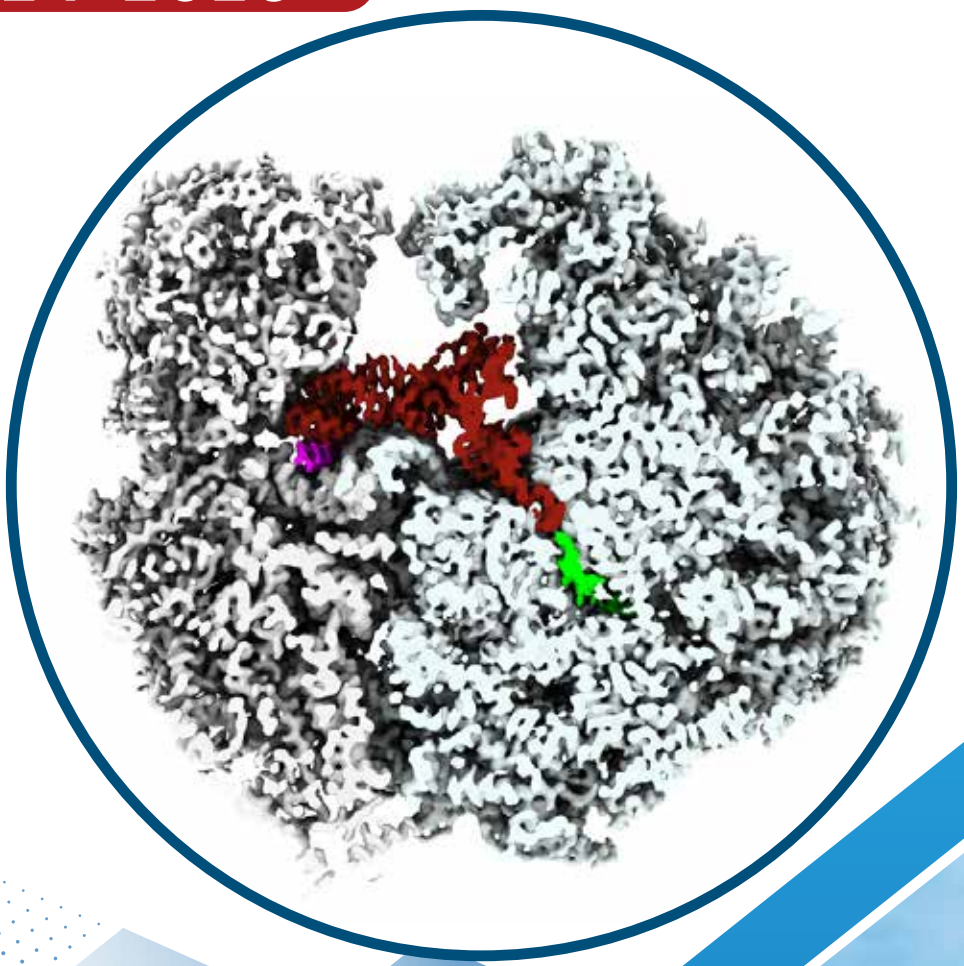
ANNUAL REPORT

2024-2025

United Nations
Educational, Scientific and
Cultural Organization

क्षेत्रीय जैव प्रौद्योगिकी केन्द्र
Regional Centre
for Biotechnology



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RCB
REGIONAL CENTRE FOR BIOTECHNOLOGY

CONTENTS

Mandate of the Regional Centre for Biotechnology

The mandate of the Regional Centre for Biotechnology (RCB) is to provide a platform for biotechnology education, training and research at the interface of multiple disciplines. The programmes of the Centre are designed to create opportunities for students to engage in multi-disciplinary research where they learn biotech science while integrating engineering, medicine and natural sciences, to provide solutions for human and animal health, agriculture and environmental technologies.

The vision is to produce human resource tailored to drive innovation in biotechnology, particularly in areas of new opportunities and also to fill talent gaps in deficient areas. The Centre is regarded as a "Category 2 Centre" in terms of the principles and guidelines for the establishment and functioning of UNESCO Institutes and Centres.

