 males, 20 females) was predominantly aged 30–50 years and represented diverse occupational backgrounds. Most reported a single lifetime sexual partner; injectable drug use was uncommon. Mean age at first detection was 38.9 ± 11.9 years. At baseline, neither HBV DNA nor quantitative HBsAg independently predicted ALT, AST, FIB-4, or APRI (all $p > 0.05$). Alcohol intake was the only independent predictor, with non-drinkers exhibiting lower AST ($B = -20.48$; $p = 0.044$). CFIR mapping revealed outer-setting barriers (distance, travel time, transport, limited family support), inner-setting inefficiencies (fragmented workflows), and individual-level factors (poor knowledge, fear of side effects, skepticism, irregular adherence). At 6 months, 8 treated patients were followed; 6 achieved "Target Not Detected," while biochemical and fibrosis responses remained heterogeneous.

Conclusions: In grey-zone CHB, short-term effectiveness is strongly shaped by real-world implementation factors. Virological control does not uniformly translate into early biochemical or fibrosis improvement. Addressing multilevel barriers is essential to optimise uptake and outcomes.

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Abstract No: SA-002

Understanding recovery variability in hepatitis C patients through mitochondrial markers in an Indian cohort



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Introduction: Chronic hepatitis C virus (HCV) infection is linked to mitochondrial dysfunction, contributing to liver injury and immune imbalance. While direct-acting antiviral (DAA) therapy achieves high sustained virological response (SVR) rates, liver recovery varies considerably among patients. Non-invasive fibrosis indices such as APRI and FIB-4 are commonly used to monitor hepatic injury, yet the biological factors driving their variable improvement remain unclear. Mitochondrial DNA (mtDNA) heteroplasmy and mtDNA copy number are emerging markers of mitochondrial integrity and cellular stress that may reflect differences in post-SVR recovery.

Objectives: To assess mtDNA heteroplasmy and relative mtDNA copy number in post-SVR hepatitis C patients and explore their association with non-invasive fibrosis indices

Methods: Mitochondrial alterations were assessed in an Indian cohort of chronic HCV patients with paired baseline and SVR12 samples. Liver recovery was evaluated using elastography, biochemistry, and APRI and FIB-4 scores. MtDNA variants were annotated using Mitomaster, mtDNA copy number was measured by qPCR, and correlation analyses are ongoing. Mitochondrial membrane potential in PBMCs is currently being assessed using JC-1 staining.

Results: Following DAA therapy, patients showed significant improvement in liver stiffness and reductions in serum ALT and AST levels ($p<0.05$), accompanied by improvement in APRI and FIB-4 scores. Preliminary mitochondrial variant profiling identified the presence of multiple low-to-moderate heteroplasmic mtDNA variants in a subset of patients, with marked inter-individual variability. Frequently observed variants included control-region changes such as m.73A>G and m.263A>G, along with heteroplasmic variants in oxidative phosphorylation–related genes including MT-ND and MT-CYB. No dominant pathogenic mtDNA mutation was observed across the cohort. Preliminary mtDNA copy number analysis revealed substantial variability at SVR12; detailed heteroplasmy burden estimation and correlation analyses are currently ongoing.

Conclusions These preliminary findings indicate persistent mitochondrial genomic heterogeneity in post-SVR hepatitis C patients, which may contribute to variability in non-invasive fibrosis indices and hepatic recovery.

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Abstract No: SA-003

Tenofovir-Associated Renal Toxicity and Mitochondrial DNA Alterations in HIV Patients



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Introduction: Tenofovir disoproxil fumarate (TDF) is a key component of first-line anti-retroviral therapy (TDF-ART) but is associated with early renal tubular dysfunction. Mitochondrial toxicity is a proposed mechanism of TDF nephrotoxicity, however clinical evidence linking renal injury with mitochondrial DNA (mtDNA) alterations in HIV patients remained limited.

Objectives: To investigate alterations in renal and tubular function, mitochondrial DNA content, and antioxidant responses associated with early renal toxicity in HIV patients receiving TDF-based ART.

Methods: Prospective observational study was conducted in 48 HIV patients receiving TDF-ART and followed for six months. Renal function, tubular injury markers and CD4 counts was assessed. Urinary β2-microglobulin (β2M) levels were done by ELISA. Analysis of mtDNA content from PBMCs and urine, antioxidant gene expression was determined using qPCR and absolute mtDNA copy number was quantified by ddPCR. Paired and correlation analyses were performed to evaluate longitudinal changes and associations.

Results: Key renal markers like serum creatinine and fractional excretion of sodium were increased with reduction in eGFR over six months ($p<0.01$). β2M levels and PBMC mtDNA ΔCt showed significant increased while urinary mtDNA declined substantially, indicating differential mitochondrial responses. Patients with renal toxicity exhibited marked changes in mtDNA, and β2M levels. ddPCR further confirmed a significant alteration in absolute mtDNA copy number in the overall cohort. Antioxidant gene expression revealed heterogeneous upregulation and downregulation of CAT and GPX, reflecting oxidative stress response variability. Weak correlation was observed between CD4 count and mtDNA.

Conclusions: TDF-ART is linked to early renal tubular dysfunction with concurrent mtDNA alterations in HIV patients, partly independent of immune recovery. In addition, heterogeneous regulation of antioxidant genes was observed, suggesting variable oxidative stress responses across individuals. These findings support mitochondrial dysfunction as a key mechanism of TDF nephrotoxicity and underscore the value of mtDNA and tubular biomarkers for early renal injury detection.

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Abstract No: SA-004

Vitamin D Receptor Targeted Modulation by Plant-Derived Bioactive Compounds: A Host-Directed Strategy against Hepatitis B Virus



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Introduction: Hepatitis B virus (HBV) infection remains a major global health problem due to persistence of covalently closed circular DNA (cccDNA) in the host genome. Current therapies including nucleos(t)ide analogues and PEGylated interferon rarely eliminates cccDNA, highlighting the need for host directed therapeutic strategies. The vitamin D receptor (VDR), a nuclear receptor regulating immune and antiviral gene expression, has been implicated in HBV control through VDR/retinoid X receptor (RXR) mediated transcription and modulation of HBV core promoter. Since natural and medicinal plant derived bioactive compounds exhibit antiviral activity and lower toxicity, this study aims to identify VDR modulating potential of phytocompounds.

Objective: To identify and characterize plant derived bioactive compounds that modulate VDR activity as a host directed therapeutic strategy for suppressing HBV replication.

Methods: A systematic literature search was conducted across PubMed, Scopus, and Google Scholar database to identify medicinal plants and phytochemicals with reported or predicted anti HBV activity. The 3D structure of human VDR was obtained from Protein Data Bank. Selected phytocompounds were docked to VDR ligand-binding domain using AutoDock Vina via SwissDock. Protein DNA docking between VDR and vitamin D response element (VDRE) was performed using HDOCK to study transcriptional regulatory potential. In silico analysis of phytocompounds was performed for their potential to influence VDR mediated transcriptional regulation associated with HBV core promoter. Binding interactions of phytocompounds with HBV polymerase was also studied.

Results: From 3,834 articles screened, 68 were included, of which *Moringa oleifera*, *Phyllanthus* species and other plants were listed. Among phytocompounds of selected plants, Quercetin demonstrated stable binding to VDR ligand binding domain (−8.27 kcal/mol), indicating VDR modulation. VDR–VDRE docking revealed a highly stable complex (confidence score 0.978), supporting functional transcriptional regulation.

Conclusion: The findings provide a mechanistic framework linking plant-derived bioactive compounds with VDR modulation and potential suppression of HBV replication.

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Abstract No: SA-005

Utility of Droplet Digital PCR for Non-Invasive Prenatal Diagnosis of Sickle Cell Disease: A Protocol Standardization Study



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Introduction: Sickle cell disease (SCD) is one of the most common inherited hemoglobinopathies worldwide and is associated with significant morbidity and mortality. Prenatal diagnosis plays a crucial role in disease prevention and informed reproductive decision-making. Non-invasive prenatal diagnosis (NIPD) using cell-free fetal DNA (cffDNA) from maternal plasma represents a safer alternative to invasive procedures; however, reliable detection of single-gene disorders such as SCD remains challenging due to the low proportion of fetal DNA and the presence of a high maternal DNA background. Droplet digital PCR (ddPCR), with its ability for absolute quantification and high analytical sensitivity, offers a promising approach for such applications (1, 2).

Aim: The present study aims to standardize and assess the feasibility of ddPCR for the NIPD of SCD.

Methods: Maternal plasma samples were processed for cffDNA extraction, and ddPCR assays targeting the HbS mutation in the β-globin gene were optimized. Key parameters evaluated during protocol standardization included DNA input concentration, Fluorescence based primer–probe specificity, thermal cycling conditions, droplet separation, and allelic discrimination between mutant (FAM) and wild-type (VIC) alleles. Assay reproducibility and analytical sensitivity were assessed across multiple experimental runs.

Results: Preliminary findings demonstrate distinct droplet clustering and consistent detection of target alleles, supporting the ability of ddPCR to detect low-abundance fetal DNA against a maternal background. The optimized assay showed reproducible performance and sensitivity suitable for further clinical evaluation. Although comprehensive clinical validation using a larger sample size is ongoing, these initial results highlight the potential applicability of ddPCR-based NIPD for SCD.

Conclusion: ddPCR appears to be a robust and sensitive platform for the development of NIPD assays for SCD. Further studies are required to validate its clinical utility and diagnostic accuracy.

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Abstract No: SA-006

Beyond Variant Detection: Integrating Functional Genomics to Improve Variant Interpretation in Diamond–Blackfan Anemia



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Introduction: Diamond–Blackfan anemia (DBA) is a rare inherited bone marrow failure syndrome caused by pathogenic variants in ribosomal protein genes. Although next-generation sequencing facilitates variant detection, interpretation remains challenging due to genetic heterogeneity and the frequent identification of variants of uncertain significance (VUS). Integrating functional evidence may provide additional biological context to support more informed variant interpretation.

Objectives: To assess the contribution of functional genomics in supporting the interpretation of genomic variants identified in patients with Diamond–Blackfan anemia.

Methods: Clinically suspected DBA patients underwent hematological evaluation and whole-exome sequencing. Variants were classified per ACMG guidelines and validated by Sanger sequencing or MLPA. Functional assessment using qRT-PCR of ribosomal stress and p53-related pathways was correlated with molecular findings.

Results: All patients exhibited pure red cell aplasia with reticulocytopenia, and elevated eADA activity was observed in six of the fourteen patients. Among fourteen patients, pathogenic or likely pathogenic variants were identified in seven cases, while seven variants were classified as VUS. Functional gene expression alterations were observed in twelve patients overall. All pathogenic and likely pathogenic variants demonstrated concordant functional changes. Notably, functional alterations were also detected in five of seven VUS cases, providing supportive biological evidence for their potential relevance. Two VUS cases did not show detectable functional perturbation, indicating heterogeneity in molecular consequences and highlighting the limitations of functional assays as standalone evidence.

Conclusions: Functional genomics provided a supportive biological context for the interpretation of most genomic variants identified in Diamond–Blackfan anemia, including a substantial proportion of VUS. While consistent functional concordance was observed for pathogenic variants, variability among VUS underscores the need for cautious, integrative interpretation. These findings reinforce the role of functional assays as complementary tools that enhance, but do not replace, sequencing-based variant classification in rare disease genomics.

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Abstract No: SA-007

Ion Homeostasis and Oxidative Injury Underlie Erythrocyte Fragility in Sitosterolemia: Evidence from an Indian Cohort



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Introduction: Sitosterolemia is a rare inherited sterol transport disorder caused by pathogenic variants in ABCG5 or ABCG8 and is frequently associated with hemolytic anemia and abnormal red cell morphology. Despite recognition of these hematological manifestations, the cellular mechanisms contributing to erythrocyte instability and variable disease severity remain incompletely understood, particularly in Indian patients.

Objectives:

1. To identify and characterize genomic variations associated with sitosterolemia
2. To study the effect of identified variants on the RBC membrane stability and functionality

Methods: Six patients with clinically diagnosed sitosterolemia and pathogenic or suspected pathogenic ABCG5/ABCG8 variants (including stop-gain mutations) underwent detailed hematological and molecular evaluation. Erythrocyte functional assessment focused on pathways implicated in hemolysis and included analysis of intracellular calcium influx, sodium accumulation, osmotic membrane stability, lipid peroxidation, and reactive oxygen species (ROS) generation. Results were compared with age-matched healthy controls.

Results: All patients exhibited varying degrees of presentation with respect to anemia with reticulocytosis. Marked dysregulation of erythrocyte ion homeostasis was observed, characterized by significantly elevated intracellular calcium and sodium levels. Increased calcium influx showed an inverse relationship with hemoglobin concentration, implicating its role in red cell dehydration and hemolysis. Osmotic swelling assays demonstrated enhanced membrane fragility, most pronounced in patients with severe anemia. Indicators of oxidative membrane injury, including lipid peroxidation and ROS generation, were substantially elevated in patients with greater disease severity, highlighting oxidative stress as an important modifier of the hemolytic phenotype.

Conclusions: This study demonstrates that erythrocyte fragility in sitosterolemia arises from a convergence of ion transport abnormalities and oxidative membrane damage, contributing to heterogeneous clinical severity. Functional red cell profiling provides mechanistic insight into hemolysis and may serve as a valuable adjunct for disease stratification and monitoring therapeutic response in sitosterolemia.

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Abstract No: SA-008

Unsupervised Machine Learning for Immune Signature-based Stratification of Systemic Lupus Erythematosus (SLE) patients from Western India



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Introduction: Systemic Lupus Erythematosus(SLE) shows marked heterogeneity in clinical manifestations, autoantibody profile, and immune activation pathways. Persistent interferon IFN) pathway activation contributed to pathogenesis and autoantibody production through B-cell activation. However, conventional clinical classifications fail to capture underlying immunological heterogeneity. Therefore, we hypothesized that unsupervised machine learning approach may identify biologically meaningful subgroups that may improve patient stratification for personalized therapeutic approaches.

Objective: To apply unsupervised machine learning to stratify SLE patients and to evaluate clinical and immunological relevance of identified subgroups.

Methodology: This cross-sectional study included clinically diagnosed SLE patients(n=115). Detailed clinical, laboratory and treatment data were recorded. Serum IFNα and IFNλ1-λ4 levels were detected using ELISA, IFNγ levels by bead-based assay, and IFN score by RT-qPCR based on expression of five ISGs. Unsupervised clustering was applied to identify autoantibody-driven patient subgroups, and cluster comparisons were performed using Kruskal-Wallis test and chi-square test.

Results: Unsupervised clustering identified five distinct clusters(A-E), while autoantibody-negative patients formed a separate seronegative cluster(Cluster F,n=15) characterized by low disease activity (SLEDAI:6(5,7)), normal complement levels, and low IFNα levels(13.64(0.00,44.68)) and IFN scores(2.97(0.98,7.36)). Cluster A(n=48), dominated by anti-dsDNA(100%), anti-nucleosome(93.8%), and anti-histone(87.5%) autoantibodies, showed marked complement consumption(54.2%) and high proportion of untreated patients(72.9%). Cluster B(n=29;anti-RNP/Sm(100%) and anti-Sm(96.6%) dominant) exhibited highest disease activity(SLEDAI:12(6,7)), high fever(58.6%), hypocomplementemia(55.2%), and high IFNα levels(112.17(51.09,303.24)) and IFN score(9.92 (4.80,17.17)). Cluster C(n=19;anti-ribosomal P(47.4%) dominant) showed moderate disease activity(SLEDAI:8(6,9)). Cluster D(n=18) showed

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low autoantibody positivity and highest proportion of treated patients(77.8%). Cluster E (n=17;anti-SSA(100%), Ro-52(82.4%), and SSB(29.4%) dominant) and was associated with renal involvement(52.9%) and lowest IFN scores(1.38(0.60,6.89)).

Conclusions: Unsupervised machine learning identified distinct immune subgroups differing in IFN pathway activation. This reflected SLE heterogeneity and supported the potential for more precise immune signature-based stratification for anti-IFN targeting therapeutic approaches.

Acknowledgement: The authors would like to thank the Indian Council of Medical Research (ICMR), New Delhi, India through the Intramural Research Programme for the financial support (Project no: IIRP-2023-0000009).

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Abstract No: SA-009

Bridging the diagnostic gap in hemophilia A patients using targeted long-read sequencing



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Introduction: Hemophilia A (HA) is an X-linked bleeding disorder caused by pathogenic variants in the *F8*. Standard diagnostic workflow including coding region sequencing and screening for intron 1 and intron 22 inversions successfully identify the majority of cases. However, approximately 1–3% of patients remain without a molecular diagnosis, creating a significant barrier to carrier detection and prenatal diagnosis. Among a cohort of 350 severe HA patients (FVIII <1%, VWF normal), conventional testing failed to identify the causative mutation in three index cases.

Objective: To identify the genetic cause in severe HA cases unresolved by standard diagnostic approach.

Methods: Targeted adaptive long-read sequencing on the ONT GridION P-solo was performed using high integrity DNA that enriched a 1.1 Mb genomic window covering whole *F8* along with the flanking regions. The bioinformatics workflow that includes variant calling, SV prioritization, and manual breakpoint curation was done using integrated the Sentieon DNAscope Long Read pipeline, Golden Helix VarSeq, Intergrative Genome Viewer respectively.

Results: In all three cases, adaptive sequencing identified three unique, non-classical structural variants:
Case 1: A 135-kb complex structural rearrangement involving a deletion upstream of *BRCC3* with an inverted insertion into *F8* intron 1, resulting in complete ablation of F8 transcription.
Case 2: A novel ~379-kb inversion encompassing the *F8* locus, leading to a large-scale genomic rearrangement.
Case 3: A cryptic 1.1-kb intronic deletion within *F8* intron 1, causing loss of transcript expression.
These findings provide the precise molecular anchors required for carrier screening and prenatal diagnosis of these families

Conclusion: By applying adaptive long-read sequencing, we resolved the molecular basis of disease in three previously unsolved families, converting ambiguous cases into clinically actionable findings and offering a roadmap for the future of precision diagnostics in hemophilia.

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Abstract No: SA-010

Comprehensive analysis of tyrosine kinase domain mutations and imatinib resistance in chronic myeloid leukemia patients



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Introduction: Chronic Myeloid leukemia (CML) is a clonal haemopoietic stem cell disorder occurs due to t(9;22); molecularly *BCR::ABL1* fusion gene. Tyrosine kinase inhibitor therapy is proved to be effective for CML patients, however ~40% patients showed resistant to imatinib after certain time. Tyrosine kinase domain mutations (TKDMs) have been reported to be associated with resistance. Understanding these mutations is critical for optimizing treatment strategies and improving patient outcomes.

Objective: To identify TKDMs in CML patients treated with imatinib for better management.

Methods: A cohort of 457 patients were studied by G-T-G banding and Fluorescence *in-situ* hybridization. The monitoring of the patients was done as per European LeukemiaNet guidelines. The TKDMs were identified through Direct and Next generation sequencing (NGS).

Results: The patients were categorized into Imatinib responder (46.20%), Warning (10.94%) and resistance (42.86%) group. Direct sequencing analysis revealed point mutations in 69.44 % (50/72), compound/ polyclonal mutations in 11.11 % (8/72) and large deletions in 4.16 % (3/72) of IM non-responder CML patients. Additionally, we have identified low level mutations in 30.55 % of warning group patients through NGS analysis, that include singly occurring point mutations (5) and polyclonal(6) mutations with mutant allele frequency ranging from 1.1 % to 14.70 %. The low-level mutations detected through NGS in warning group patients; may be responsible for suboptimal response in our study. We also identified 5 novel mutations that had not been reported in public databases which expands the spectrum of known mutations in *BCR::ABL1* fusion gene. Overall, the combinational approach together with bidirectional Sanger sequencing identified mutations in 38.30% (72/188) of Imatinib non-responder group.

Conclusions: Our study identified the large number of *BCR::ABL1* kinase domain mutations in Indian CML patients. Further our study highlights that NGS analysis can identify low frequency mutant clone in warning group CML patients which further helps in prompt treatment decision in CML.

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Abstract No: SA-011

Matrix metalloproteinase (MMP)- based clustering for unravelling heterogeneity among Indian interstitial lung disease (ILD) patients



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Introduction: ILD is a diverse group of lung disorders with varying degrees of inflammation and fibrosis. Given the complexity and heterogeneity of ILD, stratifying them into distinct subgroups based on the routine diagnostic settings becomes difficult. MMPs and TGF-β1 are key regulators of extracellular matrix remodelling. Therefore, MMP profile can differentiate among ILD patients based on the actual heterogeneity of the disease, irrespective of the subgroup diagnosis based on HRCT scan.

Objective: To investigate whether stratification of the ILD patients differ on the basis of shared MMP profile for understanding the heterogeneity of ILD subgroups.

Methods: Serum levels of 7 MMPs, TIMP1, and TGF-β1 were measured in ILD (n=105) patients by multiplex immunoassay and ELISA. Correlation network analysis among these proteins revealed two distinct sub-networks: one comprising MMP2, MMP3, MMP8, MMP13, TIMP1, and TGF-β1; the other involving MMP1, MMP7, MMP9, TIMP1, and TGF-β1. ILD patients were clustered on basis of two subnetworks of MMPs separately. Statistical analyses were done in GraphPad prism v10.4.2 and R-software.

Results: The two clustering strategies revealed distinct ILD patient subgroups. MMP7 levels were highest in the cluster enriched for fibrotic ILD and progressive pulmonary fibrosis (PPF), while MMP9 peaked in clusters dominated by fibrotic hypersensitivity pneumonitis (HP). TGF-β1 was highest in clusters with predominant ANA/ANCA autoantibody positivity. The second clustering strategy revealed that the levels of MMP3, MMP8, and TIMP1 were significantly elevated in cluster that contained fewer CTD-ILD, IIP, and no HP patients. MMP2, MMP3, and MMP8 levels, were significantly reduced in the cluster that included the highest number of CTD-ILD, HP, and IIP patients.

Conclusion: Clustering of ILD patients based on serum MMP levels suggested a newer approach in stratifying ILD patients according to the disease heterogeneity. Further studies are required to correlate these clusters with clinical and treatment details in ILD.

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Abstract No: SA-012

Viral Determinants of Occult Hepatitis B Infection Among Household Contacts: Insights from S Gene and Precore/Core Region Analysis



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Introduction: Occult hepatitis B infection(OBI) is characterized by detectable HBV DNA despite absence of HBsAg. It is frequently observed among household contacts of chronic HBV cases and presents diagnostic challenges. Mutations in surface and precore/core regions of HBV may influence immune recognition and antigen detection.

Objectives: To evaluate the role of HBV S gene and preC/C mutations in OBI among household contacts.

Methods: Sixty two HBsAg positive index cases and 243 household contacts were enrolled. Contacts were classified based on HBsAg and anti HBc status. HBV DNA detection and quantitation was performed using nested PCR and real-time PCR, respectively. The S gene and preC/C regions were amplified and sequenced by Sanger sequencing. In silico analyses included antigenicity prediction, B cell and T cell epitope mapping, and secondary structure assessment.

Results: HBV DNA was detected in 44% of index cases, 15% of HBsAg positive contacts, and 14% of HBsAg negative and anti HBc positive contacts. OBI cases showed genotype A predominance with lower median viral loads (2.55 log10IU/mL).
S gene analysis identified mutations enriched in OBI, including R122K and V194A. In silico analysis showed that this mutation combination altered B cell epitopes in C terminal region and modified T cell epitope binding affinity without major structural changes.
PreC/C mutations included epitope altering mutations (S49T, R56S, E77Q, I97F, and L116I). However, they did not show significant association with the occult phenotype.

Conclusions: S gene mutations appear to be primary viral determinants contributing to diagnostic failure and immune escape in OBI. In contrast, mutations in preC/C regions did not differentiate occult from overt HBV infection. These findings suggest that variability within the S gene has a more prominent role than preC/C gene alterations in viral mechanisms underlying OBI.

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Abstract No: SA-013

Study of molecular mechanisms and miRNA expressions in association of mitochondrial dysfunction in Aplastic anemia



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Introduction: Aplastic anemia (AA) is a hematological disease characterised by hypoplastic bone marrow (BM) resulting in pancytopenia. AA can as non-severe AA (nSAA), Severe AA (SAA) and very-severe AA (vSAA) based on Camitta's criteria. Oxidative stress leads to the bone marrow failure thereby development into AA. Hence, our study aims to understand the role of oxidative stress and their molecular mechanism thereby unfurl the pathogenesis of AA.

Objectives:
- To study the mitochondrial dysfunction in the BM of Aplastic Anemia patients.
- To investigate significant mitochondria-related miRNAs in Aplastic Anemia and associate its effect on mitochondrial dysfunction in Aplastic Anemia.
- Correlation of Mitochondrial dysfunction with the Severity of Aplastic Anemia.

Methods:
- Newly diagnosed IST naïve 12 cases of adult AA patients were recruited in the study. BM aspirate (BMA) and peripheral blood (PB) samples were collected with informed consent.
- Quantification of intracellular ROS with reduced- DCFDA dye, mitochondrial ROS with MitoSOX dye and mitochondrial membrane potential using TMRE (Tetramethyl rhodamine, thyl ester) were standardised and studied in AA patients using flow cytometry.
- Using Spectophotometric method, quantification of ATP production was also standardised.

Results: In our study, the AA patients (n=12) showed a mean increase of 61% intracellular ROS with 98% in vSAA, 52% in SAA and 32% in nSAA patients as compared to controls (26%). Quantification of mitochondrial-ROS production showed a mean increase of 65% with 97% in vSAA, 50% in SAA and 36% in nSAA patients. Flow cytometric assay for mitochondrialmembrane potential and spectrophotometric method for ATP production were also standardized on controls.

Conclusions: Our initial study showed a significant increase of intracellular and mitochondrial ROS levels in AA patients. Hence, molecular mechanism of mitochondrial dysfunction needs to be studied in a larger cohort to understand the oxidative stress associated to AA.

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Abstract No: SA-014

Providing optimum care to pregnant women with sickle cell disease: Exiting programme services, challenges, & a way forward



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Introduction: Pregnancies in women with sickle cell disease (SCD) are associated with significantly higher maternal and perinatal adverse outcomes. Recently released WHO antenatal care (ANC) recommendations for SCD need integration into existing national guidelines under the National Sickle Cell Anaemia Elimination Mission (NSCAEM). However, incorporation of these recommendations may be challenging due to contextual and health system constraints.

Objectives:

1. To identify barriers to integrate WHO ANC recommendations for SCD into existing guidelines.
2. To develop an implementation strategy for smooth incorporation into NSCAEM.

Methods: A mixed-methods implementation research study was conducted in Chandrapur district, Maharashtra. Qualitative methods included in-depth interviews with healthcare providers across cadres, focused group discussions with SCD patients until data saturation, and facility assessments of selected Primary Health Centres and Health and Wellness Centres. Quantitative data were collected through interviews with the general population (target n≈3500; interim n=666) and pregnant women (n=400, assuming 50% awareness).

Results: Among 666 respondents, 76% had heard of SCD, primarily through healthcare providers (44%). About 71% were advised screening, and a similar proportion underwent testing, predominantly at government facilities (81%). Lack of counselling was the most common reason for non-testing. Thirty-nine respondents reported a family member with SCD, of whom 76% were receiving regular modern medical care. Qualitative findings showed uniform implementation of basic SCD services such as screening and folic acid provision. However, gaps were noted in digital services, including telemedicine and portal data entry. Healthcare providers highlighted regular training as a strength, while manpower shortages, digitization challenges, and limited local governance support were key barriers. Patients reported difficulties in emergency access and referral navigation.

Conclusion: While existing programme strengths can facilitate integration of WHO ANC guidelines, health system and treatment-related challenges must be addressed. *This is an interim analysis, and findings may evolve with complete data.*

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Abstract No: SA-015

Prevalence of Clinically Significant Blood Group Antigens and rate of Alloimmunization in Sickle Cell Disease Patients and Blood Donors in Chandrapur, Maharashtra.



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Introduction: Sickle cell disease (SCD) poses a significant public health burden in India, particularly among tribal and certain non-tribal ethnic groups[1]. Red blood cell (RBC) transfusion is an essential component of SCD management; however, repeated transfusions increase the risk of alloimmunization[2.] Antigenic mismatches between donors and recipients contribute to alloantibody formation, underscoring the need for extended RBC phenotyping and provision of antigen-matched blood[3.]

Objectives: To assess the distribution of clinically significant minor blood group antigens among SCD patients and blood donors, and to determine the prevalence and specificity of alloimmunization in transfused SCD patients.

Methods: This cross-sectional pilot study included 84 SCD patients and 124 healthy blood donors. Extended RBC phenotyping for Rh, Kell, Duffy, Kidd, MNS, Lewis, and P blood group systems was performed using multiplex polymerase chain reaction assays and gel card technology. Alloantibody screening and identification were conducted in transfused SCD patients using an in-house red cell antibody identification panel.

Results: Rare Rh phenotypes, including r″r (1%) and r′r (3%), were identified among SCD patients. Significant differences in antigen frequencies between patients and donors were observed for Fya (p=0.023), Fyb (p=0.0002), K (p=0.0334), and s (p=0.014). Additional phenotype disparities were noted for Fy (a+b−), ss, Ss, Kp(a−b+), P, and Le(a+b+). The majority of SCD patients belonged to Scheduled Caste and Scheduled Tribe communities. Blood transfusion was required in 57% of patients, with an alloimmunization rate of 7%. Identified alloantibodies included anti-c (5%) and mixture of anti-c+ anti-E (2%). Antibodies of undetermined specificity and autoantibodies were each detected in 2% of patients.

Conclusion: Alloimmunization is a major complication in transfused SCD patients, due to antibodies against Rh and Kell antigens. Differences in antigen profiles between patients and donors were observed which highlight the need for extended red cell phenotyping before transfusion. Using advanced genotyping methods, such as next-generation sequencing will improve antibody detection. Providing antigen-matched blood will enhance transfusion safety in this population.

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Abstract No: SA-016

A systematic in-silico and in-vitro approach for the characterisation of RASGRP2 variants in inherited platelet disorders.



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Introduction: Inherited platelet disorders (IPDs) comprise a heterogeneous group of rare bleeding conditions in which next-generation sequencing (NGS) has markedly improved variant detection. However, widespread NGS use has also increased the identification of Variants of Uncertain Significance (VUS), complicating molecular diagnosis, genotype–phenotype correlation, and genetic counselling. This challenge is particularly prominent in platelet function disorders, where patients often exhibit clinically significant bleeding despite normal platelet counts and routine coagulation parameters, frequently accompanied by high ISTH bleeding assessment tool (BAT) scores. Preliminary genomic analyses at the ICMR–National Institute of Immunohematology in clinically suspected IPD patients revealed multiple rare and novel variants in platelet-associated genes. Among these, **RASGRP2**, a critical regulator of RAP1-mediated platelet activation and integrin signalling, emerged as a high-priority candidate due to its recurrent association with unexplained bleeding phenotypes and limited functional evidence for reported variants.

Aim: To establish an in vitro framework for functional characterisation and validation of gene variants associated with inherited platelet disorders.

Objective: To investigate the functional relevance of prioritised genes implicated in IPDs.

Methodology: The study follows a stepwise design beginning with gene and variant prioritisation. RASGRP2 variants identified in IPD patients are evaluated using population databases (gnomAD, 1000 Genomes, ExAC) and classified according to ACMG/AMP 2019 guidelines. Variant pathogenicity is assessed using in silico prediction tools (SIFT, PolyPhen-2, MutationTaster, CADD, REVEL), while splicing effects are analysed using SpliceAI, Human Splicing Finder, and MaxEntScan. Evolutionary conservation and protein domain mapping further refine prioritisation. Shortlisted variants are planned for overexpression-based functional studies in mammalian cell lines.

Results: In silico analyses enabled systematic prioritisation of RASGRP2 variants, excluding benign variants and stratifying rare variants into likely pathogenic and high-confidence VUS, thereby establishing a robust framework for downstream functional validation.

Conclusion: This study provides a structured computational foundation for interpreting rare RASGRP2 variants in IPDs, offering a scalable roadmap for precision-based variant interpretation and subsequent functional validation.

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Abstract No: SA-017

Unravelling Early-Onset Myocardial Infarction and Coronary Artery Disease (<40 Years): A Multi-Pathway Genetic and Functional Analysis



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Background: Coronary artery disease remains the leading cause of mortality in India, with a rising burden of premature myocardial infarction below 40 years. India's genetic diversity contributes to disease susceptibility through multiple biological pathways, including lipid, sarcomeric, and arrhythmogenic mechanisms. This study aims to decode the genetic architecture of early-onset MI using targeted next-generation sequencing with expression and segregation analyses.

Objectives: This study aimed to identify pathogenic and modifier variants in lipid metabolism, sarcomere, electrolyte and arrhythmogenic pathways in young MI patients, correlate genetic findings with clinical details, perform systematic family-based investigations with functional validation.

Methods: A total of 178 young CAD patients (<40 years) were recruited, of whom 123 performed whole-exome sequencing. Variant analysis was performed using the Franklin platform, applying a designed and curated UK-based cardiovascular gene panel comprising 527 genes. Variants were classified according to ACMG guidelines and correlated with clinical Parameters, angiographic, ECG. Familial cases were included, with segregation analysis conducted in 40 family members. 150 related and 25 unrelated healthy individuals. Functional validation of selected pathogenic variants was performed using ELISA and RT-PCR based expression assays.

Results: Pathogenic or disease-modifying variants were identified in 40–60% of patients. our findings uncover a balanced burden across lipid (LDLR, LRP6, ABCA1, GPIHBP1), APOE polymorphisms affects impaired lipoprotein clearance. Sarcomere (MYH7, FLNC, TPM1), variants correlated with left ventricular hypertrophy. Arrhythmogenic variants (PKP2, RYR2) were linked to ventricular arrhythmias, these exhibit gender-specific penetrance males showing earlier onset highlighting polygenic complexity underrepresented in Indian databases yet reported globally, where deleterious effects amplify young MI susceptibility

Conclusion: Premature myocardial infarction in the Indian population is a genetically complex disorder involving lipid, sarcomere, and arrhythmogenic pathways. Both rare pathogenic variants and common risk-modifying polymorphisms contribute to early disease onset with variable penetrance. Integrating genomic, clinical, and family-based data improves risk stratification and supports population-specific precision cardiovascular care.

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Abstract No: SA-018

Integrating Genomics and Transcriptomics to Resolve Variant Consequences in Monogenic Autoinflammatory Disorder



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Background: Autoinflammatory disorders (AID) are rare monogenic disorders presenting with periodic fevers and sterile inflammation. They stem from genetic mutations associated with type 1 interferon signalling (IFN), inflammasome activation (PYD) and other mechanisms (e.g. TNF signalling) causing unrestrained activation of inflammatory pathways. Genetic diagnosis is precluded by incomplete penetrance seen in approximately half the genes implicated in AID as well as the lack of definitive functional tests to stratify the patients. Transcriptomics can provide functional evidence for candidate variants by revealing their downstream effects on gene expression, thereby improving variant interpretation.

Methods: We performed an integrative multi-omics analysis combining whole-exome sequencing and transcriptome profiling in individuals with AID as per ESID 2024 criteria (n=60) and age-sex matched healthy individuals (n=30). Deleterious, rare, clinically-correlating variants were classified by ACMG guidelines. Total RNA sequencing was performed from blood collected in Tempus tubes. Gene expression and transcript-level perturbations were quantified, including differential expression and pathway enrichment.

Results: Putative disease associated variants were present in 40 cases, which were further classified as pathogenic or likely pathogenic (n=31) or variants of uncertain significance (VUS, n=19). A distinct expression signature was observed in IFN-AID and PYD-AID. While IFN-AID was characterized by dysregulation of interferon signalling, mitochondrial dysfunction, and ER stress; coagulation and metabolic dysfunction predominated PYD-IFN. Importantly, integration of RNA-seq provided functional support for 5 prioritized variants via identification of splicing disruption, reduced expression and allelic imbalance strengthening genotype–phenotype interpretation. These findings highlight strong pathway disruption despite genetic heterogeneity and differences in disease severity and treatment.

Conclusions: Our integrated genomics–transcriptomics approach improves functional interpretation of candidate variants in AID and reveals coherent downstream pathway perturbations that may drive disease pathogenesis. This multi-omics framework supports improved diagnostic confidence, refines molecular subclassification, and provides a foundation for future mechanistic studies and therapeutic exploration.

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Abstract No: SA-019

Validation of diagnostic screening test for Pharmacogenomic targets for Thiopurine drugs in Indian Pediatric acute lymphoblastic leukemia patients



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Introduction: Thiopurines such as 6-mercaptopurine (6-MP) are indispensable in maintenance therapy for pediatric acute lymphoblastic leukemia (ALL), but their narrow therapeutic index frequently results in dose-limiting myelosuppression in genetically susceptible patients. Variants in *NUDT15* and *TPMT* are the most important pharmacogenetic determinants of thiopurine intolerance, particularly in Asian populations. Although CPIC recommends pre-emptive genotyping, routine testing is rarely implemented in India due to high costs and limited access to sequencing platforms.

Objectives: To develop, standardize, and clinically validate a rapid, low-cost tetra-primer ARMS-PCR assay for simultaneous detection of the most clinically relevant thiopurine-toxicity variants-*NUDT15* c.415C>T and *TPMT 3C* (c.719A>G), prioritized through comprehensive *in-silico* analysis.

Methods: Missense variants in *NUDT15* and *TPMT* were screened using SIFT, PolyPhen-2, PROVEAN, Meta-SNP, and SNPs&GO to identify high-impact variants. A multiplex ARMS-PCR assay was optimized and applied to 61 pediatric ALL samples, with genotyping results validated by Sanger sequencing. Clinical correlations included hematologic toxicity, 6-MP dose intensity, and blast-percentage dynamics.

Results: *In-silico* analysis consistently prioritized *NUDT15* c.415C>T and *TPMT 3C* as the most deleterious variants. Among 60 successfully genotyped patients, *NUDT15* variants were detected in 16.7% (9 heterozygous, 1 homozygous), while *TPMT 3C* heterozygosity was observed in 3.3%; no double-mutant cases were identified. ARMS-PCR demonstrated 98.4% diagnostic accuracy compared with Sanger sequencing (sensitivity 90.9%, specificity 100%). *NUDT15* variant carriers showed significantly reduced 6-MP dose intensity (median 0.50 vs. 0.79; $p < 0.0001$).

Conclusions: This validated ARMS-PCR assay offers a rapid, accurate, and affordable alternative to sequencing for *NUDT15* and *TPMT* genotyping. Its low infrastructure requirements support integration into routine pre-treatment workflows in India, enabling genotype-guided thiopurine dosing and reducing treatment-related toxicity in pediatric ALL.

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Abstract No: SA-020

The PCOS Follicle at a Crossroads: Imbalance in the Glucose Metabolism Pathways



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Introduction: Oocyte maturation is dependent on nourishment from its microenvironment. Granulosa cells (GCs)- companion somatic cells of the oocyte act as its metabolic engine by metabolizing glucose and supplying oocyte with pyruvate and other metabolites; as oocyte itself cannot utilize glucose properly [1]. This follicular metabolic orchestration is harmonized by insulin and gonadotropins. PCOS is prevalent condition in women of reproductive age, characterized by hyperandrogenaemia, skewed gonadotropins, insulin resistance and other reproductive anomalies. Many of them are infertile and opt for IVF to conceive. However, IVF outcome is poor in them, which can be attributed to poor oocyte quality [2]. Disrupted metabolic cooperation in follicle can be contributing factor towards it. Hence, we investigated the metabolic nexus in the follicle of women with PCOS undergoing IVF.

Objectives: To dissect the glucose metabolism dynamics in GCs of women with PCOS.

Methods: Glucose uptake by GCs was studied. Basal GLUT4 transcript and protein expression; and its translocation were assessed in GCs by immunofluorescence. Transcript levels of genes encoding metabolic enzymes, pyruvate levels and glycation markers were assessed in follicular environment. Real-time metabolic analysis was performed using Seahorse XFe24 system.

Results: Glucose uptake, basal GLUT4 transcript and protein expression; and its insulin stimulated translocation were significantly lower in GCs from PCOS women. In PCOS, glycolysis was downregulated as indicated by decreased transcript of rate-limiting enzymes, reduced pyruvate levels and lower real-time glycolysis and glycolytic capacity in GCs. Alternatively, pentose phosphate pathway, polyol pathway, glycation were increased in GCs from PCOS women.

Conclusions: Our work reveals metabolic reprogramming in GCs of PCOS women, potentially impacting oocyte quality. Analysing follicular energy dynamics reveals pathways driving disrupted PCOS folliculogenesis, identifying essential metabolites to optimize IVF culture media and biomarkers for oocyte /embryo quality where we rely on morphological assessments for embryo selection that can be subjective.

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Abstract No: SA-021

An Ultra-Sensitive And Cost-Effective Method For Cell-Free Dna Isolation From Blood Sample



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Introduction: Cell-free DNA (cfDNA) serves as a critical biomarker for non-invasive disease monitoring, prognostication, and therapeutic surveillance in leukemia. Despite its clinical importance, widespread adoption of cfDNA-based assays is restricted by the high cost, technical complexity, and infrastructure dependence of existing commercial extraction kits. These limitations create a significant barrier for routine clinical implementation, particularly in resource-limited settings, highlighting the need for an innovative, scalable alternative.

Objectives: To develop and protect, through patent filing, a novel, ultra-sensitive, cost-effective, and rapid method for cfDNA isolation that overcomes the technical and economic limitations of existing commercial technologies.

Methods: A proprietary manual cfDNA isolation workflow was designed involving optimized plasma processing, customized lysis buffer composition, carrier RNA–assisted binding, silica membrane–based purification, and low-volume elution. The method was evaluated for cfDNA yield, purity, fragment size (<400 bp), processing time, and operational simplicity, and benchmarked against commercially available cfDNA extraction kits.

Results: The patent filed method demonstrated cfDNA yields and purity comparable to standard commercial kits while significantly reducing processing time and operational complexity. The protocol achieved reliable recovery of low-abundance cfDNA fragments and functioned effectively across samples with variable leukocyte counts. Notably, the cost per sample was reduced to approximately one-eighth of that incurred using commercial kits, without reliance on specialized collection tubes or vacuum-based instrumentation.

Conclusions: This patent-registered cfDNA isolation method represents a clinically and commercially viable innovation, enabling affordable liquid biopsy applications for leukemia monitoring. Its simplicity, sensitivity, and cost efficiency position it as a strong candidate for large-scale deployment in diagnostic laboratories and public healthcare systems, bridging the gap between advanced molecular diagnostics and real-world accessibility.

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Abstract No: SA-022

Dissecting Molecular Mechanisms of Viral Replication in Trophoblast Cells: Implications for transplacental transfer during Pregnancy



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Introduction: Viral infections during pregnancy can lead to congenital abnormalities, fetal growth restriction, and pregnancy loss. Trophoblast cells act as a barrier between maternal and fetal compartments. Several viruses like Cytomegalovirus, Herpes simplex virus, rubella, dengue, and Zika can replicate within these cells, facilitating their entry into the fetal bloodstream. The molecular pathways involved in viral infection of trophoblasts and subsequent transplacental transfer are not well understood.

Objectives: This objective of this study is to investigate the prevalence of Dengue virus (DENV) and Herpes simplex virus (HSV-2) infections during pregnancy in Central India, along with the molecular characterization of virus-exposed placental tissues. It aims to clarify how the DNA damage response (DDR) pathway regulates viral replication in trophoblast cells and to identify small-molecule inhibitors that can suppress this replication.

Methods: Trophoblast stem cell culture models are being employed to study the molecular mechanisms of virus replication, specifically focusing on DENV and HSV-2. Pregnant women showing signs of infection are screened, with confirmed virus positive cases used for viral isolation and monitoring of pregnancy outcomes.

Results: Activation of proximal DDR factors is crucial for viral replication, while suppressing downstream DDR signaling is necessary for host cell survival. A previous study found that in placental cells, the ATR and DNA-PK DDR pathways are suppressed, but the ATM pathway is active. The hypothesis posits that virus infections activate the ATM DDR pathway in trophoblast cells. Research involves trophoblast stem cell cultures and DDR pathway inhibitors to investigate their role in virus replication. Additionally, pregnant women with virus infections are being recruited and screened to analyze structural and molecular changes in the placenta throughout pregnancy.

Conclusion: In summary, this study will help in understanding how viruses replicate and cross the placental barrier by investigating DNA damage response (DDR) pathways in trophoblast cells.

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Abstract No: SA-023

DNA break mapping in placental cells reveals vulnerability of repetitive sequences in pregnancy complication



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Introduction: Placenta is a vital organ that develops during pregnancy and is essential for sustaining pregnancy and fetal growth. Placental abnormalities are leading cause of pregnancy related disorders.

Objectives: Placental trophoblast cells increase their ploidy through many rounds of replications, either by endocycle or by syncytium formation. During this process, reduced activity of the ATR (ATM and RAD3-related) DNA damage response pathway leads to DNA damage accumulation. As gestation progresses, there is a gradually DNA damage increase likely due to this. The objective of this study is to map DNA damage and associated genomic loci in the placental cells.

Methods: We performed γH2A.X chromatin immunoprecipitation (ChIP) in mouse parietal trophoblast giant cells (P-TGCs) at 9.5*dpc* stage of pregnancy and in human term placental cells. Using an in-vitro human trophoblast stem cell culture model and blood samples from different stages of human pregnancies, we developed a q-PCR based method to detect DNA breaks in cell-free DNA (cfDNA) during gestation.

Results: The analysis identified 51 reproducible DNA damage sites in P-TGCs and several repetitive DNA sequences, which are more prone to DNA damage. Our finding revealed that placental cells show more breaks in CGG repeats as compared to other repeats. Using in-vitro human trophoblast stem cell culture model and blood samples from different stages of human pregnancies, we showed that flanking sequences corresponding to CGG repeats can be detected as cell free DNA (cfDNA) and the amount of these repeats in cfDNA increases in the case of fetal growth restriction.

Conclusions: In conclusion, we have mapped DNA damage sites in placental cells, and our result suggest that repetitive CGG rich regions are highly vulnerable during gestation. we propose that detection of these repetitive DNA sequences sites in maternal cfDNA could serve as potential biomarker for early detection of pregnancy complications.

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Abstract No: SA-024

Insights from Transcriptomic Profiling into Cellular Homeostasis in Aicardi–Goutières Syndrome



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Introduction: Aicardi–Goutières Syndrome (AGS) is a rare, inherited, type I interferonopathy that is characterised by severe chronic inflammation in the central nervous system (CNS)[1]. The upregulation of type I interferons is driven by monogenic variants that alter metabolism and sensing of endogenous nucleic acids (NAs), leading to their accumulation in the cytoplasm[2]. Lysosomes maintain cellular homeostasis by clearing damaged organelles and molecules, including nucleic acids. Recent studies indicate that lysosomal nucleases and autophagy contribute to the clearance of nuclear DNA that escapes repair and accumulates in the cytoplasm, thereby preventing inflammation[3]. However, the involvement of lysosomal pathways in AGS has not been well characterised.

Objectives: To investigate the expression of genes related to lysosomal function in Aicardi–Goutières syndrome.

Methods: Transcriptome profiling was performed on clinically and molecularly confirmed AGS patients (n=6), healthy controls (n=27), and disease controls (non-AGS autoinflammatory cases) (n=8). Total RNA sequencing was carried out using peripheral blood collected in Tempus™ blood RNA tubes. Differential expression analysis was performed using DESeq2 and edgeR, and gene enrichment was assessed using Gene Ontology (GO) pathway analysis. Additionally, supervised differential analysis was performed on predefined gene sets associated with type I interferon signalling, lysosomal function, and mitochondrial homeostasis.

Results: Transcriptomic analysis revealed marked inter-individual variability among AGS patients. Additionally, AGS patients showed a significantly decreased expression of genes regulating lysosomal acidification and autophagy receptors compared with the healthy and diseased controls.
Conclusions

These findings indicate dysregulation of cellular homeostasis in AGS patients. Comparative analysis with other autoinflammatory disease controls demonstrated a significant reduction in the expression of genes involved in lysosomal pH regulation and lysosomal activity in AGS. Collectively, these data support further investigation of lysosomal function in AGS patients, which may contribute to improved clearance of accumulated nucleic acids and attenuation of aberrant type I interferon responses.

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Abstract No: SA-025

Dynamic Regulation of TLR9 during Progression of Triple-Negative Breast Cancer



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Introduction: Triple Negative Breast Cancer (TNBC) is a subtype of breast cancer (BC), which lacks hormone receptors (ER/PR/Her2), and is associated with chemo-resistance and tumor recurrence. TNBC is considered an immunogenic subtype of BC, making it a good candidate for treatment with immunotherapeutic approaches[1]. TLR (Toll-like receptor) 9 belongs to a family of pattern recognition receptors (PRR) that has been previously associated with immunoregulatory roles in several cancers[2]. But, the role of TLR9 in TNBC tumor progression and metastasis still remains to be explored. In the present study we have developed and characterized a murine syngeneic TNBC model and studied the expression of TLR9 across the stages of TNBC.

Objectives:
1.To develop a syngeneic murine TNBC model mimicking progressive stages of Human TNBC.
2.To characterize the murine progressive stages of TNBC tumors
3.To screen the expression of TLR9 in progressive stages of TNBC

Methods: To develop TNBC syngeneic mouse model, we injected 4T1 cells into 4th inguinal mammary gland via nipple by intraductal surgery. The TNBC tumours were characterized for cell proliferation index, invasiveness, and epithelial content (PCNA, alpha smooth muscle actin, Cytokeratin) and the expression pattern of TLR9 was screened by immunofluorescence staining.

Results: The mouse TNBC tumor tissues obtained were confirmed for ductal carcinoma in situ (DCIS) (preinvasive) and invasive carcinoma (IC) (invasive) and found mimicking the progressive stages of human TNBC. Further characterizing these tissues for distinct molecular markers revealed progressive loss of alpha smooth muscle actin expression, increase in proliferative cell nuclear antigen and cytokeratin expression as the tumor progressed from DCIS to IC. Additionally, screening the expression pattern of TLR9 in DCIS and IC tumor tissue revealed its significant progressive increase.

Conclusions: These results indicate that TLR9 might play an important role in TNBC tumor progression

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Abstract No: SA-026

The Moonlighting Face of HMGB1 in Endometrial Regeneration



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Introduction: Cyclic endometrial repair and regeneration encompass re-epithelialization, vascular remodelling, glandular and stromal cell proliferation. Menstrual fluid is known to facilitate this cyclic repair and regeneration of endometrium. HMGB1 has been identified in menstrual and uterine fluid. Extracellular HMGB1 is known for its role in tissue repair and promoting regeneration of different cell types. We previously demonstrated role of HMGB1-RAGE axis in endometrial repair in the rat model of induced menstruation.