The objectives of the Regional Centre are:

a. to disseminate and to advance knowledge by providing instructional and research facilities in such branches of biotechnology and related fields as it may deem fit including technology policy development,

b. to provide capacity-building through education, training, research and development in biotechnology and related academic fields for sustainable development objectives through regional and international cooperation,

c. to facilitate transfer of knowledge and technology relating to biotechnology at the regional level,

d. to create a hub of biotechnology expertise and to address human resource needs in the countries in the region,

e. to promote and strengthen international co-operation to improve the social and economic conditions and welfare of the people,

f. to promote and facilitate a network of satellite centres in the region as well as within India.

The functions of the Regional Centre are:

a. to establish infrastructure and technology platforms which are directly relevant to biotechnology education, training and research,

b. to execute educational and training activities including grant of degrees in education and research in biotechnology and related fields,

c. to produce human resource tailored to drive innovation in biotechnology, particularly in areas of new opportunities and to fill talent gap in deficient areas,

d. to undertake research and development and scientific investigations in collaboration with relevant research centres in the region,

e. to hold scientific symposia and conferences within India or in the region or outside the region and to conduct short-term and long-term training courses and workshops in all areas of biotechnology,

f. to collect universally available information with a view to setting up data banks for bio-information,

g. to collect and disseminate, through networking, the relevant local knowledge in the field of biotechnology, ensuring protection of intellectual property rights of local stakeholder communities,

h. to develop and implement a policy for intellectual property rights which is equitable and just to the stakeholders involved in research in the Regional Centre,

i. to disseminate the outcome of research activities in different countries through the publication of books and articles,

j. to promote collaborative research and development networking programme in specific areas of biotechnology with national, regional and international networks and promote exchange of scientists, at the regional level having regard to issues pertaining to intellectual property rights of collaborating institutions promoting equitable sharing of benefits with collaborating institutions.

From the Executive Director's Desk

The Regional Centre for Biotechnology (RCB) is committed to delivering world-class education, training, and research at the intersection of multiple disciplines in biotechnology. The objective is to develop highly skilled professionals and foster innovation in both core and interdisciplinary areas to address global challenges in biotechnology.

The Centre has made significant strides in fulfilling its mission, particularly in the key areas of biotechnology education, research and training.

RCB's partnership with UNESCO has remained strong, with the Centre maintaining its Category 2 centre status under UNESCO. This collaboration enhances RCB's global visibility and strengthens its capacity to participate in internationally significant programs and initiatives. It further supports the Centre's mission to advance biotechnology education, research, and training across diverse disciplines.

This annual report provides a comprehensive overview of the Centre's activities, highlighting its extensive research, education, and training initiatives that contribute to the global advancement of biotechnology, thus cultivating the next generation of competent professionals in the field.

Research-based learning is the hallmark of RCB's education and training programs. By emphasizing hands-on, inquiry-driven learning, RCB ensures that students not only gain theoretical knowledge but also develop the critical thinking, problem-solving, and skills crucial for tackling real-life challenges, thus integrating research into the learning process and fostering a deeper understanding of both fundamental and applied aspects of the discipline. While successfully running its existing academic programmes and coordinating the i3c BRIC-RCB-PhD programme in Biosciences, in January 2025, RCB successfully launched the 'Postgraduate Diploma Programme' in 'Industrial Biotechnology' (PGDIB) aimed at producing industry-ready graduates to be recruited and deployed in biopharma companies. Eighteen students registered in the first batch of the programme are currently carrying out their 6-month coursework, after which they will head on for the industrial internship.

RCB offers doctoral degree programs in the following key areas: Biotechnology, Bioinformatics, Biostatistics and Biosciences. These programs are designed to provide advanced research training through a combination of rigorous academic coursework and hands-on research, thus equipping students to contribute to cutting-edge biotechnological advancements to tackle global challenges in health, agriculture, and the environment. Currently, 123 students are pursuing their PhD in Biotechnology at RCB. During the period of this report, 12 students graduated with a PhD in Biotechnology. The interdisciplinary doctoral programme in Biostatistics and Bioinformatics is supported through collaboration with the global pharmaceutical company GlaxoSmithKline Pharmaceuticals India Private Ltd. (GSK). Currently, 07 students are pursuing the PhD Programme in Biostatistics/ Bioinformatics at RCB. Over the past year, 03 students graduated with a PhD. RCB's MS-PhD programme is also gaining popularity and attracting the best talent nationally and internationally. During 2024-2025, 08 students exited the programme with an M.Sc. degree, while 68 students are currently registered in the programme. As empowered by the RCB Act, this year, RCB has granted academic recognition to the Biotechnology Research and Innovation Council (BRIC) and, consequently, to the 13 institutions subsumed under BRIC (iBRIC). This recognition further strengthened the Centre's role in shaping a highly skilled workforce in biotechnology. A total of 94 students from these recognized centres were registered for their Master's (Biotechnology and Clinical Research) degree, 34 for the MS-PhD (Biotechnology) degree, and 695 for the PhD (Biotechnology, Medical Biotechnology, Virology, Lifesciences and Biosciences) degree with RCB.

RCB has also been entrusted with the responsibility of conducting and coordinating the 'i3c-BRIC-RCB-PhD Programme in Biosciences', a common PhD programme for all the DBT-supported autonomous institutions subsumed under BRIC (iBRIC), ICGEB, and RCB, termed now as iBRIC+. At present, 57 students are registered in the programme. Out of 57 students, 6 students are pursuing their PhD at RCB, and the remaining are pursuing PhD in various iBRIC (institutions of BRIC) and ICGEB.

RCB organized various events during the reporting period. The Design Thinking workshop organized during 25-27 October 2024 was attended by 58 i3c-BRIC-RCB PhD students. The program featured a well-structured blend of dynamic learning experiences that fostered a focused problem-solving mindset among students and highlighted the importance of aligning individual skills with broader societal needs.

The Science Communication Workshop organized during 21-25 November 2024 under the i3c BRIC-RCB PhD programme in Biosciences was attended by more than 100 students. The participants of this workshop were trained in the basics of science communication, writing a manuscript, presentation skills, writing grants, preparing CVs, etc.

The Indian Biological Data Centre (IBDC) has achieved a remarkable milestone by collaborating with the GenomeIndia consortium to archive 1 Petabyte of genomic data from 10,000 human genomes. This monumental achievement was inaugurated by the Honourable Prime Minister, Shri Narendra Modi, on January 9, 2025, at the Genomics Data Conclave in New Delhi. Additionally, IBDC, in partnership with the Data Management Group, developed the FeED protocols by DBT and a Data Access Portal for controlled-access data sharing, unveiled by the Honourable Minister of S&T, Dr. Jitendra Singh. These initiatives underscore the IBDC's leadership in advancing data accessibility and driving innovation in the life sciences.

The 1st Computational Biology Conference organized from February 19-21, 2025, was a resounding success featuring 19 distinguished speakers from five countries - India, USA, UK, Israel and Australia - who presented cutting-edge developments in computational biology and data sciences. The conference gathered 200 participants and featured 67 poster presentations by researchers from 50 organizations across 20 states of India. The event also nucleated a dialogue with EBI-EMBL (UK) for potential collaboration on data hosting, curation, and visualization.

A three-day manuscript writing workshop was organized from 5-7 March 2025 for research scholars in collaboration with Editage, wherein the basics of scientific writing through extensive exercises and discussions were introduced. The event received an overwhelming response from the scientific community of RCB.

A series of talks, titled i3c BRIC-RCB Leadership Talks, was organized for i3c BRIC-RCB PhD students to expose them to how leaders think, make decisions, and translate ideas into meaningful outcomes. Leaders included visionary scientist Prof. Vijay Raghavan, DBT/Wellcome Trust India Alliance Chief Executive Officer Dr. Apurva Sarin and entrepreneurs like Dr. Anand Deshpande and Mr. Subramani Ramachandrappa, who successfully led a team in building AI, Big Data (Persistent Systems) & Biotech (Fermbox Bio) ventures. The leaders visited RCB to engage with students and inspire a spirit of ambition toward achieving greater heights while making a positive impact on society.