Objectives: To investigate whether extracellular HMGB1 and its cognate receptor, RAGE plays any role in regenerating endometrium following menstruation.

Methods: A rat model of induced menstruation and regeneration was established. Groups of animals were treated with single dose of E2 (500ng/100µl) (n=4), single dose E2 (500ng/100µl) + combined Glycyrrhizin (100µg/g of body weight/day, HMGB1 inhibitor) and FPS-ZM1 (2µg/g of body weight/ day, RAGE inhibitor) (n=4), saline (n=4) and combined Glycyrrhizin and FPS-ZM1 (n=4). Endometrial tissues were examined at T24 and T48 post menstrual phase repair of endometrium. Histological analysis and immunostaining for markers of cell proliferation (PCNA), steroid receptors (ERα and ERβ) were assessed in all groups of animals.

Results: The animals treated with combined inhibitors revealed thinning and disintegration of luminal epithelium ($p < 0.03$) with reduced endometrial thickness ($p < 0.04$) compared to E2 group at T24. Furthermore, decline in number of glands was observed in combined inhibitors group ($p < 0.01$) compared to E2 group at T48. Immunofluorescence analysis demonstrated that combined inhibitors (with and without E2) suppressed PCNA expression in luminal and glandular epithelium in comparison to E2 alone group. The combined inhibitors (with and without E2) also lowered expression of ERα and ERβ in luminal and glandular epithelium.

Conclusions: The results indicate that the combined inhibitors counteract estrogen-driven endometrial regeneration by affecting epithelial integrity and glandular proliferation.

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Abstract No: SA-027

Understanding the Molecular Crosstalk Guiding Sperm Towards the Egg



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Introduction: Successful fertilization depends on precise molecular communication between sperm and the oocyte within the female reproductive tract. Among the mechanisms involved, sperm chemotaxis selectively guides capacitating sperm with high fertilization potential toward the oocyte. In assisted reproductive technologies such as IVF and ICSI, conventional sperm selection procedures bypass this physiological guidance. Despite its biological relevance, the molecular cues mediating sperm navigation within the oocyte microenvironment remain poorly characterized, largely due to the lack of suitable experimental platforms.

Objectives: To identify ovulation-associated metabolites in the oviductal microenvironment and to evaluate their chemotactic potential using an *in-vitro* microfluidics-based assay.

Methods: Ovulation-associated metabolites were first identified by analyzing pre-ovulatory and ovulatory-phase oviductal fluid using LC–MS/MS. Metabolites increased or exclusively present during ovulation were selected for evaluation of chemotactic potential. Capacitating sperm were exposed to gradients of these metabolites using a microfluidics-based chemotaxis assay developed in our laboratory. Sperm responses were quantified by assessing directionality, straight-line velocity, and accumulation patterns.

Results: N-formyl-L-aspartate exhibited a characteristic bell-shaped response, with maximal chemotactic activity observed at 0.01 M gradients in both rat and human sperm. A second metabolite, Compound X (name withheld; patent pending) induced a strong chemotactic response at nanomolar concentrations in both species. In contrast, cinnamyl isovalerate did not elicit chemotaxis but promoted capacitation-like characteristics in sperm, suggesting a role in sperm capacitation rather than guidance. Additionally, two other compounds, tulobuterol and ferulic acid, failed to induce chemotaxis, indicating an absence of chemoattractant activity.

Conclusion: This study identified multiple ovulation-associated metabolites with functional relevance, of which N-formyl-L-aspartate and Compound X demonstrated significant chemotactic responses in both rat and human sperm. These findings suggest the potential of chemoattractants in sperm sorting to selectively isolate good-quality sperm with maximal fertilization potential, thereby improving IVF/ICSI outcomes and ultimately increasing 'take-home baby' rates

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Abstract No: SA-028

Decoding Host-*Candida albicans* Interactions in Vaginal Infection: A Systems-Level Perspective



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Introduction: *Candida albicans* is a commensal fungus commonly present on mucosal surfaces of its human host. Under conditions of host stress, it transforms into a pathogenic state, causing localized or systemic infections. Symptomatic infections caused by *Candida* species in the reproductive tract of women are called vulvovaginal candidiasis (VVC). The treatment options for the management of VVC are limited to a few antifungal drugs, and several *Candida* species have been increasingly developing resistance to them. A better understanding of the host-pathogen interactions would pave the way to the identification of novel antifungal targets.

Objective: To understand the host-pathogen interactions in VVC using genome-scale metabolic models integrated with multi-omics data.

Methods: We used an *in vitro* model of VVC wherein *C. albicans* was co-cultured with the human vaginal epithelial cell line A-431 in conditions mimicking the host microenvironment. Untargeted multi-omics techniques were employed to gain a global overview of their interactions and help connect the host and pathogen at different biological levels. Integrated analysis of the transcriptomics, proteomics and metabolomics profiles using systems biology revealed significant perturbations in several metabolic pathways of both the host cell line as well as *C. albicans*.

Results: This multi-omics data was further integrated into genome-scale metabolic models of human and *C. albicans*. The individual models were merged using systems biology tools to create an *in silico* host-pathogen model of VVC.

Conclusions: Such a context-specific community model can help draw deeper insights into disease pathogenesis of VVC and facilitate the discovery of novel therapeutic agents.

Funding: DST-SERB (now ANRF), Lady Tata Memorial Trust

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Abstract No: SA-029

Immune and Drug Resistance Mutation Profiling of Putative HIV-1C Reservoirs in an Indian Cohort



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Introduction: While antiretroviral therapy (ART) effectively suppresses HIV, it demands lifelong use. Persistent HIV reservoirs, which may contain therapy-resistant variants, jeopardize sustained viral control and cure. Given that broadly neutralizing antibodies (bNAbs) represent a promising adjunct to ART, we aimed to evaluate the resistance patterns of reservoir-derived Indian HIV-1C from primary samples.

Objectives: To evaluate the resistance profile of reservoir-derived Indian HIV-1C viruses against bNAbs, and ART in peripheral blood mononuclear cells (PBMC) and FACS sorted CD4+T cell reservoirs from PLHIV across therapy naïve and receiving states.

Methods: HIV-1C infected participants (n=250) were classified as per their therapy status and compared with seronegative controls (n=57) to delineate degree of dysregulation in immune cells using flow cytometry. CD4+T cell putative reservoirs were sorted using FACS to estimate HIV proviral enrichment across subsets. Pseudo-viruses containing envelopes derived from PBMC or FACS sorted CD4+ central memory (CM) cells were assessed for their sensitivity to best-in-class bNAbs. Drug resistance mutations (DRMs) in archival proviruses across CD4+T cell subsets were predicted.

Results: Significantly impaired restoration of CD4/CD8 ratio, activation and exhaustion of T cells was observed, despite prolonged ART. We also observed positive association between HIV-1 proviral loads in memory CD4+T cells, activation and PD-1 expression only in the ART naïve setting. Pseudoviruses generated from central memory CD4+T cells had disparate profiles of bnAb resistance compared to those observed in PBMC and this disparity was also reflected in their DRM profiles that included instances of primary and acquired resistance to dolutegravir (DTG), a recently included drug in the national ART regimen.

Conclusions: Our results reveal limitations of current ART regimens in restoring immune profiles and eliminating reservoirs. Our DRM analyses emphasize the value of archival DNA screening to avert treatment failures and inform bnAb-based therapies.

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Abstract No: SA-030

Development and Characterization of 3D Human Placentoids and their Application in Drug Testing



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Introduction: Placenta is the organ formed during pregnancy. It helps in protection to fetus and transport of nutrients and waste between mother and the fetus**.** Medication consumed during pregnancy are associated with the risk of damage to placenta and can cause teratogenic effect. Traditional two-dimensional (2D) cell cultures often fail to capture the complex physiological environment of the human placenta. This study introduces a high-throughput 3D spheroid model to accurately simulate *in vivo* trophoblast behavior, including cellular differentiation and response to external stressors.

Objectives: To characterize human placentoids using a novel high-throughput spheroid generation device and demonstrate their utility for assessing the effects of Anti-tuberculosis therapy (Anti-Tb) drugs.

Methods: 3D placentoids were generated from BeWo and Htr-8/SVneo cell lines using a high-throughput spheroid generating device. Structural integrity was assessed via histology, while differentiation was confirmed through Beta-hCG, E-Cadherin, and Vimentin staining. Placentoids were treated with physiological doses of Anti-Tb drugs. Impact was evaluated using cytotoxicity assays and spheroid migration assays to measure functional outgrowth.

Results: Spheroids were first characterized based on the histology that showed resemblance to the human placental villi. BeWo placentoids produced Beta hCG after differentiation. Htr-8/SVneo placentoids expressed E-Cadherin. Like the human placental anchoring villus, these placentoids transitioned from epithelial to mesenchymal state was confirmed using vimentin staining. Cytotoxicity assay in response to Anti-Tb drugs showed no significant decrease in cell viability. Spheroid migration assay showed reduced spheroid outgrowth.

Conclusion: The initial Screening Anti-Tb drugs did not affect the placentoids viability but the functional assay showed these drug affects the placenta. Further this platform will be useful for predicting drugs that may be safe or unsafe in pregnancy.

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Abstract No: SA-031

Non-coding RNA-mediated Regulatory Networks in the Maternal Endometrium in Recurrent Implantation Failure and Pregnancy Loss



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Introduction: Embryo implantation is a highly selective and tightly regulated process requiring coordinated interaction between competent embryo and receptive endometrium. The endometrium functions as a dynamic biosensor that actively evaluates and selects viable embryos for implantation. Disruption of this selective mechanism can lead to reproductive failure, with evidence suggesting that recurrent pregnancy loss (RPL) is associated with endometrial under-selectivity, whereas recurrent implantation failure (RIF) reflects an over-selective endometrial response. Although extensive transcriptomic studies have delineated molecular signatures of endometrial receptivity, these datasets largely capture downstream gene expression changes and do not fully explain the regulatory mechanisms governing embryo selection. Non-coding RNAs plays a key role in post-transcriptional and epigenetic regulation of endometrial selectivity, which remains incompletely understood.

Objectives: This study aimed to identify molecular networks associated with RIF and RPL by integrating coding and non-coding RNA profiles. We explored circRNA-mRNA and lncRNA-mRNA interaction networks that are associated with RPL and RIF.

Methods: Publicly available rRNA-depleted and RNase R-treated RNA-sequencing datasets of endometrial biopsies from RPL and RIF women were analysed. Comprehensive profiling of mRNAs, lncRNAs, and circRNAs was performed. Differential expression analysis and interaction mapping were used to construct circRNA-mRNA and lncRNA-mRNA regulatory networks, with pathway enrichment analyses.

Results: Distinct transcriptomic signatures were observed across fertile, RPL, and RIF endometria. Dysregulated circRNA-mRNA and lncRNA-mRNA interaction networks were associated with key biological pathways including cytokine signalling, immune modulation, and decidualization. Perturbation of these networks were pronounced in RPL and RIF, suggesting impaired endometrial function.

Conclusions: Our integrative analysis reveals coordinated circRNA–lncRNA–mRNA regulatory networks critical for endometrial function. Disruption of these axes reflects a dysfunctional endometrium in women with RPL and RIF. These molecular signatures offer promising targets for therapeutic intervention to improve pregnancy outcomes in reproductive failure.

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Abstract No: SA-032

Maternal cellular immune determinants associated with cCMV and adverse pregnancy outcome



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Introduction: Human cytomegalovirus (HCMV) infection is highly prevalent among Indian women of reproductive age (>90% seroprevalence), yet India bears the highest global burden of congenital HCMV (cCMV), affecting >1.5% of live births. Maternal systemic and HCMV-specific cellular immune responses associated with pregnancy outcomes remain poorly defined.

Objective: To characterize maternal cellular immune signatures associated with cCMV and adverse pregnancy outcomes (APOs).

Methods: Eighty-three pregnant women were enrolled and followed longitudinally, including those with a bad obstetric history (BOH; n = 45) and without BOH (n = 38), along with 19 non-pregnant women recruited cross-sectionally. Multiparametric flow cytometry was used to assess early maternal systemic and HCMV-specific cellular immune responses across outcome groups: healthy controls, pregnancy loss (PL), congenital HCMV with symptomatic birth (cCMV+SB), cCMV, symptomatic birth (SB), and normal pregnancy outcomes (NPO). Immune profiling included enumeration of T, B, NK cells, and monocytes, assessment of activation markers and PD-1 expression across T-cell memory subsets, and evaluation of HCMV-specific recall responses to pp65, IE1, and gB. Functional analyses assessed degranulation (CD107a), chemokine (MIP-1β), and Th1 cytokine (IFN-γ, TNF-α, IL-2) responses.

Results: PL and cCMV+SB groups shared overlapping immune signatures and were enriched for recent HCMV infection, characterized by heightened immune activation, reduced PD-1 expression, increased IL-2 responses to pp65 and gB, and enhanced cytolytic activity; PL additionally showed elevated B-cell frequencies. In contrast, cCMV group was associated with viral reactivation and exhibited reduced lymphocyte, B-cell, NK-cell, and monocyte frequencies, diminished cytolytic and Th1 responses, increased MIP-1β production, and elevated activation and PD-1 expression. NPOs were enriched for signatures of past HCMV exposure.

Conclusion: Distinct maternal immune profiles are associated with cCMV and adverse pregnancy outcomes, highlighting potential immunological mechanisms underlying poor pregnancy outcomes in congenital HCMV infections.

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Abstract No: SA-033

Pancreatic β Cell Functions and Heterogeneity of Gestational Diabetes Mellitus in Indian Women



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Introduction: Gestational Diabetes Mellitus (GDM) is defined as any Degree of glucose intolerance first occurring or diagnosed during pregnancy. The prevalence of GDM ranges from 9 to 16%, and around 5-6 million pregnancies are affected in India yearly. Traditionally, GDM is considered a homogeneous condition; however, recent studies among Caucasian women have shown heterogeneity of GDM. Physiologically, GDM is classified into defect in Insulin secretion, defect in insulin sensitivity, and both defects. Asian-Indians have a distinct metabolic profile and compromised pancreatic beta cell functions, leading to increased risk of GDM at an earlier age and lower BMI compared to their Caucasian counterparts. The heterogeneity of GDM based on pancreatic β-cell physiology and glucose metabolism in Indian women with GDM has not been studied. This study aims to understand the physiological heterogeneity of GDM.

Objective: To classify physiological subtypes of GDM based on insulin sensitivity/secretion among Indian women

Methods: Pregnant women undergoing Oral Glucose Tolerance Test (OGTT) between 24th – 32nd week are recruited into the study. GDM is diagnosed by the IADPSG criteria. Surrogate markers of insulin secretion (Stumvoll Index) and insulin sensitivity (Matsuda Index) were calculated. The 25th percentile below the Stumvoll and Matsuda index was used to subtype GDM either as a defect in insulin sensitivity, secretion or mixed.

Results: In this study, n = 690 pregnant women were recruited, and the prevalence of GDM was found to be 12.5%. The distribution of subtypes is as follows: >50% women having a defect in Insulin Sensitivity, ~20% having a defect in Insulin Secretion, ~15% having Both Defects, and ~10% with no defect.

Conclusion: Physiological Heterogeneity in GDM is found in the Indian population, where individuals having defect in their insulin sensitivity are predominant

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Abstract No: SA-034

Systemic and Antigen-Specific Immune Signatures Associated with Latent Tuberculosis Infection in PLHIV



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Introduction: Active tuberculosis remains the primary cause of morbidity and mortality among people living with HIV (PLHIV). Elucidating how HIV-1–driven CD4$^+$ T cell depletion and subsequent immune dysfunction contribute to Mycobacterium tuberculosis reactivation in PLHIV with latent TB infection (LTBI) would address a major public health challenge in LMICs, where the overwhelming burden of both HIV and TB resides.

Objective: Delineation of unique systemic and TB-specific pathogenic signatures associated with LTBI and active TB in the context of ART-naïve and -receiving HIV-1 infected individuals towards developing actionable targets to minimize morbidity and mortality caused by TB reactivation.

Method: Fifty HIV-seronegative individuals and 112 ART-naïve HIV-1–infected participants were enrolled from tertiary care hospitals in Mumbai and subsequently stratified as LTBI$^+$ or active TB$^+$ based on interferon-gamma release assay (IGRA) results and clinical confirmation, respectively. Systemic and TB-specific (DosR and Rpf) immune profiling of cellular subsets was performed using flow cytometry, complemented by multi-analyte plasma analyses. PLHIV with latent TB were prospectively followed for up to two years after initiation of isoniazid preventive therapy (IPT) and antiretroviral therapy (ART).

Results: Therapy naive HLTBI+ individuals exhibited highest CD4/CD8 ratio with lowest levels of circulating intermediate monocyte counts, T cell activation and PD-1 expression with decreased frequency of T regulatory cells and higher circulating IL-10 and IL-17A levels. PD-1 expression on CD4+ T cell memory subsets together with opposing anamnestic TB specific TNF-α responses to DosR and Rpf by HLTBI+ and HTB+ individuals respectively were discriminatory signatures for these groups. Also, a distinctive signature of TB specific TNF-α production that positively correlated with CD4:CD8 ratio was preserved following ART.

Conclusion: Our findings identified a distinct immunomodulatory milieu associated with attenuated disease progression, independent of ART, in latently co-infected PLHIV, which—if maintained—may confer protection against tuberculosis reactivation

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Abstract No: SA-035

Deciphering role of novel *Salmonella Typhi* effector in controlling Host Cell Death and Intracellular bacterial Survival



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Introduction: Bacterial pathogens manipulate host cell pathway to create an environment that supports their survival and dissemination. *Salmonella enterica* serovar Typhi is a human-restricted intracellular pathogen that survives within monocytes while carefully modulating host cell death. Understanding how bacterial genes balance host cell killing and intracellular persistence is essential for unravelling *S. Typhi* pathogenesis.

Objective: To identify the novel *S. Typhi* effectors responsible for Apoptosis regulation in human monocytes

Methods: Approx one thousand transposons mutants Tn5 library of *Salmonella Typhi* were generated and screened for intracellular survival in primary human monocytes. Apoptosis was assessed by flow cytometry (FACS) following Annexin V/PI staining. Intracellular bacterial survival was assessed using the gentamicin protection assay followed by colony-forming unit (CFU) enumeration at specific post-infection time points. Through this screening, we identified three mutants M-844, M-845, and M-938 that consistently induced significantly higher monocyte Apoptosis compared to the Ty2 strain. Whole-genome sequencing (WGS) was performed to identify Tn5 insertion sites and mutated genes.

Results: All three Tn5 mutants M-844, M-845, and M-938 induced significantly higher levels of Apoptosis in primary human monocytes compared to the Ty2 strain. FACS analysis using Annexin V/PI staining revealed increased apoptotic and late apoptotic/necrotic populations in mutant-infected monocytes. Interestingly, despite causing increased host cell death, these mutants displayed distinct intracellular survival phenotypes. Mutant M-844 showed equal intracellular survival comparable to Ty2, whereas mutants M-845 and M-938 exhibited significantly reduced survival within monocytes. WGS confirmed unique Tn5 insertion sites in each mutant, implicating genes potentially involved in intracellular adaptation, stress tolerance, host–pathogen interactions and regulation of host cell death pathways

Conclusions: Overall, our findings highlight novel effector that influence monocyte cell death and intracellular survival in *Salmonella Typhi*, providing new insights into how this pathogen balances host damage with persistence during human infection.

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Abstract No: SA-036

Evaluation of Circulating MicroRNAs for Early Detection of Breast Cancer



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Introduction: Breast cancer (BC) is the most common malignancy and leading cause of cancer-related deaths worldwide. Early diagnosis remains challenging due to lack sensitive detection methods. Circulating microRNAs (miRNAs) appear as potential promising non-invasive biomarkers for breast cancer detection.

Objectives: The study objectives are to evaluate the diagnostic potential of miRNAs and explore their involvement in cancer-related pathways.

Methods: Small RNA Sequencing (sRNA-Seq) was utilized for identification of differentially expressed miRNAs (DemiRs), and validated by quantitative PCR (qPCR) in sera of 80 BC patients, 30 healthy controls, and 38 paired-tissue samples. Further, Receiver Operating Characteristics (ROC) curve analysis was performed to evaluate diagnostic potential. Target prediction and functional enrichment was done bioinformatics analysis.

Results: sRNA-Seq identified 23 significantly dysregulated miRNAs with 12 upregulated and 11 downregulated in BC patients compared to controls. Three miRNAs- hsa-miR-200a-3p, hsa-miR-125b-5p and hsa-miR-4306 that were identified as downregulated by sRNA-Seq analysis were also found to be significantly downregulated by qPCR validation analysis. ROC analysis showed strong discriminatory ability for hsa-miR-200a-3p and hsa-miR-4306. The involvement of these miRNAs in Wnt/β-catenin and Hippo pathways and key target genes including CTNNB1, YAP1, WWTR1 and GSK3B was revealed by **bioinformatics analysis.**

Conclusions: hsa-miR-200a-3p and hsa-miR-4306 hold potential as non-invasive biomarkers for early BC detection, and their potential association in oncogenic pathways emphasizes further clinical investigation.

Project funding: Project has been funded by ICMR

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Abstract No: SA-037

ART driven immune reconstitution is linked to heterogeneous longitudinal gut microbiome remodelling and TB associated dysbiosis risk in HIV+LTBI+ individuals



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Introduction: Antiretroviral therapy (ART) improves immune recovery in people living with HIV [1], yet its impact on gut microbiome dynamics and tuberculosis(TB) risk, particularly with latent TB infection (HIV+LTBI+), remains incompletely understood. Longitudinal interactions between immune reconstitution, microbial metabolism and progression toward TB-associated dysbiosis are poorly defined.

Objectives: To examine longitudinal gut microbiome changes during ART in HIV+LTBI+ individuals and their associations with immune recovery, microbial metabolites and TB reactivation.

Methods: 13 HIV+LTBI+ individuals were followed every six months for 24 months after ART initiation. Longitudinal ut microbiome profiles were compared with 15 HIV-LTBI+ (healthy latent TB) and 17 HIV+TB+ (pathological endpoint) groups. Alpha and beta diversity analyses, linear mixed-effects models, fecal short-chain fatty acid (SCFA) profiling and correlation analyses with immunological parameters were performed. Exploratory longitudinal modeling assessed effects of ART, isoniazid-preventive therapy(IPT) and TB reactivation.

Results: HIV+LTBI+ individuals showed increased alpha diversity and a transient shift of gut microbiome toward HIV-LTBI+ state and away from HIV+TB+ profile after 6 months of ART. However, individual microbiome trajectories varied widely and duration of ART alone did not predict convergence toward a healthier state. Longitudinal analyses showed that higher CD4/CD8 ratios were unexpectedly associated with increased dissimilarity from HIV-LTBI+ microbiome, whereas higher levels of butyric acids, were associated with reduced dissimilarity to this healthier state. One individual experienced TB reactivation, showed increase of uncultured taxon *QALR01 sp900552255* and poor immune recovery.

Conclusion: ART induces heterogeneous and non-linear gut microbiome remodelling in HIV+LTBI+ individuals. Immune reconstitution and microbial metabolic recovery may not occur in parallel during ART and specific microbial signatures may signal vulnerability to TB reactivation. These findings suggest that tracking gut microbiome and metabolic changes during ART could guide development of targeted interventions to support immune recovery and potentially lower risk of TB reactivation.

Acknowledgement(s) and Funding: We gratefully acknowledge extramural support from ICMR (Grant no. HIV/INDO-US/162/7/2018-ECD-II AND IEC no 348/2018). We thank study participants for the samples.

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Abstract No: SA-038

Isolation, Characterization, and Therapeutic Potential of Lytic Bacteriophage Targeting MDR *Pseudomonas aeruginosa*



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Introduction: Multidrug-resistant (MDR) *Pseudomonas aeruginosa* poses a serious threat in clinical settings for intrinsic and acquired resistance mechanisms and its ability to form protective biofilms that limit antibiotic efficacy and host immune responses. The burden of antimicrobial resistance (AMR) has renewed interest in bacteriophage therapy as a promising alternative to conventional antibiotics, particularly for biofilm-associated infections.

Objective: To assess the therapeutic potential of a lytic bacteriophage against MDR *P. aeruginosa* through biofilm disruption and phage–antibiotic synergy.

Methods: A lytic bacteriophage, PAGP25, was isolated from environmental samples collected in Kolkata, India, and characterized against clinical *Pseudomonas* isolates. Transmission electron microscopy revealed an icosahedral head with a contractile tail, placing PAGP25 within the family *Myoviridae*. Host range analysis demonstrated high specificity toward *Pseudomonas* spp., with no lytic activity against other tested clinical bacteria. The physicochemical stability of PAGP25 was evaluated across varying temperature and pH conditions.

Results: PAGP25 exhibited broad thermal and pH stability, supporting its suitability for therapeutic applications. Its antibiofilm activity against *P. aeruginosa* was evaluated using confocal laser scanning microscopy (CLSM), which showed significant biofilm disruption following phage treatment. Colistin, a last-resort antibiotic for MDR *Pseudomonas*, reduced biofilm biomass when used alone; however, combined phage–colistin treatment resulted in markedly enhanced biofilm eradication, indicating strong synergistic activity. Ciprofloxacin, to which the host strain was resistant, showed minimal antibacterial activity when applied alone. In contrast, its combination with PAGP25 restored antibacterial efficacy, demonstrating clear phage–antibiotic synergy (PAS), as evidenced by an increased zone of inhibition.

Conclusion: The potent lytic activity, effective biofilm disruption, broad physicochemical stability, and demonstrated antibiotic synergy highlight the strong translational potential of PAGP25. These findings support the development of phage-based therapies, alone or in combination with antibiotics, as a targeted strategy for managing MDR *P. aeruginosa* infections and advancing precision antimicrobial therapy.

Acknowlegement and Fundings: Arpita Sarbajana, Rishikesh Kumar

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Abstract No: SA-039

Comparative microbiome analysis in field-caught *Aedes aegypti* populations from Puducherry, India



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Introduction: The microbiota residing in the mosquito midgut plays a crucial role in shaping the host's biology, influencing processes such as nutrition, reproduction, metabolism, and immune function, and ultimately affecting mosquito fitness and vector competence.

Objectives: This study characterised and compared the midgut bacterial communities of field-collected *Aedes aegypti* from various ecological contexts, including different populations, and two different time points.

Methods: Mosquito larvae were collected from the field and reared into adults. The midgut was dissected from female mosquitoes after emergence, and water samples were pooled based on the time point, using the high-throughput Illumina NovaSeq 6000 platform to sequence the 16S rRNA gene for analysis of the bacterial diversity and composition in both the midgut and water.

Results: At the phylum level, *Pseudomonadota* (proteobacteria) is highly abundant in the midgut bacterial community, comprising roughly 72% of the total abundance in our study. Microbial richness and evenness varied among individual *Ae. aegypti* populations. Bacterial genera such as *Aeromonas, Ralstonia, Bifidobacterium, Methylobacterium, Polynucleobacter, Escherichia,* and *Sodalis* are highly abundant across the population. Samples collected during time point 1 (February) showed a consistently higher abundance of genera such as *Methylobacterium*, *Herbaspirillum*, *Candidatus Atelocyanobacterium*, and *Staphylococcus* in the *Ae. aegypti* midgut. Whereas *Sodalis*, *Ralstonia*, *Escherichia*, *Enterobacter*, *Klebsiella*, and *Ligilactobacillus* were more dominant in time point 2 (July). These seasonal shifts in abundance may be influenced by environmental factors such as temperature and climatic conditions that favour the growth of certain bacterial taxa.

Conclusion: The findings may be useful in future research on the roles of the midgut microbiome in variable vector competence, insecticide resistance, and mosquitoes' fitness. Finally, the study may help in the development of microbiome-based vector control strategies.

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Abstract No: SA-040

Nanofiber-Encapsulated *Bacillus thuringiensis* israelensis VCRC B668 for Eco-Friendly Mosquito Control



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Introduction: Mosquito-borne diseases remain a major public health concern, while prolonged use of chemical insecticides has led to environmental contamination, health risks, and resistance development. Bacterial larvicides such as *Bacillus thuringiensis* (*Bt*) offer a safer alternative, though their field efficacy is often limited by environmental degradation and formulation constraints.

Objective: In this study aims to develop and characterize a nanofiber-encapsulated formulation of *Bacillus thuringiensis* subsp. *israelensis* VCRC B668, a highly potent strain with broad-spectrum larvicidal activity and a favourable safety profile.

Methods: A nanofiber-encapsulated formulation was developed using electrospun polyvinyl alcohol–carboxymethyl cellulose (PVA–CMC) polymers. Molecular identification was performed using 16S rRNA, ilvD, and pycA phylogenetic analyses, along with cry and cyt toxin gene profiling. Whole-genome sequencing, protein characterization (SDS–PAGE and LC–MS/MS), and physicochemical analyses (SEM, zeta potential, and FTIR) were conducted. Larvicidal bioassays were performed against *Aedes aegypti, Culex quinquefasciatus, and Anopheles stephensi*, along with non-target organism assessments.

Results: Molecular identification using 16S rRNA, *ilvD*, and *pycA* phylogenetic analyses, along with toxin gene profiling of *cry* and *cyt* genes, confirmed its identity as *Bti*. Whole-genome analysis revealed a 6.25 Mb genome with 34.97% GC content and close relatedness to reference *Bti* strains AM65-52 and BGSC 4Q1. SDS–PAGE and LC–MS/MS analyses identified major toxin proteins Cry4Ba, Cry11Aa, and Cyt1Aa at approximately 130, 70, and 25 kDa, respectively. The nanofiber formulation enhanced toxin stability, enabled controlled release, improved persistence under field conditions and demonstrated structural stability as confirmed by SEM, zeta potential, and FTIR analyses. High larvicidal activity was observed, with LC_{50} values ranging from 0.0076 to 0.0098 mg/L, while no adverse effects were detected in non-target aquatic organisms.

Conclusion: Overall, this study highlights nanofiber-encapsulated *Bti* VCRC B668 as a promising eco-friendly mosquito control strategy with enhanced stability and effectiveness.

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Abstract No: SA-041

Evaluating the Immunotherapeutic Potential of rfhSP-D in LPS-induced *in vitro* and *in vivo* models of Pre-eclampsia



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Introduction: Pre-eclampsia (PE) is a pregnancy-induced hypertensive disorder characterized by a dysregulated immune response and a systemic angiogenic imbalance. Cohort studies with pregnant women that reduced serum levels of innate immune lectins, particularly Surfactant Protein D (SP-D), are associated with severe early-onset PE (EOPE). Surfactant Protein D (SP-D), a collectin expressed at the feto-maternal interface, contributes to fertility, parturition, and immune homeostasis. Data from SP-D KO mice show that sustained SP-D levels are critical during implantation and placentation. This study was conducted to evaluate the effectiveness of a recombinant fragment of human SP-D (rfhSP-D) as an immunotherapeutic agent in the treatment of PE.

Objectives: To evaluate the immunotherapeutic potential of recombinant fragment of SP-D in in vivo and in vitro models of PE

Materials and Methods: The methodology followed experimental evaluation at two levels: an *in vitro* approach to simulate PE by challenging the first-trimester trophoblast cells with ultra-low dose LPS (ULD LPS) in hypoxia, followed by assessment at transcript, protein, and functional levels, and an *in vivo* and *ex vivo* approach by generating the LPS-induced EOPE mice model (low-dose LPS administration at GD 5.5) and treating their placental explants at GD12.5 with rfhSP-D in hypoxia.

Results: *In vitro*, rfhSP-D significantly upregulated the levels of angiogenic, migration, and invasion markers, VEGF, PLGF, MMP9, N-cadherin, Vimentin, and significantly downregulated the levels of anti-angiogenic sFlt1 and sEng in HTR8 cells under hypoxia. Additionally, rfhSP-D treatment significantly downregulated the levels of inflammatory markers, IL1β, TNFα, and TLR4. The ULD LPS stimulation induced a significant pro-inflammatory response, by upregulation of TLR4, IL1β, TNFα, pNFκB, and an anti-angiogenic response, by upregulation of sFlt1 and downregulation of VEGF, PLGF, MMP9, N-Cadherin, and Vimentin in HTR8 cells under hypoxia. The rfhSP-D treatment rectified the angiogenic and inflammatory imbalance in this model. The administration of low-dose LPS in pregnant mice at GD 5.5 produced hypertension, proteinuria, placental abnormalities, kidney pathology, and aberrant placental immune cell profiles. The LPS EOPE dams also exhibited lower placental and fetal weights. In an *ex vivo* culture of the LPS EOPE placentae at GD12.5, rfhSP-D treatment under hypoxia restored the inflammatory and angiogenic balance in the placental tissue.

Conclusion: rfhSP-D sustains cell viability of HTR8 cells in hypoxia, whilst inducing a pro-angiogenic, pro-migratory, pro-invasive and anti-inflammatory effect. In the *in vitro* rescue experiment, rfhSP-D mitigated the effects of ULD LPS challenge in HTR8 cells. The treatment of LPS EOPE murine placentae with rfhSP-D in an *ex vivo* culture significantly upregulated the angiogenic markers and demonstrated its ability to be assessed as an immunotherapeutic molecule in PE.

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Abstract No: SA-042

An Integrative Epigenetic-Epitranscriptomic Landscape of PCOS: MicroRNAs at the Regulatory Crossroads



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Introduction: Polycystic Ovary Syndrome (PCOS), leading cause of anovulatory infertility, lacks a unifying genetic signature, suggesting a critical role of reversible epigenetic and epitranscriptomic alterations in its pathogenesis[1–3]. Our current research delineates a multi-level epi-regulatory cascade underpinning PCOS pathophysiology in granulosa cells (GCs), surrogates for oocyte quality and ovarian function.

Objective: To delineate the role of miRNA dysregulation in multi-level epigenetic and epitranscriptomic mechanisms driving aberrant gene expression in GCs of PCOS.

Methods: Reanalysed transcriptomic datasets and systematically curated miRNAs to identify differentially expressed genes and miRNAs in follicular environment of PCOS. Functional enrichment and network analyses identified dysregulated pathways and hub genes. Expression of hub genes and regulatory miRNAs and m6A machinery (writers, erasers, readers) was assessed by qRT-PCR, DNA methylation profiles of miRNA were evaluated by pyrosequencing in GCs, global m6A levels were measured by ELISA and correlations with androgen indices were evaluated.

Results: Regulation of Actin Cytoskeleton was the top dysregulated pathway, which may impair steroidogenesis and cumulus expansion. Hub genes, ARPC1B, ACTR2, RAC2, PIP5K1B and their regulatory miRNAs (miR-196a-5p, miR-377-5p, miR-424-5p) showed altered expression. Further, miR-mRNA dysregulation was evidenced by aberrant DNA methylation of miRNA-encoding genes. At the epitranscriptomic axis, elevated global m6A levels were accompanied by increased writers, decreased erasers, and altered readers expression in GCs of PCOS women. Differential expression of miR-20b and miR-607, targeting METTL3 and FTO respectively, suggests miRNA-mediated modulation of m6A machinery. Correlations between m6A levels, METTL3, FTO expression, and androgen indices indicate a potential androgen-m6A regulatory loop.

Conclusion: Our findings highlight complex epi-regulatory network driven by miRNA may underline ovarian dysfunction in PCOS.

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Abstract No: SA-043

Effects of Altered Levels of Extracellular High Mobility Group Box – 1 (HMGB1) on Embryo Implantation



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Introduction: The uterine immune profile during implantation adopts a tolerogenic profile that promotes embryo attachment and invasion. Variations in the frequencies or phenotypes of immune cells can lead to implantation failure. Altered levels of alarmins could be a potential source of immune profile derangements. Our group had demonstrated that an excess of one such alarmin, HMGB1, in the uterine lumen led to implantation failure in Holtzman rats.

Objectives:
1.To determine whether implantation failure due to an excess of uterine HMGB1 was associated with an altered uterine immune profile in a rodent model
2.To determine whether glycyrrhizin abrogated the effects of HMGB1 on embryo implantation

Methods: Adult female Wistar rats received intrauterine administration of recombinant HMGB1, with or without glycyrrhizin, whereas sham control animals received only a saline injection on day 3 of post-coitum (p.c.). The uterine horns were harvested on day 5 p.c. for uterine fluid collection. Part of the horn was excised for histological analyses and immunofluorescence experiments. The remaining uterine horn was slit open to prepare a single-cell suspension of the inner lining for flow cytometry.

Results: Excess of HMGB1 in the uterine milieu in the peri-implantation phase led to implantation failure in Wistar rats. Further, this was associated with impaired decidualization, as indicated by reduced immunolocalization of stromal cell decidualization markers, i.e. Prolactin and IGFBP1. These effects were mitigated by the co-administration of equal concentrations of glycyrrhizin and rHMGB1. Flow cytometric analyses revealed altered frequencies of uterine NK and regulatory T cells in the horns injected with rHMGB1. Their frequencies in the horns that received rHMGB1+glycyrrhizin were comparable to those in saline-treated horns. The proportion of anti-inflammatory M2-macrophages activated during tissue remodelling was also found to be reduced in rHMGB1-treated horns, which were restored in rHMGB1+glycyrrhizin-treated horns.

Conclusions: Excess HMGB1 in the uterine microenvironment during implantation altered the immune profile, leading to implantation failure. This opens up possibilities of interrogation of the uterine microenvironment for an excess of sterile inflammation in women experiencing recurrent implantation failure.

Funding agencies: This work was supported by Science and Engineering Research Board (SERB), Department of Science and Technology (DST) (file no. CRG/20l9/000700) and Women Scientists Scheme - A (WOS-A), DST [project no. SR/WOS-A/LS-75/2019 (G)].

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Abstract No: SA-044

Integrated Buccal Swab based Biochemical and Genetic analyses revealed 18 Novel Variants in Indian Paediatric Mitochondrial Cases



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Background: Mitochondrial disorders are clinically and genetically heterogeneous multisystemic diseases caused by mutations in mitochondrial or nuclear DNA. Although genetic investigation detects numerous variants, the pathogenic relevance of many remains unclear. Integrating mitochondrial enzyme activity analysis using non-invasive buccal swabs with genetic data is therefore essential to establish functional relevance and improve genotype–phenotype correlations.

Objective: To correlate oxidative phosphorylation (OXPHOS) complex deficiencies in buccal swabs with pathogenic variants identified in mtDNA or nDNA, establishing reference ranges for mitochondrial enzymes, comparative analysis of paired buccal and muscle enzyme activities and development of a non-invasive diagnostic tool.

Methods: Buccal swabs from 52 paediatric patients with suspected mitochondrial disorders and 37 age-matched controls were collected. Spectrophotometric assays were used to measure enzyme activities of mitochondrial complexes I–IV. Genetic analysis of blood samples included long-range PCR for detection of large mtDNA deletions and whole-exome sequencing for variant identification, with Sanger sequencing for validation.

Results: Our study demonstrated biochemical–genetic concordance in 26 of 52 patients. A significantly reduced buccal mitochondrial enzyme activities of complexes II, III, and IV ($p < 0.05$) was identified in our cohort. Enzyme deficiencies showed concordance between paired muscle biopsy and buccal swab samples ($n = 4$), and Receiver Operating Curve analysis indicated that buccal swabs could predict complex I, III, and IV deficiencies. Genetic analysis identified 51 variants across 42 genes, including 18 novel variants in our pediatric cohort(11 mitochondrial and 7 non-mitochondrial). Using genetically and biochemically concordant cases as true positives, the buccal swab approach demonstrated a sensitivity of 72.4%, making it considerable non-invasive diagnostic tool for paediatric mitochondrial disorders.

Conclusion: Integrating biochemical and molecular genetic analyses using non-invasive buccal swabs enables early and accurate diagnosis of paediatric mitochondrial disorders, helps management and treatment and genetic counselling, especially in resource-limited areas.

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Abstract No: SA-045

Development of a low-cost, rapid and ultrasensitive CRISPR-Cas12a based diagnostic kit for tuberculosis



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Introduction: Tuberculosis (TB) is a bacterial infection caused by *Mycobacterium tuberculosis*. It is the leading cause of death due to a single infectious agent claiming about 1.23 million lives and affecting 10.7 million people, of which 25% is contributed by India[1].
Current diagnostics recommended by WHO include microscopy, culture, GeneXpert, and Truenat, are constrained by sensitivity, long turnaround time, and high cost, respectively[2]. Hence, there is pressing need for a rapid, and affordable molecular diagnostic platform to advance India's TB elimination goals. CRISPR-based diagnostics provide a promising alternative, using Cas12a nucleases guided by crRNAs designed specifically to identify target sequences with high specificity. Leveraging Cas12a's collateral cleavage property, fluorescence-based probes enable detection upon target recognition[3].
CRISPR-Cas12a when coupled with PCR-based pre-amplification offers a promising solution to overcome these challenges. Thus, this study aimed to develop a rapid, low-cost, ultrasensitive, PCR-CRISPR-Cas12a detection kit 'Glow-TB_{PCR}' to address the gaps.

Objectives: To design, develop, optimise and validate a CRISPR-Cas12a based tuberculosis detection kit.

Methods:

1. Bioinformatics analysis: Target selection, primer and gRNA designing.
2. PCR and CRISPR assay optimization, manufacturing of kits.
3. Analytical and clinical validation (Sample size: ~300).
4. Statistical analysis.

Results:

1. Turnaround time: ~3-hour.
2. LOD: ~1 copy per reaction.
3. Internal validation against GeneXpert in 267 samples including 74 positives and 193 negatives:
   Sensitivity: 93.24%
   Specificity: 99.48%
   Cohen's kappa: 0.94
   Positive Predictive Value (PPV): 98.57%
   Negative Predictive Value (NPV): 97.46%
4. Estimated lab-based cost: INR 105 per test.

Conclusions: The Glow-TB_{PCR} kit when integrated with in-house developed RapidBact DNA extraction kit and RapidGlow device for real time fluorescence detection provides a rapid, low-cost, ultrasensitive, and scalable solution with comparable performance to GeneXpert and Truenat. Deployment of this technology in district TB wards, hospitals, and medical colleges could substantially enhance diagnostic accuracy, and enable timely treatment.

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Abstract No: SA-046

Distinct temporal regulation of Trop2 and EpCAM expression in rat and human placenta



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Introduction: Trop2 and EpCAM, transmembrane glycoproteins belonging to tumor associated calcium signal transducer family, are encoded by *TACSTD2* and *TACSTD1* gene respectively. They were first identified as human trophoblast surface antigens and subsequently widely studied in cancer. In cancer, they have been shown to be associated with cell survival, metastasis, and stem cell maintenance. However, their functional relevance in placentation remains poorly understood.

Objectives: This study aimed to determine the temporal patterns of expression of Trop2 and EpCAM in human and rat placenta in order to understand their importance in different stages of placentation.

Methods: Transcript and protein expression was assessed by qRT-PCR and immunoblotting. Localization in the human placenta was shown by immunohistochemistry. Human and rat *TACSTD2* and *TACSTD1* promoter sequences were compared *in silico*, and binding sites for key trophoblast-associated transcription factors were identified.

Results: In rat placenta, Trop2 and EpCAM expression increased gradually, correlating with progressive placental growth. In contrast, in human placenta expression remained same from the first trimester till term. The peak expression of these proteins coincided with the respective window of maximal trophoblast invasion - early gestation in humans and late gestation in rats. In rat placenta, Trop2 expression was restricted to the labyrinth zone, whereas EpCAM was detected in the labyrinth and junctional zones. In human placenta, Trop2 and EpCAM predominantly co-localized within villous trophoblasts. *In silico* promoter analysis revealed species-specific transcription factor binding sites. Binding sites for ASCL2, which regulates extravillous trophoblast differentiation, were identified in the human

TACSTD2 and in rat TACSTD1 promoter, while binding sites for TEAD4, which marks the proliferative trophoblast progenitors, were identified in both promoters in rat but present only in the *TACSTD1* promoter in human.

Conclusions: The findings suggest distinct roles for Trop2 and EpCAM in gestational regulation of trophoblast invasion in human and rat placentation.

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Abstract No: SA-047

Trypanothione Synthetase mediated Antileishmanial Drug Resistance and Redox Balance in *Leishmania donovani*



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Leishmania donovani is the causative agent of visceral leishmaniasis, a severe neglected tropical disease transmitted between humans and sand fly vectors which is often fatal if left untreated. The efficacy of current chemotherapeutic options, including Amphotericin B (AmpB) and Miltefosine (Mil), is increasingly threatened by the emergence of drug resistance, in addition to limitations such as high cost, teratogenicity, and complex administration routes. These challenges underscore an urgent need to identify novel therapeutic targets, capable of overcoming resistance mechanisms. Trypanothione synthetase of *L. donovani* (LdTryS), a key enzyme of the parasite-specific thiol metabolic pathway, plays a central role in maintaining redox homeostasis and has been validated as a potential drug target. In this study, the involvement of LdTryS in antileishmanial drug resistance has been investigated by analyzing its expression and enzymatic activity in Ag83 AmpB sensitive and resistant *L. donovani* parasites, including wild-type; LdWT, Amp B–resistant clinical isolate; LdAmpBRCI, Amp B–resistant laboratory-generated strain; LdAmpBRLG, and Mil-resistant laboratory-generated strain; LdMilRLG. The analysis showed an up regulation in the LdTryS protein expression as well as activity for the resistant strains indicating its role in drug resistance. Furthermore, LdTryS expression, intracellular ROS and total thiol content were evaluated under oxidative stress induced by menadione and heavy metal stress induced by cadmium in the sensitive as well as resistant parasites. The results demonstrated a significant up-regulation of LdTryS protein expression in drug-sensitive as well as drug-resistant parasites under the induced stress conditions suggesting an active role of LdTryS in stress balance. These findings highlight the contribution of LdTryS to thiol-mediated drug resistance and stress tolerance in *L. donovani*, underscoring its potential role as a promising therapeutic target for the development of new antileishmanial agents.

Keywords: LdTryS, Redox homeostasis, Drug resistance.

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Abstract No: SA-048

Identified Secreted Leishmanial protein as a novel biomarker for the diagnosis of VL, PKDL and VL co-infected cases in Bihar



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Visceral Leishmaniasis (VL) is a life threatening protozoan disease caused by *Leishmania donovani*. Bihar is the most endemic state for VL in India; an estimated 2-7% of VL cases are co-infected with HIV. HIV has been identified as one of the emerging challenge for VL control. For diagnosis of VL the rk39 strip test frequently used but in case of VL-HIV the sensitivity of rK39 decreased. In some other disease like TB and also in pregnant women it shows false positive result. Although, VL is usually associated with higher titer of antibodies against leishmanial antigens facilitating the serological diagnosis, the repression of the immune system by HIV virus reduces these significantly in co-infected patients. In case of PKDL, mostly in macular lesion the sensitivity of gold standard Parasitology test is decreased which is also reported in Bihar. To overcome this diagnosis related issues associated with PKDL and VL co-infection, we are working on to develop the novel biomarker with significant sensitivity and specificity for the detection of PKDL and VL co-infected patients. In this study, we have identified SPV16 and analyzed by Immunoblot and ELISA for the diagnosis of VL, PKDL, VL-HIV, VL-HIV-TB and VL-TB patient's serum with HIV and TB as control. Our results showed that the SPV16 identified antibodies in patient's sera samples. IgG- Isotyping was also done to know the type of immune response of antigen before and after treatment, thus our SPV16 antigen is recognized of VL, PKDL and VL-HIV patients significantly instead of control, such as HIV and TB, suggested that our antigen have higher potential or even better than rK39 test to detect PKDL and VL co-infected patients in Bihar.

Keyword- PKDL, VL-HIV,VL-TB, ELISA, Diagnosis, Biomarker

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Abstract No: SA-049

From Stigma to Suffering: Impact of Stigma on Health-Related Quality of Life and Healthcare Access in Sickle Cell Disease



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Introduction: Sickle Cell Disease (SCD) is a chronic genetic condition marked by recurrent pain, fatigue, and life-limiting complications. Beyond biomedical burden, individuals with SCD experience profound psychosocial distress driven by stigma, discrimination, and structural neglect. Stigma—manifesting as disbelief, moral judgment, social exclusion, and institutional invisibility—has emerged as a major social determinant shaping quality of life and access to care. However, existing evidence remains fragmented across regions and disciplines, limiting a comprehensive understanding of stigma as a multi-level health determinant.

Objectives: To synthesize global empirical evidence on how stigma influences health-related quality of life (HRQoL) and healthcare access among adolescents and adults living with SCD.

Methods: A systematic review was conducted following PRISMA 2020 guidelines. Searches of PubMed, Scopus, Embase, and PubMed Central identified peer-reviewed studies published between 2000 and 2025. Sixty-three studies (qualitative = 18, quantitative = 32, mixed = 13) across five regions were included. Data were extracted using a Joanna Briggs Institute matrix and analyzed through thematic and narrative synthesis.

Results: Four interlinked stigma domains emerged:

1. **Disbelieved and Dismissed** – clinical mistrust and opioid suspicion.
2. **Carrying the Mark** – internalized stigma and psychological distress.
3. **Excluded Twice Over** – intersectional marginalization by race, caste, gender, and class.
4. **Silenced and Invisible** – structural neglect and policy absence.

Across contexts, stigma was consistently associated with reduced HRQoL, delayed care-seeking, treatment non-adherence, and emotional exhaustion. An analytical model conceptualizes stigma as a reinforcing process across micro (personal), meso (interpersonal), and macro (structural) levels.

Conclusions: Stigma is not peripheral to SCD but a central structural determinant of inequity. Addressing stigma through provider training, psychosocial support, and stigma-responsive health policy is essential for improving quality of life, rebuilding trust, and ensuring equitable SCD care.

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Abstract No: SA-050

Epidemiological and Molecular Surveillance of Dengue Virus Circulating in Jodhpur District, Rajasthan, India



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Introduction: Dengue virus (DENV) is an emerging arboviral threat in India, and there is a growing need to characterise its transmission patterns in semi-arid regions such as Jodhpur, Rajasthan. Although dengue outbreaks are widely reported from urban and coastal regions, systematic epidemiological and molecular surveillance data from semi-arid areas remain limited. The present study aimed to investigate the temporal distribution, serotype diversity, and demographic characteristics of dengue infections in Jodhpur district.

Objectives: To analyse seasonal and temporal trends of dengue infections, assess age-group, gender, and urban–rural distribution of cases, and determine circulating dengue virus serotypes using molecular methods.

Methods: A retrospective observational study was conducted using data from clinically suspected dengue patients attending government healthcare facilities in Jodhpur district between July 2024 and June 2025. Dengue diagnosis was performed using ELISA-based NS1 antigen and IgM antibody tests. ELISA-positive samples were further subjected to serotyping by real-time RT-PCR. Patient footfall, fever incidence, demographic variables, and meteorological parameters were analysed to evaluate seasonal associations.