RCB successfully organized its 3rd Convocation Ceremony, where degrees were conferred to students who completed their PhD and Master's programs in the academic session 2023-24. The ceremony was graced by Prof. Ajay K. Sood (Principal Scientific Advisor, GoI) as the Chief Guest. A total of 93 scholars graduated during the ceremony. Of these, 56 students were awarded a PhD in Biotechnology and Medical Biotechnology, and 37 students received their Master of Science in Biotechnology and Clinical Research. This milestone reflects RCB's commitment to nurturing highly skilled professionals who are ready to contribute to innovations in biotechnology and related fields.

The scientific programs at RCB are broadly categorized into six major verticals: Structural Biology, Infectious Disease Biology, Molecular Medicine, Cancer and Cell Biology, Plant Biotechnology, and Systems and Synthetic Biology, focused on addressing critical challenges in biotechnology and life sciences. Throughout the year, significant advances were made across these diverse research domains. Summarized below are some of the major impactful highlights of the year.

Many prokaryotes, such as Neisseria, lack the MutH enzyme and rely on the endonuclease activity present in MutL's C-terminal domain (CTD) for mismatch repair (MMR). Dr. Deepak Nair's group revealed that the MutL-CTD endonuclease interacts with the β-clamp via the conserved motif III (QHLLIP). The NgoL-CTD–Nβ-Clamp complex shows each MutL monomer binds one clamp monomer, positioning the endonuclease dimer across the clamp's C-terminal face. This arrangement likely directs the newly

synthesized DNA strand toward the MutL active site for nicking. This study, therefore, suggests that the Neisseria achieves strand discrimination through a β-clamp–mediated structural mechanism, distinct from methyl-directed MMR in E. coli.

Current dengue virus (DENV) vaccines are limited, thus prompting the search for effective antivirals. Dr. Prasenjit Guchhait's group identified a compound 7D, a CXCR3 antagonist, that inhibits all DENV serotypes in vitro with good stability and low toxicity. In DENV2-infected mice, 7D enhanced IFN-α/β/λ production, alleviated disease symptoms, and improved survival. By inhibiting Sirt-1, 7D promoted STAT3 acetylation and phosphorylation, boosting plasmablast proliferation, germinal centre maturation, and neutralizing antibody production. Overall, 7D acts through the CXCL4–CXCR3–p38–IRF3 pathway to enhance antiviral and immune responses against dengue. Currently, they are testing the anti-viral efficacy of this drug in DENV-infected non-human primate model.

The eukaryotic 43S pre-initiation complex (PIC), containing Met-tRNA$_i^{Met}$ in a ternary complex with eIF2-GTP, scans mRNA for the AUG start codon within a favorable Kozak context. Recognition of AUG triggers a transition from an open scanning state to a closed arrested state with tightly bound Met-tRNA$_i^{Met}$. Dr. Anil Thakur's group investigated how the ribosomal protein uS11 (Rps14) regulates this process. Their study revealed that uS11/Rps14-L137 mutations, which disrupt rRNA contacts, promote initiation at suboptimal codons, whereas R135 and R136 substitutions, perturbing rRNA interactions in the closed state, enhance initiation fidelity. Thus, distinct uS11/Rps14–rRNA interactions sequentially stabilize PIC conformations, ensuring accurate start codon selection.

Mitochondrial Ca^{2+} signaling plays a vital role in pigmentation by regulating melanosome biogenesis. Dr. Rajender Motiani's research group revealed that mitochondrial Ca^{2+} uptake via the mitochondrial Ca^{2+} uniporter (MCU) promotes melanogenesis, whereas its negative regulator MCUb inhibits it. In zebrafish and mouse models, the MCU complex drives pigmentation in vivo. Mechanistically, MCU silencing activates NFAT2 thereby inducing keratin (K5, K7, K8) expression. K5 in turn enhances mitochondrial Ca^{2+} uptake and melanosome maturation, forming a feedback loop. The group showed that the MCU inhibitor mitoxantrone reduces pigmentation, revealing therapeutic potential for pigmentary disorders.

Glucuronoxylan, a key component of dicot secondary cell walls, is often O-acetylated to stabilize interactions with cellulose. Prashant M Pawar's group was working on Arabidopsis mutant of ESKIMO1 or TBL29 (Golgi-localized xylan O-acetyl transferase) and found that its loss leads to reduced xylan acetylation, stunted growth, and collapsed xylem vessels. Transcriptomic and metabolomic analyses of eskimo1 stems revealed upregulation of genes for aliphatic glucosinolate (GSL) biosynthesis, while indolic GSL pathway genes were unaffected. Correspondingly, aliphatic GSLs such as 4MSOB accumulated more in stems and seeds of eskimo1. These metabolic shifts correlated with reduced methionine, increased jasmonic acid, and altered soluble acetate levels.