Results: Out of 1,683 patients tested, 121 were NS1-positive and 44 were IgM-positive. Dengue positivity peaked in September 2024 during the post-monsoon period, with the highest NS1 antigen detection indicating acute infections. Male patients consistently showed higher positivity compared to females. The majority of confirmed cases belonged to the 15–29 years age group. Urban and semi-urban areas accounted for most dengue-positive cases. Molecular analysis revealed co-circulation of all four DENV serotypes. Among male patients, DENV-2 was predominant (n = 50), followed by DENV-3 (n = 16). Mixed serotype infections were also detected during peak transmission months. Dengue transmission showed close association with rainfall, humidity, and temperature.

Conclusion: The study demonstrates a distinct seasonal shift in dengue epidemiology in Jodhpur, a semi-arid region not traditionally considered dengue-prone. The predominance of DENV-2 and DENV-3 among male patients and the presence of mixed serotype infections highlight the potential risk for severe dengue. Continuous epidemiological and molecular surveillance is essential for early detection and effective public health response in emerging dengue-prone regions.

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Abstract No: SA-051

Proteomic and genetic characterization of a potent mosquitocidal Bacillus thuringiensis isolated from spoiled fruit for sustainable mosquito control



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Introduction: Mosquito-borne diseases continue to impose a significant public health burden, particularly in tropical regions, while increasing insecticide resistance and ecological concerns demand sustainable vector control alternatives. This study aimed to isolate and comprehensively characterize a highly potent mosquitocidal strain of Bacillus thuringiensis israelensis (Bti) for eco-friendly larval control.

Objectives: To isolate and characterize a highly potent mosquitocidal strain from spoiled fruit and evaluate its larvicidal efficacy and toxin profile for sustainable vector control applications.

Methods: Spoiled fruit samples were screened for larvicidal activity, and the most effective isolate (VCRC B633), recovered from a spoiled apple, was evaluated against late third-instar larvae of Aedes aegypti, Anopheles stephensi, and Culex quinquefasciatus following WHO bioassay protocols. Phenotypic and biochemical characterization was complemented by MALDI-TOF profiling, 16S rRNA sequencing, and PCR-based detection of cry and cyt toxin genes. Proteomic analysis of spore–crystal complexes was performed using SDS-PAGE and LC–MS to confirm toxin expression patterns.

Results: The isolate demonstrated exceptional larvicidal potency, with Ae. aegypti exhibiting the highest susceptibility (LC_{50} = 0.0017 mg/L), followed by An. stephensi and Cx. quinquefasciatus. Proteomic profiling revealed dominant expression of Cry and Cyt toxins within the 25–130 kDa range, indicating a synergistic toxin composition associated with enhanced bioefficacy. No significant adverse effects were observed in representative non-target aquatic organisms under laboratory conditions.

Conclusions: The integration of genetic confirmation with proteomic validation establishes VCRC B633 as a translationally promising biocontrol candidate. The results highlight unconventional ecological niches as promising sources of high-efficacy microbial larvicides for sustainable mosquito control.

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Abstract No: SA-052

CRISPR-Cas based detection of *Pseudomonas aeruginosa* and associated Antibiotic Resistance.



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Introduction: *Pseudomonas aeruginosa* is an aerobic, Gram-negative bacillus associated with severe health care associated infections targeting immunocompromised patients[1]. It predominantly causes nosocomial infections such as pneumonia, urinary tract infections, wounds and bloodstream infections[2]. In addition, it poses significant clinical challenge due to its intrinsic resistance mechanisms and the ability to acquire additional antimicrobial resistance genes[3]. The rapid emergence of multidrug and extensively drug-resistant strains has limited therapeutic options[4]. Therefore, early detection of *P. aeruginosa* along with the antimicrobial resistance profile is crucial for effective infection control and appropriate therapeutic intervention.

Objectives: Development of CRISPR Cas based molecular assays for the detection of *Pseudomonas aeruginosa* and AMR genes.

Methods: CRISPR-Cas–based molecular assays will be designed targeting conserved species-specific biomarker for the detection of *Pseudomonas aeruginosa* and clinically relevant antimicrobial resistance genes by sequence analysis. The assay workflow involved nucleic acid extraction followed by multiplex target amplification using specific primers and finally CRISPR-Cas mediated detection using incubator cum fluorescence detection device called RapidGlow. Analytical performance such as sensitivity, specificity, and limit of detection will be determined using reference strains and characterized clinical samples. Finally, the developed assay will be validated using culture and molecular confirmed clinical samples.

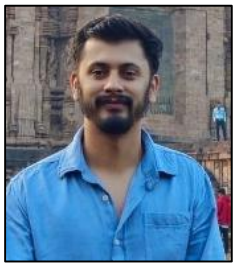
Results: Primers and gRNAs targeting conserved regions of *Pseudomonas aeruginosa* were designed and evaluated using both cloned constructs and clinical samples. Similarly, primers and gRNAs specific to antimicrobial resistance (AMR) genes were designed and tested using cloned targets. The sensitivity and specificity of the developed assay were assessed with cloned targets.

Conclusion: This CRISPR-Cas-based assay is expected to enable rapid and simultaneous detection of *Pseudomonas aeruginosa* and the antibiotic resistance genes with high specificity and sensitivity. Simultaneous detection of the pathogen and resistance markers will enable early initiation of targeted antimicrobial therapy, with potential applications in both clinical and resource-limited settings.

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Abstract No: SA-053

In Silico Drug Discovery Approach to Target Isocitrate Lyase in Dormant *Mycobacterium tuberculosis*



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Tuberculosis, caused by *Mycobacterium tuberculosis*, primarily affects the lungs but can also involve other organs. It remains a major global health concern due to the pathogen's ability to persist in a dormant or non-replicating state that is poorly responsive to first-line anti-tubercular drugs such as isoniazid and rifampicin. The enzyme isocitrate lyase (ICL) plays a crucial role in the survival of dormant mycobacteria by enabling the utilization of fatty acids as a carbon source under nutrient-limited and hypoxic conditions through diversion of metabolism from the tricarboxylic acid cycle to the glyoxylate shunt. Consequently, ICL represents an attractive target for the development of novel therapeutics against latent tuberculosis.

In this study, *in-silico* drug discovery approach was employed to identify potential ICL inhibitors. We obtained the three-dimensional structure of ICL(6XPP) from the Protein Data Bank and prepared it for molecular docking. A library of 37 natural and synthetic compounds was screened using virtual screening and molecular docking to evaluate predicted binding affinities and key interactions with the target enzyme. The top-ranked compounds were further assessed for pharmacokinetic properties and drug-likeness using ADMET predictions.

Six lead compounds demonstrated strong binding affinity relative to the covalent reference inhibitor itaconate and formed consistent interactions with key catalytic residues of ICL. These findings highlight ICL as a promising drug target in dormant *M. tuberculosis* and identify potential lead compounds for further development. Further, as a next step, we plan to run molecular dynamics simulations to check how stable the protein–ligand complexes are and how their interactions change over time. Additional in-vitro experimental validation is also needed.

Keywords: Latent tuberculosis; Isocitrate lyase; Glyoxylate shunt; In silico drug discovery; Molecular docking; ADMET.

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Abstract No: SA-054

Exploring the role of iron as a critical determinant in *Leishmania donovani* for survival, oxidative stress tolerance and infectivity



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Leishmania donovani relies on iron and heme acquisition within mammalian macrophages to sustain metabolic and redox balance. However, the precise impact of iron availability on parasite survival and pathogenesis remains inadequately understood. In this study, we systematically evaluated the effects of iron supplementation and depletion on *Leishmania* growth, oxidative stress responses, and infectivity. Our results demonstrate that low iron concentrations (0-1000 μM) enhance parasite proliferation and maintain normal morphology, whereas higher concentrations (2000-4000 μM) are toxic, inducing cell death and DNA fragmentation. Both iron excess and deficiency activated caspase-like pathways and DNA damage, implicating iron-mediated apoptosis mechanisms. Iron supplementation enhanced parasite resistance to oxidative stress by reducing reactive oxygen species (ROS) levels and maintaining intracellular thiol pools. Conversely, iron chelation using deferoxamine (0–50 μM) impaired parasite growth and disrupted redox homeostasis, thereby exacerbating oxidative damage. At the molecular level, iron-rich conditions upregulated key Fe-S cluster proteins (Nbp35, IscU) and thiol-related enzymes (TryS, TryR, CS, SAT, cTXN, cTXNPx), supporting metabolic and antioxidant functions. Conversely, iron deficiency downregulated these proteins, except for frataxin protein, which was upregulated, likely as an adaptive response. Infection assays using THP-1 macrophages showed that iron supplementation increased *L. donovani* infectivity, while iron depletion significantly reduced parasite viability. Thus, our findings highlight the pivotal role of iron in regulating parasite virulence, redox homeostasis, and host-pathogen interactions.

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Abstract No: SA-055

Evaluation of Natural Coumarins for Anti-Biofilm Activity Against *Mycobacterium smegmatis*: A Dual-Mechanism Approach



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Mycobacterial biofilms exhibit high antibiotic tolerance, showing approximately 10–1000-fold greater resistance than planktonic cells. This enhanced resistance significantly contributes to tuberculosis (TB) treatment failure and disease relapse. Current anti-tubercular drugs are largely ineffective against biofilm-associated mycobacteria, highlighting the need for alternative or adjunctive therapeutic agents. Natural compounds, particularly coumarin derivatives, have gained attention for their potential anti-biofilm properties.

In this study, the anti-biofilm activity of three coumarin derivatives-dicoumarol, imperatorin, and scopoletin-was evaluated using rifampicin as a reference drug. The compounds were assessed for their ability to inhibit biofilm formation and disrupt pre-established Mycobacterial biofilms. Dicoumarol, imperatorin, and scopoletin were tested at concentrations ranging from 100 to 12.5 µg/mL. Biofilms were incubated for 7 days, stained with crystal violet, and quantified by measuring optical density at 590 nm to determine biofilm biomass.

Imperatorin exhibited the highest activity in the biofilm inhibition assay, whereas dicoumarol showed strong biofilm disruption activity. Scopoletin did not demonstrate significant anti-biofilm effects in either assay. Rifampicin displayed high efficacy in both inhibition and disruption assays. Notably, dicoumarol was more effective in biofilm disruption than inhibition and outperformed scopoletin and imperatorin overall.

Dicoumarol demonstrated potential dual-mechanism anti-biofilm activity against *Mycobacterium smegmatis* biofilms, with efficacy comparable to rifampicin. These findings suggest that coumarin derivatives, particularly dicoumarol, are promising candidates for further investigation against biofilm-mediated persistence in *Mycobacterium tuberculosis*.

Keywords: Biofilm, Tuberculosis, Dicoumarol, *Mycobacterium smegmatis*, Coumarin derivatives

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Abstract No: SA-056

Cervical Cytology Abnormalities and High-Risk HPV Genotype Distribution Among Women from North East India



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Introduction: Cervical cancer remains the fourth most common cancer in women worldwide, with over 660,000 new cases and 350,000 deaths in 2022 (GLOBOCAN). Persistent infection with high-risk human papillomaviruses (HR-HPVs) is the primary driver of cervical carcinogenesis. Northeast India reports a disproportionately high burden of cervical cancer, yet data on HPV prevalence and genotype distribution are limited.

Objectives:
1.To investigate the prevalence of HPV infection and their association with cervical cancer
2.Identification of high-risk types of HPV from North East India
3.Clinico-pathological characteristics with early cancerous lesions prone to develop cervical cancer

Methods: We analysed cervical swab samples from 493 women from different states of NE attending obstetrician and gynaecology dept. of NEIGRIHMS Shillong. HPV detection was performed using the Xpert HPV assay on the GeneXpert platform, followed by DNA extraction and qPCR-based genotyping.

Results: Overall, 17.03% (84/429) samples were positive for HR-HPV. HPV-16 emerged as the most prevalent genotype (53.57%), followed by HPV-59 (11.9%), HPV-52 (9.52%), HPV-18 (7.14%), and other less frequent types. Both single and multiple infections were observed, with HPV-16 predominating in high-grade cytological lesions (HSIL, SCC). Cytological abnormalities ranged from ASCUS and LSIL to HSIL, SCC, and AGC.

Conclusions: These findings provide baseline evidence on genotype distribution and cytology correlations in Northeast India. The strong association of HPV-16 with severe lesions underscores the need to integrate molecular HPV testing with cytology for improved screening, early detection, and cervical cancer prevention strategies tailored to this high-burden region

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Abstract No: SA-057

Comparative analysis of Body Composition, Metabolism, Diet, and Gut microbial characteristics of Elite Indian Endurance and Resistance athletes



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Introduction: Endurance and strength training impose distinct mechanical and metabolic demands that drive modality-specific adaptations in body composition, bone health, substrate utilization, and haematological function – all key determinants of athletic performance. These adaptations are further shaped by ethnicity, diet, and environment, but there is limited data on the Indian population.

Objectives: To quantify and compare training-modality–specific differences in body composition, bone health, resting metabolism, haematological indices, dietary intake, and selected gut microbial markers in elite Indian endurance and strength athletes relative to sedentary controls.

Methods: This cross-sectional study at ICMR-NIN involved 27 Elite Endurance athletes, 25 Elite Resistance athletes, and 24 Sedentary controls. Body composition and bone mineral density were measured with DXA, while Resting Metabolic Rate (RMR) and Fasting Respiratory Quotient (RQ) were assessed via indirect calorimetry. Fasting blood samples were analyzed for complete blood count, and faecal samples were examined for specific bacterial taxa using qPCR.

Results: Appendicular skeletal muscle, total skeletal mass and total bone mass were higher in strength athletes than in endurance athletes and controls ($p = 0.001$). Absolute RMR was highest in strength athletes, then endurance athletes and controls ($p < 0.001$). When normalized to lean body mass, no differences appeared. Endurance athletes had lower body fat, greater fasting fat oxidation, and higher mean corpuscular volume. Dietary intake matched training: endurance athletes consumed more energy, and strength athletes had higher protein intake (both $p < 0.01$). Taxa like *Bacteroides, Prevotella copri, Desulphovibrio,* and *Streptococcus* were enriched in both groups ($p < 0.05$). *Methanobrevibacter smithii* was highest in endurance athletes, *Lactobacillus* in controls.

Conclusions: This study highlights the significant impact of sport-specific training on athlete's physiological traits. Varied profiles among endurance and resistance athletes reflect training adaptations. Recognising these differences is key to develop tailored training, recovery, and nutrition plans to improve health, performance, and injury prevention.

Funding: ICMR-National Institute of Nutrition intramurally funded the project.

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Abstract No: SA-058

Reduced Oral Bacterial Nitrate Reductase Activity in Hypertension : A Case Control study



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Introduction: Dietary nitrate supports vascular health by enhancing nitric oxide (NO) bioavailability through the nitrate–nitrite–NO pathway. This pathway depends on oral nitrate-reducing bacteria that convert salivary nitrate to nitrite, particularly when endogenous nitric oxide synthase (NOS) activity is impaired. In hypertension and diabetes, alterations in oral microbial redox balance may reduce nitrate reduction, lower NO availability, and contribute to endothelial dysfunction and increased cardiovascular risk.

Objectives: To evaluate oral nitrate-reducing activity in a geriatric population and compare nitrate reduction capacity between older adults with hypertension, with or without diabetes, and age- and sex-matched healthy controls.

Methods: A quantitative case–control study was conducted among adults aged ≥65 years. Participants were categorized into controls without hypertension or diabetes (n = 24), individuals with hypertension (n = 25), and individuals with both hypertension and diabetes (n = 17). Oral nitrate-reducing activity was assessed using a filter paper–based biochemical assay, with spectrophotometric estimation of nitrite formation at 540 nm using a standardized diazotization method. Nitrite concentrations were quantified using a validated calibration curve. Data normality was assessed using the Shapiro–Wilk test, and group differences were analyzed using the Kruskal–Wallis test with Dunn's post hoc comparisons. Effect size was calculated using η^2.

Results: The calibration curve showed excellent linearity ($y = 0.0106x + 0.0035$; $r^2 = 0.9998$), confirming assay reliability. Oral nitrate-reducing activity differed significantly among groups ($p < 0.0001$). Both hypertension groups showed significantly lower nitrite formation compared with controls ($p < 0.0001$), with a large effect size ($\eta^2 = 0.3487$).

Conclusion: Reduced oral nitrate-reducing activity in older adults with hypertension, particularly with coexisting diabetes, highlights the role of oral microbial function in NO bioavailability and suggests potential microbiome-targeted strategies to improve vascular health in aging populations.

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Abstract No: SA-059

Unveiling the Path to Nutrition: Factors Influencing Nutritional Resilience in Low-Birth-Weight under-five Children



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Introduction: Low birth weight (LBW) is a major public health concern in India and is strongly associated with childhood stunting and adverse health outcomes. However, a substantial proportion of LBW children attain normal linear growth during early childhood, indicating the presence of growth resilience. Understanding the determinants of such resilience is essential for designing effective nutrition interventions.

Objectives: To examine the prevalence of growth resilience and identify socio-demographic, maternal, and child-level factors associated with normal linear growth among low-birth-weight children under five years of age in India.

Methods: A cross-sectional analysis was conducted using data from the National Family Health Survey (NFHS-4: 2015–16; NFHS-5: 2019–21). Children aged 0 - 59 months with valid birth weight and anthropometric data were included (NFHS-4: n = 170,319; NFHS-5: n = 180,131). Growth resilience was defined as the absence of stunting (height-for-age Z-score ≥ −2) among LBW children (<2.5 kg). Weighted descriptive analyses and multivariable logistic regression models were used, accounting for the complex survey design.

Results: Among LBW children, 44 - 56% were not stunted by five years of age, indicating substantial growth resilience. Stunting peaked during the first two years of life and stabilised thereafter. Growth resilience varied widely across states, with higher prevalence observed in Kerala, Jammu & Kashmir, Sikkim, and Lakshadweep. Children from the poorest households had significantly lower odds of normal growth compared with the richest (NFHS-4 aOR 0.49; 95% CI 0.45 - 0.53; NFHS-5 aOR 0.53; 95% CI 0.45 - 0.62). Lower maternal education, higher birth order, and increasing child age were consistently associated with reduced odds of growth resilience, while female children had higher odds in both survey rounds.

Conclusions: A substantial proportion of low-birth-weight children in India achieve normal linear growth, underscoring the importance of postnatal social and maternal environments in mitigating early biological disadvantage. Strengthening maternal education, reducing socio-economic inequalities, and prioritising early-life interventions are critical for improving growth outcomes among LBW children.

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Abstract No: SA-060

Preconceptional paternal calorie restriction dysregulates the AMPK/SIRT pathways in diet-induced obese Wistar rats offsprings



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Introduction: Obesity is a metabolic syndrome shaped by genetic and environmental factors. Caloric restriction (CR) is an effective dietary strategy for weight loss in obesity with several health benefits; however, preconceptional parental CR without proper guidance can adversely affect offspring health. According to literature, maternal CR effects are well documented, paternal CR remains underexplored. This study investigates the effects of different preconceptional paternal CR regimens on metabolic syndrome outcomes in high-fat-diet–induced obese male Wistar rats (WNIN) and their offspring.

Objectives: To study the impact of paternal CR regimes in diet-induced obese male Wistar rats (WNIN), on their offspring and the metabolic pathways.

Methods

High-fat diet-induced obese male Wistar rats were subjected to caloric restriction of 50% (HFCR-I) and 40% (HFCR-II) and mated with normal females. The male parent's reproductive function was assessed using sperm parameters, and the expression levels of DNMTs' mRNAs were also examined. The offspring's metabolic function was assessed by physiological, biochemical and molecular parameters.

Results: The HFCR-I reduced the body weights and DNA methylation activity with compromised male fertility. HFCR-I offspring project attenuation of the AMPK/SIRT1 pathway, which in turn progresses proinflammatory status and oxidative stress. Offspring shows altered glucose and lipid homeostasis due to impaired glucose tolerance & insulin sensitivity, dyslipidemia and steatosis. In HFCR-II offspring, these effects are largely mitigated. Female offspring were more susceptible than males, suggesting that females are more prone to the effects of the paternal diet.

Conclusions: HFCR-I induced paternal undernutrition which adversely affected offspring health, whereas HFCR-II largely reversed high-fat-diet effects. Thus, moderate caloric restriction appears to be an effective weight-loss strategy with minimal intergenerational impact, highlighting fathers' shared responsibility for shaping sperm-specific epigenetic imprints that influence offspring's health

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Abstract No: SA-061

Multiepitope mRNA Vaccine Design Targeting Structural and Regulatory Proteins of HSV-2 to Induce Robust T-Cell Immunity



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Introduction: Herpes Simplex Virus type-2 (HSV-2) is a major global health concern, causing recurrent genital herpes and increasing susceptibility to HIV infection and adverse reproductive outcomes. Despite decades of research, HSV-2 vaccine development has been unsuccessful, largely due to antigenic narrowness, viral immune evasion, and inadequate induction of durable cellular immunity. Recent advances in mRNA vaccine platforms and Immunoinformatics offer new opportunities to overcome these limitations through rational multiepitope vaccine design.

Objectives: This study aimed to design and computationally characterize novel multivalent, multiepitope mRNA vaccine candidates against HSV-2 using a reverse vaccinology-based Immunoinformatics approach, emphasizing antigenicity, immune breadth, population coverage, and translational feasibility.

Methods: Key HSV-2 structural and regulatory proteins (gB, ICP0, RIR1, and VP23) were evaluated for antigenicity, toxicity, and epitope density. High-affinity B-cell, $CD4^+$, and $CD8^+$ T-cell epitopes were predicted, filtered, and assembled into five multiepitope constructs incorporating immunostimulatory adjuvant sequences and optimized linkers. Constructs were assessed for physicochemical properties, structural stability, immune receptor interactions, and population HLA coverage. *in silico* immune simulations were performed to predict humoral and cellular responses. Selected constructs were cloned into the IVT vector backbone to facilitate *in vitro* transcription for downstream experimental validation.

Results: All five constructs exhibited high predicted antigenicity, absence of toxicity and allergenicity, and broad HLA population coverage. Immune simulations indicated strong $CD4^+$ and $CD8^+$ T-cell activation, robust interferon-γ and pro-inflammatory cytokine responses, and sustained antibody production. Structural analyses supported favorable folding, stability, and compatibility with mRNA synthesis and expression workflows.

Conclusions: This study establishes a rational framework for multiepitope mRNA vaccine development against HSV-2. The designed candidates demonstrate strong immunogenic potential and translational readiness, supporting further experimental validation and highlighting the promise of multiepitope mRNA vaccines for effective HSV-2 immunization.

Funding: This research was supported by Indian Council of Medical Research (ICMR) Intramural Grant (Grant no. INTR-IM-2024-00126)
Fellowship: ICMR-Junior Research Fellowship.

Acknowledgement: The authors gratefully acknowledge the support of the Director, ICMR-NIV, Pune, for facilitating this study. We also thank the Bioinformatics Centre, Savitribai Phule Pune University (SPPU), and PARAM Brahma super computer for providing computational time and infrastructure support.

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Abstract No: SA-062

Seasonal Variation in Dietary Intake and Nutritional Parameters among Children Aged 6-23 Months: Evidence from NFHS-5 Data



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Introduction: Optimal Infant and Young Child Feeding (IYCF) practices are crucial for growth and development. But seasonal fluctuations and climatic change may influence dietary diversity and nutritional parameters. Despite its importance, seasonal variation in complementary feeding practices remains underexplored in India.

Objective: To assess seasonal variation in dietary intake and nutritional parameters among children aged 6-23 months using the data from the National Family Health Survey-5 (NFHS-5).

Methods: A secondary analysis of NFHS-5 data was conducted for children aged 6-23 months. Dietary indicators (Exclusive breastfeeding, complementary feeding, Minimum Dietary Diversity [MDD], Minimum Meal Frequency [MMF], Minimum Acceptable Diet [MAD], and nutritional parameters (underweight, stunting, wasting, Haemoglobin concentration) were compared across summer, monsoon and winter seasons.

Results: Breastfeeding was consistently high across all seasons (~82%). In contrast, complementary feeding practices varied seasonally. Egg consumption peaked during the monsoon (22.8%) but was lowest in summer (9.05%). Intake of nuts and pulses was lowest in summer (14.33%) and highest during monsoon (20.51%). MMF remained consistent across seasons (~32%). Stunting, wasting and underweight were most prevalent during the monsoon (36.43%, 23.22%, and 30.78%, respectively) while anaemia showed no seasonal variation, consistently high (~80%) across all seasons. Logistic regression analysis confirmed significant seasonal shifts in IYCF indicators. Achievement of MDD was less likely during summers (r= -0.14; 95% CI [-0.22, -0.07]) compared with winters or monsoon. MAD was more likely in winters (r= 0.08; 95% CI [0.01, 0.16]) and less likely in summers (r= -0.11; 95% CI [-0.21, -0.01]). DDS also observed a higher likelihood to be achieved during winters (r=0.06; 95% CI [0.01, 0.11]).

Conclusion: Complementary feeding practices and dietary diversity among children aged 6–23 months exhibit seasonal variation, with lower levels during summer. Given the cross-sectional design of NFHS-5, causal inferences cannot be drawn, highlighting the need for longitudinal research.

Keywords: Seasonal variation, dietary intake, Dietary Diversity Scores, Minimum Acceptable Diet, Minimum Meal Frequency, Minimum Dietary Diversity, Nutritional Parameters

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Abstract No: SA-063

MelioGlow$_{PCR}$: A Rapid, Low-cost, Ultra-sensitive CRISPR-Cas-based Molecular Diagnostic system for detecting Melioidosis in hospital settings



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Introduction: Melioidosis is a neglected tropical disease caused by *Burkholderia pseudomallei* with a fatality rate of 10–50%. In India, an estimated 20,000–52,000 new cases and 32,000 deaths are reported annually.
Melioidosis remains largely underdiagnosed due to the absence of rapid and reliable diagnostic methods. Routine diagnostics are limited by either time, cost, accuracy, or are unconventional for resource-limited regions. Melioidosis is a 'great mimicker,' often resembling symptoms of bacterial infections complicating diagnosis.
CRISPR is an adaptive immune system in bacteria and archaea. The CRISPR–Cas complex, composed of guide RNA and Cas nuclease, recognizes target genes via base pairing and triggers trans-cleavage of fluorescently labelled single-stranded probes, generating signal for pathogen detection.

Objectives: Development of CRISPR-Cas-based molecular diagnostics for detection of *Burkholderia pseudomallei*.

Methods: RapidBact; an in-house developed kit, utilizes alkaline-heat lysis method and silica column-based purification for DNA extraction from clinical samples.
MelioGlow$_{PCR}$; uses Polymerase Chain Reaction to first amplify the target DNA and the trans-cleavage activity of CRISPR-Cas12a to cleave single-stranded fluorophore-quencher labelled probes leading to fluorescence emission.
RapidGlow device, developed at ICMR-RMRCNE, provides appropriate incubation temperature for CRISPR assay and captures the fluorescence intensity which can observed by both naked eye/mobile phone camera or in real-time with RGLOW software.
Limit of detection (LOD) of the system was measured using serial dilution of standard plasmids and sensitivity and specificity was determined using clinical samples.

Results: The MelioGlow$_{PCR}$ diagnostic system is a standalone and indigenous system developed at ICMR-RMRCNE, Dibrugarh. The system provides rapid (~2.5 hours), low-cost (~80.00 INR per test), sensitive (1.6 x 10^{-3} copies/ µl), and specific solution for melioidosis detection.

Conclusions: In conclusion, this novel melioidosis diagnostic system will bring to the light the underdiagnosed cases and aid in administering fast and reliable treatment to the patients in a hospital setting.

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Abstract No: SA-064

Development of 5-FU resistant gallbladder cancer cell line and identification of predictive biomarkers associated with chemoresistance



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Introduction: Gallbladder cancer (GBC) is a heterogeneous malignancy that arises from the epithelial lining of the gallbladder. (1) GBC is often diagnosed at advanced stages and the patients carry a poor prognosis. (2) Chemoresistance contributes significantly to these poor clinical outcomes. Gemcitabine and cisplatin are the first line of drugs while 5-fluorouracil (5-FU) along with oxaliplatin (FOLFOX) are commonly used as the second-line of treatment. (3) The present study aims to understand the causes and underlying mechanisms of GBC drug resistance in response to 5-FU in GBC.

Objectives: To develop and characterize 5-fluorouracil–resistant gallbladder cancer cell line as an *in vitro* model for studying mechanisms of acquired chemoresistance.

Methods: To identify the mechanisms underlying 5-FU resistance in GBC, a 5-FU resistant GBC cell line (NOZ 5-FU R) was established by exposing the parental NOZ cell line to increasing concentrations of 5-FU. IC_{50} for 5-FU was determined for the parental and resistant cell lines and morphological changes were also evaluated.

Results: The results demonstrated that the IC_{50} of parental NOZ cells and NOZ 5-FU R cells was 11.77µM and 251.6µM respectively. The resistance index ratio was 21.37. Morphological analysis of resistant cells, showed an increased cell size, elongated and spindle-shaped morphology, with prominent cytoplasmic extensions, whereas the parental cells retained a compact and predominantly spherical morphology.

Conclusions: This study establishes an *in vitro* model to study the molecular mechanisms associated 5-FU chemoresistance in GBC. Future studies will employ global genetic, transcriptomic and proteomic analyses to identify molecules associated with 5-FU chemoresistance followed by validation in clinical samples. These proteins may serve as predictive biomarkers for 5-FU resistance in GBC enabling the decision for the appropriate drug to be used for the chemotherapy and may facilitate the development of targeted inhibitors or repurposing existing inhibitors for treatment of 5-FU resistant GBC patients.

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Abstract No: SA-065

Stage-Specific miRNA Profiling Reveals Key Regulators of EMT and EGFR-TKI Resistance in Gallbladder Cancer



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Introduction: Gallbladder cancer (GBC) is a highly aggressive malignancy characterized by a poor prognosis, particularly in its advanced stages. While microRNAs (miRNAs) regulate cancer progression, their specific role in the transition from early to advanced GBC is poorly understood.

Objectives: This study aimed to characterize the miRNA expression landscape associated with the initiation and progression of GBC. By profiling tissues from early and advanced stages against controls, we focused on identifying stage-specific miRNA signatures, unravelling their involvement in key oncogenic pathways, and determining their significance by correlating expression patterns with clinical parameters.

Methods: We performed miRNA expression profiling on 41 formalin-fixed paraffin-embedded (FFPE) tissues, including 10 gallstone disease controls, 14 early-stage GBC (stage I and II), and 17 advanced-stage GBC cases (stage III and IV), using the NanoString nCounter platform. Differentially expressed miRNAs (DEMs) were identified followed by miRNA target identification using miRTarBase.

Results: We identified 43 significantly dysregulated miRNAs in early-stage and 46 in advanced-stage GBC compared to controls. Based on the literature search, we found EMT inhibiting miRNAs (miR-200 family) to be overexpressed in early stage and downregulated in advanced stages (miR-574-3p, miR-195-5p) in our study. Pathway analysis revealed significant enrichment of the 'EGFR tyrosine kinase inhibitor resistance' pathway in both the stages. The correlation of DEMs with clinicopathological features revealed that the expression of miR-361-3p ($p=0.0003$) and miR-423-5p ($p=0.0001$) was significantly associated with tumor grade and lymph node status, respectively.

Conclusions: This study delineates distinct miRNA signatures driving GBC progression, characterized by a loss of EMT-inhibiting miRNAs in advanced stages. The enrichment of the EGFR tyrosine kinase inhibitor resistance pathway highlights a potential mechanism for treatment resistance. Furthermore, the significant correlation of miRNAs with tumor grade and lymph node status establishes their potential utility as clinical biomarkers for assessing disease severity and prognosis.

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Abstract No: SA-066

Microglial Senescence Triggered by Dolutegravir: Potential Links to Neurodegenerative Pathology



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Introduction: Microglia play a central role in maintaining CNS homeostasis, and their senescence is linked to neurodegenerative pathology [1]. Dolutegravir (DTG), a frontline integrase inhibitor in HIV therapy, has been implicated in neurocognitive disorders [2]; however, whether DTG induces microglial senescence and associated neuroinflammatory changes remains unknown. This study investigates this unexplored mechanism using combined in-silico and in-vitro strategies. In this study, we addressed this gap using both in-silico and in-vitro approaches.

Objective: To evaluate the effect of DTG in induction of Microglial senescence.

Methods: Hallmark features of senescence, including β-galactoside activity, secretion of senescence associated phenotypes, reduction in SIRT3 activity etc. are critical to be investigated. Cytotoxicity of DTG was assessed on Human Microglial cell line (HMC3) using 7.8ng/ml till 10000 ng/ml concentration by MTT and flow-based assay. DTG induced senescence was evaluated (conc.18ng/ml and 9.6ng/ml). Production of Senescence associated β-Galactosidase cells, in silico docking (Chimera, Avagadro, CB-Dock) and in vitro activity assays for SIRT3, flow cytometry for senescence-associated secretory phenotype (SASP) markers (IL-6, TGF-β, CCL2, CXCL10, CXCR2, IFN-γ, IL-8, IL-17A and IL-21R) were evaluated. Doxorubicin (DOX) was used as a positive control.

Results: DTG did not had cytotoxicity up to 10,000 ng/ml concentration. However, subtoxic concentrations of DTG induced β-galactosidase and reduction in SIRT3 activity indicating senescence. Docking studies demonstrated strong binding of DTG to SIRT3. Flow cytometric analysis revealed induction of SASP markers, including IL-6, TGF-β, CCL2, CXCL10, CXCR2, IFN-γ, IL-8, IL-17A, and IL-21R.

Conclusion: This study provides the first evidence that DTG induces microglial senescence that may lead to neurodegeneration. These findings highlight a potential link between long-term DTG treatment and neurodegenerative risk, warranting further mechanistic and in vivo investigations

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Abstract No: SA-067

Effect of Finger Millet-Based Supplementation on Anthropometry and Body Composition Among Moderately Acute Malnourished Under 5 Children in Telangana, India: A Randomized, Community-Based Trial



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Introduction: Moderate acute malnutrition (MAM) remains a major health challenge in India despite ongoing efforts of government nutrition programs. Finger millet (Ragi), a nutrient-dense, climate-resilient crop rich in calcium, fiber, and bioactive compounds, offers potential advantages over conventional cereal-based ready-to-use therapeutic foods (RUTF).

Objectives: To Determine The Effect Of Germinated Finger Millet- Based Intervention On Micronutrient Status, Weight Gain; And Body Composition Using *In Body* S10 Device Among Under 5 Yr Old Uncomplicated MAM Children

Methods: In this open-label, randomized community-based trial, 221 MAM children were allocated to receive either a finger millet-with-dates supplement (FMD) or the standard wheat/rice-based Balamrutham plus with dates (BMD) for 8 weeks in Anganwadi centers in Hyderabad, India. Anthropometry, body composition (InBody S10), dietary intake (three-day recall), biomarkers, and compliance were assessed at baseline and endpoint, with follow-ups at days 100 and 160. Growth trends were evaluated using repeated-measures ANOVA.

Results: 136 children completed the intervention (FMD: 71; BMD: 65); compliance exceeded 80%. By day 40, both groups showed significant gains in weight (6.3-6.4%), height (2.4%), and MUAC (3.5-6.2%), which continued through day 160. The FMD group showed better improvements in mineral mass, bone mineral content, and skeletal muscle mass, whereas the BMD group demonstrated higher increases in protein mass and fat-free mass. Significant improvements in serum vitamin B12 and folate were observed in both FMD and BMD groups ($p < 0.05$), whereas haemoglobin, vitamin D, and ferritin showed transient declines with follow-up recovery, with ferritin improving significantly only in the BMD group ($p < 0.001$). Dietary recall revealed markedly low micronutrient adequacy among MAM children. No major adverse events were reported.

Conclusions: Finger millet-based supplementation achieved comparable improvements to cereal-based RUTF, supporting its integration into ICDS and POSHAN 2.0 as a sustainable approach to MAM management.

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Abstract No: SA-068

Distinct FcγIIa-mediated Entry of SARS-CoV-2 Induces SYK–MAPK–AP-1–Biased Inflammatory Signalling with Delayed Innate Antiviral Responses



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Introduction: Antibody-dependent enhancement (ADE) of viral infection is mediated by Fcγ receptor (FcγR)-dependent uptake of virus and antibody immune complexes and may alter host innate immune responses compared to canonical ACE-2 receptor-mediated entry [1, 2]. However, signalling pathways involved in ADE-associated host gene expression during SARS-CoV-2 infection remain incompletely understood [3].

Objectives: To investigate the host gene expression and signalling pathways activated during FcγR-mediated antibody-dependent enhancement of SARS-CoV-2 infection.

Methods: To characterize ADE-associated signalling, FcγRIIa-mediated SARS-CoV-2 entry under MW05 monoclonal antibody-enhancing conditions was analyzed by qPCR relative to controls. Gene expression was assessed at early (6 h and 12 h), intermediate (24 h), and late (48 h) time points, focusing on inflammatory mediators, innate sensing pathways, endocytic trafficking markers, and FcγRIIa-proximal signalling components.

Results: ADE mediated by MW05 monoclonal antibody in SARS-CoV-2 infection induced a distinct gene expression signatures. Early upregulation of SOCS and MX1 at 12 h suggested initial modulation of interferon signalling. There was induction of CLTC (24–48 h) and RAB5A (48 h) at later time points, indicating clathrin-mediated endocytosis and endosomal trafficking consistent with FcγRIIa-dependent viral entry. The upregulation of FcγRIIa-associated kinases LYN and SYK, along with MAPK3, was observed at 48 h, coinciding with marked increases in pro-inflammatory cytokines IL1β, TNFα, and IL8. Delayed activation (at 48h) of innate RNA-sensing pathways was evident by increased expression of RIG-I, IFIH1 (MDA5), and interferon-stimulated genes (ISG15, IFIT1, CXCL10).

Conclusions: ADE through FcγRIIa in SARS-CoV-2 activates inflammatory signalling pathways, increasing inflammation-related gene expression. At the same time, antiviral interferon responses are delayed and suppressed, explaining how ADE shifts immune responses toward inflammation instead of effective viral control

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Abstract No: SA-069

Formulation, Characterization and Antimicrobial investigation of Nobel natural antibiotics on clinically isolated enteric bacterial strains.



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Introduction: The increasing global prevalence of antimicrobial resistance (AMR) is a critical public health concern, prompting the urgent need for novel and effective antimicrobial agents. Conventional antibiotics are becoming less effective due to the emergence of resistant bacterial strains, particularly among enteric bacteria such as Escherichia coli, Klebsiella pneumoniae, Salmonella spp., and Shigella spp. (WHO, 2021). Natural products, derived primarily from plants, have been a cornerstone of traditional medicine and a rich source of antimicrobial agents (Newman & Cragg, 2020). This project focuses on the formulation, characterization, and antimicrobial evaluation of natural antibiotics derived from selected plants to address this critical gap.

Objectives:

- To identify and select medicinal plants (*Albizia lebbeck, Terminella chebula, Aegle marmelos, Berberis aristata and Holarrhena antidysenterica*) with known traditional use for antimicrobial properties
- To compare the antimicrobial efficacy of plant-based compounds with conventional antibiotics
- To explore the potential for synergy between plant extracts and existing antibiotics

Methodology/Experimental design

i) Screening for Antimicrobial Potential
Agar Diffusion Method:
Minimum Inhibitory Concentration (MIC):
ii) Isolation and Characterization of Bioactive Compounds.
iii) Anti-microbial Synergy Study and Formulation Development

Results: Preliminary study shows antimicrobial activity of *Terminella chebula and Berberis aristata* in multidrug resistant Shigella species among 5 selected medicinal plants in disc diffusion and agar dilution methods.

Conclusions: The anti-microbial synergy study and formulation development will lead to the creation of more effective antimicrobial treatments, potentially offering a new and innovative solution to combating enteric bacterial infections. By harnessing the power of plant-derived compounds and their synergistic effects, this approach could reduce the reliance on synthetic antibiotics, minimize the development of antibiotic resistance, and provide a safer, more sustainable alternative for treating infectious diseases.

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Abstract No: SA-070

Lyme borreliosis in Assam: A study among acute febrile illness cases and animal farm workers



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Introduction: Lyme borreliosis commonly known as Lyme disease (LD) is an emerging tick-borne disease caused by *Borrelia burgdorferi* (*sensu lato*) complex and transmitted by deer ticks of *Ixodes* sps[1]. It typically presents with "erythema migrans" and flu-like symptoms. It was first reported in 1977 in Lyme town of Connecticut, United States in children suffering from arthritis[2]. In India, there are a few reported cases of LD and the probability of missing out of suspected cases is very high due to its typical features with other tick-borne diseases[3]. In North east region a local backyard farming is mostly practiced. It promotes close human-animal contact and exposure to tick-infested environments, facilitating *Borrelia* transmission.

Objectives:

1. To determine the case load of LD among AFI patients in selected hospital of Assam.
2. To calculate the seroprevalence of LD among animal farm workers.

Methods: Blood samples were collected from AFI patients from hospital and farm workers from community. Serological diagnosis of LD was done using CDC standard two tire testing algorithm *i.e.,* EIA recombinant ELISA for both IgM and IgG antibodies against *Borrelia burgdorferi* (*sensu lato*) followed by IgM and IgG recombinant immunoblot

Results: A total of 249 AFI patients and 100 animal handlers were enrolled during January 2022 to December 2024. Seropositivity was recorded in 14.85% of AFI cases (IgM: 6.02%, IgG: 7.63%, both: 1.20%) and in 10% of animal handlers (IgM: 4%, IgG: 6%).

Conclusions: Detection of IgM and IgG antibodies to *Borrelia burgdorferi* among suspected patients and farm workers indicates presence of LD in the study area. The rising trend of reported cases highlights the need for improved clinical awareness and early diagnosis at the primary healthcare level. This study highlights the human–animal–vector interface, contributing to a One Health understanding of Lyme borreliosis in Assam.

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Abstract No: SA-071

Clinical Relevance of Differentially Methylated Sperm Long-noncoding RNA Genes in Male Partners of Couple Experiencing Idiopathic Recurrent Pregnancy Loss



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Introduction: Recurrent pregnancy loss (RPL) is condition wherein woman experiences two or more consecutive miscarriages within 24th week of gestation. In Indian-population it is reported to be 7.46%. There are several known maternal factors however, 50% of cases remain idiopathic (iRPL). Early nuclear transplant experiments have highlighted importance of paternal genome in early embryo-development and placentation. Therefore, there is need to focus on paternal factors for their implications in iRPL. Through whole genome bisulphite sequencing (WGBS) we obtained list of differentially methylated CpG site (DMC) within long non-coding RNA (lncRNA) genes. Methylation of CpG sites within gene regulatory region regulates gene expression. Sperm epigenome undergoes episodes of demethylation and re-methylation, which could be aberrantly altered in-case of pathophysiology of iRPL. LncRNA epigenetically regulates trophoblast cell-function by regulating gene-expressions. Therefore understanding methylation of sperm lncRNA genes involved in early development process is of utmost importance.

Objective: Selection of lncRNA genes having role in early developmental processes for methylation analysis.

Methods: GEO datasets of chorionic-villi from RPL studies were analysed to identify commonly differentially expressed genes (DEGs) and compared with existing WGBS data to identify differentially methylated lncRNAs. In parallel, literature mining was used to shortlist developmentally relevant lncRNAs from existing WGBS list to assess methylation status by pyrosequencing.

Results: 481 DEGs were found to be common between 2 or more datasets. Pathway analysis revealed cell division pathways to be affected. A total of **3** genes (*SNHG14*, *TCL6* and *MIR3142HG*) were identified as common with our existing list of DM lncRNA genes. DMCs within lncRNA genes *FIGNL2*, *INTS9*, *NUP50* and *ZRANB2* were found to be altered.

Conclusions: DEGs across data sets highlighted dysfunction in cell division processes, which is vital during early embryogenesis. While altered DMCs further support potential epigenetic contribution of lncRNAs to pathophysiology of recurrent pregnancy loss.

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Abstract No: SA-072

Genomic Landscape of Gastric Cancer Patients from North East India



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Introduction: Gastric cancer ranks as fifth most common malignancy and fourth leading cause of cancer mortality globally (GLOBOCAN 2020) (Sung et al., 2021). In North East India, PBCR data indicates higher incidence and mortality than national averages, e.g., Aizawl (44.2/100,000 men) and Papumpare. Males exhibit 2-3x higher risk (Shanker et al., 2021). Risk factors include *Helicobacter pylori*, diet (smoked foods), and genetics. Despite rich epidemiology, somatic genomic data remain scarce. one study in Mizoram reported unique TP53/ARID1A mutations, suggesting region-specific profiles amid ethnic heterogeneity (Lalrotlua et al., 2023).

Objectives

1. To detect somatic mutations in gastric cancer patients by whole exome sequencing.
2. To identify tissue subtypes of gastric cancer based on molecular classification.

Methods: A case-based observational study enrolls 120 gastric cancer patients from hospitals across Assam, Mizoram, Nagaland, and Manipur, following ethical approval and informed consent and Demographic, lifestyle, dietary, and clinical data is collected using structured questionnaires. Paired tumor tissues and peripheral blood samples are obtained. Tumor samples are histologically evaluated and stored at −80°C. Genomic DNA is extracted, quantified, and quality-checked. Whole exome sequencing is performed using Roche KAPA HyperExome V2 on Illumina NovaSeq 6000, followed by analysis of somatic variants, tumor mutational burden, and mutational signatures with comparison to TCGA and COSMIC databases.

Results: Analysis of 24 samples revealed 416,088 somatic mutations across 16,829 genes, including 2,945 novel variants, indicating high genomic diversity. Recurrent mutations involved TP53, TTN, MUC16, KRAS, and PIK3CA. Tumor mutational burden was high (75–97 mutations/Mb). Mutation patterns showed predominant missense and C>T transitions, with immune and signaling pathways implicated, highlighting IL36RN and ITPKB as potential therapeutic targets.

Conclusions: The study reveals marked genetic heterogeneity and region-specific mutational patterns, with high tumor mutational burden indicating immunotherapy potential. Expanded analyses will refine regional molecular subtypes and enable tailored precision and immunotherapeutic strategies.

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Abstract No: SA-073

Gut Microbial Dysbiosis and Elevated Mucosal Inflammation in Severe Acute Malnutrition: A Case-Control Study from India



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Introduction: Severe Acute Malnutrition (SAM) in early days of life remains a concerning global health challenge, contributing to high child mortality and morbidity. The mechanistic role of the gut microbiota in its pathophysiology remains incompletely understood.

Objectives: To profile the gut microbiota of pre-school children with SAM and healthy controls, and to assess dietary intake, fecal inflammatory markers (MPO, CAL, NEO), and fecal sIgA levels in relation to clinical and dietary parameters.

Methods: This matched case-control study included 115 pre-school children (52 SAM and 63 Healthy) aged 6–59 months residing in Hyderabad, India. Gut microbiota was profiled using 16S-rRNA sequencing of the V3–V4 region. Dietary data was collected using 24-hour diet recall and a food frequency questionnaire (FFQ). Fecal inflammatory markers, MPO (Myeloperoxidase), CAL (Calprotectin), and NEO (Neopterin), along with fecal sIgA levels, were analysed and correlated with clinical parameters and dietary intake.

Results: Dietary diversity was good in both healthy and SAM children. Children with SAM showed a higher probability of micronutrient inadequacy and had significantly lower carbohydrate and protein intake compared to healthy children. Gut microbial diversity showed a significant difference in ChaoI index, indicating reduced richness in the SAM group ($p<0.001$). Children with SAM exhibited reduced abundance of beneficial taxa such as *Blautia*, *Akkermansia*, and *Ruminococcus gnavus*, with an expansion of opportunistic taxa including *Enterococcus*, *Staphylococcus*, and *Turicibacter*. Inflammatory markers indicated elevated inflammation in SAM children compared with healthy controls. Reduced fecal sIgA levels in the SAM group suggested an impaired immune response, with male children being at a higher risk of inflammation and immune dysfunction.

Conclusions: Children with SAM show gut microbial alterations, increased mucosal inflammation, and reduced immune response. Targeting these specific taxa and their associated metabolic pathways may help in tailoring future interventions.

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Abstract No: SA-074

Impact of Different Emicizumab Doses on Clinical Outcomes and Global Coagulation Profiles



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Introduction: Emicizumab is a non-factor, bispecific monoclonal antibody that restores haemostasis by mimicking activated factor VIII (FVIIIa), achieving near-zero annualized-bleeding-rates in HemophiliaA. Its high cost limits widespread use in low- and middle-income countries, prompting lower-dose regimens[1]. Both our retrospective-cohort and a randomized controlled trial have shown that a low-dose-regimen(3mg/kg/q4w) is clinically non-inferior to the standard--regimen (loading-dose:3mg/kg/wk×4w;maintenance:6mg/kg/q4w)[2]. Given these equivalent clinical-outcomes, it is important to assess whether comparable haemostatic profiles are achieved at with the two doses.

Aim: To compare haemostatic profiles associated with standard-dose and low-dose emicizumab using gold-standard and global coagulation assays.

Materials and Methods: Plasma samples were analyzed both *in vivo* and *in vitro*. *In vivo*, samples were obtained from patients receiving standard-dose and low-dose emicizumab prophylaxis with trough plasma levels of ~45µg/mL & ~20µg/mL, respectively. *In vitro*, emicizumab was spiked into FVIII-deficient plasma to achieve concentrations corresponding to standard and low-dose regimens. Activated partial thromboplastin time(APTT), FVIII-activity(one-stage assay), rotational thromboelastometry(ROTEM) clotting-time, thrombin-generation assays, and confocal microscopy for fibrin-clot-network analysis were performed in triplicate.

Results: Emicizumab markedly shortened APTT, with no statistical difference between low-dose (27.2 ± 0.43 s) and standard-dose (24.2 ± 1.06 s). ROTEM clotting times were comparable between standard-dose (1010±108s) and low-dose (1231±581.8s). Surrogate FVIII-activity was substantially overestimated, measuring 336±42 IU/dL and 206.5±32.08 IU/dL in standard and low-dose groups, respectively. Thrombin-generation parameters showed no significant differences between dosing regimens. Confocal microscopy demonstrated marked differences in fibrin network density between healthy controls and untreated Hemophilia A; analysis in emicizumab-treated patients is ongoing.

Conclusion: Despite lower circulating emicizumab concentrations, low-dose prophylaxis achieves haemostatic profiles comparable to standard dosing across global coagulation assays. These findings provide mechanistic support for dose-optimization strategies, particularly in resource-limited settings, without compromising haemostatic efficacy.