Targeting specific RNA conformations essential for SARS-CoV-2 replication offers a promising antiviral strategy. The viral genome contains G-rich sequences, e.g. RGQ-1 sequence derived from nucleocapsid gene, which adopt dynamic hairpin–G-quadruplex (Hp-GQ) secondary structures. In the current study conducted by Dr. Ambadas Rode's group, two tetraphenylethene (TPE) derivatives, TPE-MePy and TPE-Allyl Py, were shown to bind and stabilize RGQ-1 by 8.56°C and 12.54°C, respectively. Furthermore, treatment with these compounds in infected cells shifted the Hp-GQ equilibrium toward the GQ form and significantly reduced the expression levels of viral RNA, spike, and nucleocapsid proteins. These findings reveal that the TPE derivatives exert their antiviral effect during postentry replication stages, underscoring their potential as effective SARS-CoV-2 inhibitors.

Additionally, RCB not only continued to participate in the multi-institutional project such as GRBHIni, aimed at understanding the biology of preterm birth to identify possible biomarkers to predict birth outcomes, but also initiated the following new multi-institutional projects: 1) Mitigating Potato leafroll virus (PLRV) incidence through genetic and chemical interventions and 2) Addressing Neurodegeneration in Diabetes.

As detailed in the report, BSC BioNEST Bio-Incubator (BBB), a BIRAC's Associate Partner, continues to foster Bio entrepreneurship as a leading startup ecosystem enabler in the National Capital Region. The year was eventful with BBB bagging the best incubator award in Tier 1 category at Global Bio India 2024. Besides, the start-ups incubated at BBB performed exceptionally well, with Dharaksha Ecosolutions Pvt Ltd. grabbing the Startup Grand Challenge 2.0 award and seed fund by Avaana Capital; Techinvention Lifecare Pvt. Ltd. receiving the Coveted Startup 50 Award and Inte-e-labs Pvt. Ltd. receiving NASSCOM EMERGE 50 Awards 2024.

The Advanced Technology Platform Centre (ATC) at RCB offers state-of-the-art equipment and technical support to researchers from startup, industry and academia across India, facilitating cutting-edge scientific work and innovation. The Biosafety Support Unit (BSU) at RCB continues to provide support to the Department of Biotechnology, Govt. of India, in its regulatory activities. The Human Resource Development (HRD) Project Management Unit at RCB has been effectively overseeing and managing a range of HRD initiatives supported by the Department of Biotechnology (DBT), Government of India, contributing to the development of skilled professionals and advancing biotechnology research in the country. Currently, the following programmes are being managed by the DBT-HRD PMU: Ramalingaswamy Re-entry Fellowship (RRF) Programme, Biotechnology Career Advancement and Re-orientation (BioCARe) Programme, Junior Research Fellowship (JRF) Programme, DBT Research Associateship (RA) Programme, Post-Graduate Teaching (PG) Programme, Biotech Industrial Training Programme (BITP) and DBT-TWAS Fellowship Programme (TWAS).

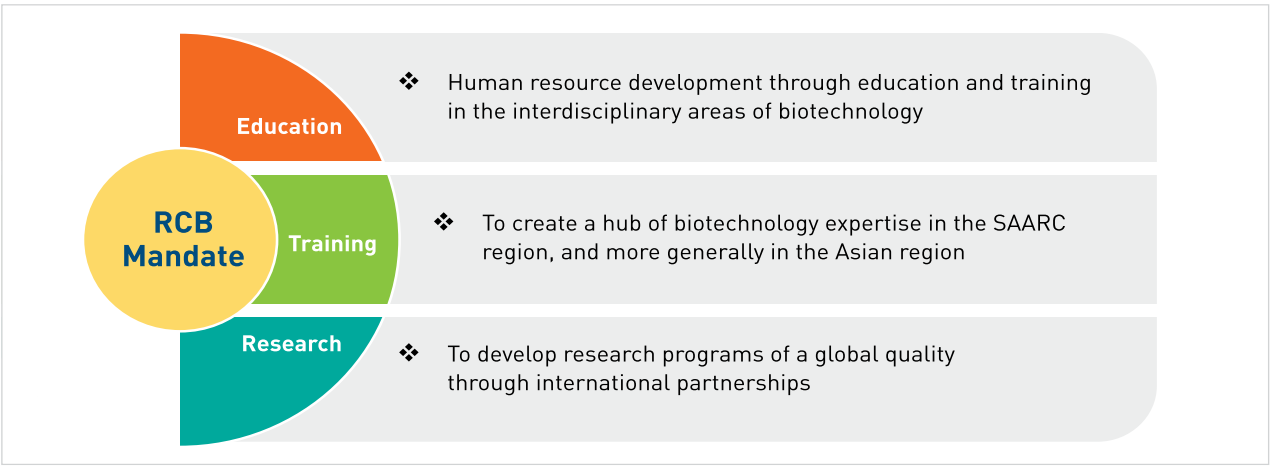
IBDC, established by RCB with support from the DBT, is the country's first national repository for life science data. The centre is a collaborative project of RCB, NII, ICGEB and NIC. It has a data storage capacity of about 4.5 petabytes with a disaster recovery storage site located in NIC, Bhubaneshwar, of 1 petabyte. The centre houses the 'Brahm' High Performance Computing (HPC) facility with a computing capacity of 961 teraFLOPs. IBDC has created portals for the storage and dissemination of nucleotide, crop phenome, proteome, imaging, macromolecular structure, and metabolomics data. IBDC has a total of 589271 cumulative submissions, amounting to 1070 terabytes of storage. IBDC supports large-scale genomics projects like INSACOG, GenomeIndia, ODOG, PRaGeD, the Indian Human Microbiome Initiative and Mission Mode projects (Chickpea, Safflower, Sesame, Linseed, Wheat, and Rice) of multiple crops by managing, analyzing, and sharing datasets per government guidelines, empowering the research community with high-quality resources. IBDC personnel also contributed to the development of the FeED (Framework for Exchange of Data) Protocols, which are used to implement the Biotech-PRIDE (Promotion of Research and Innovation through Data Exchange) Guidelines. These guidelines regulate the submission and sharing of life science data within India. IBDC conducted numerous webinars for dissemination and online training sessions for data deposition during FY 2024-25. IBDC has also implemented an Integrated Computing Environment (ICE) developed by CDAC for training purposes. In addition, the computational biology conference (CBC 2025), which is now an annual event, was held in February 2025.

At the end, I would like to extend my heartfelt thanks to all my colleagues for their outstanding cooperation. I also acknowledge the continued support of the Department of Biotechnology (DBT) and UNESCO, as well as the invaluable contributions of the RCB Board of Governors, the Programme Advisory Committee, and the various other statutory committees, whose guidance has been crucial in helping us achieve the Centre's scientific and academic objectives.

Arvind Sahu
Executive Director

Executive Summary

Photo Credit: Rohan Rajiv Babar



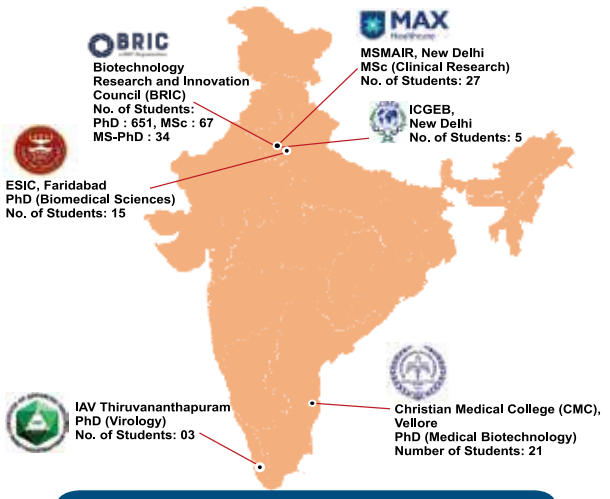
Academic and Training Activities

- Post-doctoral Training
- Young Investigator Awards
- EMR grant Fellows
- Doctoral Research Programs
  - Biotechnology
  - Bioinformatics, Biostatistics
- Pre-doctoral Programs
- MS-PhD program
- Research Interns