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Abstract No: SA-075

Role of climate on Dengue and Malaria in Thane, India



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Introduction: Climate change has exacerbated vector-borne diseases including dengue and malaria globally. India hosts a large burden of dengue, accounting for more than one million cases between 2015 and 2022, and is highly climatically sensitive. Thane, a coastal city adjacent to Mumbai, experiences changing monsoon trends associated with the variation in the low-level jet stream from Kerala (8°N) to Maharashtra (15°N), which enhances rainfall along the coast and could possibly drive disease dynamics.

Objectives: The objective of the study is to access the role of climate factors on the occurrences of Dengue and Malaria in Thane district and undertake climate-driven disease modelling to explain the disease dynamics.

Methods: In this study, we assessed the influence of climatic factors on dengue and malaria incidence in over a ten-year period (2015–2024). We applied time-series analyses to monthly occurrences data against meteorological variables including maximum, minimum, and mean temperatures, rainfall (RF), and relative humidity (RH). Disease data were obtained from the Maharashtra State Health Department, while climate data were sourced from the India Meteorological Department (IMD).

Results: Our findings indicate pronounced seasonality in both dengue and malaria, with incidence peaks during the monsoon months (June–October). Statistical analyses revealed significant associations between disease occurrences and various climatic variables. Incorporating lagged effects of meteorological parameters into time-series models substantially improved forecasting accuracy.

Conclusions: This work adds to growing evidence that climate variability directly influences vector-borne disease transmission and underscores the importance of climate-informed early-warning and public health strategies to mitigate outbreaks in coastal environments.

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Abstract No: SA-076

Intra-Articular Delivery of Nanoemulsified Curcumin Ameliorates Joint Degeneration in a Chemically Induced Model of Osteoarthritis



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Introduction: The pathogenesis of knee osteoarthritis (OA) is multifaceted and involves the complete joint microenvironment. Inflammation is a key pathophysiological aspect of osteoarthritis (OA) and is present before radiographic changes like joint space narrowing, cartilage degeneration or osteophyte formation occur. Despite beneficial evidence of curcumin, the mechanistic insights of nanoemulsified curcumin (n-Cur) delivery to the knee-OA microenvironment are limited.

Objectives: The study aimed to establish localized delivery of curcumin nanoemulsion in the knee joint of OA rats. Further, the study aimed to evaluate the effects of curcumin nanoemulsion in ameliorating osteoarthritis in vivo and in vitro.

Methods: Curcumin nanoemulsion was prepared using neutral oil and surfactant. Adult (5 mo) male SD rats were intra-articularly delivered 40 mg/mL of monoiodoacetate (MIA) to induce OA in the left knee and further treated with n-Cur (30 mg/mL). To further study the molecular pathways related to osteoarthritis, IL-1β-induced OA model was used. In vitro, chondrocytes were cultured and treated with IL-1β (10ng/mL) or combination of IL-1β and n-Cur. The effect of n-Cur on macrophage recruitment was evaluated using a co-culture model of CHON 001 and RAW 264.7 cells.

Results: In the MIA model, localized delivery of n-Cur significantly reduced knee joint edema and joint space narrowing in the target site. Curcumin ameliorated cartilage degeneration by reducing fibrillation, hypocellularity, and restoring matrix proteoglycan, as evidenced by histology. n-Cur was found to mitigate MIA-induced systemic oxidative stress and synovial inflammation in rats. Nanocurcumin effectively modulated the expression of matrix regulators and lowered macrophage recruitment in vitro.

Conclusions: Reduced synovial inflammation displays the effect of curcumin on the synovium, possibly by lowering the recruitment of macrophages in chemoattractant-stimulated chondrocytes. Thus, curcumin nanoemulsion can act as a chondroprotective agent, modulating the OA microenvironment by reducing joint edema, synovial inflammation, and oxidative stress in the OA model.

Acknowledgements: The work is part of a research project sponsored by the ICMR National Institute of Nutrition (**Grant number: 23-BS08**). K.S.N.H. was supported by the DST Inspire Fellowship, Department of Science and Technology, Government of India. We appreciate the efforts of Syeda Farhana in carrying out the animal trial and Raviprakash in imaging. The authors acknowledge Varinder Singh Raina for his technical expertise and assistance in performing X-ray imaging.

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Abstract No: SA-077

Impact of Lead and Amyloid-β Co-exposure on ER Stress and ER Stress-Associated Cell Death in Human Neuronal Cells



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Introduction: Alzheimer's disease (AD) is a progressive neurodegenerative disorder characterized by gradual loss of memory and cognitive function. Amyloid-β (Aβ)–induced neurotoxicity is considered a key pathological feature of AD. In addition to Aβ pathology, growing evidence suggests that exposure to environmental pollutants, particularly lead (Pb), may contribute to the development and progression of AD. Pb exposure is known to induce cellular oxidative stress (OS) and importantly, Endoplasmic reticulum (ER) dysfunction, especially ER stress, has emerged as a key contributor to neuronal degeneration in AD.

Objective: In this study, we aimed to investigate the individual and combined toxic effects of lead, Aβ (25–35), and Aβ (1–40) in the SH-SY5Y human neuroblastoma cell line, with a focus on OS, ER stress signaling pathways, and ER stress-mediated apoptosis.

Methods: SH-SY5Y cells were treated with Pb and Aβ (25–35) and Aβ (1–40), either alone or in various combinations. Cellular and molecular changes were analysed using western blotting, RT-PCR, scanning electron microscopy, and flow cytometry.

Results: Our results showed that exposure to Pb and Aβs caused significant alterations in cellular morphology, along with a marked increase in reactive oxygen species (ROS) generation leads to OS. We observed a significant upregulation of ER stress-related gene and protein expressions (GRP78 and CHOP) in treated cells. Moreover, co-exposure to Pb and Aβ peptides induced significant ER stress, through activation of all three major unfolded protein response (UPR) pathways like PERK–eIF2α, IRE1α–XBP1s, and ATF6. The upregulation of phosphorylated JNK, caspase-4, and caspase-3 further indicated the engagement of ER stress–driven apoptotic mechanisms.

Conclusion: Findings demonstrate that Pb and Aβs exposure induce OS, ER stress, and ER stress-dependent apoptosis in neuronal cells. These results suggest that Pb toxicity may act as an important environmental factor contributing to AD progression by aggravating ER stress.

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Abstract No: SA-078

Prevalence of Malnutrition in Visceral Leishmaniasis and its Association with Relapse Frequency and LD Body Positivity: A Retrospective Cohort Study



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Background: Visceral leishmaniasis (VL), a neglected tropical disease, often coexists with malnutrition in endemic regions. Malnutrition compromises immune function, potentially increasing treatment failure, relapse, and parasite burden. However, its impact on VL outcomes such as relapse frequency and Leishman-Donovan (LD) body positivity remains insufficiently explored.

Objectives: This study aimed to determine the prevalence of malnutrition among VL patients and examine its association with relapse risk, relapse frequency, and LD body positivity.

Methods: A retrospective cohort analysis was conducted using hospital records of 266 VL patients, categorized into malnourished (n=124) and non-malnourished (n=142). Relapse occurrence, relapse frequency, and LD body positivity (graded scale) were assessed. Statistical analyses included chi-square tests, odds ratios (95% CI), independent samples t-tests with Levene's correction, and Mann-Whitney U tests.

Results: Malnutrition was identified in 46.6% of patients. Relapse occurred in 62.9% of malnourished patients compared to 40.8% of non-malnourished patients (χ^2=12.9, p<0.001; OR=2.46, 95% CI 1.50–4.03). Relapse frequency was significantly higher in the malnourished group (median 1.00, range 0–3) versus the non-malnourished group (median 0.00, range 0–3; t=5.27, p<0.001; Mann-Whitney U=6090, p<0.001). LD body positivity was also elevated in malnourished patients (median 3.00, range 1–6) compared to non-malnourished patients (median 2.00, range 1–5; t=3.50, p<0.001; Mann-Whitney U=6815, p=0.001).

Conclusion: Nearly half of VL patients were malnourished, and malnutrition was strongly associated with increased relapse risk, higher relapse frequency, and greater parasite load. These findings highlight the need to integrate nutritional assessment and support into VL management strategies to improve treatment outcomes and reduce relapse rates.
Keywords: Visceral leishmaniasis; Malnutrition; Relapse; Parasite burden; LD bodies

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Abstract No: SA-079

Phytochemical warfare: Exploring Catharanthus roseus leaf extract as a natural insecticide for Sandfly management



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Vector control remains a cornerstone of visceral leishmaniasis (VL) elimination programs; however, sustained reliance on chemical insecticides has led to the widespread development of resistance in vector populations, particularly Phlebotomus argentipes. This challenge necessitates the exploration of alternative, eco-friendly, and sustainable vector control strategies. Plant-derived insecticides offer a promising solution due to their biodegradability, reduced environmental impact, and lower risk of resistance development. The present study evaluated the adulticidal efficacy of Catharanthus roseus leaf methanolic extract against P. argentipes under laboratory conditions. Wild-caught sandflies were collected from Patna district, Bihar, India, and reared to the F1 generation under controlled insectary conditions. Adult susceptibility was assessed using the CDC bottle bioassay at different concentrations (25, 50, and 100 mg/ml). Knockdown and mortality were recorded after 1 hour of exposure followed by a 24-hour holding period. Probit analysis was employed to determine lethal concentrations. The results demonstrated a clear dose-dependent increase in mortality, with LC_{50} and LC_{90} values estimated at 50.22 mg/ml and 272.18 mg/ml, respectively. No mortality was observed in the solvent control, confirming the specificity of the extract's effect. Qualitative phytochemical screening revealed the presence of flavonoids, terpenoids, and phenolic compounds, while alkaloids were absent. The observed adulticidal activity is likely attributable to these bioactive secondary metabolites. This study is among the first to report the insecticidal potential of C. roseus against P. argentipes, highlighting its promise as a botanical alternative for sandfly control. Further investigations focusing on compound isolation, mode of action, and field applicability are warranted to support its integration into integrated vector management programs.

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Abstract No: SA-080

Prevalence of TB among the inmates of a prison in Patna district



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Background - The burden of communicable diseases is higher in population residing in closed setting than the general population. It is more among the prison inmates. Close contact between inmates in prison cell would aid transmission of infectious diseases rapidly within prisons. The risk of transmission of pulmonary tuberculosis disease depends on situational and environmental vulnerabilities in prison setting.

Methodology - The study was conducted in the Beur jail of Patna district in Bihar. The inmates (both male and females) incarcerated in the jail during the survey period and willing to participate in the study were included. The present study is a pilot study conducted for a period of one week in the prison to understand the feasibility of doing this activity in all the prisons of Bihar. The inmates were subjected to the chest X-ray by hand held X-ray and X-ray suggestive of TB were requested to give sputum sample for TB testing by CBNAAT. The diagnostic algorithm was followed as per the NTEP guidelines. The data was entered in MS excel and analysed using the SPSS software.

Result – Out of 745 inmates screened by the X-ray, 42 were found to be suggestive of TB. Sputum samples of 22 inmates could be collected and sent for CBNAAT testing. Samples of 3 inmates was found positive for MTB and no drug resistance was detected. Treatment was initiated for all 3 inmates according to the NTEP guidelines.

Conclusion – The Active Case Finding is important in all the vulnerable population especially the jail inmates. Regular screening will help in early case detection and treatment initiation. TB Preventive Therapy can be advised to all the inmates after ruling out active TB

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Abstract No: SA-081

PKDL- Challenges to early diagnosis



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Post-Kala-Azar Dermatosis Leishmaniasis (PKDL) is a major public health problem in South Asia with epicentre in Indian sub-continent. In India, Bihar & Jharkhand are the most effected states. PKDL, a sequel to visceral leishmaniasis (VL) is considered as reservoir of VL; effective in hampering the elimination of kala-azar and disease spread. PKDL manifests as hypo-pigmented nodules or papulonodular lesions, causing diagnostic confusion with leprosy or vitiligo. The conventional modalities of diagnosis of formalin-fixed paraffin-embedded biopsy material are insensitive, particularly for muscular forms, leading to under-reporting. Molecular tests (quantitative PCR) is more sensitive and its acceptance in diagnostics is increasing, but it requires specialized lab settings and skilled personals. The clinical therapy challenges include the high half-life and presence of side effects in therapy, miltefosine and liposomal amphotericin B (AmBisome) as potential drugs, between the lack of patient compliance. Studies of combination short-course therapy and newer drugs have some potential but need to be validated in multiple sites. Host biomarker- and immune marker-based tests for diagnosis and treatment monitoring are under investigation. Recent advances, such as point-of-care diagnosis using molecular assays and the new short regimen(s) of treatment, are under trial. Research and development on new diagnostic methods, their adoption, policy support, and human resources comprise the key components to address the challenges of PKDL and its diagnosis and treatment

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Abstract No: SA-082

A Pipeline for Analysis of Therapeutic Potential of phytomedicines: In-silico analysis



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Background: Phytomedicines have been a great source of inspiration and elixir of curative compounds for various complex diseases including cancer. Recent studies show a greater potential in phytomedicines as additive and adjunct therapy, known to improve control of a variety of biological processes such as cell proliferation, induced apoptosis, regulated cell growth, oncogenic differentiation and better patient survival. Multiple evidence suggests that phyto-medicines are promising source for cancer treatment and management. In past years, computational databases, bioinformatic tools and artificial intelligence-based methods have been proven to be an invaluable tool for anticancer compound research, curation, analysis and validation too, in the field of oncology.

Method: In the present study we have explored a pipeline for in-sillico analyses for screening of drug/phytomedicine to particular protein targets with phytomedicines using freely available tools such as IMPPAT, STITCH, STRING, cBioPortal, ULCAN, Cytoscape, CytoHubba, miRNet, GEPIA3, TIMER3, Human Protein Atlas, DAVID and KEGG pathway analysis before going to validate results in in-vitro and in-vivo models.

Result: Pipeline for in-vitro analyses of phytomedicines in cancer research, aligning open-source tools in a manner to replicate the biological evidences. This study provides a framework to the basic science researcher to build confidence in bioinformatics and computational biology as their supporting evidence in oncology therapeutics research and drug repurposing scope.

Conclusion: Though nothing could beat in-vivo evidences and trials in therapeutic research, but they have time constraints and many hurdles including ethical clearance, confounding factors, drop-out rates, adverse impacts, non-specific targets and many more hidden challenges. In-sillico analyses comes into play there as a way to save resources, manpower and time, aligned approach in cancer research clubbed with AI tools and several bioinformatic techniques could help in development of future drugs and save the time, resources and cost. Further in-vitro and in-vivo validation be required through several functional assay before using the drug for clinical purposes.

Keywords: In-sillico analysis, Phytomedicines, IMPPAT, Cancer

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Abstract No: SA-083

An Impediment to Breast Carcinogenesis: Bioinformatic Analysis with Molecular characterization of a long unappreciated factor SALL2 in Breast Carcinogenesis



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Background: Aberrant alterations in transcription factors often disrupt key signaling pathways, contributing to oncogenesis, including breast cancer. The *SALL* Family of transcription factors has been shown to play an important role and has emerged as a crucial player in carcinogenesis. Despite its pivotal role, limited studies have been carried out to explore its role in Breast Cancer. Following similar lines of Inquiry, *SALL2* has emerged as a potential tumor suppressor in various malignancies; however, its role in Breast Cancer remains underexplored.

Methods: With the help of omics databases and bioinformatic tools such as cBioPortal, UALCAN, and the Human Protein Atlas, an extensive bioinformatic–based characterization of the *SALL2* transcription factor in breast carcinogenesis was undertaken, followed by in vitro validation and downstream molecular characterization.

Results: Our analysis revealed several crucial predictive molecular signatures, with differential mRNA and protein levels and survival status observed for the SALL2 transcription factor across different breast cancer subtypes. For instance, *SALL2* exhibited significantly lower expression in aggressive breast cancer subtypes (TNBC – Triple Negative Breast Cancer). Moreover, we observed that the *SALL2* gene was significantly linked with survival (HR=0.68, (0.53-0.85) P=9e–04 for overall survival. Subsequently, it is also observed that it may induce apoptosis in breast cancer cell lines.

Conclusion: This work underscores the potential of the *SALL2* transcription factor as a novel biomarker and therapeutic target, and it may contribute to the development of transcription-based interventions for breast cancer management.

Keywords: Breast cancer, Spalt-like transcription factor, oncogenes, biomarkers

Acknowledgement/funding – We would like to acknowledge AcSIR for the support PhD program of Manvi Naugain.

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Abstract No: SA-084

Prevalence of leptin-specific epigenetic modulation in preterm cord blood and its correlation with neonatal adiposity



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Introduction: Preterm neonates often show rapid compensatory catch-up growth, which can predispose them to obesity in later life. Although leptin regulates adiposity, its epigenetic role in predicting the risk of obesity in preterm neonates' later in life remains unclear.

Objectives: This study aims to understand the epigenetic interplay between preterm birth and predictive risk of adiposity using cord blood from preterm (n=67) and term (n=71) mothers.

Methods: Umbilical venous blood was collected from 138 pregnant women from Rainbow Children's Hospital, Hyderabad. Global DNA methylation levels were estimated using a methyl flash ELISA kit, and leptin promoter methylation was assessed by methylation-specific PCR. Leptin and IGF-1 levels were determined by ELISA, and real-time PCR was used to measure *LEP, LEPR, IL6,* and *TNFα* mRNA levels.

Results: The pregnant women were categorized into term (n=71) and preterm (n=67) based on gestational age and birthweight. Preterm cord blood exhibited significantly reduced genome-wide ($p<0.001$) and *LEP* promoter methylation ($p=0.001$), increased *LEP* ($p=0.05$), *LEPR* expression ($p=0.05$), and elevated circulatory leptin ($p=0.02$). In preterm, birth weight was positively associated with leptin ($r=0.288$, $p=0.03$). *LEP* methylation was inversely associated with IGF1 ($r=-0.506$, $p=0.03$) in preterm. The mRNA expression of *IL6* ($p=0.05$) and *TNFα* ($p=0.01$) was significantly increased in preterm cord blood. In preterm, *IL6* expression positively correlated with circulatory leptin ($r=0.318$, $p=0.05$), and *LEP* expression ($r=0.278$, $p=0.03$).

Conclusions: The hypomethylated state of global DNA, as well as *LEP* promoter observed in our study, suggests preterm neonates carry an altered epigenomic fingerprint in their subsequent life that might affect gene expression response to the various stimuli, including the neonate's metabolic health and energy homeostasis. The interplay between *LEP* methylation and pro-inflammatory cytokines can influence each other in promoting inflammation in preterm neonates, which might predispose to obesity in later life.

Acknowledgements: The work is part of a research project sponsored by the ICMR-National Institute of Nutrition (grant number 22-BS05). Navya Sree Boga was supported by the DST-Inspire Fellowship, Department of Science and Technology, Govt. of India. We appreciate the contribution of KSN Hridayanka during laboratory experiments and Kiran Teja during sample processing.

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Abstract No: SA-085

Malaria vector bionomics in highly endemic district Dantewada, Chhattisgarh



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Malaria continues to be a significant health problem in India. 80% of malaria reported in India is from the tribal, hilly and forested areas. Despite the decrease in Prevalence few state like Chhattisgarh still report very high malaria incidence. Vector control is one of the essential components of the malaria elimination program. The study aimed to study bionomics and behaviour of malaria vectors in Dantewada, Chhattisgarh. Adult mosquito were collected from indoor as well as outdoor by catch, total catch and human landing. Vector surveys were carried out in pre-monsoon, monsoon and post-monsoon period for vector density and their bionomics. *Anopheles* species are morphotyped and sibling species of *An. cullicifacies* and *An. fluviatilis* were identified using PCR. All the female anophelines were tested for sporozoite positivity and blood meal sources using PCR. A total of seven different Anopheles species were collected in the survey. *An. subpictus* (n- 3234) is the predominant species followed by *An. cullicifacies* (n-1023) and *An. fluviatilis*(n-216). Indoor resting behaviour is more common as compare to outdoor. In indoor, the vector were resting mainly in human dwelling and cattle shed. Sporozoite positivity of *A. cullicifacies* in pre-monsoon is 0.4854%, in monsoon 1.3245%, zero sporozoite positivity in post-monsoon season. Blood meal source of all Anopheline mosquito is mainly cow, in addition they also fed on human and goat. Sibling species of *An. cullicifacies* in all three different seasons were mainly B followed by E while *An. fluviatilis* sibling species were mainly U followed by S. *An. cullicifacies and An. fluviatilis* are the key malaria vector in district Dantewada of Chhattisgarh.Vectors were having indoor resting behaviour with preference to human dwelling compared to Cattle sheds.

Keywords ; Vector Bionomics, Sibling species, Sporozoite and Blood Meal

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Abstract No: SA-086

Sero-epidemiological Landscape and Clinico-Demographic Determinants of HAV and HEV Infections in Jabalpur, Madhya Pradesh: A 2024–2025 study



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Introduction: Hepatitis A (HAV) and Hepatitis E (HEV) viruses are the primary etiological agents of enterically transmitted acute viral hepatitis in India. In Jabalpur, these infections present a persistent public health challenge. This study evaluates shifting epidemiological trends and clinical presentations during 2024–2025 to improve diagnostic accuracy and patient outcomes in tertiary care settings.

Methods: This study was conducted at SL-VRDL, ICMR-NIRTH, Jabalpur. The study analysed patient sera referred from NSCB Medical College. Samples were screened for anti-HAV and anti-HEV IgM antibodies using ELISA. Statistical analyses, including Chi-square tests, determined correlations between viral positivity and demographic factors (age, sex, and urban/rural distribution).

Results: Seroprevalence increased over the study period; HAV rose from **9.21% to 14.11%**, and HEV from **5.94% to 9.78%**. A strong correlation appeared between age and virus type ($p < 0.01$). HAV clustered in pediatric/adolescent groups (1–18 years), while HEV was more prevalent in adults (18–40 years), with the **5–18 years** group showing the highest overall positivity. Urban areas exhibited significantly higher seropositivity (n=19) than rural regions (n=10, $p < 0.05$). Primary symptoms included fever and jaundice, though 2025 saw rare complications like encephalitis and altered sensorium.

Conclusion: Jabalpur remains hyper-endemic for enteric hepatitis, with rising urban prevalence and severe clinical manifestations. These data underscore the need for targeted vaccination and improved sanitation. Future phases will utilise **RT-PCR, Digital Droplet PCR**, and **Sanger sequencing** to quantify viral loads and identify regional genotypes. In future studies, we plan to check:

1. **Genotype Determination:** Using **Sanger sequencing** to identify regional circulating genotypes and track viral evolution.
2. **Viral Load Quantification:** Utilising **RT-PCR** and **Digital Droplet PCR** to correlate viral titers with clinical severity.
3. **Molecular Surveillance:** Establishing a genomic baseline to improve outbreak prediction and public health response.

Acknowledgements: The authors express their gratitude to the SL-VRDL staff for their technical expertise and support in sample processing and diagnostics.

Funding: This work was supported by the Department of Health Research (DHR) Virus Research & Diagnostic Laboratory (VRDL) Scheme.

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Abstract No: SA-087

Harnessing Structural Biology and Computational Tools for the Screening of Broad-Spectrum Antimalarials



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Malaria continues to pose a major public health burden in India despite significant advances in control strategies, with emerging drug resistance in the *P. falciparum* and *P. vivax* threatening existing therapeutic options. To contribute towards India's malaria elimination programme, our research focuses on the rational design of novel antimalarials employing a multi-target inhibition strategy. Instead of restricting drug action to a single protein, we are exploring pharmacophores and scaffolds that can selectively engage multiple essential enzymes or proteins with overlapping binding pocket features. This approach not only increases the likelihood of achieving higher efficacy but also reduces the risk of resistance development.

Through *in silico* pharmacophore modelling, molecular docking, and comparative binding site analysis, we have shortlisted several *Plasmodium* targets of high therapeutic relevance, including enzymes of the glycolytic pathway (*Pf*FBP, *Pf*PGM1), mitochondrial electron transport chain (cytochrome bc_1, *Pf*MQO), and metabolic regulators such as *Pf*PMT, *Pf*LPL3, and *Pf*GluPho. Common structural motifs that interact across these targets were identified, enabling the construction of prototype scaffolds with dual or triple binding activity. Lead prioritisation was guided by potency, drug-likeness, and predicted pharmacokinetic properties, with particular emphasis on extending half-life and overcoming cardiotoxic liabilities such as QTc prolongation.

This multi-target scaffold-based strategy provides a promising framework for next-generation antimalarials, combining rational design with mechanisms to prevent resistance. Ongoing efforts include optimising hits into leads, *in vitro* validation, and integrating ADME-Toxicity profiling. By aligning molecular innovation with national elimination goals, our work underscores the potential of multi-target inhibitors as viable candidates in India's roadmap towards malaria elimination.

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Abstract No: SA-088

Aflatoxin B1 Exposure Decreases Hepatic Iron Intake: Potential Cause for Global Anaemia Prevalence



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Introduction: Anaemia is a major global public health challenge. Common causes of anemia include haemoglobinopathies, infectious diseases, and nutritional deficiencies, especially the deficiency of iron. Specific intervention programs including Iron-Folic Acid (IFA) supplementation, and deworming for improving hemoglobin levels, were initiated to reduce anemia prevalence. Despite these immense efforts, over the decades, anemia prevalence has been constantly increasing. Aflatoxin B1 (AFB1) is identified as a potent hepatocarcinogen. It is estimated that approximately 4.5 billion people are at risk of chronic exposure to aflatoxin-contaminated food, and according to the US Food and Drug Administration (FDA), AFB1 is an unavoidable food contaminant. In non-cirrhotic conditions, iron overload in the liver plays a major role in hepatocarcinogenesis. The exact role of iron metabolism in AFB1-induced hepatocarcinogenesis is not known.

Objective: Elucidate the effect of AFB1 on hepatic iron homeostasis.

Results: In the present manuscript, we show that AFB1 upregulates the Let-7 microRNA expression, leading to cMyc downregulation in human liver cells. Through cMyc, AFB1 downregulates Transferrin Receptor (TFRC), and upregulates (Ferritin Heavy chain) FTH1 expression, leading to impairment in iron import in these cells. Overexpression of Lin28b, which blocked the AFB1-mediated Let-7 upregulation, was sufficient to reverse the blockade in iron uptake in these cells.

Conclusions: The present study elucidates the plausible reason for having an anaemia burden, despite immense efforts to eradicate this problem globally, and signals the necessity to supply “healthy meals.”

Keywords: Aflatoxin B1, hepatocytes, Iron intake, hsa-Let-7a-5p microRNA, cMyc, TFRC, and FTH1.

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Abstract No: SA-089

Vitamin D3 outperforms Vitamin D2 in regulating specific classical functions in a rat model



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Introduction: Vitamin D deficiency is prevalent globally, and food fortification with either D2 or D3 is one strategy to combat this. The structural differences in the side chains of D2 and D3 directly affect their metabolism, with D3 showing a greater half-life than D2. However, the differential effect of these vitamers on classical functions remains unclear. Therefore, the present study was designed to explore the impact of D2 vs D3 and their combination, on classical target organs—involved in calcium homeostasis.

Objectives: To decipher the impact of vitamin D2 vs D3 when used independently or in combination, at different levels, on the functions of classical target organs (intestine, bone and kidney), using animal models.

Methods: Weanling male SD rats received diets containing either D3 (2000 IU/kg or 400 IU/kg) or D2 (2000 IU/kg or 400 IU/kg) or D2+D3 (1000 IU+1000 IU/kg) or no vitamin D, for 18-weeks. Vitamin D-depleted rats, were rehabilitated with the same diets from 9th week. Serum parameters were quantified using HPLC, ELISA, and spectrophotometry. Fractional calcium absorption (^{45}Ca) was determined using liquid scintillation counting. Bone quality was evaluated by DEXA, digital force testing, and histopathological analyses. Gene expressions were assessed using RT-qPCR.

Results: A ~2-fold increase in serum 25(OH)D was observed in D3-fed groups than in D2-fed groups, while concurrent supplementation had a declining effect. A trend of higher intestinal calcium absorption was observed in the D3-fed groups ($P<0.05$). D3 was more efficacious ($P<0.05$) in improving bone mineral content, bone strength, articular cartilage thickness and collagen deposition, especially during recovery. Additionally, the expression of genes involved in calcium reabsorption were better corrected with D3 than D2 during recovery.

Conclusions: D3 improved 25(OH)D levels, calcium absorption and bone quality more efficiently than D2. D3 could be a better alternative to D2 for food fortification and supplementation programs.

Funding: This work was funded by a research grant from the Department of Biotechnology (DBT) [Project #BT/PR33124/PFN/20/1444/2019], GoI, to Ayesha Ismail. We also acknowledge University Grants Commission (UGC), GoI, for providing research fellowship to Soumam Dutta.

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Abstract No: SA-090

Metabolomics-Driven Discovery of Metabolite Biomarkers in PKDL



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Post Kala-azar Dermal Leishmaniasis (PKDL) is a sequela of Visceral leishmaniasis (VL), presented as macular, papular or nodular skin lesions, transmitted by phlebotomine sandflies. Though, PKDL does not jeopardize survival aspects of patients, but PKDL patients form an infectious reservoir that sustains *Leishmania* transmission, directly undermining visceral leishmaniasis (VL) elimination. Currently, no clinically validated prognostic biomarker exists to identify VL patients who are at high risk of developing PKDL. Using untargeted metabolomics by LC-MS/MS, initial assessment and profiling of metabolites in serum and tissue samples of patients with VL and PKDL was done. In the study, T-test was applied to find significant metabolite features at p-value < 0.05. It was followed by analysing fold change at threshold value FC ≥ 2.0 that identified 54 upregulated and 65 downregulated metabolite features in PKDL group in comparison to VL group for serum sample and 14 upregulated and 42 downregulated for the tissue samples. Differential metabolites were found on the basis of combined consideration of VIP score greater than or equal to 1.0 from OPLS-DA model and FC threshold value greater than or equal to 2.0. Further, we identified Resolvin D1, 13-KODE, 8,9-DiHETrE, 11-HETE, Prostaglandin G2, 9Z-9-Octadecenamide, Leukotriene B4, His-Tyr, His-Pro, 13(S)-HpOTrE and Linoleamide, Kynurenic Acid among 35 annotated metabolite biomarkers (AUC > 7.0) from each sample-type using ROC-curve analysis on the basis of three machine-learning techniques support vector machine and random forest. Pathway enrichment analysis mapped the pathways exhibiting significantly high impact ($p \leq 0.05$) to be involved in Glycine, serine and threonine metabolism (PI 0.23934), Glycerophospholipid metabolism (PI 0.15033), Arachidonic acid metabolism (PI 0.14496) among others. Further, the metabolite panel can be quantified by targeted metabolomics to make it clinically qualified. The validated signature will be translated into a standardized, field-compatible diagnostic platform supported by a practical risk-scoring system.

Keywords: PKDL; untargeted metabolomics; biomarkers

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Abstract No: SA-091

Unraveling the impact of maternal deficiencies of protein and folic acid in critical windows of embryonic development in mice



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Introduction: Embryonic development is a strictly regulated genetic program. The nutrients reprogram epigenetic pattern during critical windows of embryonic development. Thus malnutrition perturbs developmental gene expression. Protein or folic acid deficiency affects development of heart or neural tube. In mice embryos, the perturbed gene expression during development can be tested between embryonic day (E) a 7.5 to E11.5 in neural tube and between E7.5 to E18.0 in heart.

Objective: To analyze the impacts of maternal deficiencies of protein or folic acid in embryonic heart and neural tube during the critical windows of development.

Methods: Well fed male and female mice (C57BL/6) were pre-selected. The control mice were fed standard diet (n=6). For Test cases females were provided deficiency nutrition: T1-Protein (7% instead of 20%) or T2-folic acid (70% instead of 100%). The males never fed deficiency feed were used for timed-mating. The plugged mice were staged for embryonic day E10.5. The pregnant mice were euthanized by CO_2 to extract embryos for histological and gene expression analyses. The molecular markers of the neural tube development were done using RT- qPCR.

Results: The mother fed deficiency diet had lesser litter size than the control (4-5 vs 7-8). The abortion rate was high in deficient groups. The molecular markers (Shh, Olig2, Pax3, Pax6, Nkx2.2, and Nkx6.1) of the neural tube development were affected in the embryos under maternal malnutrition.

Conclusion: The preliminary data indicated that the malnutrition affected the embryonic development in mice by altering gene expression.

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Abstract No: SA-092

Exploring the molecular architecture and function of 3-MST in *Leishmania donovani* for Drug Target



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Leishmaniasis affects millions worldwide and remains a major public health concern, with declining efficacy of current therapeutics such as amphotericin B and miltefosine threatening sustained disease elimination. Resistance is characterized by the parasite's heightened capacity to withstand host oxidative insults, enabling escape from chemotherapeutic action. 3-Mercaptopyruvate sulfurtransferase (3-MST) is an enzyme that plays integral roles in various biological processes. In the realm of *Leishmania*, the role of 3-MST is less explored. It is a critical player in maintaining oxidative homeostasis in *Leishmania* during stress for survival. This highlights the potential of *Leishmania donovani* 3-MST (*Ld*3-MST) as an appealing drug target. However, recognising structural disparities becomes essential when a protein is present in the host and parasite. This study delves into the structural distinctions between *Ld*3-MST and *Homo sapiens* (*Hs*3-MST), providing valuable insights with direct implications for drug design. A standout feature of *Ld*3-MST is the elongated 70 amino acid C-terminal mainly contributing to a lid-like domain above the active site cavity, setting it apart from *Hs*3-MST. The root mean square deviation (RMSD) analysis shows fluctuation due to the extended tail, while radius of gyration (Rg) and solvent accecable surface area (SASA) confirm the open and solvent-accessible nature of Ld3-MST, especially in its active site, suggesting its ability to accommodate larger molecules. Principal component (PC) and free energy landscape (FEL) analysis reveals unique internal molecular dynamics of Ld3-MST, particularly in its active site. Docking studies demonstrate that *Ld*3-MST's active site can effectively accommodate molecules, highlighting its potential as a drug target. In our study we also observed significantly elevated *Ld*3-MST expression in resistant *L. donovani* isolates compared to sensitive counterparts, confirming its role in resistance. This comprehensive investigation lays the foundation for developing precise *Ld*3-MST inhibitors with promising therapeutic applications.

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Abstract No: SA-093

Bioactive compounds of *Azadirachta indica* as promising antileishmanial agents with defined molecular targets and immunoregulatory effects.



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Background: Leishmaniasis remains a major global health challenge, worsened by rising resistance to drugs like miltefosine and amphotericin B, underscoring the need for new therapies. Phytomedicine offers promise, as our prior study showed *Azadirachta indica* leaf extract had strong antileishmanial activity. LC-MS/MS analysis revealed bioactive compounds such as azadiradione (AZD) and nimbolide (NB), with unexplored therapeutic potential against leishmaniasis.

Results: Both AZD and NB exhibited dose-dependent growth inhibition along with structural disruption and DNA fragmentation in promastigotes with an IC_{50} of 17.09 and 22.67 µM, respectively. In silico docking and simulation with AZD identified *Leishmania* peroxidases (e.g., APx and TXNPx) as probable molecular targets, with subsequent downregulation of their expression confirmed in vitro. Whereas NB inhibits parasite proliferation and motility by targeting the microtubule protein dynein (in silico), and induces oxidative killing through increasing ROS production. The CC_{50} on human macrophages (MΦs) and EC_{50} on intracellular amastigotes were determined as 56.32 µM and 11.67 µM for AZD, respectively. The dose- dependent reduction in MΦs' infectivity demonstrates the drug potential of AZD. However, the selectivity index 4.83 indicates its moderate *Leishmania*-specific drug potential. The decrease in IL-10, IL-1β, and arginase and increase in IL- 12 and iNOS expressions reinforce the immunoregulatory potential of AZD in favour of the host. Further investigations are required to optimize the dosage and improve the selectivity of AZD.

Conclusion: This study demonstrated the novel findings related to the drug potential of AZD with defined targets of *Leishmania* and host protective cytokine response. Studies on intracellular amastigotes with NB and on animal models with both AZD and NB are in progress, which may deliver further insights into their therapeutic potential.

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Abstract No: SA-094

Molecular Surveillance of *Rickettsia felis* in Ticks from Tripura: Insights from India's Northeast Border



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Introduction: *Rickettsia felis* is an intracellular pathogen responsible for rickettsioses[1]. It is a causative organism of spotted fever group rickettsia (SFGR) and typhus group rickettsia (TGR)[2]. Its primary vectors are fleas, particularly *Ctenocephalides felis*. However, recent studies have implicated ticks as potential vectors or reservoirs for *Rickettsia felis* in various parts of the world, including a study from Tamil Nadu, India[3].
Tripura, a northeastern state in India, shares ecological features that are conducive to vector-borne diseases. However, the role of ticks in the transmission of rickettsial pathogens remains underexplored. Moreover, limited research has been conducted on the molecular diversity of *Rickettsia* spp. in arthropod vectors.

Objectives

1. Detect *Rickettsia* spp. in ticks collected from Tripura using molecular methods targeting the 17 kDa gene specific to SFGR and TGR.
2. To assess the potential role of ticks as vectors or reservoirs for *Rickettsia felis* in northeastern India.

Methods: Between June 2023 and May 2024, 424 ticks (72 pools) were collected from various host animals and the environment (through flagging and dragging) in Tripura. The ticks were identified morphologically up to the genus level. DNA extraction was performed, followed by heminested PCR amplification targeting the 17 kDa gene specific for SFGR and TGR using primers R17kM61F, R17k31F, and Rr2608R. Positive amplicons were sequenced and analysed phylogenetically.

Results: Of the 72 pools examined, 8.3% (6/72) tested positive for 17 kDa gene. BLAST analysis revealed 99% nucleotide sequence similarity of all six positive samples with *Rickettsia felis*.

Conclusions: This study provides the first molecular evidence of *Rickettsia felis* in ticks from Tripura. It also highlights a potential role of ticks as vectors or reservoirs for this zoonotic pathogen in the region. Further studies are warranted to elucidate the epidemiological significance and transmission dynamics of *Rickettsia felis* in India's northeastern border areas.

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Abstract No: SA-095

Development and evaluation of peptide-based vaccine candidate targeting immunodominant regions of the envelope protein of Kyasanur Forest Disease Virus



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Introduction: Kyasanur Forest Disease (KFD) is an acute viral haemorrhagic fever affecting humans and monkeys. The causative agent, KFD virus (KFDV), is a tick-borne flavivirus first identified in the Western Ghats of southern India (*Work et al. 1957*). The disease is primarily transmitted by the hard tick *Haemaphysalis spinigera* (*Varma, Trapido, and Rajagopalan 1957*). Despite of the discovery of KFDV for over than six decades, the available formalin-inactivated vaccine showed limited efficacy, highlighting the need for better vaccine candidates.

Objectives: This study aims to develop a protective, non-allergenic and immunogenic peptide-based vaccine candidate against KFDV.

Methods: In this study, a systematic immunoinformatic pipeline was applied to identify novel peptide vaccine candidates. As available KFDV protein sequences exhibit more than 99% similarity, the reference envelope protein sequence was considered representative and used for all downstream analyses. The sequence was analysed for homology against the human proteome, gut-microbiome, and human anti-targets to ensure safety. Multiple algorithms were employed to predict B-cell epitope, while MHC-I and MHC-II epitope predictions were performed using Indian population-specific HLA using the NetMHCPan servers. Additionally, the predicted epitopes were screened for antigenicity, allergenicity, toxicity, and immunogenicity. High-scoring, overlapping epitopes were then assembled into multi-epitope vaccine constructs. Their 3D structures were modeled and docked with receptors, including the TLRs and MHCs, followed by molecular dynamics simulations to assess stability.

Results: This systematic immunoinformatics approach revealed multiple multi-epitope, vaccine candidates as promising interventions against KFDV, demonstrating robust in-silico immunogenicity.

Conclusions: The resulting immunoinformatics analysis identified several multi-epitope vaccine candidates as promising interventions against KFDV, exhibiting high structural stability, favourable receptor interactions, and strong in-silico immunogenicity. These candidates warrant further *in vitro* validation to confirm their protective potential.

Acknowledgement and Funding: I would like to sincerely thank Council of Scientific & Industrial Research (**CSIR**), India, for their financial support. I would also like to thank ICMR-National Institute of Virology.

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Abstract No: SA-096

Development of CAR NK cells to target latent HIV-1 reservoirs



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Introduction: Despite effective antiretroviral therapy (ART), human immunodeficiency virus (HIV) persists in latent form in cell reservoirs, posing a major challenge to complete eradication. Reactivation of latent HIV alone is insufficient, as infected cells are inefficiently cleared by endogenous $CD8^+$ T cells and rapidly evade immune recognition. Chimeric antigen receptor (CAR)–engineered immune cells offer a promising alternative strategy for eliminating reactivated HIV reservoirs. This study explores a modular approach to developing CAR-engineered natural killer (NK) cells to target gp160-expressing cells following latency reversal.

Objectives: To develop CAR NK cells to target reactivated latent HIV-1 reservoirs.

Methods: An anti-DNP CAR construct comprising a CD8α signal peptide, HA tag, scFv region specific to the HIV antigen, CD28 hinge and transmembrane domains, and CD28 and CD3ζ intracellular signaling domains was cloned into the lenti-ZsGreen lentiviral vector. Correct cloning was confirmed by restriction digestion and sequencing. Lentiviral particles were produced in HEK293T cells using packaging and VSV-G envelope plasmids, concentrated, and used to transduce NK cells. CAR expression on NK cells was evaluated by flow cytometry using an anti-HA antibody. CAR NK cell–mediated killing of reactivated HIV reservoirs will be assessed by multicolor flow cytometry based on the reduction of p24-expressing cells.

Results: The CAR lentiviral construct was successfully designed, cloned, and validated. Functional lentiviral particles were generated, and optimization of viral titers enabled efficient NK cell transduction with detectable CAR expression.

Conclusion: This study demonstrates the feasibility of generating allogeneic CAR NK cells, providing a promising platform for redirecting NK cell–mediated cytotoxicity toward reactivated HIV reservoirs and supporting further evaluation of this approach for HIV cure strategies

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Abstract No: SA-97

Relative Validation of Telephonic Versus In-Person 24-Hour Dietary Recalls Among Primary School Children: A Pilot Study



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Introduction: Childhood obesity is a growing public health concern in India, driven by rapid urbanization, dietary changes, reduced physical activity and obesogenic environments. Accurate dietary assessment is essential for surveillance and evaluating dietary interventions, however, minimizing participant burden is challenging. Dietary intake fluctuates significantly day-to-day, requiring multiple measurements, particularly in young children who snack frequently and consume mixed dishes. Technology-enabled methods such as telephonic 24-hour recalls offer a scalable alternative to household visits, yet evidence on their relative validity among primary school children (6-9 years) in India remains limited.

Objectives: To assess agreement between telephonic and in-person 24-hour dietary recall methods for estimating daily energy intake and macronutrient intake (carbohydrate, protein, dietary fibre and fat) among children aged 6-9 years.

Methods: A relative validation study was conducted among children aged 6-9 years (n=15) from a government school in urban Hyderabad. Each child completed six recalls: three in-person (reference method) and three telephonic (test method), covering two non-consecutive weekdays and one weekend day per method. Standardized cup sizes aided in-person interviews, while 2-D images of the same cups were used telephonically. Nutrient analysis was performed using standardized cooked-food databases. Planned statistical analyses include paired t-test, intraclass correlation coefficients (ICC) and Bland-Altman analysis with 95% limits of agreement.

Results: Pilot data from 15 children (mean age : 7.67 ± 1.05 years; 46.7% boys; mostly lower-to-middle socioeconomic strata), generated 90 recall days (45 in-person and 45 telephonic). A ~190-item food/recipe database was developed, covering homemade foods, out-of-home items, and ultra-processed/packaged products. Agreement analyses between the two methods is currently underway.

Conclusions: This study offers preliminary evidence on the feasibility and relative validity of telephonic 24-hour recall for estimating energy and macronutrient intake among young children, supporting scalable dietary assessment approaches for childhood obesity research and school-based nutrition interventions.

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Abstract No: SA-98

Potential of Secondary malaria vectors in malaria transmission dynamics across North-eastern states of India



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Introduction: Malaria is endemic in the North eastern regions of India, in which a variety of ecological variables promote diverse vector species. The major primary malaria vector in this region has long been considered to be *Anopheles minimus* and *Anopheles baimaii*, both closely associated with forest ecosystems. Despite the reduced abundance of these primary anopheline vectors, the persistence of malaria suggests the involvement of additional anopheline species and also play a role in transmitting malaria, along with primary vectors, and are widely distributed across northeastern India. These vectors have significantly lower sporozoite rates compared to primary vectors. This study aimed to investigate the sporozoite positivity of secondary anopheline species in the high-malaria-endemic district of Kokrajhar, Assam, in northeastern India.

Methods: During the study period, 1,794 female mosquitoes representing five genera in *Anopheles*, *Culex*, *Aedes*, *Mansonia*, and *Armigeres* were collected from Kochugaon PHC in Kokrajhar, Assam. The three methods of collection were using: CDC light trap collection, Indoor resting collection using the mouth aspiration method, and pyrethrum spray collection.

Results: The *Plasmodium* positivity (Percent, number/total number) was highest in *An. maculatus* (4%; 5/80), followed by *An. minimus* (4.8%; 1/21), and *Anopheles kochi* (4.6%; 1/22). All the Plasmodium- positive samples of mosquito were identified as *P. vivax*. The highest human blood index form in *An. minimus* and then *An. maculatus* is 0.86 and 0.42 respectively. These results suggest that anopheline species beyond the traditionally recognized primary vectors, may play a role in sustaining malaria transmission in endemic areas of northeastern India.

Conclusion: The study highlights the spatiotemporal variability in the density of primary malaria vectors and reconfirms that multiple *Anopheles* species carry malaria parasites in the international border areas of Kokrajhar (Assam, India). A reassessment of vector control priorities is essential for achieving malaria elimination in the northeastern region of India.

Acknowledgments and Funding: Authors acknowledge to ICMR- NIMR and Acsir to conduct the study and UGC for funding the research work.

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Abstract No: SA-99

Unraveling the Symphony of HSP 70 in Indian Malarial vector- A Molecular Ballet Shaping Mosquito Development and Influencing *Plasmodium* Transmission



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Introduction: HSP's are critical molecular chaperones, categorized into various classes based on their molecular mass, which assist in protein folding and support organisms in adapting to extreme environmental conditions. Despite their importance, the role of HSPs in the stress response of mosquitoes remains insufficiently understood. This study investigates HSP70 in two primary Indian malaria vectors, *Anopheles culicifacies* and *Anopheles stephensi,* aiming to elucidate its role in stress response mechanisms and its potential application in vector control.

Objectives: Our aim and objective is to elucidate the role of HSP70 in *anopheles* in developmental regulation and parasite transmission.

Methods: The investigation involved a comprehensive bioinformatics analysis of HSP-70 in *Ac* and *As* using tools such as BLASTP, tBLASTn, and Pfam for sequence analysis, and phylogenetic and syntenic analyses to explore evolutionary relationships. Experimental validation included qPCR to examine HSP70 expression across developmental stages and under various stress conditions, alongside recombinant protein expression and characterization. Functional studies involved RNAi-mediated silencing of HSP70-1 in *Ac* larvae, coupled with selective inhibition of HSP70 to evaluate effects on developmental cycle of mosquito and *Plasmodium* development inside mosquito.

Results: Seven distinct subcellular localizations of HSP70 isoforms were identified. Notably, HSP70-1 exhibited increased expression at the L3 larval stage, underscoring its role in larval development. Silencing HSP70-1 led to significant upregulation of other HSP70 isoforms indicating compensation of stress. In *P.berghei*-infected mosquitoes, HSP70 inhibition markedly impaired oocyst development, suggesting its critical role in parasite survival within the mosquito.

Conclusion: This study provides novel insights into the function of HSP70 in malaria vectors, particularly how its inhibition impacts mosquito development and malaria parasite progression. The findings suggest that targeting HSP70 could serve as a potential vector control strategy. By examining the interactions between HSP70 and malaria parasites, this research identifies exploitable vulnerabilities that may aid in reducing malaria transmission.

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Abstract No: SA-100

Burden and distribution of *Pfhrp2* and *Pfhrp3* gene deletions in *Plasmodium falciparum* in India: a systematic review and meta-analysis protocol



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Introduction: Accurate diagnosis of *Plasmodium falciparum* malaria is essential for effective case management and malaria control. However, the performance of histidine-rich protein 2/3 (HRP2/3)-based rapid diagnostic tests (RDTs) is threatened by deletions in the *P. falciparum* histidine-rich protein 2 and 3 (*Pfhrp2* and *Pfhrp3*) genes, leading to false-negative results (*World Malaria Report 2025*). Although several studies have reported the presence of these gene deletions across India, the available evidence remains fragmented, heterogeneous, and regionally variable (Krishna et al., 2024 (PLoS ONE); (Nema et al., 2025).

Objective: This protocol outlines a systematic review and meta-analysis to estimate the national prevalence, geographical distribution, and temporal trends of *Pfhrp2* and *Pfhrp3* gene deletions in India.

Methods: This systematic review will be conducted in accordance with the Preferred Reporting Items for Systematic Review and Meta-Analysis Protocols (PRISMA-P) guidelines and is registered with PROSPERO (CRD420251150598). A comprehensive literature search will be performed in PubMed, Scopus, and Web of Science to identify observational studies published between September 2010 and December 2025 reporting molecular confirmation of *Pfhrp2* and/or *Pfhrp3* gene deletions in *P. falciparum* isolates from India. Two reviewers will independently screen studies, extract data, and assess methodological quality using the Joanna Briggs Institute (JBI) Critical Appraisal Checklist for proportion Studies. A random-effects meta-analysis will be conducted to estimate pooled proportion, and subgroup analyses will be performed based on geographical region, malaria transmission intensity, study period, and diagnostic methodology to explore sources of heterogeneity.

Conclusion: This review will provide a robust national estimate of *Pfhrp2* and *Pfhrp3* gene deletions in India, generating critical evidence to guide diagnostic policy decisions, particularly regarding WHO recommendations on RDT selection, and to support malaria elimination efforts by 2030

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Abstract No: SA-101

Assessment of antibody responses to *Plasmodium falciparum* antigens for malaria serosurveillance in India



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Introduction: Global malaria control is hindered by diagnostics that only detect active infections, whereas serosurveillance overcomes this limitation by identifying past exposure and enabling better monitoring of transmission. This study assessed antibody responses to key *Plasmodium falciparum (Pf)* antigens, including CSP (Circumsporozoite Protein), EBA-140 RIII-V (Erythrocyte Binding Antigen-140 RIII-V), $MSP1_{19}$ (Merozoite Surface Protein 1_{19}), and MSP-6 (Merozoite Surface Protein 6), in malaria patients to advance serosurveillance capabilities for improved malaria control strategies.

Methods: Archived serum samples from Jagdalpur, Chhattisgarh:180 Pf-positive cases, 150 exposed group from endemic areas, 10 non-endemic controls for threshold determination, and 10 *Plasmodium vivax* (Pv) samples for cross-reactivity evaluation. Antibody responses were assessed using ELISA, with seropositivity thresholds established as mean optical density plus two standard deviations of non-endemic controls.

Results: $MSP1_{19}$ exhibited highest seropositivity in Pf-positive cases (160/180; 88.89%), followed by CSP (142/180; 78.89%), MSP-6 (51/180; 28.33%), and EBA-140 RIII-V (26/180; 14.45%). In exposed group, CSP showed the strongest reactivity (91/150; 60.67%), followed by $MSP1_{19}$ (82/150; 54.67%), EBA-140 RIII-V (38/150; 25.33%), and MSP-6 (13/150; 8.67%). A significant positive correlation was observed between age and $MSP1_{19}$ antibody levels in Pf-positive individuals suggesting increasing antibody titre with repeated exposure.

Conclusion: $MSP1_{19}$ demonstrated strong potential as serological markers for malaria surveillance, showing consistent antibody responses in both active infections and exposure scenarios. CSP showed higher antibody titers in both Pf-positive and exposed groups, but might interfere with vaccine-induced responses. MSP-6 captures more recent or active infection, consistent with short-lived antibody responses. Interestingly, EBA-140 RIII-V exhibited higher antibody titre in exposed individuals versus Pf-positive cases, indicating its potential for estimating past exposure. These findings warrant further evaluation of these antigens across diverse Indian endemic regions for developing multiplex sero-assays

KEYWORDS: Serosurveillance, CSP, EBA-140 RIII-V, $MSP1_{19}$, MSP-6, ELISA

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Abstract No: SA-102

Assessment of pathogenicity of 2.3.4.4b HPAI H5N1 virus and evaluation of inactivated virus as a vaccine candidate



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Introduction: Highly pathogenic avian influenza (HPAI) H5N1 virus is a major pandemic threat, which is a global cause of public health concern. HPAI H5N1 virus was isolated from Kerala, India in 2024 belonged to clade 2.3.4.4b. This clade of H5N1 virus is spreading globally and has shown spill-over and adaptation to mammalian hosts is concerning. The present study was conducted to assess the pathogenicity of 2.3.4.4b HPAI H5N1 virus and use of β-propiolactone (BPL)-inactivated virus as a vaccine candidate.

Objectives:

- Challenge BALB/c mice with infectious HPAI H5N1 homologous virus to study pathogenicity.
- To study safety, immunogenicity of BPL inactivated highly pathogenic avian influenza (HPAI) H5N1 virus in BALB/c mice and evaluate as a potential candidate vaccine.

Methods:

- A/Chicken/India/240008/2024 (H5N1) virus titration was performed using 50% egg infectious dose (EID_{50}).
- β-propiolactone (BPL) was used to inactivate the virus.
- 6-8 weeks of BALB/c mice were immunized with the inactivated virus and infectious virus were challenged through intra-nasal route.

Results:

- Both immunized as well as non-immunized mice showed symptoms such as shivering, ruffled fur and cuddling for 3-4 days, after which immunized mice were recovered.
- Prolonged symptoms were seen in the non-immunized mice. Neurological signs such as Convulsions, ataxia and tremors were seen. Presence of the virus in the brain was also noted.

Conclusions:

- HPAI H5N1 virus was seen to be highly pathogenic in BALB/c mice causing neurotropism and mortality.
- There was 100% protection in mice immunized with inactivated, adjuvanted H5N1 virus preparation.
- This preliminary study shows the potential of BPL-inactivated H5N1 virus as a vaccine candidate, highlighting further studies.

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Abstract No: SA-103

Isolation and virological characterisation of Respiratory Syncytial Virus from clinical samples



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Introduction: Respiratory syncytial virus causes respiratory tract infection in infants and older adults. Studies on RSV are hampered due to the difficulties in virus isolation and revival and consistent quantification. A reliable method is essential for research and antiviral screening for RSV.

Objectives: To establish the protocols for RSV isolation from clinical samples and to standardise the protocols of plaque assay, and growth kinetics.

Methods: RSV RT-PCR positive clinical samples were inoculated onto Hep-2 and Vero CCL-81 cells to standardize the isolation procedure. Plaque assay was performed in Vero CCL 81 with both agarose and CMC overlays. Plaque purification was carried out through two serial passages, and viral replication was evaluated by qRT-PCR. Growth kinetics were studied in Hep-2 cells at MOI 1 and 5.

Results: RSV clinical isolates representing both RSV A and RSV B subgroups were successfully obtained from patient samples. Following isolation, plaque assay was successfully optimised for RSV. Titre obtained from plaque assay was 6×10^7 PFU/mL for RSV A isolates and 8.4×10^5 PFU/mL for RSV B isolates. Plaque purified RSV isolate shows robust amplification measured by qRT-PCR and plaque assay. RSV replication cycle began at 24 hours, viral growth peaks at 5-6 days for MOI 1 and MOI 5. The declining phase starts after 5 days for MOI 1, thus exhibiting reproducible replication kinetics for both MOI. Whole genome sequencing of RSV isolates was performed using Illumina Mi-Seq platform, and it confirmed RSV A and RSV B isolates.

Conclusions: These protocols improve the research, enable RSV isolation and quantification and support further studies like antiviral screening, immunological studies, and strengthen the RSV research in India

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Abstract No: SA-104

Isolation of Coxsackievirus B4 from a Case of Acute Gastroenteritis: A Rare Occurrence



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Introduction: Coxsackievirus B4 (CVB4), a member of *Enterovirus B* (family *Picornaviridae*), is associated with type 1 diabetes mellitus, myocarditis, hand, foot and mouth disease but is rarely reported in acute gastroenteritis (AGE). Molecular and biological data on CVB4 circulating in India remain limited. Host- directed factors, including cellular kinases and epigenetic regulators, are increasingly recognized as critical for enteroviral replication and represent promising antiviral targets.Objectives: The present study aimed to isolate and characterise Coxsackievirus B4 from diarrheal samples and to evaluate the role of selected host kinases and epigenetic regulators in modulating viral replication.

Methods: Diarrheal stool samples were subjected to virus isolation in susceptible cell lines. CVB4 was identified by RT-PCR and VP2 sequencing, followed by phylogenetic analysis. Viral growth was assessed through cytopathic effect and replication kinetics. Host involvement was evaluated using kinase and epigenetic inhibitors, with viral replication quantified by plaque assay and qPCR.

Results: We report isolation and molecular characterization of CVB4 from a stool sample of a 4-year-old female with acute gastroenteritis in Pune, India. Routine bacteriological, parasitological, and rapid viral tests were negative. Pan-enterovirus RT-PCR (5′UTR) was positive, and VP2 sequencing showed >97% nucleotide identity with reference CVB4 strains. Phylogenetic analysis placed the isolate in CVB4 genogroup B. Virus isolation in RD cells showed characteristic cytopathic effects, qRT-PCR indicated a high viral load, and whole- genome sequencing confirmed CVB4 identity.

Conclusions: The absence of co-infecting enteric pathogens and a consistent clinical presentation suggest CVB4 as probable etiological agent. This finding adds to limited evidence linking CVB4 to gastrointestinal disease, previously reported only sporadically. Our results underscore the need to include enteroviruses in the diagnostic evaluation of unexplained pediatric AGE and support enhanced molecular surveillance and genotyping to better define the epidemiology and public health impact of CVB4 infections.

Acknowledgement(s) and Funding: This work was supported by ICMR-National Institute of Virology, Pune. Pooja acknowledges the University Grants Commission (UGC), Government of India, for providing financial support in the form of a research fellowship.

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Abstract No: SA-105

Towards Exploring Novel Inhibitors Against *Leishmania donovani*



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Introduction: Visceral leishmaniasis (VL), caused by *Leishmania donovani*, fatal protozoan disease across in the Indian subcontinent, Asia, and Africa. With ~30,000 (WHO) new VL cases occur annually, with nearly 1 billion people at risk, the lack of a vaccine and dwindling treatment options necessitate the urgent discovery of novel, efficacious inhibitors. This study utilized an integrated approach through *in-silico*, *in-vitro*, and *ex-vivo* methodologies to identify potential antileishmanial compounds.

Objectives: To identify and evaluate potent inhibitors against *Leishmania donovani* by integrating *in-silico*, and *in-vitro* wet lab experiments.

Methods: A 3-D protein target model was constructed and validated, with structural stability confirmed through Molecular Dynamics (MD) simulations. High-throughput virtual screening and molecular docking identified high-affinity leads, which were then evaluated for binding energy, ADMET pharmacokinetic profiles, adherence to Lipinski's "Rule of 5" and subjected to additional MD simulations of complexes. An anti-leishmanial efficacy was validated through *in-vitro* assays against promastigotes and *ex-vivo* assays against intracellular amastigotes. To assess safety, cytotoxicity was measured via MTT assays on THP1-derived monocytes and PBMCs to determine IC_{50} and LD_{50} values. To characterize the mode of parasite death and ensure hemocompatibility, mode-of-action analyses were performed, including DNA fragmentation, Oxidative burst evaluation via DHR analysis, & Hemolysis assays.

Results: *In-silico* result demonstrated that selected top-ranked inhibitors possessed favorable pharmacophore features comparable to the control drugs while *in-vitro* and *ex-vivo* assays confirmed that the selected compounds effectively inhibited parasite growth & markedly reduced intracellular parasite burden without inducing significant host-cell toxicity and were also safer for Nucleic acids, WBCs and RBCs.

Conclusions: The integrated approach identified promising inhibitors with potent antileishmanial activity and minimal host toxicity, suggested that the identified inhibitors can be utilized as a promising lead molecule and therapeutic candidate for further exploration against VL.

Acknowledgement(s) and Funding: I would like to express my heartfelt gratitude to ICMR-RMRIMS Patna for providing an opportunity to access the research facilities. I am grateful to the Department of Science and Technology (DST) for INSPIRE fellowship and to the ICMR Ad-hoc for providing Research Grant.

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Abstract No: SA-106

Co-exposure to Lead and Aβ peptides disrupt Autophagy and Synaptic Protein Homeostasis via CDK5 and CRMP1 Dysregulation in SH-SY5Y cells



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Introduction: Autophagy is a crucial cellular mechanism for maintaining neuronal homeostasis, synaptic integrity, and protein quality control. Dysregulation of autophagic flux has been implicated in neurodegenerative disorders, including Alzheimer's disease. Environmental toxins such as lead (Pb) and amyloid-β peptides (Aβps) are known to disrupt neuronal function, but the molecular interplay between these insults, autophagy, and synaptic proteins remains unclear.

Objective: This study aimed to investigate the effects of Pb and Aβps (25-35 and 1-40) on autophagy and key cytoskeletal and synaptic regulatory proteins-CRMP1, LC3, endophilin, syntaxin, synapsin-and the kinase CDK5 in human SH-SY5Y neuronal cells.

Methods: SH-SY5Y cells were exposed to Pb, Aβps, or their combination. Autophagic activity was assessed using autophagy detection kit. Protein expression and distribution of LC3, CRMP1, endophilin, syntaxin, synapsin, and CDK5 were evaluated by western blot.

Results: Exposure to Pb and Aβps significantly impaired autophagy, as evidenced by altered LC3 expression and autophagosome accumulation. CRMP1 and CDK5 levels were dysregulated, indicating disrupted cytoskeletal dynamics and kinase signaling. Synaptic proteins-endophilin, syntaxin, and synapsin-showed aberrant distribution, reflecting impaired vesicle trafficking and synaptic function. Co-exposure produced more pronounced effects, suggesting synergistic neurotoxicity.

Conclusion: Pb and Aβps synergistically impair neuronal autophagy and disrupt cytoskeletal and synaptic regulatory networks. These findings highlight the mechanistic link between environmental and pathological insults, autophagy dysfunction, and synaptic pathology, providing insights into early events in neurodegenerative disease progression.

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Abstract No: SA-107

Integrative Network Analysis of Metabolic Syndrome



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Introduction : Prevalence of Metabolic Syndrome (MeS) is rising in all walks of life. Previous studies have explored gene expression alterations in isolated metabolic conditions, yet these efforts lack integrative analysis across multiple datasets and fail to capture the interplay between metabolic and inflammatory pathways.

Objectives: We aimed to unravel the genetic landscape and gene expression pattern under Metabolic Syndrome (MeS) by identifying differentially expressed genes (DEGs) of various pathways through integrated bioinformatics approaches.

Methods: Publicly available gene expression datasets related to obesity, insulin resistance, and diabetes were retrieved from the Gene Expression Omnibus (GEO) database. Samples were categorized into MeS-related conditions and healthy controls for comparative analysis. Differential gene expression analysis was performed using established bioinformatics tools. Common differentially expressed genes across datasets were identified through integrative intersection analysis. Network-based approaches were employed to construct and analyze protein-protein interaction networks, followed by functional enrichment and pathway analyses. In addition, drug-gene interaction analysis was conducted to assess potential therapeutic relevance.

Results: The resulting PPI network comprised 131 proteins corresponding to the DEGs, and 10 hub proteins were identified. These hub proteins were mainly involved in phosphatidylinositol signaling, actin cytoskeleton regulation, inositol phosphate metabolism, and phospholipase D signaling, highlighting their roles in cell signaling, membrane trafficking, and metabolic regulation.

Conclusions: In the present study, PIK3R2 and PIK3CB emerged as major hub genes with identifiable interacting drug molecules, underscoring their therapeutic relevance and potential for targeted modulation of PI3K signaling in MeS. In contrast, the remaining hub genes showed no existing drug interactions, highlighting promising avenues for future research and novel compound discovery to address unexplored molecular targets in the management of MeS.

Keywords: Metabolic syndrome, differentially expressed genes, obesity, diabetes, insulin resistance, integrative bioinformatics analysis.

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Abstract No: SA-108

Somatic Mutation Profiling of Esophageal Cancer in Northeast India: An Ongoing PhD Study



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Esophageal cancer persists as a major global health concern, with distinct geographic variations in incidence and mortality rates. Despite the increasing burden of cancer in Northeast India, genomic studies from this region remain scarce. The PhD study aims to comprehensively characterize the somatic mutation profile of esophageal cancer in patients from Northeast India to enhance the current understanding of esophageal cancer in this population.

Following institutional ethical approval and informed consent, a total of 60 histologically confirmed primary esophageal cancer patients from Northeast states were enrolled and sociodemography and clinicopathological data were recorded. Genomic DNA was extracted from tumor tissues and matched peripheral blood samples and assessed for quality and concentration using commercial DNA extraction and Quantification kits. Whole exome sequencing of 20 tumor samples was carried out on the Illumina platform and analysis using a customized Linux-based pipeline is currently underway. On the basis of mutational frequency and oncogenic relevance, the top three mutated genes will be selected for mutational screening on the remaining samples.

As per GLOBOCAN 2022, esophageal cancer ranks fifth in India for both the incidence and mortality. Data from ICMR - National Center for Disease Informatics and Research (ICMR-NCDIR) indicates that in the northeast, esophageal cancer is the leading cancer site in males and the fourth cancer site in females. The probability of developing esophageal cancer is highest for males (1:54 males) and fourth highest in females (1:113 females). Additionally, the region has a high relative proportion of tobacco-related cancers, among which the leading site is esophageal cancer.

Considering the epidemiological relevance, high disease burden and limited genomic data, this study is significant as it addresses a critical gap in the genetic understanding of esophageal cancer in the high-risk region of Northeast India. The findings could lead to improved diagnostic, prognostic, and therapeutic strategies

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Abstract No: SA-109

Epitope centric mutational profiling of Dengue virus serotype 3 envelope protein with relevance to vaccine design



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Introduction: Dengue virus serotype 3 (DENV-3) continues to drive outbreaks in India, with frequent antigenic variation in the envelope protein altering key neutralizing epitopes and potentially undermining existing immunity and vaccine efficacy. The absence of long-term, epitope-level molecular surveillance of circulating Indian DENV-3 strains over the past decade limits our understanding of these evolutionary changes.

Objectives: To investigate how DENV-3 envelope protein epitope mutations influence immune recognition, viral evolution, and vaccine effectiveness.

Methods: In this study, 136 dengue RNA-positive plasma samples collected from West Bengal between 2016 and 2023 were subjected to whole-genome amplification using serotype-specific multiplex RT-PCR, followed by Illumina-based next-generation sequencing. Consensus sequences of DENV-3 isolates were generated and compared with the reference strain (NC_001475) and vaccine strains Dengvaxia, TV003, and TAK003. Epitope prediction for B-cell, MHC class I, and MHC class II regions was carried out using the Immune Epitope Database (IEDB). Identified epitope-associated mutations were further evaluated for antigenicity, immunogenicity, allergenicity, and toxicity using established *in silico* tools.

Results: Epitope mapping revealed recurrent amino acid substitutions within immunodominant regions of the E protein. Notably, substitutions such as I380T and K383N were identified within the EDIII domain, both located in exposed B-cell epitopes, suggesting immune-driven selective pressure. Additionally, mutations including V169T in EDII and multiple substitutions within predicted T-cell epitopes were observed, potentially affecting HLA-binding affinity while remaining non-toxic and non-allergenic. Comparative analysis demonstrated antigenic divergence between circulating local DENV-3 strains and vaccine-represented sequences, indicating possible implications for vaccine efficacy in the regional context.

Conclusion: This epitope-focused analysis of Eastern Indian DENV-3 strains reveals region-specific mutations in key B- and T-cell epitopes, emphasizing the need for pan India continuous epitope-level surveillance to guide vaccine efficacy and better diagnostic development.

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Abstract No: SA-110

Exploration of Epitope Ensembled Chimera to Boost Immunity to Leishmaniasis



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INTRODUCTION: VL is pathophysiological condition of Leishmania and regulated by cellular immunity. Dominance of MHC polymorphism and antigens variability is the factor of HLA-specific epitope discovery.

AIM/OBJECTIVE: Universal multiepitope construct targeting VL with broad population coverage.

METHODS: Screening of MHC class-I and II–restricted epitopes of Leishmania donovani identified a consensus HLA A 02: 01, HLA-DRB1*01 01-restricted epitopes respectively. Based on in silico screening, followed by population coverage analysis, HLA cross-presentation ability, docking and MD simulation best epitopes in each class were identified. In vitro assays to evaluate the immunogenicity of these peptides by isolating peripheral blood mononuclear cells (PBMCs) from healthy donors and VL patients with respect to HLA Type were performed. Peptide stimulation, proliferation, and cytokines secretion assay are being conducted.

RESULT: The analysis revealed that the set of epitopes presented by diverse MHC class-I and II alleles having maximum population coverage using IEDB software.IL-10Pred signify the immunopathogenic nature of the shortlisted peptides. Selected epitopes have potential to generate significantly higher proinflammatory cytokine (CD4+, CD8+ IFN-γ).This comprehensive approach allowed us to identify potential Th1 stimulatory peptides that could effectively stimulate a protective immune response, thereby highlighting their potential as immunoprophylactic candidates.

CONCLUSION: Protein fragment identified in this study can be further evaluated for the development of prophylactic or therapeutic study. Stimulation with the cocktail of epitopes against VL-treated subject will provide an enhanced CD4+and IFN-γ level. The selected epitopes having potential to generate Th1 immune responses rather than Th2 that is important for suppressing leishmania infection.

Acknowledgement(s) and Funding: I would like to express my heartfelt gratitude to ICMR-RMRIMS, Patna for providing research facility support & guidance. This study has been Financially supported from ICMR Delhi; Govt. of India as extramural Project.

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Abstract No: SA-111

Iron homeostasis and reproduction: Unveiling the Microbiome-Gut-Brain-Axis connection in the mosquito *Anopheles culicifacies*



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Introduction: Our study investigated how adult female mosquitoes regulate systemic iron homeostasis after blood feeding, a process essential for reproduction, and revealed striking parallels to iron deficiency disorders in mammals.

Objectives: Our aim and objective is to elucidate a coordinated transcriptional regulation of *Ferritin (Fer)* and *Transferrin (Trf)* plays a crucial role in follicle development and egg maturation.

Methods: The investigation involved a comprehensive bioinformatics analysis of *Ferritin* in Anopheles culicifacies using tools such as BLASTP, tBLASTn, and Pfam for sequence analysis, and phylogenetic and syntenic analyses to explore evolutionary relationships. Experimental validation included qPCR to examine *Ferritin* expression across developmental stages and under various stress conditions and functional studies involved RNAi-mediated silencing of Ferritin transcription expression analysed with the help of real time polymerase chain reaction in different tissues and their effect on phenotype.

Results: Silencing of both genes using RNA interference (RNAi) led to severe reproductive impairment, including ovarian arrest in 50% of females, 40% reduction in oocyte number, and a decrease in first instar larval size. These outcomes correlate with increased reactive oxygen species (ROS) and altered serotonin receptor (5-HTR) expression in the brain, possibly driven by microbial Gut-Brain-Axis communication alteration due to disrupted iron metabolism. Additionally, we also report the discovery of a previously unknown mosquito gene encoding a hepcidin-like peptide (*AcHep*), expressed in the fat body.

Conclusions: This finding reflects the role of mammalian hepcidin, a central regulator of iron homeostasis, suggesting a conserved evolutionary mechanism. In summary, our research provides the first molecular proof and new conceptual understanding that iron metabolism disorders may affect mGBA communication and, in turn, reproductive outcomes.

Acknowledgement(s) and Funding: We would like to thank the ICMR-National Institute of Malaria Research insectary staff members for mosquito rearing. Laboratory work was supported by the ICMR Grant (Ref # VBD/NIMR/Intra/002-ECD-II). Pooja Yadav is the recipient of UGC fellowship (Ref # 191620022266). The funders had no role in study design, data collection and analysis, decision to publish, or preparation of the manuscript.

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Abstract No: SA-112

Addressing Antimicrobial Resistance: Challenges and Opportunities in Nursing Practice



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Introduction: Antimicrobial resistance (AMR) is a growing global health challenge that threatens infection prevention and treatment across healthcare systems. Nurses play crucial role in addressing AMR through infection prevention and control practices, patient education, and surveillance activities. Nursing care is influenced by knowledge, personal attitude and clinical practice that affect antimicrobial use, in the context of evolving healthcare demands and public health emergencies.

Methodology: PubMed was searched for the articles on Challenges and opportunities in nursing practices in the context of AMR in last 5 years. The articles relevant to topic were included for the synthesis of review. The article whose full text were freely available were included. It includes articles from everywhere. The settings include care homes, ICUs and hospital settings.

Findings

Challenges: The challenges that limit the effectiveness of nursing practices in addressing AMR, includes insufficient training, resulting in varied knowledge, attitude and practices among nurses and their decision-making. Staffing shortages and limited autonomy further constrain nurses' ability to adhere to infection prevention and control guidelines. System-level factors of inconsistent implementation of evidence-based policies. Pandemic and outbreaks disrupt AMR surveillance and alter prescribing practices, exacerbating resistance patterns and complicating stewardship efforts.

Opportunities: The opportunities to strengthen nursing contributions to AMR prevention, nursing education programs have demonstrated improvements in stewardship competencies and infection prevention practices. The implementation of evidence-based practices, such as optimized glove use and evidence-based care bundles. Advancements in surveillance systems, epidemiology, and machine learning offer innovative tools to support early detection of resistance patterns and informed decision-making. Strengthened interdisciplinary collaboration present additional opportunities to enhance AMR control efforts.

Conclusion: Addressing educational barriers while leveraging technological and policy-level opportunities is essential to enhance nursing contributions to AMR prevention. Empowering nurses is critical for improving antimicrobial use, patient safety, and global efforts to combat AMR.

Acknowledgement and Funding: The authors like to acknowledge ICMR- National Institute for Research in Bacterial infections. No Funding received.

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Abstract No: SA-113

Artificial Intelligence in Infectious Disease Research: An Analysis of Global Trends and Applications



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Introduction: Infectious diseases remain a major global health challenge demanding scalable, and accurate diagnostic solutions. AI is rapidly advancing healthcare through applications such as medical imaging, disease surveillance and predictive analysis; however, global research landscape of AI-driven diagnostics for infectious diseases remains insufficiently characterized.

Objectives: This study examines the global research trends, key contributors, and thematic shifts in the field of AI-driven diagnostics for infectious diseases.

Methods: Publications obtained from Web of Science database reveal an exponential growth with 5,465 publications from 2005 to 2024. The search included studies on human, animal, and environmental health using keywords related to infectious disease, machine learning and artificial intelligence. Bibliometric parameters like publication trends, prolific authors, and geographical distribution were assessed and core journals, institutions were identified. Keyword co-occurrence analysis highlighted major research themes. Analyses were conducted using pyBibX, bibliometrix, and VOSviewer to map collaborations and thematic areas.

Results: USA leads AI-driven infectious disease research, contributing 1,687 publications and 72732 citations, surpassing the combined contributions of China and India. The Chinese Academy of Science (China), University of Oxford (UK), and Harvard Medical School (USA) emerged as the top institutions. 'Scientific Reports' turned out to be the top journal with 157 publications followed by 'PLOS One' (144). Citation network analysis highlighted regional disparities, with low-income countries like Gambia and Mozambique underrepresented. Keyword clustering identified six key research themes, with machine learning as a central theme across diagnostics imaging, epidemiology modelling, outbreak surveillance, and drug discovery.

Conclusions: AI is transforming infectious disease research in healthcare, yet its significant contributions remain unevenly distributed. However, emerging collaborations in lower middle-income countries highlight the need for equitable AI adoption. Addressing these disparities in infrastructure, funding, technological and computational capability through global collaborations is important.

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Abstract No: SA-114

Prevalence of linezolid resistance among Multidrug-Resistant *Mycobacterium tuberculosis* isolates recovered from pulmonary tuberculosis patients in Uttar Pradesh, North India



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Drug resistant tuberculosis (TB) remains a major global health concern, with India accounting for highest (32%) global burden of the disease. Recently, BPaLM regimen has been introduced in India under National TB elimination Program (NTEP) for effective management of drug-resistance TB. Linezolid is the core component of BPaLM regimen. The resistance to linezolid has been reported in several countries, however information from India remain limited. This study aimed to investigate the frequency of Linezolid in clinical isolates of *Mycobacterium tuberculosis* from pulmonary tuberculosis patients in Uttar Pradesh, a high drug resistant-TB burden state in India**.** A total of 65 MDR-TB isolates recovered from sputum samples of pulmonary TB patients from various districts of Uttar Pradesh were included. All the MDR-TB isolates were processed to phenotypic drug susceptibility testing for linezolid at WHO defined critical concentration (1µg/ml) using MGIT 960 system. The results were compared with demographic data and analyzed statistically. Out of 65 MDR-TB isolates, 12 (18.46%) isolates were found resistant to linezolid. The prevalence of linezolid resistance was found higher among female patients (20%) compared to male (16%). Age-wise analysis revealed the high prevalence of linezolid resistance among patients with age group 25-35 years (26.6%) followed ≤ 25 years (20.83%) and >35 year (11.5%). The findings of the study demonstrated high prevalence of linezolid resistance among MDR-TB patients in Uttar Pradesh and highlight the need to strengthen routine drug susceptibility testing services for linezolid under the NTEP to ensure early detection and effective management of linezolid resistant TB cases in Uttar Pradesh, North India.

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Abstract No: SA-115

Development and Validation of High-Throughput TaqMan Probe-Based Multiplex qPCR Assays for Pathogen Monitoring in Laboratory Rodent Colonies



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Introduction: Laboratory rodents, particularly mice and rats, are essential models for biomedical research. The presence of viral, bacterial, or parasitic infectious agents can significantly impact experimental reproducibility, animal welfare, and research integrity. Routine health monitoring is therefore mandatory in accredited animal facilities. Traditional pathogen screening methods, such as serology, culture, or single plex PCR, are limited by throughput, turnaround time, and sensitivity. In this context, high-throughput TaqMan probe-based multiplex real-time PCR panels provide a robust platform for rapid, sensitive, and simultaneous detection of multiple rodent pathogens.

Objectives:

1. Design, develop, and validate a high-throughput TaqMan probe-based multiplex PCR panel for comprehensive health surveillance (viruses and bacteria) in mouse colonies.
2. Design, develop, and validate a high-throughput TaqMan probe-based multiplex PCR panel for comprehensive health surveillance (viruses and bacteria) in rat colonies.

Methods: The FELASA list of viral and bacterial pathogens for health monitoring in mice and rats will is being used to develop multiplex PCR panels (5 agents/panel) using TaqMan probes and oligonucleotide primers. The sensitivity and specificity will be assessed in silico and in vitro. The developed panels will be validated in a large cohort of rodent samples, evaluating its performance, sensitivity, and specificity.

Results: The development and validation of the proposed multiplex TaqMan probe-based qPCR panel is currently in progress, with optimization and performance evaluation studies underway.

Conclusion:

Development and validation of multiplex qPCR panels for comprehensive rodent colony surveillance. These assays will provide,

- Rapid and sensitive detection
- High specificity
- Scalable surveillance capacity
- Improved animal welfare and research reproducibility

Such diagnostic platforms are critical for modern SPF rodent facility management.

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Abstract No: SA-116

Uncovering Inhibitory Mechanisms of HIF-1α Signaling to Enhance Mesenchymal Stem Cell Efficacy in Myocardial Ischemia–Reperfusion Injury



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Introduction: Hypoxia-inducible factor-1α (HIF-1α) serves as a crucial regulator of cellular adaptation to low oxygen levels. However, limited information is available on the cardio-protective effects of hypoxia-responsive signaling during ischemia–reperfusion. This paradox implies the existence of inherent inhibitory mechanisms that restrict effective adaptation to hypoxia. Mesenchymal stem cells (MSCs) offer promising therapeutic potential for cardiac repair through paracrine effects, yet their survival and functional efficacy within the ischemic microenvironment remain suboptimal. Discovering regulatory checkpoints that hinder hypoxia signaling may open up new avenues to enhance stem cell-based cardiac therapies.

Objectives: This proposed study intends to examine the regulatory mechanisms that restrict functional HIF-1α signaling in hypoxic and ischemia–reperfusion and to investigate whether altering these mechanisms can enhance MSC survival and therapeutic capacity for myocardial repair. Finally, MSC will be delivered by intramyocardial route by direct injection into peri-infarct myocardium and intravenously for tail vein injection

Methods: Isolation, Culture, and Characterization of MSCs Derived from Mouse Adipose Tissue. Hypoxia will be induced by 1% O_2 and 5% CO_2 (in a modular hypoxia chamber). Then, the assessment of transcriptional activity of HIF-1 is being performed by quantitative real-time PCR (qRT-PCR) for the HIF-1 target genes VEGF, GLUT-1, LDHA, and PGK1.

Results: Mechanistic insights for hypoxia-induced protective signaling during myocardial ischemia–reperfusion. Identifying regulatory factors that diminish effective hypoxic adaptation and restrict MSC performance under ischemic stress, and mesenchymal stem cells (MSCs) as promising therapeutic potential for myocardial ischemia–reperfusion repair.

Conclusions: This proposed research aspires to deepen the understanding of inhibitory regulation within hypoxia-responsive pathways during myocardial ischemia–reperfusion. The insights obtained may contribute to the formulation of strategies aimed at enhancing endogenous cardio protection and refining mesenchymal stem cell-based therapeutic methods for ischemic heart disease.

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Abstract No: SA-117

Antiviral activity of bacteriocins against the dengue virus in different cell lines.



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Introduction: *Orthoflavivirus denguei* or dengue virus (DENV) with four distinct serotypes (DENV 1-4) belongs to the *Flaviviridae* family and is a threat for global health, affecting more than 100 million people annually. There is presently no approved antiviral treatment for DENV. However, some repurposed drugs and plant-derived molecules have been tested for antiviral efficacy. Bacteriocins a type of antimicrobial peptides produced by bacteria represent a promising alternative.

Objective: The purpose of the study is to assess how well bacteriocins supress the dengue virus in different cell lines.

Methods: In the present study, five bacteriocins were screened for their antiviral activity against DENV- 2 using Vero CCL-81 and Huh-7.5 cell lines. The cytotoxicity activity of all compounds was evaluated by 3-(4,5-dimethylthiazol-2-yl)-2,5-diphenyltetrazolium bromide (MTT) assay in both cell-lines, and the CC_{50} value were calculated. Primary antiviral screening of all compounds was performed under three treatment conditions (pre-, co- and post-treatment) in both cell lines. For compounds that exerted promising activity against DENV, dose-dependent studies were performed to calculate the IC_{50} values. Antiviral activity was screened using foci forming unit (FFU) assay.

Results: The results suggested that Nisin and Plantaricin-A showed >50% inhibitory activity against DENV under pre-treatment condition, with a selectivity index (SI) of 157.14 for Nisin.

Conclusion: Limited antiviral activity of Nisin and Plantaricin-A was observed against the DENV.

Acknowledgment and Funding: I would like to sincerely thank University Grant Commission (UGC), India, for their financial support. I would also like to thank ICMR-National Institute of Virology.

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Abstract No: SA-118

Coinfection Dynamics and Pathogenic Interplay between Parasitic Microorganisms and *Helicobacter pylori* for Unravelling the Complex Microbial Interrelationship



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Introduction: *Helicobacter pylori* is a highly prevalent gastric pathogen in developing countries, where enteric protozoan infections are also endemic. Although both organisms inhabit the gastrointestinal tract, they are generally studied in isolation. Evidence of faecal shedding of *H. pylori* suggests potential interaction with intestinal microbes; however, the biological consequences of *H. pylori*-parasite coinfection remain poorly characterized. Understanding such polymicrobial interactions is important for explaining variability in disease manifestations in endemic settings.

Objectives: This study aimed to investigate interactions between *H. pylori* and enteric parasites by detecting their co-occurrence in stool samples, establishing *in vitro* coculture models, and analysing transcriptional changes associated with coinfection.

Methods: Stool samples from patients with gastrointestinal symptoms were screened for *H. pylori* and enteric protozoan parasites using PCR-based assays. In vitro coculture experiments were performed to assess direct interactions between *H. pylori* and *Entamoeba histolytica*. Transcriptomic analysis was conducted to compare gene expression profiles under mono-culture and coculture conditions.

Results: *In vitro* coculture demonstrated that the presence of *Helicobacter pylori* modulated pathogenic traits of *Entamoeba histolytica*, including altered phagocytic activity compared to parasite-only cultures. Transcriptomic analysis revealed differential expression of genes associated with virulence and cellular uptake processes under coinfection conditions, indicating that bacterial interaction influences parasite pathogenic potential.

Conclusions: The findings indicate that interaction with *H. pylori* can modulate key pathogenic features of enteric parasites under *in vitro* coinfection conditions. Combined stool-based detection, coculture experiments, and transcriptomic analysis provide insight into pathogen–pathogen interactions within the gastrointestinal environment. These observations highlight the relevance of polymicrobial interactions in gastrointestinal infections, particularly in high-burden regions.

Acknowledgement: This work is supported by an ICMR grant. The authors gratefully acknowledge the Director, ICMR-NIRBI, for providing the necessary institutional facilities and administrative support to carry out this study.

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Abstract No: SA-119

Antiviral Activity of anti-psychotic drugs against dengue and chikungunya viruses



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Introduction: Dengue and chikungunya viruses transmitted by the bite of *Aedes* mosquitoes are a concern for the global public health. Infection with dengue virus (DENV) can lead to wide spectrum of clinical manifestations ranging from febrile illness to dengue shock syndrome (DSS), which is fatal. Similarly, infection with CHIKV leads to fever, rash and severe joint pain (arthralgia). Arthralgia may persist for months. Infection with these viruses will also lead to overlapping clinical symptoms that complicates clinical diagnosis. Currently, no approved antiviral drugs are available, and existing vaccines have notable limitations. Repurposing of drugs is a viable strategy to address this gap, as it can bypass preliminary phases in clinical trials

Objectives: In the present study, we evaluated 17 FDA approved anti-psychotic drugs for their antiviral potential against both DENV and CHIKV

Methods: The cytotoxicity of the drugs was investigated using MTT assay. The maximum non-toxic concentration of the drugs was used to screen the antiviral activity against DENV and CHIKV in Vero CCL-81 cells under pre, co and post infection treatment conditions

Results: Notably, Pimozide, a diphenylbutylpiperidine derivative, at a concentration of 3.125 µM demonstrated antiviral activity against DENV under post treatment condition. The EC50 value was 0.17 µM, with selectivity index of 72.

Conclusions: The results suggest that Pimozide can be exploited for treatment of DENV infection. However, further in-vivo studies are required and mechanism of action needs exploration.

Acknowledgements: I gratefully acknowledge the University Grants Commission (UGC) for awarding the fellowship that supported my research work.

I also express my sincere thanks to the National Institute of Virology (NIV) for providing funding support and necessary research facilities.

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Abstract No: SA-120

Detection of high-risk human papillomavirus using molecular assays.



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Introduction: Human Papillomavirus (HPV) is a sexually transmitted DNA virus with more than 450 types, with the high-risk types (such as HPV-16, HPV-18, and HPV-52 etc.) and the low-risk types (such as HPV 6, HPV 11 etc.). The common screening tests available in the past have been the Pap test, as well as the latest technological molecular based analysis.

Objectives: To detect HPV DNA and analyse its genetic diversity by PCR targeting of the L1, E6 and E7 genes.

Materials and methods: A total of 202 samples were collected from patients from NSCB Medical College, Jabalpur, India between March 2024 and October 2025, which were subjected to DNA isolation (QIAamp DNA kit), PCR amplification L1, E6, and E7 genes, and Sanger sequencing. Genotyping 48 samples has been completed so far in this ongoing work.

Results: Analysis with PCR showed that 15 samples out of 202 (7.4%) were positive for L1, and 23 samples (11.4%) were positive for E6 and 18 samples (8.9) were positive for E7. From sequencing, it was confirmed that 36 samples (75%) belonged to HPV 16, and 4 samples (8.3%) belonged to HPV 52. These are among the high-risk types of HPV that cause cervical carcinogenesis.

Conclusions: This study effectively detected and confirmed HPV-16 and HPV52 genotypes from clinical samples in central India. The inclusion of the L1 genes and along with the oncogenes E6 and E7 genes, increased molecular coverage and enhanced detection accuracy. This study also provides molecular evidence of the presence and distribution of high- risk HPV types in central India. Further, the friendly molecular test/POCT can make the screening more practical with widespread coverage in remote areas, thereby enabling timely detection and management of cervical cancer.

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Abstract No: SA-121

An AI-Driven Voice Assistance System to Improve Medication Safety in Visually impaired



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Introduction: Medication errors are a leading cause of preventable harm worldwide, especially among visually challenged and elderly populations. According to the World Health Organization (WHO), unsafe medication practices and medication errors cause at least one death every minute globally. In India, visual impairment affects nearly 5 million people, and millions more are elderly or illiterate, the simple act of taking medicines correctly becomes a daily challenge. Our proposal supports the Government of India's initiative, led by the CDSCO, to improve medication accessibility for visually impaired persons as per notification dated September 9, 2025 by the Central Drugs Standard Control Organization (CDSCO). Our project advances the national mandate for implementing Braille labelling validated by NIEPID, by integrating a digital accessibility layer through QR-coded prescriptions and AI-based voice assistance.

Objective: We propose an innovative, low-cost digital solution that integrates QR codes on medicine strips with an AI-based voice chatbot to deliver accessible, personalized medication guidance with the following objective of the study is to improve medication safety and accessibility for visually challenged using a QR code–based digital system.

Methods: We are developing a system based on a scalable Django-based backend with strong data security measures, the solution complements existing Braille labelling initiatives by adding a dynamic digital accessibility layer. An AI-based chatbot layer is integrated to enable natural language interaction, healthcare-specific queries and medication-related information.

Results: The AI chatbot interface allows users to repeat instructions on demand, reducing dependence on caregivers and minimizing anxiety associated with medication intake. Multimodal alerts (audio, vibration, visual) enhance usability across varying degrees of sensory impairment.

Conclusion: This AI-assisted QR-based medication support system has the potential to substantially reduce medication errors, improve adherence, and empower vulnerable populations, making it a strong candidate for large-scale deployment within India's evolving digital healthcare ecosystem.

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Abstract No: SA-122

Utility of Mathematical Models of Dengue Vaccination for Public Health Decision-making: Critical Elements and Evidence Gaps



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Introduction: Mathematical models of dengue vaccination need to integrate immunology and clinico-epidemiology with operational contexts, to generate evidence useful for policy-level decisions on optimal introduction and implementation strategies.
Dengue vaccine modelling is further complicated by spatio-temporal changes in circulating serotypes, and limited availability of approved vaccines, each with a unique profile. As the science of dengue vaccination evolves, models too must adapt to answer the key policy questions: "*who*, *where*, and *when* to vaccinate".

Objectives: To review the existing modelling evidence on dengue vaccines, and identify:
(a) critical elements (biological, operational, and economic) that might determine potential utility of models in informing public health policy; and
(b) evidence gaps in existing models.

Methods: A systematic search yielded 102 publications; 48 publications addressing the objectives were included in final analysis after screening.
We extracted data on biological, operational, and economic elements, and applied deductive thematic analysis techniques to identify:
(i) elements which were critical to determine clinical safety, population-level impact, operational feasibility and economic value of dengue vaccination; and
(ii) data requirements and areas where key model assumptions lacked supporting evidence.

Results: Over the years, modelling studies have identified and increasingly incorporated key elements that addressed clinical safety (dengue serostatus, antibody-dependent enhancement risk), and population-level impact (strain-specific efficacy, duration of protection), and assessed operational considerations (age-targeting, screening requirements, integration with vector control), and economic value (cost-effectiveness thresholds).
Models required high-resolution, age-stratified data on local seroprevalence, circulating serotypes and vector dynamics to inform locally-relevant, optimal vaccination strategies. Evidence gaps included comprehensive data on infectiousness of subclinical/asymptomatic cases, long-term immunity and waning, cross-virus interactions, and local/regional entomological and environmental heterogeneities.

Conclusions: Key elements and data requirements essential to inform safe and cost-effective public health policy were identified. These will be used while developing mathematical models of dengue vaccination specific to the Indian context.

Acknowledgement(s) and Funding (if any): ICMR-AcSIR Research Activity - Research Grant for PhD Work

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Abstract No: SA-123

Antimicrobial Resistance Patterns of Enteric Bacterial Pathogens Isolated from Acute Diarrhoeal Cases: Evidence from a Hospital-Based Surveillance System



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Introduction: Acute diarrhoeal diseases remain a significant public health concern, especially among children and vulnerable populations. Enteric bacterial pathogens are major causes, and rising antimicrobial resistance due to antibiotic misuse complicates treatment. This study aims to determine the prevalence and antimicrobial resistance patterns of enteric bacterial pathogens in hospital-based acute diarrhoeal cases.

Objectives: To estimate the prevalence of enteric bacterial pathogens among patients presenting with acute diarrhoeal disease at a paediatric tertiary care hospital

1. To determine the antimicrobial resistance patterns of the pathogens
2. To assess the antimicrobial susceptibility profiles of the isolates
3. To estimate the proportion of multidrug-resistant enteric bacterial isolates among the study population

Methods: Data were collected from indoor and outdoor patients (aged below 18 years) with acute diarrhoeal illness. Clinical samples were transported to the laboratory and analysed in collaboration with ICMR-NIRBI, Kolkata. Samples were processed using standard microbiological methods for isolation, identification, and antimicrobial susceptibility testing of enteric bacterial pathogens.

Results: A total of 364 patients presenting with acute diarrhoeal illness were included in the study. *Vibrio cholerae* was identified in 1.37% of cases. Among other bacterial isolates, non-typhoidal Salmonella (NTS) was detected in 3.84% of cases (n = 14). The most common serotypes were *Shigella sonnei Type II* accounting for 21% of cases, followed by *Shigella sonnei Type I* (14%).
Vibrio cholerae isolates showed the highest resistance to trimethoprim/sulfamethoxazole (100%), followed by streptomycin (80%) and cefotaxime (40%). Among NTS isolates, highest resistance was observed for ciprofloxacin (57%) followed by ofloxacin (42%), and ampicillin (36%).
MDR isolates were identified in 100% of the total enteric bacterial isolates.

Conclusions: These findings provide baseline data for a diarrhoeal disease database, support targeted patient care and preventive measures, and can inform future research and early warning systems for outbreak preparedness.

Acknowledgement(s): We are thankful to Dr. Dilip Kr Pal, Principal, DR BC Roy PGIPS for continuous support and cooperation.

Funding: Funding: ICMR-NIRBI, Kolkata Institutional Fund.

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Abstract No: SA-124

Determination of host preference in malaria vector an Anopheles culicifacies in Madhya Pradesh



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Background: The transmission of Malaria is strongly influenced by the host-feeding behaviour of mosquito vectors. *Anopheles culicifacies*, the principal rural malaria vector in central India, exhibits considerable variability in host preference across ecological settings. This study aimed to determine the host preference of *An. culicifacies* using PCR-based molecular techniques in a malaria-endemic tribal region of central India.

Methods: Wild caught Adult female *Anopheles* mosquitoes were collected from selected villages of Bihar CHC in Balaghat district, M.P using mouth aspirator in early morning hours from cattle shade(CS) and mixed dwellings in December 2024. Mosquito Specimens were morphologically identified to species level following WHO taxonomic key as *An. Culicifacies*. The genomic DNA was extracted from blood-fed mosquitoes using DNA extraction kit from Qiagen as per manufacturers' protocol. The extracted DNA was quantified and subjected to species-specific and multiplex PCR assays for detection of various vertebrate hosts DNA, including human, bovine, pig, dog, and chicken.

Results: PCR analysis demonstrated that 80% (n=50) of the examined mosquitoes had fed on human blood, indicating strong anthropophagic behaviour. Bovine blood meals were detected in 24% of samples, while no evidence of remaning hosts. The high presence of human blood meals indicates higher human–vector contact in the study area, consequently adding to malaria transmission.

Conclusion: Molecular analysis provides valuable insights into vector behavior and supports evidence-based malaria control planning in tribal and rural settings. The findings in our study demonstrate a marked preference of *Anopheles culicifacies* for human hosts in the study region, emphasizing the importance of human-cantered vector control interventions such as insecticide-treated nets and indoor residual spraying. Further, the sample size of the study is small therefore studies with large samples sizes are required for validation of results.

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Abstract No: SA-125

Exploring strategic interventions targeting antibiotic resistance from One-Health perspective



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Introduction: AMR is a difficult ecological problem. Close interaction between human, animal and environmental systems coupled with widespread use of antibiotics across domains call for integrated one-health approach. Traditionally strategies are mostly vertically aligned, which suit implementers at higher tiers. However, at ground level, the distinction between three systems is often blurred and fragmented efforts fail to have lasting impact.

Objectives: To explore the current landscape of one-health interventions aiming reduction in antibiotic resistance.

Methods: Literature search was undertaken in pubmed and clinical trials.gov databases. For Pubmed, MeSH term "One Health" and "drug resistance, bacterial" were used. For clinicaltrial.gov database "antibiotics" was used along with identifier like "animal", "environment" to look for ongoing interventions in one-health domain, as "One-health" terminology was not recognised by the website. The contents were analysed to understand the spectrum of interventions.

Results: The Pubmed search identified 20,311 hits with MeSH term drug resistance, bacterial and 1237 with One-health in last 5 years. But when combined, the yield is 198 and none of those was a clinical trial[1]. In clinical trials database of NIH, 49 intervention projects were registered on topics related to antibiotic usage among animal and environment. Interventions are varied, like drugs (20%), devices (20%), behavioural (16%) and specific procedures (4%) and multi-pronged (40%)[2]. However, projects are at different stages of implementation and results are awaited. Global agencies are encouraging implementation research for optimal use of antibiotics across sectors, robust surveillance and discovery of newer vaccines/diagnostics/drugs[3].

Conclusions: Global agencies are encouraging for greater investment in one-health based intervention to reduce antibiotic resistance, but till date, evidence from published literature on effective interventions is scanty. Ongoing studies with multipronged packages hold promise and locally optimised models should be tested in our country, too.

Acknowledgement(s) and Funding: ICMR intramural Ignition grant: INTR-IG-2025-00101 (ACsIR Reg No. 40MR24A81005)

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Abstract No: SA-126

Metabolic Syndrome in a Particularly Vulnerable Tribal Group: A Study among the Bharia Tribe of Chhindwara



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Introduction: Metabolic syndrome is a cluster of metabolic abnormalities that significantly increases the risk of cardiovascular diseases and type-2 diabetes mellitus. The syndrome includes hypertension, hyperglycemia, dyslipidemia, and central obesity. Traditionally considered a problem of urban populations, metabolic syndrome is now emerging among tribal and central Indian communities, undergoing rapid lifestyle transitions[1,2]. Studying the prevalence of metabolic syndrome in tribal populations is essential to understand disease burden and to guide targeted public health interventions.

Objective: To estimate the prevalence of metabolic syndrome among adults of the Bharia tribe population of Chhindwara district, Madhya Pradesh**.**

Methods: The present study is a community-based cross-sectional study conducted among 210 respondents belonging to the Bharia tribe of Chhindwara district, Madhya Pradesh, India. Villages were selected using cluster sampling (07 adults from 30 tribal dominated villages of Chhindwara), and respondents aged 18–65 years were selected through simple random sampling (after getting the list of eligible adults in selected villages, random number table were used). Metabolic syndrome was defined according to the National Cholesterol Education Program – Adult Treatment Panel III (NCEP ATP III) criteria. Data collection was carried out using the WHO STEP-wise approach to NCD risk factor surveillance questionnaire. Blood samples were collected for biochemical investigations including fasting blood glucose and lipid profile.

Results: The prevalence of metabolic syndrome among the Bharia tribe of Chhindwara district was found to be 7.61% in which males accounted for 4.29 % and females for 3.33 %. Among the components, central obesity and hypertension were the most commonly observed abnormalities. The findings indicate that metabolic syndrome is emerging as an important health concern among the Bharia tribal population.

Conclusion: These findings highlight the urgent need for early screening, culturally appropriate health education, and integration of non-communicable disease prevention strategies into tribal health programs**.**

Acknowledgements: The authors express their gratitude to the Director, ICMR-NIRTH, CO-PIs in project and NCD Division staff for their support.

Funding: This work was supported by the ICMR.

Abstract No: SA-127

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Tempo-spatial pattern and risk factors of Gender disparity in Infant and Child Mortality in India



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Introduction: India has made notable progress in child survival, yet it continues to record the highest number of under-five deaths globally. While male children are biologically more vulnerable to early-life mortality, persistent gender bias in India has resulted in excess female child mortality, particularly in northern states. Sex differentials in child mortality remain a key challenge for achieving gender equity and Sustainable Development Goal (SDG) targets.

Objectives:

- Tempo-spatial pattern of gender disparity in infant and under five mortality in India
- To assess the change in the risk of infant and under five mortality by gender in India

Data and Methods: The study uses data from three rounds of the National Family Health Survey—NFHS-3 (2005–06), NFHS-4 (2015–16), and NFHS-5 (2019–21). Infant and under-five mortality were examined across time and regions. Logistic regression analysis was employed to assess gender-specific mortality risks controlling for socio-economic, demographic, and maternal healthcare factors.

Results: Results indicate a substantial decline in child mortality over time. Under-five mortality declined from about 74 deaths per 1,000 live births in NFHS-3 to around 42 in NFHS-5, while infant mortality reduced from nearly 57 to 35 deaths per 1,000 live births. Despite overall improvement, regional disparities persist. Kerala exhibits consistently low mortality levels, whereas Uttar Pradesh, Bihar, and Chhattisgarh continue to face high mortality burdens. Gender gaps have narrowed nationally, but emerging female disadvantages in rural areas are evident. Maternal education and adequate antenatal care significantly lower mortality risks.

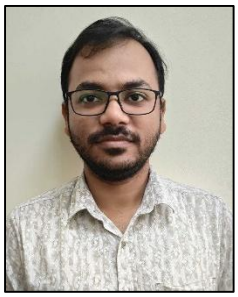
Conclusion: Focused investments in maternal and child healthcare, especially in rural and high-mortality states, alongside improved primary healthcare and family planning services, are essential to further reduce child mortality and address gender disparities.

Keywords: Infant mortality; Under-five mortality; Gender; NFHS

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Abstract No: SA-128

Access and utilization of Maternal and Child Health services during covid19 pandemic: Findings from Odisha, India



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Introduction: The COVID-19 pandemic disrupted essential health services globally, with maternal and child health (MCH) services particularly affected in low- and middle-income settings. Evidence is essential to understand service utilization patterns and health system responses during public health emergencies.

Objectives: The overall aim of this study was to assess and understand the status of maternal and child health (MCH) services during COVID-19 pandemic; barriers and challenges and thereby formulate a mitigation strategy for ensuring quality MCH care during a disease pandemic.

Methods: The study adopted a mixed-methods approach comprising four components: (i) a systematic review to identify challenges in provisioning and ensuring quality MCH services during the COVID-19 pandemic and similar health emergencies; (ii) secondary analysis of HMIS data to compare changes in key indicators between pre-COVID and COVID periods; (iii) qualitative inquiry through in-depth interviews and focus group discussions with MCH beneficiaries, community health workers, healthcare providers, and programme managers; and (iv) a quantitative assessment using structured schedules and Likert-scale questionnaires among antenatal and postnatal mothers.

Results: HMIS analysis indicated declines in several key MCH service indicators during the COVID-19 period, including full antenatal care coverage, TT booster coverage, institutional deliveries, postnatal home-based newborn care visits, immunization coverage, and family planning services. Early antenatal registration and safe delivery rates remained relatively stable. Primary data identified major barriers such as mobility restrictions, fear of COVID-19 infection, transport constraints, financial hardship, and diversion of healthcare workforce. Continuity of services was supported through community-based outreach, telephonic consultations, task shifting, and special service delivery sessions led by frontline health workers.

Conclusions: The pandemic adversely affected utilization of essential MCH services in Odisha; however, adaptive health system responses mitigated severe disruptions. Strengthening community-based service delivery, integrating telehealth approaches, ensuring uninterrupted emergency transport, and supporting frontline health workers are critical for improving MCH services during future public health emergencies.

Acknowledgements: ICMR-RMRC Bhubaneswar: Dr. Sanghamitra Pati, Dr. Subrata Kumar Palo, Dr. Bijaya Kumar Mishra, Dr. Srikanta Kanungo

UNICEF: Dr. Monika Nielsen, Dr. Meena Som, Dr. Brajesh Raj Merta, Dr. Soumen Ray
Department of Health and Family welfare Govt of Odisha
All the Participants of the study Project staff: Dinesh Bhuyan, Sumit Kumar Dash, Aparna Aparajita Dash, Kripalini Patel, Mili Sahay, Sapna Negi, Snehasish Tripathy, Sonam Karna, Shubhankar Dubey, Subhashree Panda and Subhralaxmi Dwivedy

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Abstract No: SA-129

Developing an integrated tiered Molecular Diagnostic and DST Framework for Nontuberculous Mycobacteria



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Introduction: The rising burden of nontuberculous mycobacterial infections[1] and their overlap with tuberculosis demands an accurate species-level diagnosis.[2] Conventional methods are non-specific, while line probe assays are costly and limited in resolving mixed, subspecies, or rare infections.[3] Predominantly non-Indian DST data is available, underscoring the need for region-specific evidence on drug susceptibility to guide NTM management in India. Standardisation of diagnostic methods and DST are the need of the hour.

Objectives: i) Standardisation of methods for species-level identification ii) precise detection of rare and mixed infections using NGS platforms iii) establish standardised DST for both clinical isolates and reference strains.

Methods: We collected NTM-suspected samples and performed PRA hsp65, LPA (GenoType CM/AS KIT), and NGS (both WGS and tNGS Deeplex Myc TB), to identify NTM species. Drug susceptibility testing was employed for NTM isolates using the Resazurin microtitre assay.

Results: PRAhsp65 provides cost-effective differentiation of TB and NTM and requires basic infrastructure, but has lower species-level resolution than LPA and NGS. Of 28 samples, this method identified 13 samples precisely, as confirmed by both LPA and NGS. LPA identified all samples, while NGS differentiates species and subspecies at the level of closely related NTM and in mixed infections. It also provides information for phylogeny and AMR determinants. But it requires specialised infrastructure, expertise and longer turnaround times. The initial setup cost is high. *M. avium* and *M. abscessus* clinical isolates exhibited resistance to most tested drugs. Most species were susceptible primarily to doxycycline, kanamycin, and clarithromycin.

Conclusions: This study establishes an integrated, tiered diagnostic framework combining hsp65 PCR–PRA and next-generation sequencing (NGS). PRA hsp65 serves as a first-tier method for TB–NTM differentiation, LPA as a second-tier tool for NTM species identification, and NGS for resolving rare or mixed infections. DST revealed that *M. avium* and *M. abscessus* clinical isolates were largely drug-resistant. Most of the other NTM species were susceptible to doxycycline, kanamycin, and clarithromycin.

Acknowledgement(s) and Funding: The authors thank ICMR, India for intramural funding and also ICMR–RMRCBB for providing infrastructure and laboratory facilities. We acknowledge our collaborating centres for their contributions to patient recruitment and sample referral.

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Abstract No: SA-130

Dietary Influence on Oral Microbial Taxa: Vegetarian vs. Omnivorous



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Diet is one of the major environmental determinants in shaping the human microbiome, which is crucial for maintaining both oral and systemic health. Variations in dietary habits, particularly vegetarian and omnivores diets, lead to differences in nutrient composition, substrate availability, and food texture, all of which can shape oral microbial communities. The present investigation explores the variation in salivary microbiome across distinct dietary patterns. The study relies on 16S rRNA sequencing analysis on oral saliva samples collected from vegetarian and omnivores individuals. The further QIIME2 pipeline was used to analyze the downstreaming processing, and taxonomic assignment was done by using the SILVA database. The result revealed that, at the phylum level, *Firmicutes* was the most dominant phylum, followed by *Bacteroidota, Proteobacteria, Actinobacteria* and *Fusobacteria*. While at the genus level, *Streptococcus* was predominant, followed by *Prevotella, Veillonella, Neisseria, Hemophilus, Rothia,* and *Fusobacterium,* and at the species level, *Streptococcus infantis* was the most abundant, followed by *Prevotella melaninogenica, Haemophillus parainfluenzae, Veillonella dispar, Streptococcus salivarius,* and *Prevotella nanceiensis.* Comparative analysis revealed that the genera *Actinomyces, Corynebacterium, Streptobacillus, Kingella,* and *Mogibacterium* were significantly enriched in the omnivorous group; however, at the species level *Schaalia odontolytica, Actinomyces viscosus, Prevotella salivae, Rothia dentocariosa, Actinomyces dentalis* were significantly enriched in the omnivorous group, while *Rothia aerie* was significantly enriched in vegetarians, indicating a diet-driven selection for nitrate-reducing taxa, which is important in promoting vascular homeostasis. The enrichment of *Actinomyces*, *Prevotella*, and *Corynebacterium* in the omnivorous group suggests that animal-derived substrates select for taxa associated with stable dental biofilms and a heightened potential for periodontal inflammation. Diversity indices showed significant differences in alpha and beta diversity between vegetarian and omnivores groups. This study identifies taxonomic groups that drive the associated shifts between the two different dietary patterns. Overall, the findings indicate the variation in the oral microbiome is influenced by dietary habits (vegetarian or omnivores lifestyle). This understanding may pave the way towards developing strategies to sustain healthy and resilient oral microbiota through dietary patterns.

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Abstract No: SA-131

Meta-analysis of Oral Microbiome Dysbiosis in Oral Potentially Malignant Disorders



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Oral Potentially Malignant Disorders (OPMDs) are a heterogeneous group of oral lesions with an increased chance of developing oral squamous cell carcinoma. Emerging studies suggest that dysbiosis of the oral microbiome leads to chronic inflammation and epithelial dysplasia and subsequently malignant transformation. This study is a meta-analysis using oral microbiome datasets sourced from PubMed, Google Scholar, Embase, and Web of Science. From seven research papers, eight raw 16s RNA sequences were processed using the QIIME 2 (v2024.10) pipeline. Quality filtering, denoising, and taxonomic assignment were performed using standard QIIME parameters and the SILVA database. Across the included studies, OPMD samples showed distinct microbial shifts as compared to healthy controls. At the phylum level, the enriched taxa *Proteobacteria*, *Firmicutes*, *Bacteroidota*, *Fusobacteriota*, and *Actinobacteriota* were shared between OPMD and healthy samples with differences in their abundance. Genus-level analysis revealed that the taxa *Streptococcus*, *Neisseria*, *Haemophilus*, *Fusobacterium*, and *Provetella* were enriched in OPMD patients as compared to the Healthy control. And species level analysis also showed the enrichment of *Streptococcus infantis*, *Haemophilus parainfluenzae*, *Neisseria perflava*, and *Prevotella melaninogenica*, in OPMD patients, whereas *Porphyromonas pasteri* in Healthy and *Streptococcus parasanguinis* in OPMD were uniquely present. Overall, OPMD dominated microbial shifts were observed which further led to inflammation and malignant transformation. The results highlighted unique taxonomic findings in OPMD, suggesting the role of oral microbiome dysbiosis in its development.

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Abstract No: SA-132

Developing a Respectful Maternity Care Tool: A Delphi Based Consensus Approach



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Introduction: Over the past two decades, there has been a surge in research on disrespect and abuse faced by women during childbirth. However, the knowledge generated in published literature indicates considerable variation in how mistreatment is defined and measured, with the current tools lacking the cultural depth and validation necessary for diverse settings.(Bohren et al., 2015)

Objective: To obtain expert consensus on the relevance and framing of questions intended to measure Respectful Maternity Care for our upcoming study using a Delphi approach.(Brown, 1968; Dalkey & Helmer, 1963)

Method: A two-round prospective Delphi study was conducted to develop a Respectful Maternity Care questionnaire through expert consensus. The panel comprised 30 participants, including researchers, obstetricians, and recently delivered women from public and private facilities. In Round 1, participants rated item relevance on a 9 point likert scale and provided qualitative feedback guided by a rights-based approach using Google Forms. Items rated 7-9 by more than 50% across all groups were retained. In Round 2, a Python based platform with graphical summaries of group responses alongside their previous scores to encourage convergence. Consensus was defined as ≥70% agreement (ratings 7-9) in at least two groups and <10% disagreement (ratings 1-3).

Result: Thirty participants completed Round 1 with a 100% response rate. All 67 items met the inclusion criteria, with over 50% of participants across all three stakeholder groups rating them between 7 and 9. Based on feedback, 41 items were rephrased. In Round 2, the overall response rate was 76%, with group-wise rates of 90%, 80%, and 60%. Using predefined consensus criteria, all 67 items achieved consensus in Round 2.

Conclusion: We have now developed a single, comprehensive tool with 67 questions across eight core domains. It clears up the previous inconsistencies in how respectful maternity care was tracked, giving us a reliable way to measure what true respectful maternity care means.

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Abstract No: SA-133

Analyses of the oral microbiome in OSCC patients using metaproteomics and Metagenomics reveal enrichment of pathobionts and abundance of immunosuppressive proteins



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Oral squamous cell carcinoma (OSCC), the most common malignancy of the head and neck region, develops due to a combination of genetic changes, environmental factors, and alterations in the oral microbiome. Recent evidence suggests that oral microorganisms play an important role in the development of OSCC. Metagenomics and metaproteomics are complementary approaches for characterizing the taxonomic composition and functional activity of oral microbial communities. The present study investigated the oral bacteriome from the saliva samples of oral cancer patients using a metagenomics approach based on 16S rRNA gene amplicon sequencing. Sequencing data were processed using the QIIME2 pipeline for quality control, sequence alignment, and taxonomic classification. Taxonomic assignment was performed using the SILVA reference database. Additionally, a metaproteomics approach was used in which LC–MS/MS data were analysed using UniPept to characterize the taxonomic composition and functional activity of the oral microbiome. A distinct bacterial community in OSCC was identified, which includes Firmicutes as the dominant phylum, followed by Bacteroidota, Proteobacteria, and Fusobacteriota. Predominant genera included *Streptococcus, Prevotella, Veillonella, Haemophilus* enriched in healthy groups while *Neisseria, Fusobacterium,* and *Capnocytophaga* dominant in OSCC groups. The species comprised of *Streptococcus infantis, Haemophilus parainfluenzae, Prevotella melaninogenica, Prevotella intermedia, Veillonella dispar* were enriched in the saliva of OSCC patients, whereas *Capnocytophaga sputigena, Neisseria perflava,* and *Actinomyces viscosus* were highly abundant in healthy groups. Metaproteomic analysis of saliva samples further identified a distinct OSCC-associated bacterial profile, with Bdellovibrionota as the most abundant phylum, followed by Mycoplasmatota and Bacteroidota. The genus included *Pelodictyon, Afipia, Staphylococcus, and Kosmotoga,* with notable species and strains such as *Clostridium perfringens, Mycobacterium tuberculosis,* and *Pelodictyon luteolum* DSM 273. Several identified taxa are linked to oral

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inflammation and carcinogenesis. The predominance of *Streptococcus* and *Prevotella* suggests roles in metabolic interactions and biofilm-driven chronic inflammation, while *Fusobacterium* and *Porphyromonas* are known to induce genotoxicity and activate pro-inflammatory pathways and promote tumor progression. The abundant immunosuppressive proteins (IgA1, IgA2, immunoglobulin superfamily member 3, immunoglobulin lambda variable 7–46, and neutrophil elastase) were identified in the patients. Overall, this investigation revealed distinct yet complementary OSCC-associated oral microbiome profiles and abundant immunosuppressive proteins in the patients are linked to OSCC progression The combined approach provides deeper insights into microbiome dysbiosis and its potential role in OSCC pathogenesis.

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Abstract No: SA-134

Prevalence Of Substance Abuse Among Tribal Population of Asia: A Systematic Review and Meta-Analysis



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Introduction: Substance abuse has emerged as a significant public health concern across Asia. Studies suggest that substance use rates are disproportionately higher among indigenous populations compared to their non-indigenous counterparts. Asia is home to world's largest population of indigenous and tribal peoples.

Objectives: This review aims to identify and synthesize relevant literature on the prevalence of substance abuse among indigenous populations in Asia and provide a pooled prevalence estimate for these communities.

Methods: A comprehensive systematic search was conducted across PubMed, EMBASE and Google Scholar, encompassing all available literature from inception until April 20, 2024. The eligibility Criteria were structured using the CoCoPop (Condition, Context, Population) framework with the Condition defined as Substance Abuse, Context as Asia and the population as tribal communities. The methodological quality of each study was assessed using JBI's critical appraisal tools and meta-analysis was performed using MetaXL.

Result: A total of 35 studies with significant data were included in the systematic review. Meta-analysis was conducted on a subset of 20 studies that reported the prevalence of overall substance abuse. Additionally, 12 studies provided data on alcohol use prevalence, 12 studies on smoking prevalence, and 6 studies on the prevalence of smokeless tobacco use. Pooled prevalence of overall substance abuse, alcohol, smoking and smokeless tobacco was found to be 53%, 35%, 29% and 53% respectively.

Conclusion: Targeted interventions are required to address the high prevalence of substance abuse among indigenous populations in Asia. This requires a collaborative effort from policymakers, healthcare providers, and community leaders to ensure that interventions are accessible, culturally sensitive and tailored to the specific needs of indigenous populations.

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Abstract No: SA-135

Emerging Resistance in Colistin and mcr Gene Distribution in Gram-Negative Bacteria from a Tertiary Care Hospital in Odisha, India



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Introduction: Due to the misuse of antibiotics, the incidence of multidrug resistant gram-negative bacteria is increasing rapidly, limiting the treatment choices leading to dependence on colistin again. This further increases the prevalence of resistance in colistin which is known as the last resort of antibiotics in clinical samples.

Objective: This study aimed to determine the prevalence rate of colistin resistance among gram-negative bacteria isolated from clinical samples. And also, to evaluate their antimicrobial susceptibility patterns.

Methods: The work was carried out during 2024-25 on 366 isolates obtained from SUM Hospital, Bhubaneswar. The isolates were identified by biochemical test like IMVIC. Antimicrobial susceptibility was checked by Kirby Bauer disc diffusion with colistin 10-50µg disks, following CLSI guidelines, and mcr-1 to mcr-9 genes were detected by PCR and gel electrophoresis.

Results: The predominant bacteria isolates were *E. coli* (36.88%) and *K. pneumoniae* (19.67%), while the highest rate of colistin resistance was in *K. pneumoniae* (59.72%), followed by *P. aeruginosa* (29.62%) and *E. coli* (8.14%). The multiple mcr genes were detected in *K. pneumoniae*, *E. coli*, and *A. baumannii*.

Conclusion: The present study emphasizes the increasing detection of colistin, as well as multidrug-resistant gram-negative organisms, in the region of Odisha, India. Ongoing surveillance is imperative to inform clinical case management and foster targeted public health interventions.

Acknowledgements: This work is part of the PhD thesis in Biotechnology of Ms. Shreya Singh at SOA University (PhD Registration No. 2381611018). The authors sincerely acknowledge the Dean (Research), SOA University, for providing academic support and research guidance. The authors are also grateful to the Director, ICMR–Regional Medical Research Centre (RMRC), Chandrasekharpur, Bhubaneswar–751023, Odisha, India, for providing the necessary laboratory facilities, infrastructure, and technical support to carry out this research.

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Abstract No: SA-136

ISSR-PCR Based Molecular Surveillance of Multidrug-Resistant Bacteria from Street-Vended Foods and Evaluation of *Costus igneus* as a Natural Antibacterial Alternative



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Introduction: The emergence of antimicrobial resistance a problem that has been worsening rapidly remains a critical threat to global public health, especially in developing countries where food hygiene, as well as sanitary conditions, are often inadequate. Vended foods are a potential source of MDR bacteria and help in their spread to humans. This has created a growing interest in the use of plant-derived antimicrobials.

Objectives: The objectives of this study were to isolate and identify MDR bacterial isolates from street-vended panipuri in Bhubaneswar, Odisha; to determine their antimicrobial resistance pattern and diversity by ISSR-PCR; and to test in vitro antibacterial efficacy of *Costus igneus* extract against relevant MDR gram-negative bacteria.

Methods: A total of 100 samples of panipuri was obtained from roadside vendors. Routine biochemical examinations and antimicrobial susceptibility testing was performed. Genetic diversity of MDR strains was demonstrated using ISSR-PCR coupled with dendrogram and principal component analysis. The antibacterial potential of *C. igneus* was assessed employing the techniques of agar well diffusion, minimum inhibitory concentration using the broth microdilution technique, minimum inhibitory concentration (MIC) and minimum bactericidal concentration (MBC).

Results: The bacterial contaminants were found 92% and leading to the yield of 187 isolates. High resistance was observed for ampicillin, cefixime, and azithromycin, where $bla_{CTX\text{-}M}$ gene were detected in some of the isolates. High degree of genetic diversity was implicated by ISSR-PCR, implying that there were many sources of contamination. *C. igneus* extract demonstrated broad-spectrum antibacterial activity (MIC: 0.9–7.5 mg/mL) showing strongest effects against *Acinetobacter*, *Pseudomonas aeruginosa*, and *Klebsiella pneumoniae*.

Conclusions: Street foods have become a source harbouring these bacteria, which can be said to be genetically diverse and multidrug-resistant. Therefore, this situation demands urgent interventions using a 'one-health' approach. Moreover, the significant antibacterial activity shown by *C. igneus* indicates its potential as a non-conventional antimicrobial agent.

Acknowledgement(s): This work is part of the PhD thesis in Biotechnology of Ms. Alisha Sinha at SOA University (PhD Registration No. 2381611006). The authors sincerely acknowledge the Dean (Research), SOA University, for providing academic support and research guidance. The authors are also grateful to the Director, ICMR–Regional Medical Research Centre (RMRC), Chandrasekharpur, Bhubaneswar–751023, Odisha, India, for providing the necessary laboratory facilities, infrastructure, and technical support to carry out this research.

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Abstract No: SA-137

Molecular Identification and Antifungal Susceptibility Profiling of *Candida* Species from Vaginal Infections with PCR-Based Detection of Resistance Genes



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Background: Vulvovaginal candidiasis (VVC) is a prevalent fungal infection in women of reproductive age. *Candida albicans* has been the primary cause of this infection for many years, but lately, a rise in non-albicans *Candida* infection from *C. glabrata* and *C. tropicalis* has been documented. The main problem with non-albicans *Candida* infection is that it presents a certain level of resistance to commonly applied treatment agents.

Objectives: The aim of this study was to identify the distribution of *Candida* species involved in VVC, determine antifungal susceptibility pattern, and detect antifungal resistance genes by using PCR and to study their relation with phenotypic resistance.

Methods: The samples were collected from 900 symptomatic patients attending the tertiary-care hospital in Odisha, India. These samples were cultured on Sabouraud Dextrose Agar (SDA) and Candida Differential Agar (CDA). Preliminary identification by gram staining and colony morphology was performed. Antifungal susceptibility testing was done by a disk diffusion method using nine antifungal agents as per CLSI guidelines. PCR was performed to detect ten antifungal resistance genes in *C. tropicalis* and *C. glabrata* isolates. Gene functions were analysed by KEGG pathway analysis.

Results: Out of a total of 900 samples, *Candida* growth was seen in 500 samples (55.5%). The common species of *Candida* were *C. albicans, C. glabrata, C. tropicalis*, etc. The sensitivity of nystatin was high, at 83.21%, but resistance to azoles, particularly in *C. glabrata* and *C. tropicalis*, was observed. Through PCR, all resistance genes such as CDR, PDH, CgAqR, CDUr were frequently amplified, found particularly in NAC.

Conclusion: The rise of antifungal-resistant NAC species in VVC shows the need to combine molecular diagnostics with antifungal susceptibility testing for effective and focused treatment.

Acknowledgement: This work is part of the PhD thesis in Biotechnology of Ms. Utkalika Mallick at SOA University (PhD Registration No. 2381611022). The authors sincerely acknowledge the Director, ICMR–Regional Medical Research Centre (RMRC), Bhubaneswar for providing the necessary laboratory facilities, infrastructure, and technical support to carry out this research and Dean (Research), SOA University, for providing academic support and research guidance.

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Abstract No: SA-138

Integrated Molecular Surveillance and Eco-Friendly Control of Aedes Mosquitoes: Detection of Dengue Virus Serotypes and Evaluation of Plant-Based Biopesticides in Bhubaneswar, India



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Introduction: The dengue virus (DENV), which is mostly spread by *Aedes* mosquitoes, is a serious public health concern. For the early detection and management of outbreaks, early identification of viral circulation within vector populations is essential. At the same time, the growing resistance to synthetic insecticides emphasizes the need for environmentally friendly, sustainable mosquito control methods.

Objective: This study aimed to (i) detect circulating DENV serotypes in *Aedes* larvae collected from Bhubaneswar, and (ii) evaluate the larvicidal, pupicidal, and adulticidal efficacy of selected plant extracts against *Aedes* mosquitoes.

Methods: 8,257 *Aedes* larvae were gathered from 60 sites and combined into 390 groups. A pan-dengue test was used to extract viral RNA, which was then subjected to real-time PCR and serotype-specific RT-PCR (DENV-1–4). In parallel, Soxhlet extraction was used to prepare plant extracts of *Vitex negundo*, *Clerodendrum viscosum*, *Callistemon citrinus*, *Acorus calamus*, *Nyctanthes arbor-tristis*, *Lantana camara*, and *Salvadora persica* using various solvents. Larvicidal bioassays were performed in accordance with WHO guidelines to determine the values of LC_{50}, and LC_{90}.

Results: 60 out of total 390 pools tested positive for DENV, with DENV-1 predominating throughout the year and DENV-2 co-circulating during the wet season. In places like Dashpur and Acharya Vihar, low Ct values (20–25) suggested a high viral load. *C. citrinus* aqueous extract demonstrated the strongest dose-response correlation ($R^2 > 0.98$) and the best efficacy across extracts (LC_{50}= 29.31 ppm; LC_{90}.= 158.49 ppm).

Conclusion: This integrated surveillance and control method emphasizes the dual value of larval DENV monitoring and plant-based biopesticides. Together, they help achieve the SDG targets for sustainability and health and promote environmentally sustainable vector management within the One Health framework.

Acknowledgement: This work is part of PhD thesis in Biotechnology of Miss Aditi Pal at SOA University (PhD Reg. No 2381611004). The authors are grateful to Director, ICMR-RMRC, Bhubaneswar for the extended facility in research and Dean Research, Siksha 'O' Anusandhan (Deemed to be University), Bhubaneswar.

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Abstract No: SA-139

The Gendered Burden of Care: Experiences of Female Family Caregivers in Sickle Cell Disease and Thalassemia



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Introduction: Sickle Cell Disease (SCD) and Thalassemia are chronic genetic blood disorders with severe health conditions that require regular treatment, long-term management, and continuous care (Bernell et al., 2016). The care burden is primarily managed by informal family caregivers (Mumuni et al., 2023). According to the Centres for Disease Control and Prevention (CDC), the statistics show that around 58% of family caregivers are women. Global evidence shows that there is a gendered burden in caregiving responsibility (Besser et al., 2020; Hoyt et al., 2024).

Objective: To understand the experience of gendered caregiving burden among primary informal female family caregivers in SCD and Thalassemia

Method: A qualitative study was conducted using in-depth interviews with female-caregivers aged 15-65 years in selected hospitals in Bhubaneswar, Odisha. Participants were recruited through purposive sampling. Interviews were transcribed and analysed using thematic analysis.

Results: A total of 28 female-caregivers participated, including caregivers of individuals with SCD(n=13) and Thalassemia(n=15). Six major themes emerged from the study: daily caregiving routines and exhaustion; changes in family roles and social relationships; lack of social and institutional support; emotional challenges; stigma and social judgment; caregiving impacts on education and work. Most caregivers were mothers(90%), followed by sisters(8%) and grandmother(2%). Participants belonged to Scheduled Tribes(n=8), Scheduled Castes(n=11), Other Backwards Classes(n=7), and General(n=2). Most participants were from low-income households (≤₹15,000/month) with low educational attainment. Factors like younger patient age, smaller household size, availability of family support, disease-related knowledge, and caregiving experience affected the caregiving burden.

Conclusion: This study provides an in-depth understanding of women carrying the major caregiving burden in chronic genetic blood disorders such as SCD and Thalassemia in India. There is a need for a policy framework for protecting the well-being of the caregivers engaged in such chronic disease care. This will also have a positive influence on the long-term health outcomes for the patients.

Acknowledgement(s): We sincerely express our gratitude to all the caregivers for generously sharing their time, experiences, and insights, which made this research possible. Their invaluable contributions provided essential perspectives that deepen understanding of caregiving experiences and will help inform efforts to address the challenges faced by caregivers.

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Abstract No: SA-140

Whole Genome Sequencing and Genomic Characterization of Dengue Virus Circulating in Odisha during 2024–2025



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Introduction: Genomic characterisation of circulating dengue virus (DENV) lineages across serotypes is crucial for understanding their molecular evolution, effective disease management, and vaccine development. This study focuses on the lineage distribution, evolutionary patterns, and mutations of DENV circulating in Odisha from 2024 to 2025.

Materials and methods: Serotype-positive dengue samples confirmed by multiplex real-time RT-PCR (DENV1 n=37, DENV2 n=97, DENV3 n=6) were subjected to WGS using the Oxford Nanopore Mk1C platform. Base calling and variant calling were conducted, and analysis was performed using the Commander-NGS software. Reads were mapped to reference genomes using minimap2, followed by variant calling and consensus sequence generation using the Samtools & Bcftools, annotated with SnpEff. Lineages and phylogenetic analysis were performed using Nextclade and Dengue virus typing tool. FASTQ files were submitted to GISAID EpiArbo™, and mutations were detected using Dengue Server.

Results: Phylogenetic analysis of 33 DENV-1 samples revealed that 7 samples belonged to DENV-1 genotype III_A and 26 samples from genotype III_A.3 lineage. Several key mutations associated with virulence and antigenic drift were identified mainly in envelope (E) gene (K204N, S305P, T473A, D37N, T88A, and I114L) and NS2B gene (K55R and I106V).

Similarly, among 92 DENV-2 samples, 79 were identified as genotype II_F.1.1 and 6 as genotype II_F.1.1.5. Mutations suchas Q52H, M6I, E71A, R120T, V129I, H149N, I164V, I322V in E gene and F112L, L52X, and T244A in NS4B gene were found in DENV-2 strains which are associated with virulence, antigenic drift, reduced cytopathic effects, and the generation of a novel N-glycosylation site. In case of DENV-3, 5 samples were classified as genotype III_B.3, and 1 sample was III_B.3.1 and mutations in the envelope protein (K128R, A219T, and V158I) as well as in NS4B and NS5B (I115V, M151I, S157P, and F160Y) were observed that linked to altered infectivity and virulence.

Conclusion: The study provided useful insights into evolutionary dynamics of the Dengue virus circulating in Odisha and highlighted the functional importance of key gene mutations in lineages. Continued genomic surveillance is essential for tracking the evolution of emerging variants, enabling early detection and supporting vaccine development.

Acknowledgement:

1. Team VRDL, ICMR - RMRC Bhubaneswar, 2. NVBDCP, 3. DHR-ICMR

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Abstract No: SA-141

Evaluating the gut-brain axis in parkinson's disease: integrating clinical non-motor symptoms with microbiota



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Parkinson's disease (PD) is a progressive neurodegenerative disorder characterized by dopaminergic neuronal loss and α- synuclein aggregation along with motor and non-motor symptoms. Emerging evidence suggests that bidirectional communication of the gut-brain axis plays a crucial role in PD pathogenesis. This case control study evaluates the frequency, type, and severity of NMS and their correlation with gut health of the patients diagnosed with PD.

A total of 50 patients have been recruited to date. Clinical assessment utilized validated tools: MoCA, HAM-A, HAM-D, PD-NMS, MDS-NMS, and PDQ-39. Additionally, dietary and medication histories were recorded, alongside assessments for constipation scores, pesticide exposure, and previous head trauma etc. To investigate the gut microbiome, stool samples were collected for 16S rRNA sequencing via the Oxford Nanopore MinION MK1C platform for long reads and Ion Torrent for short reads. Alpha and beta diversity indices, taxonomic composition, and differential abundance analyses will be performed. Additionally, serum biomarkers for gut inflammation and permeability (calprotectin and zonulin) will be assessed using ELISA.

Preliminary data indicate an average disease onset between 50–70 years, with 5% of cases being early-onset. Notable environmental and gastrointestinal factors include pesticide exposure (30%) and constipation (45%). Autonomic NMS were prevalent: urinary urgency (62%), weight loss (29%), swallowing difficulties (25%), and bowel incontinence (12%). Psychological and cognitive burdens were high, with 63% reporting low mood, 58% reporting memory recall issues, and 38% experiencing anxiety.

The high prevalence of gastrointestinal and psychological symptoms supports the hypothesis that NMS may precede motor dysfunction. These findings aim to identify specific microbial and biomarker signatures, potentially offering a pathway for early detection and novel therapeutic interventions targeting the gut-brain axis.

Funding- Department of Health Research

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Abstract No: SA-142

Childhood Immunisation in India During COVID-19: An Interrupted Time Series Analysis of Health Management Information System (HMIS) Data



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Introduction: During and after the SARS-CoV-2 (COVID-19) pandemic, many countries experienced a decline in child immunisation rates that has not fully returned to pre-pandemic levels.

Objectives: This study utilises routine Health Management Information System (HMIS) data to estimate variability in post-pandemic recovery of child immunisation services in India.

Methods: Secondary data on childhood immunisation indicators for infants under 12 months of age were extracted from the Health Management Information System (HMIS) and analysed using an interrupted time series design and linear generalised estimating equations. To assess the impact, two time periods were considered: pre-COVID from April 2017 to February 2020 (35 months) and the COVID period from March 2020 to May 2021 (15 months). The relative percentage change of the observed child immunisation indicator from the expected child immunisation indicator volume for March was assessed and compared.

Results: The study observed a substantial decline in childhood vaccination coverage during the COVID-19 pandemic. The largest decline occurred in April 2020, and while rates improved afterwards, they remained below pre-pandemic levels. Notable reductions were seen in OPV and Pentavalent vaccines, with declines of up to 43% and over one-third, respectively. IPV doses fell by up to 42%, and Rotavirus vaccine coverage dropped by up to 36%. The MR-1 vaccine experienced a reduction of up to 41%, and the number of fully immunised children decreased by nearly 50% during the second and third quarters of 2020.

Conclusions: This study reveals significant declines in children's immunisation in India during the early stages of the COVID-19 pandemic.

Acknowledgement(s) and Funding: The authors acknowledge the Indian Council of Medical Research (ICMR), Delhi, for providing financial assistance for the study. The study is funded by the Indian Council of Medical Research, New Delhi, India.

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Abstract No: SA-143

Identifying Latent groups within rural populations and exploring their phenotypic differences in relation to infant mortality rate



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Introduction: The Infant Mortality Rate (IMR) is a critical indicator of public health, reflecting complex interactions among various socio-economic factors. While the rural–urban divide is generally used to explain disparities in infant survival, it often overlooks intra-regional heterogeneity. Households differ in economic standing, education, and access to health services, which creates distinct profiles that shape infant health outcomes. Identifying latent household-level groups can provide insight into how the risk for infant mortality is distributed across the rural population.

Objectives: The objective of this study is to identify potential latent groups within rural households in terms of infant mortality rate outcomes.

Methods: The study utilized data from the National Family Health Survey (NFHS-5), which provides nationally representative information on demographic, socioeconomic, and health indicators of women and children in India. Latent Class Analysis (LCA) was employed to identify unobserved, homogeneous household-level subgroups.

Results: The LCA identified five distinct latent household clusters within the rural population, each exhibiting a unique risk profile. The analysis revealed that "High-Risk" clusters were characterized by low maternal education, poor sanitation, and low income, correlating with significantly higher infant mortality rates. Conversely, "Low-Risk" clusters demonstrated that improved socioeconomic standing and maternal health literacy provided a protective effect.

Conclusions: The rural-urban binary provides an incomplete picture for understanding infant survival. This study highlights the necessity for interventions to prioritize high-risk socio-environmental profiles, focusing on maternal education and environmental health to effectively reduce infant mortality.

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Abstract No: SA-144

Infertility care pathways and lived experiences of care seekers in Tamil Nadu: A rapid qualitative analysis



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Introduction: Infertility is a concern in public health worldwide and is more common in couples in low- and middle-income countries, where access to fertility care is limited.[1-2] In India, the fertility care system is mainly in the private sector, resulting in high out-of-pocket expenditure, treatment abandonment, and economic burden on couples.[3]

Objectives: To explore the experiences of care seekers with infertility, treatment pathways, access to care, and perceived gaps in fertility care provision in the public health system in Tamil Nadu.

Methods: We conducted a rapid qualitative analysis using framework-based synthesis of in-depth interviews of 17 infertile care seekers from the Chennai and Kanchipuram districts of Tamil Nadu. The transcripts were analyzed using a structured matrix approach over pre-defined domains of treatment pathways, cost, social and family experiences, awareness of public services, perceived quality of care, distress, and expectations. Data synthesis was carried out by cross-case pattern analysis and domain comparison.

Results: Participants reported prolonged and fragmented treatment journeys, mainly in the private sector, involving repeated testing, multiple treatment changes, and discontinuation due to financial constraints. Treatment-related costs led to long-term economic hardship. Awareness of government infertility services remained low, and referral pathways to public facilities were negligible. Social experiences involved stigma, family pressure, relationship conflict, social isolation, and gendered attribution, intense emotional dependence on spouses and religious beliefs. Care seekers identified a specific need for government-based fertility services, including intra-uterine insemination and in vitro fertilisation, counselling, fertility education, and decentralised referral systems.

Conclusions: Infertility care among care seekers in Tamil Nadu is shaped by structural exclusion from affordable services, limited public-sector integration of fertility care, and heavy financial and psychosocial burdens. Strengthening public-sector infertility services, increasing community-level awareness, integrating psychosocial support, and establishing clear referral pathways are essential to reducing inequities and improving access to ethical, affordable fertility care.

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Abstract No: SA-145

Development of a *novel* Direct Drug Susceptibility Testing Protocol for *M. tuberculosis* Using Phage Lysin: A Pilot Study



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Introduction: Liquid culture and drug susceptibility testing (DST) of *Mycobacterium tuberculosis* (MTB) using conventional methods typically require a turnaround time (TAT) of approximately 30 days. A pilot study was conducted using phage lysin as an antimicrobial agent, on smear positive direct sputum samples for DST of MTB in an attempt to reduce the TAT using MGIT 960 instrument.

Objective: To evaluate the utility of using phage lysin as an antimicrobial agent on smear positive direct sputum samples for DST using MGIT 960 instrument for reduction of TAT

Methods: A total of 12 DSTs to MTB for rifampicin and isoniazid were conducted on smear-positive direct sputum samples using the phage lysin. A pinch of N-acetyl-L-cysteine (NALC) was added to facilitate homogenization of the samples. Each specimen was diluted at a ratio of 1:2 for the test samples and 1:200 for the control. The diluted samples were inoculated into MGIT tubes supplemented with OADC and phage lysin, following which the tubes were loaded into the MGIT 960 instrument for incubation.

Results: Drug susceptibility testing results for all 12 samples were available within an average of 12 days. All samples were found to be sensitive to both rifampicin and isoniazid. The DST results obtained using phage lysin were fully concordant with those received by standard DST performed on MTB culture isolates.

Conclusion: Promising results have been obtained in this pilot study when DST was performed using phage lysin on smear positive direct sputum samples. The results are in concordance with the results obtained using standard DST protocol. There was a reduction in TAT up to 15-17 days. We plan to extend this study further with a larger sample size in order to be able to define the phage lysin DST protocol with better clarity

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Abstract No: SA-146

Advanced HIV disease and associated factors among HIV infected individuals registered in a programme clinic at Pune: a retrospective study



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Introduction: WHO defines advanced HIV disease (AHD) as CD4 cell count <200cells/mm^3 or WHO stage 3 or 4 in adults and adolescents [1]. People with AHD are at significantly higher risk of tuberculosis (TB) co-infection, severe clinical disease, and mortality [2].

Objectives: This study aimed to assess the proportion and factors associated with advanced HIV disease among newly registered HIV infected individuals in a programme clinic at Pune.

Methods: This secondary data analysis was conducted among HIV infected individuals, registered between January 2017 and August 2025. A binary logistic regression model assessed the associated factors of advanced HIV disease. Odds ratios (OR) with 95% confidence intervals (CI) were reported.

Results: Among 765 registered individuals, 355 (46.1%) were females and 639 (83.1%) were literate. Their median age and CD4 count were 40 years (IQR:31-47) and 223 cells/mm^3 (IQR: 100-401) respectively. Half of the HIV infected individuals, 390 (50.9%) presented with advanced HIV disease. Age above 40 years (OR = 1.80; 95% CI: 1.35–2.40), having weight ≤55 kg at ART registration (OR = 2.33; 95% CI: 1.74–3.12) and HIV viral load (VL) greater than 1000 copies/ml (OR = 1.88; 95% CI: 1.05–3.37) (median duration of VL: 12 months) were factors significantly associated with AHD. The overall mortality among the HIV infected individuals was 13.2% as compared to 19.5% among individuals with advanced HIV disease.

Conclusions: Proportion of advanced HIV disease is high despite treat all strategy. Studies to identify reasons and design interventions to prevent advanced HIV disease will be very crucial to reduce mortality and associated opportunistic infections. Promoting early HIV testing, rapid ART initiation, strong retention, adherence support, health system strengthening, and community engagement will reduce stigma and improve access to timely care and management among HIV infected individuals.

Acknowledgement: The authors acknowledge the support of Care, Support and Treatment (CST) division of National AIDS Control Programme, CST officials at the Maharashtra State AIDS Control Society and staff of NARI ART centre. Authors sincerely thank the Director, ICMR-National Institute of Translational Virology and AIDS Research for support and acknowledge people living with HIV attending NARI ART centre.

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Abstract No: SA-147

Are hemoglobinopathies important contributors to anemia during pregnancy in Assam? Insights from an observational study in a population-based cohort



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Introduction: Anemia during pregnancy is a major public health problem in Assam, and the most important determinant for adverse pregnancy outcomes. Despite policy interventions (*viz.*, iron-folic acid supplementation and anti-helminthic medications), burden of anaemia during pregnancy is considerable in Assam. The current study examines the role of hemoglobinopathies in this context.

Objectives: To determine the association of hemoglobinopathies with anemia during pregnancy in Assam.

Methods: A community-based study was conducted in the catchment area of MRHRU Assam. Overall, 429 pregnant women were enrolled. They underwent blood tests for anaemia (through complete blood counts in hematology analyzer), status of iron and folic acid (through serum ferritin and folate immunoassays), inflammation (through serum CRP and α-1-acid glycoprotein nephelometric assays), and hemoglobinopathies (through HPLC). Further, stool specimens were examined for helminthiasis. Role of various etiologies in relation to anemia were investigated using univariate and multivariate approaches. A two-sided $P < 0.05$ threshold was applied for statistical significance.

Results: Anemia was detected in 75.3% pregnant women, out of which nearly half were of moderate-to-severe intensity. Mean hemoglobin levels were 10.2±1.1 mg/dL. Commonly implicated anemia etiologies, *viz.*, iron deficiency, folate deficiency, and helminthiasis were present in 27.6%, 15.6%, and 2.7% pregnant women, respectively. Besides, hemoglobinopathies were detected in 27.2% participants. These included various defects such as HbE-trait, HbE-disease, sickle cell trait, sickle cell disease, and β-thalassemia trait. Distribution of these genetic disorders exhibited ethnicity-specific segregation. Hemoglobinopathies predicted hemoglobin concentrations and anemia status in statistically significant manners ($P < 0.01$ and < 0.05, respectively), even after accounting for other covariates.

Conclusions: Hemoglobinopathies are important and independent cause of anaemia (in addition to other common etiologies) during pregnancy in Assam. Policy measures should include strategies for addressing these disorders for successful anemia control in Assam

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Abstract No: SA-148

Seasonal patterns & Risk factors of Respiratory Syncytial Virus among Nicobarese Tribal Populations of Andaman & Nicobar Islands



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Introduction: Respiratory Synctial virus (RSV) is the leading cause of acute respiratory infection (ARI) in children worldwide with an estimate of 33 million cases(1). Human respiratory virus infections also produce wide range of respiratory symptoms and severe sickness. The Global Burden of Disease (GBD) 2019 report states that 17.2 billion people worldwide suffered from respiratory infections(2).

Objectives: This study ams to understand the seasonal pattern and risk factors of ILI related RSV among the aboriginal Nicobarese tribes.

Methods: This is a hospital based prospective study conducted among Nicobarese tribes. Epidemiological data was collected using study questionnaire. Nasal swab was collected and RNA was extracted according to the manufacturer protocol (Qiagen). qRT PCR was carried out to identify the RSV and statistical analysis was performed using SPSS version 28.

Results: A total of 7,910 ILI cases reported from June 2019 to August 2025 and 2,271 cases were given consent and enrolled in the study. Overall 152 cases of RSV reported in the Nicobar group of islands. RSV A was more frequently recorded than RSV B(RSV A-143 vs RSV B-9). According to age-wise analysis, children between the age of 0 and 4 were more likely to have RSV(N=96). RSV A cases was highly reported in the month of October(N=79) and November(N=58)2021. In contrast, a few cases of RSV A were recorded in October 2019(N=2), April 2022(N=1), April 2024(N=2) and December 2024(N=1). Following this, very few RSV B cases were reported in September 2023(N=1) and October (N=8).

Conclusions: The respiratory synctial virus reported on this island had a significant association with age factors and climatic conditions. This type of research is necessary for improving and optimizing diagnostic strategies as well as developing approaches for preventing emerging respiratory viral infections especially for the health benefit of the tribal nontribal population of these islands.

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Abstract No: SA-149

Evidence of *Leptospira* spp. in the soil of Andaman Islands



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Introduction: Leptospirosis remains highly endemic in tropical regions, and understanding its environmental distribution and associated factors is crucial for effective disease management. The Andaman and Nicobar Islands are an endemic region for leptospirosis; however, the environmental prevalence of *Leptospira* spp. in soil in Andaman Island has not been well characterized. The survival and dissemination of pathogenic *Leptospira* are influenced by soil characteristics, surface substrates, and microenvironmental conditions. Soil and water are recognized reservoirs, but limited information is available on the role of plant debris and artificial contact surfaces in environmental persistence and exposure risk.

Objectives: To detect *Leptospira* from different environmental matrices and assess its association with surface type, soil characteristics, and key environmental parameters in endemic areas of Andaman.

Methods: Soil samples were collected from selected endemic locations across Andaman Island representing diverse surface types and environmental conditions, and metadata were recorded using Epicollect5. Genomic DNA was extracted using a kit-based method. Molecular detection was performed by PCR using genus-specific 16S rRNA PCR for *Leptospira* spp. and LipL32 PCR for pathogenic *Leptospira*. PCR amplicons were analysed by agarose gel electrophoresis.

Results: Pathogenic *Leptospira* DNA was detected in 8.8% (95% CI: 6–13) samples by LipL32 PCR (20/228), while genus-level PCR showed 28.9% positivity (95% CI: 24–35). Higher detection was observed in Rangat (14.9%) compared with Mayabunder (11.5%) and Diglipur (2%). Positivity was slightly higher in exposed areas (11.8%) than shaded areas (8.2%) and was comparable between abiotic (9.6%) and biotic (8.4%) samples. Higher detection was associated with near-neutral pH (7.0–7.9), moderate soil temperature (26.0–29.9°C), relative humidity of 85–94%, and fine soil texture.

Conclusions: This study provides the first evidence of environmental presence of *Leptospira* spp. in soil from endemic areas of Andaman, highlighting spatial heterogeneity and environmental conditions favoring persistence.

Acknowledgement: We thank the Director, ICMR-RMRC, Sri Vijaya Puram, for facilities & support, and all technical staff, and PhD Scholars.

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Abstract No: SA-150

Structural, Biochemical, and Functional Insights into the Periplasmic Serine Protease MucD (LIC_12812) of *Leptospira interrogans*



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Introduction: Leptospirosis is a neglected tropical disease caused by *Leptospira* spp., which is re-emerging due to climate change, rapid urbanization, and its persistence in reservoir hosts such as rodents and other animals. Leptospirosis remains a global health challenge because of its complex pathophysiology and the limited availability of effective vaccines and diagnostics. This study characterizes the serine protease MucD (LIC_12812) as a periplasmic virulence-associated protease of *Leptospira interrogans* with regulatory, pathogenic, and immunogenic roles.

Objectives:

1. To bioinformatically characterize the serine protease MucD (LIC_12812) of *Leptospira interrogans* with respect to its structure, subcellular localization, physicochemical properties, and virulence potential.
2. To clone, express, purify, and generate antibodies against recombinant MucD (r-LIC_12812).
3. To evaluate the functional and immunogenic roles of r-LIC_12812 by assessing its interaction with host extracellular matrix (ECM) components and immune cell responses.

Methods: MucD (LIC_12812) was bioinformatically analyzed for signal peptide, localization, structural features, physicochemical properties, and virulence. The gene was cloned and heterologously expressed in *Escherichia coli*, and the recombinant protein was purified for polyclonal antibody generation in rabbits. Immunogenicity was assessed by lymphocyte proliferation (MTT assay) using peripheral blood mononuclear cells. Functional interactions were evaluated through dose-dependent binding to ECM components.

Results: Bioinformatic analysis revealed a cleavable signal peptide (SignalP 5.0) and an N-terminal transmembrane helix (TMHMM 2.0) anchoring the mature protein (30–388) in the periplasm (PSORTb: 9.44; CELLO: 1.874). MucD exhibited high solubility (SOLpro: 0.8201), moderate antigenicity (VaxiJen: 0.5977), non-allergenicity, non-toxicity, virulence potential, and a predominant random coil structure (SOPMA: 42.53%). Physicochemical indices indicated stability and slight hydrophilicity (Instability Index: 34.24; GRAVY: −0.042). Recombinant MucD showed low lymphocyte proliferation in the MTT assay.

Conclusions: The bioinformatic profile, ECM-binding ability, and immunogenic characteristics suggest that serine protease MucD is an important molecule with potential application as an anti-leptospirosis target.

Acknowledgement: Funded by ICMR (Intramural project). We thank the Director, ICMR-RMRC, Sri Vijaya Puram, for facilities & support, and all technical staff, and PhD Scholars. We are grateful to Dr. T. Jebasingh (Madurai Kamaraj University) for plant sciences collaboration, PhD scholars,other technical and nontechnical staff.

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Abstract No: SA-151

Emergence and re-emergence of the Chikungunya in the Andaman and Nicobar Islands



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Introduction: Chikungunya, a re-emerging arboviral disease, continues to pose a significant public health risk in the Andaman & Nicobar Islands (ANI). In this 14-year retrospective surveillance study (2010–2023), we analysed laboratory-confirmed chikungunya cases. Chikungunya virus (CHIKV) belongs to the Family *Togaviridae.* Disease transmission is through the mosquito species *Aedes aegypti* and *Aedes albopictus*. The common symptoms include sudden onset of fever, severe arthralgia, rash, and may persist as chronic arthritis. It was first reported as an outbreak in 2006[1] (sporadic cases), and a major upsurge was observed in 2010[2]. Later, it has occasionally been present in the population. The genotype identified in the 2006 outbreak was the East/Central/South African (ECSA) genotype.[3]

Objectives:

- To assess the trend of chikungunya positivity rates in the Andaman and Nicobar Islands over 14 years (2010–2023).
- To correlate chikungunya positivity with rainfall in the region.

Methods: A retrospective surveillance analysis was done. Data Source – SL-VRDL, ICMR-RMRCSVP.

Results: The Overall positivity was 15.07% (608 positives out of 4035 tested), with variations in positivity seen across years. After the initial outbreak in 2006, a major peak in cases occurred in 2010 (34.7%), and a subsequent increase was noted in 2022 (25%). In retrospect, the increase in Chikungunya cases in the ANI was consistently observed following an upsurge on the mainland of India. From 2019, the number of suspected cases of Chikungunya reduced gradually, with only 3 cases in the year 2023. However, in 2025, from January to November, 11 cases tested positive out of 166.

Conclusions: These findings highlight the rainfall-driven dynamics of chikungunya in ANI and the need for strengthened surveillance and proactive vector control strategies to control transmission of the disease.

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Abstract No: SA-152

Designing a multi-stage malaria vaccine against *Plasmodium falciparum*



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Introduction: Malaria caused by *Plasmodium falciparum* remains a significant global health burden, particularly in sub-Saharan Africa. Vaccine development against this complex protozoan parasite has historically faced challenges due to antigenic diversity, immune evasion, and a multi-stage life cycle.

Objectives: My research work would focus on designing recombinant malaria subunit vaccine for targeting the two population bottleneck stages of *P. falciparum* development: 1. Blocking the liver-stage infection; and 2. Blocking the mosquito development stage.

Methods: Recombinant subunit vaccine candidates will be designed based on immunodominant antigens pre-erythrocytic (liver-stage) and mosquito-stage *P. falciparum* antigens (e.g. CSP, Pfs230, Pfs48/45). Selected antigen fragments will be codon-optimized, cloned into suitable expression vectors, and expressed in heterologous systems, followed by purification and biochemical characterization. Immunogenicity will be evaluated in murine models using optimized adjuvant formulations, and functional activity will be assessed through bioassays (*in vitro* & *in vivo* challenge experiments) for liver-stage inhibition and standard membrane feeding assays for transmission-blocking activity.

Results: The multistage recombinant vaccine is likely to elicit robust, antigen-specific humoral and cellular immune responses. *In vitro* and *in vivo* challenge models are expected to demonstrate reduced hepatocyte invasion by sporozoites and significant inhibition of *P. falciparum* development in the mosquito midgut, indicating dual-stage efficacy.

Conclusions: This study is expected to provide proof-of-concept that a rationally designed, multistage recombinant subunit vaccine can simultaneously target the liver-stage and mosquito-stage bottlenecks of *P. falciparum* development. By combining conserved antigens from distinct life-cycle stages, the proposed strategy may enhance overall protective efficacy, contribute to both individual-level protection and community-level transmission reduction, and inform the next generation of malaria vaccine design.

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Abstract No: SA-153

Healthcare Accessibility and Utilization of Facility- and Community-Based Health Services among Tribal Populations in Odisha: A Cross-Sectional Study



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Introduction: Tribal communities in India continue to face substantial disadvantages in accessing essential health services, largely due to remoteness, health system limitations, and social marginalisation. Odisha, which has a high concentration of tribal and particularly vulnerable tribal groups, shows persistent gaps in maternal, child, and non-communicable disease (NCD) indicators. However, evidence on how varying levels of healthcare accessibility influence utilisation of facility-based and community-based services in tribal settings remains limited.

Objectives: This study examined the association between healthcare accessibility and coverage of essential health services among tribal populations in Odisha.

Methods: This cross-sectional study analysed data from the Odisha Tribal Family Health Survey (OTFHS), conducted between 2021 and 2023 in 13 tribal-dominated districts of Odisha, India. The survey used multistage stratified random sampling and included 10 230 households and 40 921 individuals from 53 Scheduled Tribe communities, including 13 Particularly Vulnerable Tribal Groups. A composite healthcare accessibility score was constructed using availability of health personnel, health facilities, and distance to referral centres, and then categorised into quartiles. Outcome-specific analytical samples included women aged 15–49 years, children younger than 5 years, children aged 12–23 months, and adults aged 20 years or older. Outcomes included utilisation of antenatal care (≥3 visits), institutional delivery, met need for modern contraception, child immunisation (DPT3 and MCV1), diarrhoea treatment, insecticide-treated net use, and prevalence and awareness of hypertension and diabetes. Survey-weighted multivariable logistic regression models were used to estimate adjusted odds ratios (AORs) with 95% CIs.

Results: Higher healthcare accessibility was strongly associated with increased use of facility-based maternal health services. Compared with the lowest accessibility quartile, women in the highest quartile were more likely to receive at least three antenatal care visits (AOR 3·82, 95% CI 2·59–5·61) and to deliver in health facilities (2·14, 1·21–3·76). Met need for modern family planning showed limited improvement and was significantly higher only in the second quartile (1·29, 1·01–1·66). Coverage of outreach-based services varied: immunisation levels were consistently high across quartiles, insecticide-treated net use was greater in highly accessible areas (1·83, 1·22–2·75), and diarrhoea treatment remained suboptimal without a clear accessibility gradient. Both prevalence and awareness of hypertension and diabetes increased with accessibility, with significantly higher odds observed in the highest quartile.

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Conclusions: Greater healthcare accessibility improves utilisation of facility-based maternal health services among tribal populations, but alone is insufficient to ensure equitable coverage of all essential interventions. Persistently low uptake of family planning and child illness management, alongside rising detection of NCDs in better-connected areas, underscores the need for health system approaches that go beyond physical access. Strengthening culturally appropriate outreach, continuity of care, and community engagement will be critical to achieving equitable health gains in tribal setting.

Acknowledgement(s) and Funding (if any): The Odisha Tribal Family Health Survey (OTFHS) was supported by the Scheduled Castes and Scheduled Tribes Research and Training Institute, Government of Odisha.

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Abstract No: SA-154

Targeting Regulatory T Cells to Improve Cancer Immunotherapy



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Introduction: Regulatory T cells (Tregs) are a specialized subset of $CD4^+$ T lymphocytes that play a crucial role in maintaining immune homeostasis and preventing autoimmunity. However, in the context of cancer, Tregs accumulate within the tumor microenvironment and contribute to immune evasion by suppressing antitumor immune responses of the effector T cells. The presence of Tregs has been correlated with poor prognosis in several malignancies, making them a critical focus in cancer immunology and targeted therapeutic development.

Objectives: My research plan aims to explore various therapeutic intervention strategies for blocking Treg-function for enhancing anticancer immunity.

Methods: My research would explore *in vitro* co-culture systems of human tumor-infiltrating lymphocytes and autologous tumor cells to assess the impact of Treg depletion or functional blockade using various inhibitors targeting key Treg signalling pathways. Parallel *in vivo* studies will utilize syngeneic murine tumor models treated with Treg-modulating agents, alone and in combination with established immune checkpoint inhibitors, to evaluate changes in tumor growth, immune cell composition, and effector T-cell function. Flow cytometry, multiplex cytokine profiling, and immunohistochemistry will be used to quantify Treg frequency, phenotype, and suppressive capacity within the tumor microenvironment and peripheral lymphoid organs.

Results: Selective blockade or depletion of Tregs is likely to reduce their frequency and suppressive function within the tumor microenvironment, leading to enhanced activation and proliferation of tumor-specific effector T cells. These interventions are expected to result in increased production of pro-inflammatory cytokines, improved cytotoxic activity against tumor cells, and delayed tumor progression in preclinical models.

Conclusions: This study is expected to provide mechanistic insights into how therapeutic targeting of Tregs can modulate the tumor immune landscape and potentiate antitumor immunity. The findings will support the development of rational Treg-focused immunotherapeutic strategies and may inform the design of future clinical interventions aimed at improving outcomes for patients with cancer.

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Abstract No: SA-155

High Burden of Bacterial Childhood Diarrhoea and Emerging Antimicrobial Resistance in the Nicobar Group of Islands



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Introduction: The Nicobar group of islands, inhabited by indigenous tribal populations, represents a unique geographically isolated and epidemiologically underserved region of India(1). Their socio-cultural practices, including consumption of raw or undercooked seafood, may facilitate the introduction and circulation of diverse enteric pathogens (2). Access to these islands are extremely limited, restricting evidence-based clinical decision-making and public health planning. The findings from this study contribute essential data for guiding rational antimicrobial therapy, strengthening outbreak preparedness, and informing targeted prevention programmes.

Objectives: The present study aimed to assess the prevalence of diarrhoeal disease in the Nicobar group of islands and to identify the bacterial aetiologies and their antimicrobial resistance patterns.

Methods: A hospital-based prospective study was conducted from August 2023 to July 2025 among children aged 0–12 years presenting to the local PHCs with acute and chronic diarrhoeal symptoms across five groups of islands in the Nicobar District. Stool samples were collected from 277 enrolled children from 563 reported cases and processed using standard microbiological culture, microscopy, and molecular methods for pathogen confirmation. Antimicrobial susceptibility testing was performed using the Kirby–Bauer disc diffusion method in accordance with standard CLSI guidelines.

Results: Of the 277 diarrhoeal stool samples analysed, Zoonotic food borne *Escherichia coli* was the predominant isolate (78.4%), among them 4.3% were EPEC and 11.9% were EAEC, followed by *Klebsiella spp.* (12.8%), *Shigella spp.* (4.8%), and *Proteus spp*. (4.0%). Enterobacteriaceae isolates showed high resistance to penicillin (55–65%) and Quinolones/Fluoroquinolones (50–60%), with moderate resistance to aminoglycosides (40–45%) and third and fourth-generation cephalosporins (30–35%). In contrast, lower resistance was observed to carbapenems (15–20%) and β-lactam/β-lactamase inhibitor combinations (25–30%).

Conclusions: The study highlights a substantial diarrhoeal burden among children in the Nicobar groups of islands, predominantly driven by bacterial pathogens with concerning antimicrobial resistance patterns.

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Abstract No: SA-156

Chitosan Nano-scaffold to combat MDR strain for Chronic Wound Healing Applications



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Introduction: Chronic wounds are a major global health concern due to prolonged healing, leading to significant morbidity, mortality, and frequent amputations, particularly from diabetic, arterial, and pressure ulcers. The global incidence ranges from 1.51–2.21 per 1,000 individuals. Conventional antibiotic-based wound management has contributed to antimicrobial resistance (AMR), delayed tissue regeneration, and poor healing outcomes. AMR caused 1.27 million direct deaths globally in 2019 and contributed to 4.95 million deaths overall. The rise of multidrug-resistant (MDR) pathogens necessitates development of innovative, biocompatible antimicrobial materials that avoid further resistance. Chitosan (CS), a cationic biopolymer, exhibits cytocompatibility, hemostatic properties, and intrinsic antibacterial activity. In this study, a chitosan–copper (CSCu) nano-scaffold was developed via coordination of Cu^{2+} ions with chitosan amine and hydroxyl groups, demonstrating high antimicrobial efficacy and biocompatibility.
Objectives: To design a CSCu nano-scaffold, characterize its physicochemical properties, and evaluate antibacterial activity through in vitro and in silico analyses.

Methods: CSCu nano-scaffold was synthesized in situ by coordination crosslinking of chitosan with Cu^{2+} ions. Physicochemical characterization was performed using SEM, FTIR, XRD, DLS, and zeta potential analysis. Antibacterial efficacy against Gram-negative standard and MDR Escherichia coli was evaluated using bacterial viability and metabolic inhibition assays. Hemocompatibility was assessed through hemolysis assays. Molecular docking was performed to assess interaction with E. coli outer membrane protein C (OmpC).
Results: SEM showed increased crosslinking with higher chitosan concentration. XRD revealed reduced crystallinity due to Cu^{2+} coordination. FTIR confirmed functional group interactions. DLS and zeta potential indicated increased particle size and positive surface charge. The CSCu nano-scaffold showed strong antibacterial activity, metabolic suppression, excellent hemocompatibility, and high binding affinity to OmpC.
Conclusion: The CSCu nano-scaffold demonstrates strong antimicrobial efficacy, biocompatibility, and potential as a next-generation biomaterial for chronic wound therapy.

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Abstract No: SA-157

Immunology and Nanotechnology Synergy to Combat Multi-Drug Resistant Pathogens



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Introduction: Multidrug-resistant (MDR) bacterial infections in wounds are caused by persistent biofilm-forming pathogens that evade host immunity, antibiotic treatment and contribute approximately 40–60% of chronic wound infections worldwide. The overuse of traditional antibiotics accelerates multidrug resistance in bacteria, highlighting the need for alternative methods. In this regard, peripheral blood mononuclear cells (PBMCs) play a critical role in the immune defense process. However, MDR pathogens can escape phagocytosis and impair immune signalling pathways. To address such challenges, nanoparticle integration with PBMC have the potential to combat MDR pathogens. In this study, PBMC combine with with Zeolitic Imidazolate Framework (ZIF-8) nanoparticle to combat MDR *E. coli for* chronic wound healing.

Objectives:

- Isolation of PBMCs from human blood and synthesis of ZIF-8 nanoparticles.
- Isolation of MDR *E. coli* from a chronic wound sample collected from AIIMS, Bhubaneswar.
- Evaluation of the synergistic antimicrobial effect of human PBMCs and ZIF-8 nanoparticles against MDR pathogens.

Methods: PBMCs were isolated from human blood using HiSep media through the density gradient centrifugation method. The ZIF-8 nanoparticles were synthesized using a mortar–pestle–based solid-state synthesis method. Antimicrobial assays of PBMCs and ZIF-8 nanoparticles were conducted against multidrug-resistant E. coli. In addition, a hemolysis assay was performed to evaluate the hemocompatibility of ZIF-8.

Results: PBMCs were confirmed by trypan blue and giemsa staining. PBMCs did not show a strong antimicrobial effect against MDR *E. coli* even in highest tested concentration 150µl, whereas ZIF-8 nanoparticles exhibit a potent antibacterial and anti-biofilm activity at 1mg/ml concentration which is hemocompatible. So, different concentrations of PBMCs with low concentration of ZIF-8 (0.5mg/ml) are being evaluated to investigate their synergistic antimicrobial effect against MDR which is an ongoing study.

Conclusion: PBMC was effectively isolated and ZIF-8 was successfully synthesized to enable combined antimicrobial applications. This is an ongoing research work. So further studies will be focused on antimicrobial activity against multiple MDR strains along with ZIF-8 characterization, and detailed PBMCs cytotoxicity and immune response analysis.

Acknowledgement(s) and Funding: The authors acknowledge the DEBAMURTI project (PROJECT NO. VIR/Intra/042024/CD) of the Indian Council of Medical Research, Government of India, for providing necessary funding. The authors also thank the AcSIR-ICMR (Order No. ICMR/BEM/2025-26/ACSIR), ICMR-Regional Medical Research Centre, Bhubaneswar, for providing a scientific platform.

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Abstract No: SA-158

Epigenetic Regulation of Chikungunya Virus Replication by Chaetocin-Mediated H3K9me3 Inhibition



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Introduction: Chikungunya virus (CHIKV), which causes chikungunya fever, is an arbovirus of public health concern with no approved antiviral therapies. A major limitation of attempts in the area of direct acting antiviral development is the possible emergence of drug resistance. In this context, exploring host-directed approaches such as targeting epigenetic RNA modifications (H3K9me3) by chaetocin that influence viral replication and host responses offers promising alternative avenue for antiviral development.

Objective: The purpose of the study is to assess the antiviral activity of chaetocin and its mechanism of action.

Methods: The highest non-toxic concentration of chaetocin was used to evaluate its therapeutic anti-CHIKV activity, and dose-dependent antiviral effects were assessed to determine the 50% inhibitory concentration. Time-of-addition, attachment, entry, and release assays were performed to define the stage of viral inhibition. Viral output was quantified by focus-forming unit assay, while qRT-PCR and Western blotting were used to assess viral RNA and protein expression. H3K9me3 levels in control and treated cells were analyzed by Western blotting. The role of SUV39H1 in CHIKV replication was examined using siRNA-mediated knockdown. Global m6A methylation of viral and cellular RNA was quantified, and m6A sites in structural and non-structural viral RNA were predicted using in silico analysis. Long-term sequential viral passaging (P = 25) was conducted to assess the emergence of drug resistance.

Result : The results suggested that Chaetocin markedly suppressed CHIKV replication at post-entry stages by reducing viral RNA amplification, viral protein expression, H3K9 trimethylation, and global m6A RNA methylation, without affecting viral attachment, entry, or release and knockdown of SUV39H1 significantly reduced CHIKV replication, recapitulating the antiviral effect of Chaetocin, without the emergence of drug resistant CHIKV variants.

Conclusion: The study proposed that host-directed epigenetic inhibition by Chaetocin represents a promising antiviral strategy with reduced chance of resistance development.

Acknowledgements and funding: This work was supported by the Indian Council of Medical Research (ICMR), New Delhi, under the project titled *'Development of Novel Host-Directed Antivirals Against Arboviruses: Elucidating the Molecular Mechanism of Action and Drug Resistance Considerations'* and fellowship from the Department of Biotechnology (DBT).

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Abstract No: SA-159

In-Silico Design and Validation of RT-LAMP Primers Targeting the 3′UTR of Dengue, Japanese Encephalitis, and West Nile Viruses



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Introduction: Rapid and specific detection of mosquito-borne flaviviruses, including Dengue virus, Japanese encephalitis virus, and West Nile virus, is essential for effective surveillance and diagnosis. In this study, reverse transcription loop-mediated isothermal amplification (RT-LAMP) was employed for the detection of these viruses using highly specific primers designed in silico to target conserved regions of the 3′ untranslated region (3′UTR) of the viral genome. Primer specificity and functionality were validated using viral gene fragments.

Objectives:

- Designing of RT-LAMP primers specific for DENV, JEV, and WNV.
- Validation of primers for DENV, JEV, and WNV using viral gene fragments

Methods: An *in-silico* approach was used to design RT-LAMP primers for DENV, JEV, and WNV. The viral genome sequences were obtained from the NCBI database and aligned using MEGA software to determine the conserved and specific regions in the 3′UTR.
Primers were designed using web based PrimerExplorer v5. Primer characteristics and cross-reactivity were analyzed using NetPrimer, and target specificity was estimated by NCBI BLAST analysis. The designed primers and synthetic gene fragments were submitted for synthesis to use as positive controls and was validated using RT-LAMP assay.

Results: Six RT-LAMP primers were designed for each virus (F3, B3, FIP, BIP, LF, and LB) with optimized GC content (40–60%) and closely matched melting temperatures (60–65 °C for outer primers and 64–68 °C for inner primers). All primers exhibited ΔG values above the accepted threshold (ΔG > −4 kcal/mol), indicating minimal secondary structure formation. RT-LAMP amplification using viral gene fragments produced characteristic ladder-like banding patterns in positive controls, resulting from concatemeric stem–loop DNA structures, thereby confirming assay specificity and robustness without cross-reactivity.

Conclusions: This study focuses on designing as well as validation of set of primers specific for detection of flavivirus infections namely JEV, DENV and WNV using RT-LAMP assay without cross-reactivity.

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Abstract No: SA-160

Aetiology of Enteric Viruses associated with Childhood Diarrhoea among Tribal and Non-Tribal Population of Nicobar Islands



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Introduction: Childhood diarrhoea, caused by enteric viruses remains a major challenge, in remote and tribal settings of the Nicobar group of islands which are home to indigenous tribes living in geographically isolated region where access to safe water and food, sanitation, and healthcare is limited. The distinctive ecological location shapes the epidemiology, disease pattern, and antimicrobial resistance among children, where if left untreated increases fatality risk. Proper surveillance and targeted intervention are thus highly necessary in this unique environment.

Objectives:

1. To identify the etiology and risk factors of viral childhood diarrhea among the children of the Nicobar group of islands.
2. Molecular characterisation of major enteric viruses associated with childhood diarrhoea among children from the Nicobar group of islands.

Methods: A hospital based prospective surveillance study was conducted on children suffering with diarrhoea (0-12 years), across five islands of the Nicobar from August 2023 to July 2025. Stool samples were collected and processed for viral detection. ELISA, Nucleic acid extraction, screening by PCR and qRT-PCR for Rotavirus A, Norovirus, Astrovirus, and Adenovirus was done. Multiplex-PCR amplification was done using the primers targeting different viral pathogenic characterization and molecular genotyping was performed.

Results: Out of the enrolled 277 childhood diarrhoeal cases, Car Nicobar reported the highest burden of diarrheal cases mostly among children <5 years with higher positivity among non-breastfed and non-vaccinated. Rotavirus was the most common virus detected, followed by Astrovirus, Adenovirus while Norovirus was the least. Both Rotavirus and Norovirus genotypes were identified. Most of the viral cases was linked to tap water usage, indicating contaminated domestic water supplies.

Conclusion: Rotavirus contribute the most to the burden of childhood diarrhoea in the Nicobar group of islands. The circulation of the multiple genotypes indicates active viral transmission and for pathogenic genotyping, the sequencing has to be further done.

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Abstract No: SA-161

Screening for potential inhibitory molecules against KIF4A to target breastcancer stem cells



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Introduction: Kinesin Family Member 4A (KIF4A) is essential for chromosome condensation and segregation during mitosis. Its overexpression is associated with poor prognosis, drug resistance, and enhanced stemness in breast cancer and other malignancies [1-4]. Despite its therapeutic potential, no specific KIF4A inhibitors are currently available. Therefore, this study aims to identify potential inhibitory molecules targeting KIF4A.

Objectives: To identify novel inhibitory molecules against KIF4A by molecular docking to combat breast cancer stem cells and the development of resistance to chemotherapy

Methods: As the crystal structure of KIF4A is unavailable in the Protein Data Bank (PDB), its 3D structure was predicted by homology modeling and validated using a Ramachandran plot. Virtual screening of the DrugBank library was performed using the Schrödinger Suite 2021 Virtual Screening Workflow. The binding site was defined by the centroid of conserved residues Y79, L2562, and Y321. Compounds were screened sequentially using HTVS, SP, and XP docking, and the top hits were further evaluated by 100 ns molecular dynamics simulations using the Desmond module.

Results: In the present study, Capecitabine, Cladribine, Axitinib, Vorinostat, and Bortezomib were identified as potential KIF4A inhibitors, exhibiting docking scores between –7 and –5 kcal/mol. These compounds were further evaluated using MMGBSA binding free energy calculations and subjected to 100 ns molecular dynamics simulations using the Desmond module. Capecitabine, Cladribine, Axitinib, and Vorinostat demonstrated stable binding and sustained interactions with key residues within the KIF4A binding pocket throughout the simulations.

Conclusions: The present study identified 4 potential binders to after molecular docking and MD simulations, which might serve as potential binders to the KIF4A protein, inhibition of KIF4A protein might help in efficiently combating development of chemo-resistance and formation of cancer stem cells.

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Abstract No: SA-162

Identification of Vaccine targets in *Leptospira* using Convalescent Serum (CS) and validation of Immunoprotection



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Introduction: *Leptospira*, once limited to rural and agricultural setting, is emerging in urban area as well [1]. The population is bound to encounter *Leptospira* in their home and work environment and get re-infected multiple times. Vaccination is the effective measure to encounter particularly in such condition. The leptospiral proteins detected by the convalescent serum antibodies will be useful as vaccine candidates [2]. The aim is to pull down leptospiral proteins using antibodies from the convalescent serum, identify, make recombinant protein and evaluate the immunoprotection as a successful vaccine.

Objectives:

1. To identify leptospiral target proteins using convalescent sera with binding study.
2. To clone, express, isolate and purify the target leptospiral protein.
3. To validate the vaccine candidate using the recombinant protein by *in vitro* and *in vivo* study.

Methods: Initial part of the study involves collection of convalescent sera from individuals previously diagnosed with leptospirosis and using the sera for finding respective antigens from *Leptospira*. Then collection and analysis of the antibody-protein complex for identification of target and further developing the *Leptospira* protein into potential vaccine molecule by cloning and expression in suitable vector and validating in animal model.

Expected outcome: The results of this study will greatly help to understand the defence mechanism opted by the host body of recovered patients against *Leptospira*. As a result, a protein-based vaccine candidate can be developed which is expected to work against most serovars of *Leptospira*. The outcome of the study might greatly profit the population living in sub-urban and rural area where leptospirosis is already a threat, given that a potent vaccine candidate can be developed.

Acknowledgement: We are very thankful for the research facilities provided by ICMR-RMRCSVP and academic support provided by Pondicherry University.

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Abstract No: SA-163

In Vitro antiviral activity of extracts of medicinal plant, *Euphorbia hirta,* against Chikungunya



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Introduction: Chikungunya virus (CHIKV), which is a mosquito-borne alphavirus, induces fever, rash, and acute joint pain, and continues to pose a major global health problem. WHO reports of 2025 claim cases of transmission occurring in more than 119 countries and an estimated 5.6 billion people at risk worldwide. To date, there are no licensed antiviral compounds for CHIKV. Hence, it is pertinent to investigate the antiviral activity of potential medicinal plant extracts and bioactive compounds against the CHIKV.

Objective: To assess the *in vitro* activity of different solvent-based extracts of *E. hirta,* a medicinal plant of interest, with known anti-inflammatory and antiviral activity.

Methods: In the present study, cytotoxicity of different solvent-based *E. hirta* extracts and their fractions was determined on Vero CCL-81 cells by using the MTT assay to determine maximum non-toxic concentration. Antiviral activity was assessed through pre-treatment, co-treatment, and post-treatment strategies, where viral titers were quantified through focus forming unit (FFU) assay and Immunofluorescence assay. For extracts that exerted promising activity against CHIKV, dose-dependent studies were performed to calculate the IC_{50} values.

Results: EH-Chloroform extract showed anti-chikungunya activity reducing viral titers in all three treatment conditions while among 12 EH-chloroform fractions, ten fractions exhibited anti-CHIKV activity in the post-treatment condition. EH-Hexane extract reduced CHIKV titers in co- and post-treatment conditions while eight of 16 EH-hexane fractions exhibited anti-CHIKV activity in post-treatment conditions.

Conclusion: Findings confirm anti-CHIKV activity of *E. hirta* extracts (hexane and chloroform), supporting their antiviral potential (prophylactic, therapeutic and virucidal activity) and the need to identify active phytochemicals for antiviral drug development.

Acknowledgment and Funding
I sincerely thank ICMR, New Delhi, India, for their financial support, and I also thank the ICMR–National Institute of Virology for their support.

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Abstract No: SA-164

Identification of diagnostic target from Leptospiremic urine sample and development of Point-of-Care Test (PoCT) based on Lateral flow Assay (LFA)



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Introduction: Leptospirosis is a zoonotic disease caused by *Leptospira* spp. [1]. A major diagnostic challenge is its clinical similarity to other common febrile illnesses. Conventional diagnostic methods such as Microscopic Agglutination Test (MAT), IgM ELISA, and PCR are limited by issues of sensitivity, specificity, and the need for trained personnel and sophisticated instrumentation [2]. Hence, a rapid, non-invasive, and cost-effective diagnostic approach is desirable. Early detection using urine samples through a lateral flow assay (LFA) is a promising alternative, as it is simple and inexpensive [3]. Our proteomic analysis has identified several secretory molecules associated with *Leptospira* infection. Detection of these urinary proteins and their incorporation into an antibody-based LFA could improve early diagnosis and reduce disease severity and transmission.

Objectives:

1. To identify leptospiral proteins in human urine.
2. To generate recombinant proteins and antibodies against leptospiral urinary proteins.
3. To develop an antibody-based LFA for detection of leptospiral proteins in urine.

Methods:

I. **Identification of leptospiral proteins in urine-** Urine samples from qPCR-positive leptospirosis patients (infected and not cured) will be selected. Fresh urine will be concentrated using ultrafiltration spin columns, enriched by precipitation, and analysed by LC–MS/MS. Identified proteins will be shortlisted using secretory proteome data and bioinformatic analysis.

II. **Antibody generation and LFA development**-Antibodies will be generated against highly antigenic peptides of selected proteins and used to develop an LFA platform. In-house validation and optimization will be performed to achieve high sensitivity, specificity, PPV, and NPV.

III. **LFA-based point-of-care testing**-The LFA will be standardized, scaled up, and validated through nationwide multicentric studies, followed by analysis of validation data.

Expected Outcome: The urine-based LFA will detect *Leptospira*-specific proteins, providing evidence of active infection. This rapid, cost-effective, non-invasive test will support early diagnosis and can be used by non-trained individuals in resource-limited settings.

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Abstract No: SA-165

Study of biofilm formation of *Leptospira* and its role in the survival of *Leptospira* in the environment



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Introduction: Leptospirosis is a re-emerging zoonotic disease caused by spirochetes belonging to the genus *Leptospira*. Leptospires are known to remain infective in the environment for prolonged periods, although their survival strategies are not fully understood. One key mechanism is biofilm formation, which enhances resistance to environmental stresses and enables long-term survival [1,2]. In addition, multispecies biofilms formed through microbial interactions may further enhance stability, virulence, and persistence. Biofilms formed in association with other microbial species provide a more stable environment for survival [3].

This study aims to understand biofilm formation in *Leptospira* and its role in environmental persistence. By cultivating biofilms under controlled in vitro conditions, the research will examine biofilm formation parameters, the influence of co-existing microbial species, and factors involved in biofilm development and disruption to the planktonic state. Understanding how these organisms and molecules influence *Leptospira* behaviour may help identify potential targets to disrupt biofilms, thereby reducing long-term environmental persistence.

Objectives:

1. To isolate and identify leptospiral biofilms and associated organisms from the environment.
2. To establish biofilm formation and disruption to the planktonic form in vitro.
3. To characterize differentially expressed molecules and the role of microbial partners influencing biofilm formation and disruption.

Methodology: Leptospiral biofilms will be collected from soil and water samples from high-prevalence areas. *Leptospira* and associated organisms will be identified from isolated biofilms. In vitro studies will assess biophysiological factors influencing biofilm formation and disruption, followed by identification of molecules expressed during biofilm development and transition to the planktonic form. The role of associated organisms in modulating these processes will also be evaluated.

Expected Outcome: The study will identify potential targets to disrupt or prevent biofilms, reduce environmental persistence of *Leptospira*, lower infection risk, and ultimately decrease disease burden.

Acknowledgement: We thank the facility and support provided by ICMR-RMRCSVP and Pondicherry University.

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Abstract No: SA-166

Spatial Distribution and Habitat Preference of Dengue Vectors Across Tribal and Non-Tribal Settlements in the Andaman and Nicobar Islands



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Introduction: Dengue and Chikungunya are two arboviral infections prevalent in Andaman and Nicobar Islands. With no vaccine or specific treatment available for dengue, vector control is the only effective measure to prevent dengue outbreaks such as *Aedes aegypti* and *Aedes albopictus* Studies recommend eliminating the most productive breeding sites and targeting key container habitats to keep dengue vector populations below critical thresholds.

Objectives:

1. To determine the proportion of the two vectors species in the area.
2. To identify container types significant for dengue vector breeding in both the areas.

Methods:

1. An immature survey for dengue vectors was conducted by inspecting various water-holding containers in and around 200 households.
2. The emerged adult mosquitoes were identified based on the morphological characters using standard taxonomic identification key

Results: Inspection of 100 households revealed 46 *Aedes*-positive containers out of 394 in the non-tribal area of Dollygunj, Sri Vijaya Puram, whereas the tribal area of Chowra Island, Nicobar district showed markedly higher infestation, with 781 positive containers out of 972, predominantly from outdoor habitats.

Conclusions: *Aedes albopictus* dominates the local vector population, with both species exploiting diverse container habitats. High Stegomyia indices confirm significant dengue outbreak potential, warranting urgent and sustained vector control measures.

Acknowledgement: We are very thankful for the research facilities provided by ICMR-RMRCSVP and academic support provided by Pondicherry University.

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Abstract No: SA-167

Socio-epidemiological Burden of Malaria in Central India: A Biocultural Anthropological Perspective



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Introduction: Malaria is a serious public health challenge, specifically in the tribal regions of India. Despite several ongoing national-level malaria elimination programs in India, the number of malaria cases in India has consistently been rising since 2021. Most of the malaria cases have been reported from districts in Central India dominated by the tribal population, which exposes the lack of proper healthcare facilities and neglected public healthcare services in these areas. It is expected that the number of asymptomatic malaria patients in this region is also high, who contribute heavily to the malaria transmission chain.

Objectives: To understand the epidemiological burden of malaria in Central India with special reference to the tribal areas.

Methods: Secondary data has been collected and analysed from reports available in the public domain, like the World Malaria Report and Annual reports of the National Centre for Vector Borne Diseases Control.

Results: The study has found that India has continuously reported an increase in malaria cases after 2021. There is a 58% increase in Malaria cases in India in 2024 compared to 2021. The top six contributors, namely, West Singbhum Kalahandi, Kandhamal, Godda and Bijapur, which are tribal-dominated districts, have together contributed to roughly 30% malaria cases in the country in 2024.

Conclusions: India's national goal is to achieve zero indigenous malaria cases by 2027 and complete malaria elimination by 2030. Currently, the situation is alarming, so it is necessary to understand the role of existing health posts in malaria elimination efforts. Also, frontline workers like ASHA are key players in malaria programs, but whether they are adequately equipped to handle the challenges needs evaluation. Additionally, there is a strong need to create a mechanism for detecting asymptomatic malaria cases, which act as silent reservoirs of the disease.

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Abstract No: SA-168

Novel genomic markers for accurate identification of *M. leprae* genotypes and drug resistance mutations



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Introduction: Leprosy caused by *Mycobacterium leprae* and *Mycobacterium lepromatosis* still poses challenge to public health particularly in endemic regions. *M. leprae* has such minimal genetic variability that standard genotyping methods frequently fail to provide sufficient resolution for strain distinction. Recent genomic breakthroughs and sequencing of multiple *M. leprae* strains have enabled development of advanced molecular tools, providing deeper insights into the global epidemiology of leprosy.

Objectives: This study aims to develop a genotyping algorithm that can properly identify previously reported and newly described genomic markers based on Whole Genome Sequences (WGS) variable positions of *M. leprae* strains from around the world.

Methods: The integrated bioinformatics workflow begins by retrieving WGS raw data for various *M. leprae* isolates from the database repository and mapping of *M. leprae* TN reference genome using the Burrows-Wheeler Alignment (BWA) tool. A list of Single Nucleotide Variations (SNVs) is generated using a standardized variant calling tool. Finally, a custom, in-house script is employed to identify genotype-specific genomic markers of the strains.

Results: This ongoing study provides comprehensive information on *M. leprae* genetic diversity from the genomes sequenced so far from the various countries, with a primary focus on the evolution and refinement of molecular genotyping framework. Nineteen genotypes (1A to 4P) of *M. leprae* have been identified with specific markers, and the resolution of previous genotyping scheme has been enhanced with these markers.

Conclusions: The updated genotyping scheme developed in our study is particularly valuable for geographic regions dominated by low *M. leprae* genotypic diversity. Our detailed compilation of genomic markers facilitates a precise identification of genotypes through WGS variable regions. Furthermore, these markers serve as ideal candidates for the development of machine learning and artificial intelligence-driven frameworks to accurately identify of genotypes and predict drug resistance from *M. leprae* genomic datasets.

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Abstract No: SA-169

Anti-Hepatitis B Virus Activity of Terminalia chebula Mediated by Reverse Transcriptase Inhibition and Modulation of Host Inflammatory Pathways



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Background: Hepatitis B virus (HBV) infection remains a major global health burden, leading to chronic liver inflammation, fibrosis, and hepatocellular carcinoma with limited therapeutic options. *Terminalia chebula*, a traditional medicinal plant, is reported for hepatoprotective and antiviral activities; however, its molecular mechanism against HBV is still unknown.

Objective: To elucidate the anti-HBV mechanism of *Terminalia chebula* hydroalcoholic extract using integrated *in-vitro* and *in-silico* approaches.

Methods and Materials: *In-vitro* evaluation included phytochemical profiling, antioxidant activity, cytotoxicity, hepatoprotective markers, antiviral assays, antigen quantification, and gene expression analysis in HBV expressing cells (HepG2.2.15). 51 phytocompounds were screened using Molsoft (DLS >0). Compound targets were predicted via SuperPred and HBV-associated targets were retrieved from GeneCards. Gene enrichment was performed using STRING and KEGG. Network construction, and docking against NF-κB was conducted using Cytoscape and Schrödinger, followed by 100 ns dynamics simulation.

Results: The extract showed high total phenolic and flavonoid content, antioxidant activity, and low cytotoxicity (CC_{50} = 1455.84 µg/mL). Significant anti-viral activity was evidenced by time and dose dependent reduction of HBsAg up to 83.31%, HBeAg up to 80.98% levels and by 90.82% reverse transcriptase inhibition, also HBcAg inhibition was observed when co-cultured with THP-1 cells (62%). Further, IL-6 secretion was inhibited by 75% with modulation of HBV associated genes. Network analysis identified NF-κB signaling as the key pathway. Docking and molecular dynamics confirmed stable interactions.

Conclusion: *Terminalia chebula* exerts anti-HBV activity through combined viral inhibition and host-directed immunomodulatory mechanisms, highlighting its potential as a complementary therapeutic candidate for HBV management.

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Abstract No: SA-170

Hepatoprotective potential of *Tamarindus indica* L. against isoniazid–rifampicin-induced hepatotoxicity: an integrated *in-vitro* and *in-silico* Study



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The current study evaluated the phytochemicals composition, antioxidant capacity, and hepatoprotective potential of the hydroalcoholic extract of *Tamarindus indica* L. against isoniazid–rifampicin (INH–RIF)-induced hepatotoxicity. *T. indica* was selected based on previous reports supporting its traditional medicinal use and hepatoprotective properties. INH and RIF, are widely employed as first-line anti-tubercular drugs, induce liver injury primarily through metabolic activation, excessive generation of reactive oxygen species (ROS), and subsequent oxidative stress. Phytochemicals analysis revealed substantial phenolic (25–180 mg GAE/g) and flavonoid content (7.29–22 mg QE/g) in the extract. The antioxidant activity assessed by the DPPH assay demonstrated strong free radical scavenging potential, with IC_{50} values as low as 3.12µg/ml comparable to or exceeding that of ascorbic acid (42.84µg/ml). In vitro studies using HepG2 cells showed that pretreatment with *T. indica* significantly improved cell viability and attenuated INH–RIF-induced cytotoxicity. This protective effect was associated with a significant reduction in hepatic injury biomarkers (AST, ALT, ALP, and LDH), suppression of oxidative stress, and modulation of key genes involved in drug metabolism. Notably, the extract restored cytochrome P450 activity and regulated the expression of detoxification-related genes, indicating a mechanistic role in counteracting drug-induced metabolic stress. Furthermore, *in silico* analyses, including molecular docking, 100-ns molecular dynamics simulations, and MM-PBSA calculations, identified *Proanthocyanidin* as a stable, high-affinity ligand of AADAC (ΔG = –10.3 kJ/mol), providing molecular-level support for the observed hepatoprotective effects. Overall, these findings demonstrate that *Tamarindus indica* L. exhibits significant antioxidant and hepatoprotective potential and may serve as a promising natural adjuvant for mitigating anti-tubercular drug-induced hepatotoxicity.

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Abstract No: SA-171

Triclosan-induced activation of ERK/NF-kB signaling pathways drives the inflammatory responses in epithelial cells and macrophages



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Introduction: Triclosan (TCS), an antimicrobial agent, is widely dispersed and detected in various environmental matrices and organisms including human tissues and biological samples. A sustained inflammatory response is an important priming event in various disease pathogenesis. TCS-induced inflammatory response and its underlying molecular mechanisms remain largely unexplored.

Objectives: In this study, the effect of TCS exposure on inflammatory activation was investigated in both non-malignant and malignant lung epithelial cells (BEAS-2B and A549) as well as in murine macrophages (J774).

Methods: Inflammatory activation was assessed using cell viability assays, RT-qPCR, ELISA, and western blotting to evaluate cytokine expression and ERK/NF-κB signalling.

Results: The results revealed that TCS treatment could significantly induce various pro-inflammatory cytokines and chemokines in all cell types compared to the corresponding vehicle-treated cells. Furthermore, TCS-mediated inflammatory response is associated with the activation of extracellular-signal-regulated kinase (ERK)1/2 and nuclear factor-kappa B (NF-kB) p65 signaling pathways. As expected, inhibitors specific for ERK1/2 (PD98059) and NF-kB p65 (IMD0354) signaling pathways effectively attenuated TCS-induced inflammatory response in BEAS-2B cells.

Conclusion: This study demonstrates that ERK/NF-kB pathways contribute to the inflammatory response induced by TCS. Further, *in-vivo* studies are needed for a better understanding of TCS-induced inflammation-associated diseases in various organs, including the lungs.

Acknowledgement(s) and Funding: The authors acknowledge the support of Department of Science and Technology (DST), Ministry of Science and Technology, India, for the award of INSPIRE Fellowship (DST/ INSPIRE Fellowship/[IF240038]) to the first author.

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Abstract No: SA-172

Machine Learning Driven Spatiotemporal Prediction of Dengue Vector Dynamics from Landscape and Microclimatic Variables



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Introduction: Urbanization alters local climate and land-cover patterns, creating heterogeneous environments that strongly influence mosquito population dynamics. Conventional vector studies often rely on coarse climatic indicators and linear analyses, limiting their ability to capture species-specific responses within rapidly changing urban systems. Integrating microclimate, landscape structure, and predictive modelling is therefore essential for improved urban mosquito risk assessment.

Objectives: This study aimed to (i) characterize the spatiotemporal dynamics of *Aedes aegypti* and *Aedes albopictus* across an urban landscape, (ii) identify species-specific microclimatic and land-cover drivers of mosquito density, and (iii) develop predictive machine-learning models for urban mosquito risk classification.

Methods: Monthly adult mosquito collections were conducted at 29 georeferenced sites in Bhopal (2020–2022), with abundance quantified using man-hour density (MHD). Environmental predictors were grouped into monthly microclimatic variables and site-level landscape variables, each analysed using principal component analysis (PCA) with k-means clustering. PCA-derived cluster coefficients were then used as composite predictors in supervised machine-learning models (Random Forest, Neural Network, and XGBoost).

Results: Microclimatic PCA identified three clusters: Cool-Moderate, Warm-Moist, and Hot-Arid with distinct mosquito density patterns. Landscape PCA revealed three clusters: Green Buffer, Urban Core, and Transitional Niche. Neural network models performed best for both species (AUC 0.94 for *Ae. aegypti*; 0.92 for *Ae. albopictus*). Permutation importance showed contrasting drivers: *Ae. aegypti* abundance was primarily driven by daytime land surface temperature, minimum air temperature, and urban microclimatic regime, while *Ae. albopictus* depended more on nighttime land surface temperature, vegetation cover (NDVI), and relative humidity.

Conclusions: These findings reveal distinct species-specific urban microclimates: *Aedes aegypti* is strongly linked to thermally stressed, densely urbanized areas, while *Aedes albopictus* prefers vegetated, humid, and nocturnally moderated conditions. By combining dual-domain PCA with machine-learning models, this study offers a predictive, climate-informed framework for urban mosquito risk assessment and targeted vector control.

Acknowledgement(s) and Funding
The study was funded by Indian Council of Medical Council, New Delhi to Dr. Devojit Kumar Sarma (award number 6/9-7(208)/2019-ECD-II) and fellowship to Deepanker Das (award number: Fellowship/109/2022-ECD-II).

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Abstract No: SA-173

Isolation and characterization of lytic bacteriophages against multi drug-resistant *Acinetobacter baumannii*



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Introduction: *Acinetobacter baumannii*, a Gram-negative opportunistic pathogen, is a leading cause of hospital-acquired infections (HAIs) like pneumonia, bacteremia, meningitis, and urinary tract infections. The growing resistance of *A. baumannii* to multiple antibiotics, including last-resort drugs like tigecycline and colistin, poses a significant threat to global health.

Objectives: The study aimed to isolate and identify bacteriophages specific to drug-resistant *Acinetobacter baumannii* from hospital sewage, while also characterizing the phenotypic and genotypic resistance mechanisms of the bacterial isolates, including efflux pump activity and biofilm formation.

Methods: *A. baumannii* strains were isolated from hospital sewage and confirmed via PCR targeting the blaOXA-51-like gene. Antibiotic susceptibility testing was performed to determine resistance profiles. Efflux pump activity, biofilm formation, and molecular resistance determinants were assessed. Lytic bacteriophages targeting MDR *A. baumannii* were isolated from sewage and characterized via TEM, RAPD-PCR, host range and bacterial reduction assay, one-step growth and stability analyses.

Results: Four identified *A. baumannii* isolates exhibited MDR and extensively drug-resistant (XDR) profiles, with the coexistence of blaOXA-23 and blaNDM-1 genes. Efflux pump activity was detected in two isolates, and biofilm formation varied depending on sugar sources. Five bacteriophages were isolated, showing lytic activity against two MDR *A. baumannii* isolates. Phage Abp1 demonstrated strong bacterial reduction with a 30-min latent period and burst size of 68 PFU/cell with the highest titre at 37 °C and near neutral pH.

Conclusion: This study provides the first report of bacteriophage isolation and characterization against MDR *A. baumannii* in Bhopal, Madhya Pradesh (India), filling a significant research gap in this region. The findings highlight the potential of bacteriophages as therapeutic agents against MDR *A. baumannii* infections, particularly in hospital settings. By linking bacterial resistance traits with phage efficacy, this study reinforces the role of phage therapy as a promising alternative to conventional antibiotics.

Acknowledgement(s) and Funding: The authors highly acknowledge the support from Council of Scientific and Industrial Research (CSIR) for granting CSIR-SRF for the first author (17/12/2017(iI1 EU-V).

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Abstract No: SA-174

In-Silico Analysis of Genomic Diversity and Mutational Landscape of Human Astrovirus



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Introduction: Human astroviruses (HAstV) are one of the major etiological agents of acute gastroenteritis, affecting young children, the elderly, and immunocompromised individuals. Despite their global impact, evolutionary dynamics and genomic diversity remain incompletely characterized.

Objectives: To study genomic diversity and mutation profiles of HAstV using *in-silico* methods.

Methods: In this study, a comprehensive *in-silico* analysis of 179 complete HAstV genomes was performed. Complete genomes were retrieved from different public databases to investigate the phylogenetic structure and mutation density patterns. Sequences were screened with a custom Python script, then aligned with MAFFT and refined with TrimAI, followed by IQTREE3, to construct a maximum-likelihood phylogenetic tree, and the mutation density distribution map was visualized using a Python script.

Results: Phylogenetic analysis revealed three well-supported lineages corresponding to the Classical, MLB, and Virginia (VA) genogroups, with major internal nodes supported by high bootstrap values and genetic distances. Our data show HAstVs are circulating globally, MLB clade forming a compact yet highly diverse lineage, characterized by long branch lengths, indicating rapid diversification. In contrast, the VA clade represents a distinct, stable, and less prevalent lineage. Mutation density analysis revealed hypervariability at the 3′ terminal region, while ORF1a/1b remained highly conserved, suggesting functional constraints; major variation was observed in capsid proteins. However, the nonstructural protein, RdRp, remained relatively conserved.

Conclusion: These findings suggest the HAstVs comprise multiple evolutionary lineages with extensive diversification, and a phylogenetic framework facilitates understanding their global molecular epidemiology and evolutionary dynamics. These findings may be useful in future diagnostic and vaccine development.

Acknowledgement(s) and Funding: The authors highly acknowledge the support from Indian Council of Medical Research for granting ICMR-JRF for the first author (3/1/3/JRF-2023/HRD-74(144243)).

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Abstract No: SA-175

Biomonitoring of Serum Endocrine-Disrupting Chemicals (EDCs) Exposure and Type 2 Diabetes Risk: A Case-Control Study



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Introduction: Type 2 diabetes mellitus (T2DM) is a multifactorial disorder driven by genetic, lifestyle, and environmental interactions. While endocrine-disrupting chemicals (EDCs) are increasingly recognized as metabolic disruptors, epidemiological evidence linking serum EDC concentrations to T2DM risk in the Indian population remains limited.

Objectives: The study aimed to estimate serum levels of selected EDCs (eight phthalates and two phenolic compounds) and to explore their association in type 2 diabetes cases and controls.

Methods: We conducted a case-control study involving 388 participants (194 clinically diagnosed T2DM cases and 194 non-diabetic controls) in Bhopal, India. Fasting serum levels of eight phthalates and two phenolic compounds were quantified using validated GC-MS methods. To account for multicollinearity and mixture effects, we applied a robust statistical framework including multivariable logistic regression, Least Absolute Shrinkage and Selection Operator (LASSO), and Bayesian Kernel Machine Regression (BKMR) to assess the role of EDCs in diabetes and other metabolic variables.

Results: Of the analytes measured, seven phthalates showed detection rates exceeding 70%, with DBP exhibiting the highest geometric mean concentration. DMP and DEP levels were significantly elevated in T2DM cases compared to controls ($p < 0.05$). Convergence across multivariable, LASSO, and BKMR models consistently identified DMP and DEP as significant predictors of T2DM risk. Furthermore, DBP exposure was distinctively associated with obesity and dyslipidemia phenotypes.

Conclusions: This study provides multiparametric evidence identifying specific phthalates (DMP and DEP) as potential environmental risk factors for T2DM in India. From a public health perspective, these findings underscore the necessity for stricter regulatory oversight of plasticizers and suggest that environmental chemical screening should be integrated into national non-communicable disease (NCD) prevention strategies to mitigate the growing diabetes burden.

Acknowledgement(s) and Funding: The study was funded by Indian Council of Medical Council, New Delhi to Dr. Devojit Kumar Sarma (ICMR extramural grant no. 5/4/5-12/Diab.20-NCD-III) and Lokendra Rathod received a fellowship (#DBTHRDPMU/JRF/BET20/I2020/AL/272) from the Department of Biotechnology (DBT).

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Abstract No: SA-176

Small Area Estimation of Cognitive Impairment among Older Adults in India: A Multi-level approach



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Introduction: Given the share and growth of the ageing population in India, the increasing prevalence of cognitive decline among older adults is a grave concern. In this study, we examine the underlying factors of cognitive impairment among older adults (60+ years) at the individual, household, and community levels in India.

Methods: We used the first wave of the Longitudinal Aging Study in India (LASI-1) conducted in 2017-18 in the States and Union Territories of India. The outcome variable, cognitive impairment, was constructed as the lowest 10th percentile of five domains (memory, orientation, arithmetic function, executive function, and object naming). The total score across the five domains ranges from 0 to 43. Descriptive statistics (univariate and bivariate) were used along with multilevel logistic regression to estimate the variations at different levels.

Findings: There were 15% [SD = 0.36] of the total older population was found to be in poor cognitive condition. The highest variation (46%) in cognitive impairment was found at the household level. Almost 13% of the households reported that all elderly members were cognitively impaired, and in 7% of households, half of the elderly members had cognitive impairment. The covariates at the individual, household, and community levels, such as wealth status and living arrangements, significantly explained the variation in cognitive impairment among the older population.

Discussion: The findings from this study highlight that cognitive decline among the older population is not only a biomedical issue; rather, it is intertwined with socioeconomic and living conditions and mental health burden. The role of education, mental health, social protection, and chronic disease management is critical in mitigating the growing prevalence of cognitive decline. Future studies from the second wave of LASI can address the important question of how early and mid-life risks translate into later cognitive conditions.

Keywords: Cognitive decline, Older adults, India, LASI-1, Mental health

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Abstract No: SA-177

Oral Health Inequity in India: Magnitude, Determinants, and Policy Imperatives



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Background: Oral diseases remain among the most prevalent non-communicable diseases in India and represent a significant yet under-prioritized public health challenge. Despite being largely preventable, oral health outcomes are unequally distributed across socio-economic groups, geographic regions, and states. Addressing oral health inequity is central to advancing universal health coverage (UHC) and the WHO Global Oral Health Action Plan.

Methods: This oral presentation synthesizes evidence from Global Burden of Disease (GBD) estimates, national surveys, and published literature to assess the magnitude of oral disease burden in India, examine key social and health system determinants of inequity, and identify policy and implementation gaps.

Results: GBD estimates indicate that oral disorders a ect a majority of India's population, with disproportionately higher burden among socio-economically disadvantaged and rural populations. Marked inter-state variation reflects disparities in income, education, health infrastructure, and service availability. Utilization of dental services remains low, out-of-pocket expenditure is high, and the dental workforce is concentrated in urban areas. Behavioral risk factors, particularly tobacco use, further exacerbate inequities, especially in relation to oral cancer.

Conclusion: Oral health inequity in India is driven by structural, social, and systemic determinants. Aligning national policies with the WHO Global Oral Health Action Plan—through integration of oral health into primary healthcare, improved workforce distribution, strengthened prevention, and enhanced financial protection—is essential to reduce inequities and achieve equitable oral health outcomes.

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Abstract No: SA-178

Antibiotic-resistant Enterobacterales colonization among children in a sub-urban community in South India



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Background: Enterobacterales resistant to third-generation cephalosporins and carbapenems are classified as high-priority antimicrobial-resistant (AMR) pathogens by the WHO. Resistance mediated by extended-spectrum β-lactamase (ESBL) enzymes compromises the efficacy of β-lactam antibiotics and is frequently associated with co-resistance to multiple antibiotic classes. Data on community-level gut colonization with resistant Enterobacterales among children in India remain limited.

Objective: This study aimed to estimate the prevalence of gut colonization with extended-spectrum cephalosporin-resistant Enterobacterales (ESCrE), carbapenem-resistant Enterobacterales (CRE) and colistin-resistant Enterobacterales (Col-RE) phenotypes among children in a community setting.

Methods: Stool samples were collected from children enrolled from households in a sub-urban community in South India. Samples were plated on CHROMagar selective for ESCrE, CRE and Col-RE. Bacterial identification and antibiotic susceptibility testing were done using Vitek-2 Compact and disc-diffusion testing. Colistin susceptibility was assessed by broth microdilution for a subset of isolates. Prevalence estimates were calculated with 95% confidence intervals (CIs).

Results: Between December 2022 and April 2023, 390 households were approached and 127 children provided stool samples following informed consent. The median age was 8 years (IQR: 5-10), with an equal male-to-female ratio. A total of 452 Enterobacterales were identified, with *Escherichia coli* (67.7%) and *Klebsiella pneumoniae* (22.3%) being the predominant species. The prevalence of colonization with ESCrE was 79.5% (95% CI: 71.7% – 85.6%), CRE was 6.3% (95% CI: 3.2% – 11.9%), and Col-RE was 3.1% (95% CI: 1.2% – 7.8%). Overall, 79.5% (95% CI: 71.7% – 85.6%) of children were colonized with at least one resistant phenotype.

Conclusion: High prevalence of gut colonization with antibiotic-resistant Enterobacterales highlights children as an important reservoir within community settings. These findings underscore the need for strengthened community-based AMR surveillance and interventions targeting early-life exposures.

Acknowledgement: I sincerely thank ICMR for awarding me Senior Research Fellowship to conduct my doctoral research work, and the ICMR National Institute of Epidemiology for hosting me and providing the facilities to carry out my doctoral studies.

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Abstract No: SA-179

Isolation, detection & characterization of exosomes from HIV-1 infected and uninfected CD4+ T cells



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Abstract Background: Exosomes are nano-sized extracellular vesicles that mediate intercellular communication by transferring proteins and nucleic acids. In HIV-1 infection, exosomes derived from $CD4^+$ T cells are being increasingly recognized as potential modulators of viral persistence and immune regulation. Variability in isolation protocols and the biophysical similarity of exosomes and HIV virions remain major technical challenges to the isolation and characterization of exosomes of HIV-infected cells.

Objective: This study aimed to compare various isolation protocols to obtain high quality exosomes from HIV-1–infected $CD4^+$ T cells suitable for downstream molecular analyses.

Methods: Exosomes were isolated from conditioned media of $CD4^+$ T cells using polyethylene glycol (PEG6000) precipitation, differential ultrafiltration combined with size exclusion chromatography, and exoRNeasy Midi and Maxi kits that work on the principle of membrane affinity . The size distribution and concentration of the isolated exosomes were assessed by nanoparticle tracking analysis (NTA). Exosomal identity was confirmed by immunoblotting for canonical EV markers (CD63, CD9) and the absence of cellular contaminants. Potential HIV-1 contamination was ruled out by testing the mixture HIV-1 p24 protein. Exosome-associated RNA was isolated and analysed by host and viral transcript sequencing.

Results: All isolation methods yielded vesicles within the expected size range (50–150 nm), with method-dependent differences in yield and purity. PEG6000 precipitation-based isolation provided higher particle concentrations, whereas exoRNeasy-based isolation enabled robust recovery of exosome-associated RNA. Differential ultrafiltration method showed minimal detectable viral contamination and reduced non-vesicular background. Comparative analyses revealed distinct extracellular vesicle profiles between HIV-1 infected and uninfected CD4+T cells.

Conclusion: The differential ultrafiltration method combined with size exclusion chromatography yielded reliable characterization of exosomes and their RNA cargo, providing a robust framework for studying exosome-mediated mechanisms in HIV pathogenesis.

Acknowledgement: I sincerely thank ICMR for awarding me Senior Research Fellowship to conduct my doctoral research work, and ICMR National Institute of Epidemiology (ICMR-NIE) for hosting me and providing the facilities to carry out my doctoral studies.

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Abstract No: SA-180

Exploring non-parenteral routes for delivery of peptide therapeutics.



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Introduction: Peptide therapeutics are an important class of drugs due to their high specificity, potency, and favorable safety profiles. However, their clinical application is often limited by poor oral bio-availability, rapid enzymatic degradation, and low membrane permeability. To overcome these challenges, alternative routes of administration are being explored to enhance therapeutic efficacy and patient compliance.

Objectives: To evaluate alternative delivery strategies for peptide therapeutics to improve their clinical applicability.

Methods: My research work will focus on non-parenteral peptide delivery approaches. These include various administration routes, formulation strategies, and enhancement technologies will be analyzed. Approaches such as skin penetration enhancers, carrier systems, and device-assisted delivery methods such as inhalers (for intranasal delivery). *In vitro* studies will be conducted to evaluate peptide stability, permeability, and release characteristics using suitable biological membrane models. *Ex vivo* permeation studies using appropriate animal model or synthetic membrane models will be performed to assess epithelial transport efficiency. Additionally, formulation optimization will be carried out to improve peptide stability and bio-availability. The outcomes will be analyzed to identify the most promising delivery strategies for improving clinical applicability of peptide therapeutics.

Results: Parenteral routes such as subcutaneous and intravenous administration remain the most established methods, offering high bioavailability and predictable pharmacokinetics. Non-invasive routes including nasal, pulmonary, buccal, and transdermal delivery have shown promising outcomes by bypassing first-pass metabolism. Advanced strategies such as cell-penetrating peptides, ionic liquids, microneedles, and permeation enhancers significantly improve epithelial transport and systemic absorption. Several peptide drugs delivered via these routes have progressed to clinical use, demonstrating improved patient adherence.

Conclusions: Alternative delivery routes play a crucial role in expanding the therapeutic potential of peptide-based drugs. Continued advancements in formulation technologies and delivery systems are expected to further improve bioavailability, reduce dosing frequency, and enhance patient compliance, thereby broadening the clinical applicability of peptide therapeutics.

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Abstract No: SA-181

Perception and determinants leading to antimicrobial (mis)use in the rural communities of Odisha, India



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Introduction: Antimicrobial resistance (AMR) has emerged as a major global public health threat, driven largely by inappropriate antimicrobial use in human, animal, and environmental settings. Low- and middle-income countries, including India, face a disproportionate burden due to high antibiotic consumption, easy over-the-counter availability, and limited community awareness. Understanding community-level knowledge, attitudes, and practices (KAP) related to antimicrobial use is essential for designing effective antimicrobial stewardship and public health interventions, particularly in rural settings where evidence remains limited.

Objectives:

1. To assess the knowledge, attitudes, and practices related to antimicrobial use and antimicrobial resistance among rural communities of Tigiria block in Odisha, India.
2. To examine healthcare utilization patterns and quality of life (QOL) among the study population.

Methods: A community-based cross-sectional study was conducted between November 2021 and January 2022 across 25 rural villages of Tigiria block, Cuttack district, Odisha. A total of 1,003 adult participants were selected using cluster and systematic random sampling. Data were collected using a semi-structured questionnaire covering socio-demographic characteristics, antibiotic use, awareness of AMR, healthcare utilization, and quality of life assessed using the WHOQOL-BREF scale. Data were analyzed using descriptive statistics, independent t-tests, and one-way ANOVA, with statistical significance set at $p < 0.05$.

Results: Only 44.5% of participants had heard of antimicrobial medicines, and awareness of antimicrobial resistance was extremely low (0.1%). Approximately 14.8% reported purchasing antibiotics without prescription, and 20.1% discontinued antibiotics before completing the full course. Antibiotics were commonly used for conditions such as cold and diarrhoea. The physical domain of quality of life recorded the lowest mean score. QOL scores varied significantly across age, gender, education, and ethnicity.

Conclusion: The study reveals substantial gaps in community knowledge and inappropriate practices related to antimicrobial use in rural Odisha. These findings highlight the urgent need for community-focused education, strengthened antimicrobial stewardship programs, and policy-driven interventions to improve rational antibiotic use and curb the growing threat of AMR.

Acknowledgement(s) and Funding: I would like to thank to Indian Council of Medical Research, New Delhi for their support

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Abstract No: SA-182

Monocyte TNF-Superfamily Signalling Dysregulation in Tuberculosis–Type 2 Diabetes Mellitus Comorbidity



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Background: Type 2 diabetes mellitus (T2DM) increases susceptibility to tuberculosis (TB) and contributes to dysregulated immune responses, partly through altered monocyte signalling. Although our earlier work has demonstrated that T2DM alters monocyte subsets and promotes hyperinflammatory responses during TB, the mechanisms underlying dysregulated TNF-superfamily pathways in TB-T2DM comorbidity are underexplored.

Methods: Study cohort of 176 individuals comprising TB(44), TB–T2DM(44), T2DM-only(44), and healthy controls(44) were evaluated. Peripheral blood mononuclear cells (PBMCs) (20 samples per study group) were analysed by multicolour flow cytometry to assess classical monocyte ($CD14^{+}CD16^{-}$) expressing activation markers and intracellular cytokines following stimulation with purified protein derivative (PPD), whole-cell lysate (WCL), and TLR2/4 ligands. Plasma samples (44 samples per study group) were used to measure TNF-superfamily receptors and quantified using Human ProcartaPlex 12-plex multiplex ELISA. Further, Spearman correlation analysis was performed between soluble TNF-superfamily molecules and monocyte cytokine responses.

Results: Flow cytometric analysis demonstrated a distinct phenotype, with significant increase of net frequencies of intercellular cytokines [Interleukin(IL)-6, IL-12, IL- 1β, IL-1α, Tumour Necrosis Factor (TNF) - α and IL-10) and activation markers (Programmed Death ligand-2(PDL-2), Cluster of Differentiation(CD)163 and CD206] in TB-T2DM compared to TB or T2DM groups upon TB-specific antigen stimulation (PPD, WCL) ($p<0.05$). Multiplex ELISA revealed alterations in TNF-superfamily receptor expression, with significant decrease in CD137, CD40, GITR, TNFR1/2, TRAIL-R1/R2 and increase in CD27, CD30, Fas (APO-1) expression in TB-T2DM compared to TB or T2DM groups. Correlation analysis revealed distinct association pattern among TNF receptors, cytokine-associated and activation markers. Weak to inverse associations were observed between cytokine-associated markers (including IL-6, IL-1β, TNF-α and IL-10) and activation markers (CD86 and PD-L1) in unstimulated and antigen stimulated (PPD, WCL) monocytes responses across multiple TNF receptor superfamily members ($p<0.05$).

Conclusion: Together, our results suggest that monocyte dysfunction linked with hyperglycaemia leads to dysregulated TNF-superfamily receptor expression and defective receptor–cytokine integration, which may contribute to impaired immune regulation in TB–T2DM comorbidity.

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Abstract No: SA-183

Hybrid Artificial Intelligence Modelling of Longitudinal Cough Acoustics for Early Treatment Response in Pulmonary Tuberculosis



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Background: Pulmonary tuberculosis (TB) remains a major global health burden, with wide variation in early recovery despite standardized treatment. Although infectiousness often declines within the first two weeks, this critical early phase is poorly understood because routine monitoring relies on microbiological and radiological tests performed later. Cough, a key driver of transmission, may change earlier than these markers and could indicate early treatment response. Advances in Artificial Intelligence (AI) and audio signal analysis enable objective evaluation of cough acoustics as digital biomarkers. Since much clinical data are unstructured, leveraging them in trials could improve early efficacy assessment.

Methods: We developed a hybrid AI-statistical modelling framework to objectively quantify early treatment recovery in microbiologically confirmed pulmonary tuberculosis patients through cough sound analysis, facilitating early treatment response evaluation and supporting strategies to reduce infectiousness. Cough audio from the Coda TB dataset was segmented into 0.5-second clips during the first two weeks of therapy. Statistical time and frequency-domain acoustic features were extracted and combined with deep neural audio embeddings to construct a digital Cough Severity Index (d-CSI). Longitudinal trajectories of d-CSI were analysed using linear mixed-effects models for population-level trends and Latent Class Mixed Models (LCMM) for subgroup stratification.

Result & Discussion: Population-level modelling demonstrated significant early improvement in cough severity (β = -0.021/day; median 14-day change: -0.26 [IQR: -0.32 to -0.18]; $p < 0.001$). LCMM revealed three latent recovery phenotypes with distinct slopes: a rapid improvement group (37%), a gradual improvement group (41%), and a minimal improvement group (22%) characterized by persistently elevated d-CSI. These findings reconcile the strong average treatment response with heterogeneous individual trajectories.

Conclusion: This hybrid framework offers an objective **cough based** digital biomarker of early treatment response, providing short-term prognostic insights during the critical infectiousness window.

Keywords: Tuberculosis, Cough acoustics, Digital biomarkers, Treatment response, Phenotyping.

Acknowledgment:
We sincerely acknowledge and thank ICMR-NIRT for granting permission to present this work at SANVAD-2026 at ICMR-NIMR. This study utilizes the CODA TB dataset, which is publicly available TB cough audio dataset accessed through Synapse platform.

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Abstract No: SA-184

Profiling of Circulating Inflammatory Biomarkers in Individuals with Latent Tuberculosis Infection Compared with Healthy Controls



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Introduction: Latent Tuberculosis Infection (LTBI) is an asymptomatic state marked by immune containment of *Mycobacterium tuberculosis* (Mtb) but may involve persistent low-grade inflammation. Interferon-gamma release assay (IGRA) widely used for LTBI diagnosis, cannot distinguish latent infection from active disease and do not reflect inflammatory or immune activation status. Therefore, identification of complementary biomarkers is needed to better characterize immune responses in LTBI.

Objective: To evaluate the various inflammatory markers such as acute phase proteins, complement proteins and adhesion molecules and assess the immune status among LTBI.

Methodology: In this study, healthy volunteers were recruited from in and around Chennai during 2023-2025. Sample size was calculated and a total of 84 participants were enrolled and equally allocated into two groups (LTBI-positive & LTBI-negative). This is a longitudinal prospective study and the present analysis reports data from baseline only. Baseline demographic characteristics were comparable between groups. Circulating inflammatory markers, including acute-phase proteins (C3, haptoglobin, α1-acid glycoprotein, α2-macroglobulin), innate markers (MBL, RBP-4), adhesion molecules (VCAM-1, ICAM-1), and chemokines were quantified using ELISA and multiplex assays. Group comparisons and correlation coefficients (ρ) with p-values were calculated.

Results: We found a significant difference in the C3 protein, which is significantly downregulated ($p<0.001$), and α2 macroglobulin which is significantly upregulated ($p<0.0001$) in LTBI positive group. Correlation analysis demonstrated coordinated inflammatory regulation, with moderate positive associations among chemokines and adhesion markers, including IL-8–MCP-1 ($\rho = 0.54$), GRO-α–RANTES ($\rho = 0.49$), Eotaxin–IL-8 ($\rho = 0.39$), Eotaxin–MCP-1 ($\rho = 0.48$), and ICAM-1–IP-10 ($\rho = 0.31$) (all $p < 0.05$). These findings indicate network-level immune interactions rather than isolated biomarker changes.

Conclusion: LTBI is associated with a characteristic inflammatory signature marked by downregulated C3 and upregulated α2-macroglobulin, indicating altered complement and acute-phase responses. These circulating proteins may serve as indicators of immune status and hold potential for risk stratification or adjunctive screening along with IGRA, although validation in larger longitudinal cohorts is required before clinical or public health application.

Acknowledgment: HG work supported by CSIR fellowship

Funding: This work was funded by ICMR intramural funding.

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Abstract No: SA-185

A CRISPR-Cas13a- Based Molecular Assay for Rapid and Accurate Detection of *Mycobacterium tuberculosis*



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Background: Rapid, simple, and highly sensitive diagnostic methods are essential for effective 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* (*M.tb*) and to evaluate its analytical and clinical performance in clinical specimens.

Methods: The assay was designed using CRISPR-derived RNAs (crRNAs) targeting a conserved region of the *rpoB* gene of *M.tb*. Pre-amplification was performed using both polymerase chain reaction (PCR) and recombinase polymerase amplification (RPA). Analytical sensitivity, specificity, and limit of detection (LOD) were determined using cultured *M.tb* isolates and non-tuberculous mycobacteria (NTM). Clinical validation was carried out using sputum samples, with mycobacterial culture as the reference standard.

Results: The assay demonstrated a limit of detection of 20 copies/µL and 100 CFU/mL, with no cross-reactivity observed with NTMs or other bacterial species. PCR-based amplification achieved 100% sensitivity in cultured isolates. In clinical sputum samples, the assay exhibited a sensitivity of 95.56% and a specificity of 93.3% compared to culture.

Conclusion: The CRISPR-Cas13a based assay provides high sensitivity and specificity for the detection of *M.tb* in sputum samples, highlighting its potential as a promising molecular diagnostic tool for tuberculosis.

Keywords: Tuberculosis; *Mycobacterium tuberculosis*; CRISPR-Cas13a; crRNA; diagnosis

Acknowledgement: I sincerely thank the Lady Tata Memorial Trust (LTMT) for awarding me a doctoral fellowship, and the ICMR-National Institute for Research in Tuberculosis (ICMR-NIRT) for hosting me and providing the facilities to carry out my doctoral studies.

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Abstract No: SA-186

RAPID AND COST EFFECTIVE DETECTION OF BEDAQUILINE AND LINEZOLID DRUG RESISTANCE IN *MYCOBACTERIUM TUBERCULOSIS* BY LUCIFERASE REPORTER PHAGE ASSAY



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Introduction: A simple, rapid, cost-effective, in-house and bio-friendly method is required for detection of drug resistance in *Mycobacterium tuberculosis* (Mtb). Luciferase reporter phage (LRP) assay has the potential to develop a standardised drug susceptibility testing (DST) of Bedaquiline (BDQ) and Linezolid (LZD)

Objective: To validate LRP assay for rapid detection of BDQ and LZD drug resistance in *M. tuberculosis*

Methodology: The LRP phAETRC202 was used for the validation and propagated using standard protocol. A total of 153 MTB isolates were used for testing DST of BDQ and LZD by LRP assay. DST by Mycobacterium growth indicator tube (MGIT) 960 liquid culture is used as control for BDQ and LZD resistance.

Results: The sensitivity, specificity, positive and negative predictive values and efficiency of LRP assay for BDQ drug resistance was found to be 100%, 98.6%, 86.7%, 100% and 98.7% respectively compared to MGIT 960. The specificity, negative predictive value and efficiency of LRP assay for LZD DST was found to be 98%, 100% and 98%, respectively. Since none of the isolates exhibited LZD resistance by MGIT 960, the sensitivity and positive predictive value could not be calculated. The turnaround time for the detection of drug resistance for LRP for any drug is 3 days compared to 4-12 days by MGIT 960 and the test cost for LRP is approximately INR 200 (Indian Rupees) for a drug compared to INR 1000 by MGIT 960.

Conclusion: The LRP assay can be used for rapid and cost-effective detection of Bedaquiline and Linezolid drug resistance in *Mycobacterium tuberculosis*.

Funding: ICMR Intramural

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Abstract No: SA-187

TB-INDUCED IMMUNOSENESCENCE CONTRIBUTES TO INCREASED MORTALITY AMONG SUCCESSFULLY TREATED AND CURED TB PATIENTS



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Background: Several studies have documented a roughly three-times higher all-cause mortality rate in cured TB patients as compared to their counterparts who have never had TB. Key contributors of increased mortality include chronic lung diseases (COPD), cardiovascular disease, and cancer, often driven by underlying metabolic abnormalities. The present study is based on the hypothesis that persistent immune activation and prolonged inflammation associated with TB contribute to accelerated immunological senescence and early onset of metabolic diseases in cured TB patients, leading to significantly higher mortality rates in this population.

Methods: Individuals aged 18-59 years were enrolled into two groups namely previously treated and cured TB patients (Group A) and age, sex and lifestyle matched healthy controls with no prior TB history (Group B). Thirty participants from each group were included in this analysis. Peripheral Blood Mononuclear Cells (PBMCs) were isolated from whole blood and used to assess apoptosis, frequency of regulatory T cell population, T cell exhaustion markers and telomere length. Statistical analyses were performed using GraphPad Prism and $p < 0.05$ considered statistically significant.

Results: PBMCs from Group A demonstrated a significantly higher rate of apoptosis compared to Group B ($p<0.0001$). Myeloid derived suppressor T cells and regulatory T cells were significantly increased in Group A ($p=0.01$ and $p=0.001$ respectively) compared to group B. Expression of T-cell exhaustion markers CD95 and CD95L were significantly elevated in Group A compared to group B in different subsets of memory $CD4^+$ T cells like central memory (CD95; CD95L- $p<0.0001$, $p<0.0001$), effector memory ($p<0.0001$, $P=0.001$) and Terminally Differentiated Effector Memory RA (TEMRA) cells ($p= 0.04$, $P<0.0001$). Additionally, PBMCs from Group A exhibited significantly shorter telomeres (2-3 kb) compared to Group B (5-15kb) ($p=0.0358$).

Conclusion: Cured TB patients exhibit features of accelerated immune aging, including increased apoptosis, expansion of suppressor cell phenotypes, T-cell exhaustion markers and telomere attrition. These findings suggest that TB may induce long lasting immune alterations despite clinical cure, highlighting the need for long term immune monitoring in TB survivors.

Acknowledgment: The authors thank Indian Council of Medical Research (ICMR) for funding this study and sincerely acknowledge participation of all the volunteers who took part in the study. The first author also thanks the C-TRIUMPh study team for their valuable contributions.

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Abstract No: SA-188

DESIGN AND CHARACTERIZATION OF PEPTIDO-MIMETICS OF BROADLY NEUTRALIZING ANTIBODIES TARGETING VULNERABLE SITES ON THE HIV-1 ENVELOPE



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Background: Broadly neutralizing antibodies (bNAbs), which target conserved epitopes on the HIV-1 envelope and neutralize diverse viral strains, have gained attention as potential adjuncts to therapy. Alongside antibodies, therapeutic peptides and proteins have emerged as promising candidates due to their specificity and selective mechanism of action. This study is based on the hypothesis that short peptides derived from the paratopes of bNAbs could serve as potent peptide-mimetics.

Methods: Using *in silico* approaches like molecular modelling, interface analysis, and molecular dynamics simulations, we identified eleven potential peptide candidates from the established bNAbs targeting five conserved epitopes on the HIV-1 envelope. *In vitro* assays, including cytotoxicity, hemolysis, anti-HIV activity, Time-of-Addition (TOA), and improvement of neutralization and inhibitory potential of different peptide cocktails were performed to validate their efficacy.

Results: PBMC cytotoxicity and hemolytic assays demonstrated that these peptides were safe and non-toxic. All eleven peptides exhibited anti-HIV activity against the laboratory-adapted HIV-1 strain NL4-3. The mean IC_{50} values of these peptides were within optimal inhibitory ranges (1.5–17 µM), and the peptides effectively blocked viral entry. Furthermore, no significant improvement in inhibitory potency was observed when the peptides were used in cocktails against NL4-3, although two peptide cocktails achieved >61% inhibition.

Conclusion: These findings suggest that short bNAb-derived peptides retain neutralization capacity and may serve as promising HIV-1 entry inhibitors, warranting further validation in primary isolates and *in vivo* models.

Acknowledgement: I sincerely thank the Department of Biotechnology (DBT) for awarding me a doctoral fellowship, and the ICMR–National Institute for Research in Tuberculosis (ICMR-NIRT) for hosting me and providing the facilities to carry out my doctoral studies.

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Abstract No: SA-189

Plasma and TB Antigen Stimulated Immune Signatures associated with treatment outcomes in Pulmonary Tuberculosis



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Background: Tuberculosis (TB) remains a major global health challenge, with India contributing nearly 26% of global cases. Persistent disease burden is driven by latent infection, comorbidities such as diabetes and Human Immunodeficiency Virus (HIV), and considerable rates of treatment failure, recurrence, and mortality. Identifying reliable immunological biomarkers before and during anti-TB treatment (ATT) could enable early risk stratification and improve disease management.

Aim: To examine the association between host immune responses and unfavourable treatment outcomes in pulmonary TB (PTB) and identify blood-based immune signatures predictive of adverse outcomes.

Methodology: This retrospective study (2014–2019) evaluated 446 newly diagnosed, smear- and culture-positive, drug-sensitive PTB patients followed for 12 months during ATT. Sixty-eight experienced unfavourable outcomes (treatment failure, relapse/recurrence, or death). A nested case–control design matched these cases with 108 recurrence-free cured controls based on age, sex, BMI, diabetes, smoking, and alcohol use. Circulatory immune markers (plasma complement proteins, acute phase proteins, MMPs, and TIMPs) and TB antigen–stimulated chemokines (QuantiFERON Nil, TB Antigen, and Mitogen) were measured at baseline and Month 2 using Luminex platform.

Results: Patients with unfavourable outcomes exhibited significantly distinct immune profiles. Baseline and Month 2 levels of complement proteins (C3, C3b, C4b, C5, C5a, C1q; $p < 0.05$), MMP-2, MMP-9, and CRP ($p < 0.0001$) were elevated, while TIMP-1 and TIMP-2 were higher only at baseline ($p < 0.0001$). TB antigen–stimulated chemokines—CCL3 ($p = 0.008$) and CXCL10 ($p = 0.0194$) at baseline, and CCL1, CCL2, CCL3, CXCL9, and CXCL10 at Month 2 ($p < 0.0001$)—were significantly higher in cases, indicating strong TB antigen-specific associations with adverse outcomes.

Conclusion: Distinct pre- and early-treatment immune signatures—including complement components, CRP, MMP-2, and MMP-9—are strongly associated with unfavourable TB outcomes. Early assessment of these markers may aid in risk stratification and improve treatment management.

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Abstract No: SA-190

STRUCTURAL INSIGHTS INTO RIFAMPICIN INTERACTION ALTERED BY BORDERLINE *rpoB* MUTATIONS: AN INSILICO STUDY



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Introduction: Drug-resistant *Mycobacterium tuberculosis (Mtb)* represents a major obstacle to effective tuberculosis (TB) control. Rifampicin, a first-line anti-TB drug, targets the β-subunit of RNA polymerase, and resistance is primarily mediated by mutations in the *rpoB* gene. While most diagnostic assays focus on the Rifampicin Resistance Determining Region (RRDR), borderline mutations outside this region may also contribute to resistance but remain poorly characterized.

Objective: This study aimed to evaluate the structural and functional impact of borderline *rpoB* mutations at residue S441 (S441Q, S441L, S441M, and S441P) on RNA polymerase stability and rifampicin binding.

Methods: The *M. tuberculosis* H_{37}Rv *rpoB* sequence (UniProt ID: P9WGY9) and RNA polymerase crystal structure (PDB ID: 5UH5) were used. Missing residues were resolved by pairwise sequence alignment. Mutations were introduced using FoldX PositionScan, and structural refinement was performed with RepairPDB. Protein stability, protein–protein interactions, and protein–ligand interactions were assessed using mCSM, mCSM-PPI, and mCSM-lig, respectively. Changes in energy and hydrogen bonding were analyzed using FoldX.

Results: The S441Q mutation was predicted to destabilize RNA polymerase (mCSM $\Delta\Delta G = -1.244$ kcal/mol) and disrupt rifampicin binding (mCSM-lig $\Delta\Delta G = -1.200$ kcal/mol). mCSM-PPI analysis indicated that this mutation occurs at the protein–protein interface and is destabilizing. In contrast, S441L, S441M, and S441P exhibited stabilizing effects. Structural analysis implicated steric clashes and entropic alterations.

Conclusion: The S441Q borderline mutation significantly compromises RNA polymerase stability and rifampicin binding, supporting its role in rifampicin resistance and improving interpretation of *rpoB* missense mutations.

Funding: ICMR Intramural.

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Abstract No: SA-191

LOW-FREQUENCY OF HIV-1 PROTEASE RESISTANCE MUTATIONS IN A PI-NAÏVE AND PI-EXPOSED HIV-INFECTED COHORT



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Background: HIV-1 protease inhibitors (PIs) play a crucial role in salvage therapy for patients who fail the first-line antiretroviral treatment regimen. PIs act as competitive inhibitors by binding to the active site of the HIV-1 protease enzyme, which cleaves the Gag polyprotein into functional structural proteins. Consequently, the effectiveness of PIs is critically influenced by the frequency of mutations in the HIV-1 protease gene. This study aimed to evaluate the frequency of drug resistance mutations in HIV-1 protease among PI-naïve individuals and PI-treated individuals.

Methods: A retrospective cross-sectional analysis of DRMs in the HIV-1 protease (PR) gene was performed in three groups of HIV-1 infected individuals: PI-naïve group comprising of individuals not exposed to PIs (n= 95), PI-treated responder group comprising of individuals on a PI-based regimen responding well through viral suppression (n=19), and PI-treated non-responder group comprising of individuals failing on PI-based regimen (n=52). The HIV-1 PR gene was sequenced using the 3500 Genetic Analyzer (Applied Biosystems), and drug resistance mutations were interpreted using the Stanford HIV Drug resistance database. A chi-square test of homogeneity was performed to compare the frequency of mutations across the three groups.

Results: The frequency of PI-associated DRMs was 3.16% in PI-naïve, 5.26% in the PI-treated responder, and 11.54% in the PI-treated non-responder groups respectively. Statistical analysis however indicated no significant differences in the frequency of mutations between the groups (Chi-square test, $p > 0.05$ at the 5% significance level).

Conclusion: The observed low frequency of PI mutations in the non-responder group (11.54%) could possibly suggest the presence of either unreported mutations in the PR gene or mutations outside the PR region such as in the HIV gag gene which is the natural substrate of the **protease enzyme.**

Acknowledgment: The authors thank Indian Council of Medical Research (ICMR) for funding this study and sincerely acknowledge technical support rendered by the staff of Department of Virology & Biotechnology, ICMR-NIRT. Also, the first author thank all the all the volunteers who took part in the study.

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Abstract No: SA-192

Drug susceptibility profiling of pulmonary Nontuberculous mycobacteria (NTM) isolated from Presumptive pulmonary tuberculosis patients



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Introduction: With the introduction of newer molecular diagnostic tools, an increasing number of nontuberculous mycobacteria (NTM) are being identified with isolation rates increasing from 0.9% (2001–2010) to 1.6% (2011–2020). However, the drug resistance patterns that is crucial for treatment of the identified NTM species remains poorly explored.

Objective: To determine the drug resistance patterns of NTM using an in-house drug susceptibility testing (DST) by the minimum inhibitory concentration (MIC) method.

Methodology: A total of 1121 samples from presumptive pulmonary TB patients were processed and subjected to MGIT culture and LPA for species identification. Of the 135 (12%) NTM species, 50 (37%) underwent DST by the microdilution method using Clarithromycin, Amikacin, Moxifloxacin, and Linezolid for both rapid growers (RG) and slow growers (SG) of NTM. Additional drugs tests included Rifabutin and Ethambutol for SG, and Ciprofloxacin, Tigecycline, Imipenem, and Trimethoprim-sulfamethoxazole for RG. The drugs were serially diluted according to (Clinical and Laboratory standards Institute(CLSI) guidelines 2024 in a 96-well plate, incubated, and read after 48 hours for RG and after 1 week for SG.

Results: Out of 50 isolates subjected to DST, results could be obtained in 42 isolates comprising 30 RG (*M. fortuitum* (12), *M .abscessus* (16), and *M. gordonae* (2)) and 12 SG (*M.intracellulare*). The remaining isolates turned out be either negative (3) or contaminated (5). Of the 30 RG, 24 were sensitive to Amikacin and Clarithromycin, and 18 were sensitive to Linezolid. Of 12 SG, 8 were sensitive to Amikacin, 10 to Clarithromycin, 7 to Linezolid, and 8 to Rifabutin. The isolates were resistant to other drugs.

Conclusion: An appropriate drug resistance testing method is essential to prompt the initiation of appropriate treatment for the increased NTM pulmonary infections. The inhouse method of testing developed seems to be promising and needs to be validated in a large sample size before implementation.

Funding Details: Intramural grant

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Abstract No: SA-193

Strengthening Continuum of Care (COC) for Patients of Hypertension and Diabetes in Dibrugarh District, Assam, using Hybrid-III Interrupted Time Series Design



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Hypertension and diabetes are major contributors to morbidity and premature mortality in India, yet the effective Continuum of Care (CoC) remains weak despite standardized guidelines under the National Programme for Prevention and Control of Non-Communicable Diseases (NP-NCD). Gaps in screening, diagnosis, treatment initiation, referral, adherence, and long-term follow-up lead to poor disease control, particularly in resource-constrained settings such as Assam.

This study aims to assess and strengthen the CoC for hypertension and diabetes in Dibrugarh district, Assam. Using a mixed-methods approach, the study will identify demand-side, supply side, and process-level barriers affecting CoC at the patient, community, and health-system levels. A Hybrid Type III effectiveness–implementation design combined with an Interrupted Time Series approach will be used to evaluate implementation processes and service delivery outcomes.

The study will develop and test a standardized, quality-assured CoC implementation model aligned with NP-NCD guidelines. Findings will inform district and state-level planning and provide a scalable framework for strengthening chronic disease management within public health systems.

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Abstract No: SA-194

Morbidity profile, patterns and determinants of healthcare utilization and out of pocket expenditure on healthcare among elderly in India: A secondary analysis of Longitudinal Ageing Study of India (LASI) Wave 1



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Background: The research in domain of inequity in healthcare utilization in India for geriatric population is limited. Therefore, the present study was undertaken to study the morbidity profile, pattern of health care utilization and out of pocket expenditure for healthcare and to determine the factors (socio-demographic, economic and clinical) associated with health care utilization and out of pocket expenditure for healthcare.

Methods: Secondary data analysis of elderly population in Longitudinal Ageing Study of India (Wave 1) (LASI) (cross-sectional study design) was done.

Results: The study revealed that the commonest health condition reported was urogenital diseases. Only one third of the respondents who received care in outpatient in last 12 months, had visited public health facility for the same while 58% utilized private sector health facility for inpatient care. The determinants of healthcare utilization included religion, caste, MPCE, no health insurance, geographic locations and marital status. The health insurance coverage among elderly was 20.9%. The median expenditure during hospitalization was Rs.787.22 and during OPD visit was Rs.806.05. The OOPE in both inpatient and outpatient care also varied with age (75-79 years), gender (male), non-working status, education status (graduate & above) richest quintile of MPCE, marital status, region (NE) and living arrangements (living with children and spouse) in our study. Overall Catastrophic Health Expenditure-10 is reported by 35.1% elderly people in LASI (2017-18).

Conclusions: The study highlight that elderly suffer from multi-morbidities. Only one third of elderly are receiving care in public healthcare system. Catastrophic Health Expenditure-10 is reported by 35.1% elderly people in LASI. It is therefore recommended to direct the public policy that needs to be grounded with an understanding of the vulnerabilities related to old age and inequities related to social, economic, medical and demographic factors.

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Abstract No: SA-195

PMCA4b: The host switch controlling malaria parasite growth and artemisinin resistance



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The ATP2B4 gene encodes the PMCA4b Ca^{2+}-ATPase, a key regulator of calcium homeostasis in erythrocytes. Genome-wide association studies have identified variants in ATP2B4 as protective against malaria infection, yet the underlying mechanism remains unresolved. While earlier studies suggested that reduced PMCA4b activity leads to calcium mediated red cell dehydration, emerging evidence indicates that altered calcium and redox balance may play a more direct role in parasite survival and drug sensitivity. This study investigates the association between ATP2B4 genotypes and PMCA4b expression in malaria susceptibility and artemisinin sensitivity. Genotyping of 230 samples from severe malaria, uncomplicated malaria, and healthy controls was performed. PMCA4b expression, intra-erythrocytic calcium, ROS levels, Gardos channel activity, and P. falciparum growth were evaluated in donor RBCs. Artemisinin sensitivity was determined using IC_{50} growth inhibition and ring-stage survival assays, establishing functional links between calcium homeostasis, oxidative stress, and parasite response to treatment. ATP2B4 genotypes showed no significant association with malaria protection. However, low PMCA4b expression, irrespective of genotype, was linked to elevated intra-erythrocytic calcium, increased oxidative stress, and reduced in vitro parasite growth. Gardos channel activity inversely correlated with PMCA4b but did not cause dehydration, suggesting that oxidative-stress regulation by PMCA4b plays a pivotal role in malaria protection. Importantly, reduced PMCA4b expression also decreased P. falciparum artemisinin sensitivity, which was strongly associated with heightened oxidative stress, providing the first evidence that host red cell variations modulate both malaria susceptibility and antimalarial drug response. These findings suggest PMCA4b's role in oxidative stress and drug response as critical to malaria pathophysiology. We further emphasize that many redox modulating RBC polymorphisms in malaria endemic areas, could also influence artemisinin efficacy and serve as potential biomarkers for predicting therapeutic response.

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Abstract No: SA-196

Essential Oil Nano-Formulation for Prolonged and Sustainable Mosquito Vector Control



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Introduction: Mosquito vectors transmit several vector-borne diseases and pose a major global public health concern, particularly in tropical and subtropical regions. Sustainable mosquito control remains essential for reducing disease transmission, with malaria continuing to contribute significantly to global morbidity and mortality. Although synthetic repellents such as N,N-diethyl-m-toluamide (DEET) are widely used due to their high efficacy, concerns regarding toxicity, skin penetration, and environmental persistence limit their long-term acceptability. Therefore, safer and eco-friendly alternatives are urgently required.

Objectives: The present study aimed to develop and evaluate an essential oil–based nano-formulation with improved stability and prolonged repellent activity for sustainable mosquito vector control.

Methods: An essential oil–based preconcentrate was prepared using simple and conventional formulation techniques. Selected essential oils were mixed with suitable surfactants and co-surfactants under continuous stirring at ambient conditions until a homogeneous and stable system was obtained. The prepared formulation was evaluated for physicochemical stability and mosquito repellency to assess its effectiveness and durability.

Results: A stable and homogeneous essential oil–based nano-formulation was successfully developed. The formulation exhibited improved dispersion, reduced volatility, and controlled release of essential oil constituents compared to conventional essential oil preparations. These properties contributed to sustained repellent activity against mosquito vectors, indicating enhanced effectiveness and prolonged protection.

Conclusion: The developed essential oil–based nano-formulation provides a simple, cost-effective, and environmentally sustainable alternative to synthetic chemical repellents. The formulation demonstrates strong potential for integration into mosquito vector management and malaria prevention programs and may contribute to reducing dependence on synthetic insecticides while supporting eco-friendly public health interventions.

Acknowledgement and Funding: The authors acknowledge the Academy of Scientific and Innovative Research (AcSIR) and the Council of Scientific and Industrial Research (CSIR), India, for financial support.

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Abstract No: SA-197

Addressing Multilevel Barriers to Lifestyle Change in Obesity: Development and Validation of a Behavioural Intervention



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Background: Obesity is a growing public health challenge in India, particularly in urban and semi-urban settings, driven by complex interactions between individual behaviours, family environments, and socio-cultural contexts. Most existing interventions focus narrowly on individual behaviour change and show limited sustainability. This study aims to develop and validate a culturally appropriate multilevel behavioural intervention module to address personal, familial, and societal barriers to lifestyle modification among adults with obesity. The objectives are to identify multilevel barriers, co-develop an intervention module, assess its acceptability and feasibility, and evaluate its preliminary effectiveness on obesity-related outcomes.

Methods: A mixed-methods study will be conducted in four phases in urban and semi- urban areas of Delhi NCR. Phase I includes focus group discussions and a cross-sectional survey of approximately 500 adults aged 18–60 years with BMI ≥25 kg/m² to identify multilevel barriers. Phase II involves participatory co-development of the intervention and expert validation using Delhi techniques, followed by pilot testing. Phase III comprises a pilot randomized controlled trial (n≈250) comparing the multilevel intervention with standard care over 12 weeks. Outcomes include changes in BMI, waist circumference, and perceived barriers, analysed quantitatively, alongside thematic analysis of qualitative feedback. Phase IV focuses on dissemination and scalability.

Results: The study is expected to produce a validated, feasible, and acceptable multilevel behavioural intervention module, demonstrating preliminary improvements in obesity- related anthropometric measures and reduced perceived barriers to lifestyle change.

Conclusion: This study will generate a scalable, grounded intervention aligned with the socio-ecological model for obesity management in India.

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Abstract No: SA-198

Development of a Recombinase Polymerase Amplification Assay for Spotted Fever Group Rickettsia



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Background: Spotted fever group (SFG) *Rickettsia* are a neglected group of zoonotic bacteria belonging to the genus *Rickettsia* and are transmitted to humans through arthropod vectors such as ticks, fleas, and mites. In India, SFG *Rickettsia* are increasingly recognized as important yet underdiagnosed causes of acute febrile illness (AFI), and acute encephalitis syndrome (AES). Untreated rickettsial infections have high mortality, requiring timely diagnosis. Serological assays have limited sensitivity in the acute phase due to delayed antibody responses. While PCR-based methods enable sensitive early detection, their reliance on sophisticated infrastructure and trained personnel restricts use in resource-limited and decentralized settings. Recombinase polymerase amplification (RPA) is a highly sensitive and selective isothermal nucleic acid amplification technique operating at 37–42 °C, requiring minimal sample preparation and capable of amplifying low copy numbers of target DNA within a short time, making it suitable for field-adaptable diagnostic applications.

Aim: The aim of this study was to develop and optimise an isothermal RPA assay for the rapid detection of spotted fever group *Rickettsia*.

Methods: Conserved genomic regions specific to SFG *Rickettsia*, targeting the 23S–5S intergenic spacer region, were identified. Multiple RPA primer sets were designed using NCBI primer-Blast software. The synthesised primers were screened for optimal performance using cloned positive control of *Rickettsia conorii targeting 23s–5s* gene. Assay optimization was performed using different copy number on cloned positive *Rickettsia* DNA control by evaluating reaction temperature and incubation time to determine optimal amplification conditions.

Results: The study designed 5 pair of primers, and from them one primer pair showing best performance was selected for further evaluation. This screened primer set showed reliable amplification of the cloned control DNA down to 10^5 copies. Under optimized conditions, the developed RPA assay successfully amplified SFG *Rickettsia* DNA within 20 minutes at 39 °C. Consistent amplification was observed across replicate experiments, while no amplification occurred in negative controls, indicating assay specificity. The assay in current stage demonstrated reproducible performance under the optimized conditions.

Conclusion: This study has developed an isothermal amplification assay for the detection of SFG *Rickettsia*. The optimized RPA assay provides a foundation for further evaluation using clinical samples and holds promise for future adaptation into point-of-care diagnostic platforms to improve detection and surveillance of rickettsial infections in endemic regions of India.

Keywords: Isothermal Amplification; Recombinase Polymerase Amplification; *Rickettsia*; Point-of-Care Testing.

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Abstract No: SA-199

Determination of Methicillin-Resistant *Staphylococcus aureus* from clinical samples in a tertiary care hospital of Eastern Uttar Pradesh by phenotypic and molecular methods.



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Introduction: Antimicrobial resistance has become a global health challenge due to the misuse, overuse or underuse of antimicrobials. A 2024 Lancet report estimated 7.7 million deaths due to bacterial infections annually, out of which 4.95 million are associated with antibiotic-resistant bacteria. The Lancet systematic review states that in 2019, *S. aureus* was the second leading pathogen associated with more than 1 million deaths in 135 countries. In 2022 prevalence of methicillin-resistant *S. aureus* (MRSA) was 35% in 76 countries, highlighted by the 2022 GLASS report.

Objective: The proposed study is conceptualized to determine the prevalence of MRSA in clinical settings for guiding appropriate therapeutic strategies and to explore the mechanism of resistance.

Methodology: 100 clinical isolates were collected from patients admitted to a tertiary care setting in the Eastern region of Uttar Pradesh. Gram staining was performed from isolated colonies. To confirm *S. aureus*, the coagulase test was performed. Screening of MRSA among coagulase-positive strains was done by CLSI recommended method, i.e., Disc diffusion with oxacillin (1 µg). Confirmatory testing was done using the Automated Microbial Identification System (VITEK 2.0 compact). The presence of the mecA gene was determined by real-time PCR.

Results: A total of 100 clinical isolates were subjected to Gram staining. All Gram-positive isolates were subjected for coagulase test, of which 47 were found positive. Among 47 isolates, 25 isolates were found resistant to oxacillin. All 25 isolates were confirmed MRSA when analysed with the Automated Microbial Identification System (VITEK 2.0 compact). The presence of the mecA gene was detected in all MRSA isolates using real-time PCR. After analyzing as per CLSI guidelines for disc diffusion against 22 antibiotics, AST profile revealed a varied susceptibility pattern with a high level of resistance against beta-lactams, fluoroquinolones and aminoglycosides. The obtained disc diffusion data were parallel to the result of the antimicrobial susceptibility testing system, which validates our results.

Conclusion: The study identified a significant prevalence 53.19% of MRSA suggesting the colonisation of this resistance isolate clinical settings. Antimicrobial susceptibility profiling revealed multidrug resistance in MRSA isolates, highlighting limited therapeutic options. Therefore, strict monitoring and targeted infection control are essential to limit the spread of these resistant strains.

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Abstract No: SA-200

A Comprehensive Scoping Review of Biochemical Newborn Screening Landscape in India (1985 - 2025)



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Introduction: India faces a significant public health challenge from congenital and inherited disorders, yet lacks a national newborn screening (NBS) programme leading to fragmented efforts. This scoping review systematically maps Indian NBS landscape from 1985-2025 to inform evidence-based recommendations.

Objectives: To map the epidemiological characteristics of congenital, inherited and other biochemically screenable conditions included in NBS; identify biochemical diagnostic technologies used in NBS; examine the implementation of public health initiatives and NBS programs, including the challenges, barriers, failures, opportunities, facilitators and successes; highlighting areas needing further research for strengthening NBS in India.

Methods: Following PRISMA-ScR and JBI Methodology, a literature search was conducted across PubMed (9805), Scopus (10260) and Embase (7745). 22,210 unique articles after de-duplication underwent title/abstract screening. Following a full-text review of 320 articles, 270 studies included for data extraction and analysis.

Results: 270 included studies comprised original research (180,67%), reviews (68,25%) and expert perspectives/policy documents (22,8%). Reported prevalence of screened disorders showed significant variation, with CH affecting 1 in 1388 newborns, CAH 1 in 4074 and G6PDD 1 in 80 newborns. Dried blood spot most frequently utilized sample type; screening technologies evolved from ELISA and colorometric assays to advance platforms like Time-Resolved Fluoroimmunoassay and Tandem Mass Spectrometry. Qualitative analysis identified successful, cost-effective pilot programs (Karnataka, Chandigarh) as key facilitator. However, universal implementation is absent due to lack of national policy. Major barriers included sociocultural and awareness gaps, failures included inadequate sample transport, no quality assurance guidelines and treatment gap where screening occurs without guaranteed access to affordable care, particularly in rural and tribal areas.

Conclusion: This scoping review reveals a critical disconnect between India's disease burden and fragmented NBS landscape. There is an urgent need for a unified national NBS policy establishing a core screening panel with equitable access from diagnosis through treatment to reduce preventable disability.

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CLOSING NOTE

This compilation of abstracts represents the creativity, dedication, and scholarly contributions of PhD scholars from across the Indian Council of Medical Research (ICMR) network. The conclave has provided a unique platform for peer learning, academic exchange, and interdisciplinary collaboration, reflecting the spirit of SANVAD 2026.

We extend our heartfelt thanks to all participating scholars, AcSIR coordinators, mentors, and staff for their enthusiasm and commitment. Your engagement continues to strengthen India's research ecosystem and inspires future innovation in biomedical and public health research.

We hope this compendium inspires continued exploration, collaboration, and innovation in scientific research.

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2. Scientific Review and Advisory:

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संवाद (SANVAD) 2026

Scholar's Assembly for Next-gen Ventures to Advance their Development

SANVAD 2026 Souvenir
ISBN:978-93-5737-992-2

Website: sanvad.nimr.org.in, Email: sanvad.nimr@gmail.com

Published by:
ICMR - National Institute of Malaria Research, Sector 8 Dwarka, New Delhi -110077

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