No. of Students studying at RCB

123	PhD (Biotechnology)	MS-PhD (Biotechnology)	68
07	PhD (Bioinformatics & Biostatistics)	PGDIB	18
06	i3c BRIC-RCB PhD	PhD Awarded	15

RCB Recognized Centres



Total number of students registered at RCB: 823

DATE	EVENT ORGANIZED
JUNE 03 – JULY 01, 2024	Summer Research Internship Programme Facilitated by Gujarat State Biotechnology Mission (GSBTM)
SEPTEMBER 23-26, 2024	Swachhata Campaign 4.0 at RCB
SEPTEMBER 14 - 30, 2024	Hindi Pakhwada 2024
OCTOBER 28 – NOVEMBER 2024	Vigilance Awareness Week 2024
OCTOBER 25 – 27, 2024	Design Thinking Workshop
NOVEMBER 21-25, 2024	Science Communication Workshop
DECEMBER 16, 2024	3rd Convocation Ceremony 2024

DATE	EVENT ORGANIZED
JANUARY 09, 2025	Genomics Data Conclave
FEBRUARY 19-21, 2025	1st Computational Biology Conference 2025
FEBRUARY 28, 2025	National Science Day 2025
MARCH 01, 2025	RCB Foundation Day 2025
MARCH 05-07, 2025	Manuscript writing workshop
MARCH 08, 2025	International Women's Day 2025
1 APRIL 2024-31 MARCH 2025	30 webinars/ seminars by visiting scientists
1 APRIL 2024-31 MARCH 2025	06 Leadership Talks

Research Areas

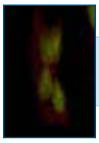
Structural Biology

Molecular Medicine

Infectious Disease Biology

Cancer & Cell Biology

Plant Biotechnology



Systems and Synthetic Biology

Publications : 67
Patent Applied : 3, Granted : 3

Research Highlights

Characterized the Myh8 gene, which is associated with musculoskeletal diseases such as Trismus-pseudocamptodactyly. Myh8 function is crucial for proper skeletal muscle differentiation, metabolic properties and regeneration.

Drought tolerance in rice is tightly regulated at the translational level, with specific polysome-bound mRNAs orchestrating stress-responsive pathways. The findings highlight translational control as a key mechanism for enhancing crop resilience under water-limited conditions.

Developed RNA G-quadruplex(G4) stabilizing TPE derivatives as antivirals against the SARS-CoV-2 infection. G4 stabilization blocks viral replication, thereby reducing viral RNA and protein levels, suggesting TPE derivatives potential as antiviral agents.

An evolutionarily conserved role of mitochondrial Ca 2+ uptake in vertebrate pigmentation was revealed. Further, it was demonstrated that mitoxantrone, an FDA approved drug that inhibits mitochondrial Ca 2+ uptake, decreases physiological pigmentation.

Introduced a simple and cost-effective spray inoculation method for uniformly applying *Erysiphe pisi* conidia on pea leaves, enabling consistent and reproducible infection for disease assessment. A semi-automated, open-source image analysis approach and RT-qPCR validation to accurately quantify powdery mildew severity at both visual and molecular levels was also presented.

Highlighted the potential of targeting RNA G-Quadruplexes (GQs) with small molecules like BRACO-19 as a novel therapeutic strategy against Japanese encephalitis virus (JEV), which currently lacks specific antiviral treatments. BRACO-19 stabilizes JEV GQs, inhibits viral replication, reduces infectious virus titres, and suppresses viral protein expression.

Identified a possible unique link between the plant cell wall and secondary metabolism using omics approaches. Fundamental understanding of such cross-regulation will help to fine-tune plant lignocellulosic biomass properties with reduced polysaccharide acetylation and glucosinolate levels.

Xylan and lignin represent significant barriers during the process of saccharification. One of the study utilized a genetic stacking approach in Arabidopsis to simultaneously modify both of these cell wall components. Improvement was observed in the digestibility of both cellulose and xylan, without compromising plant growth or immunity.

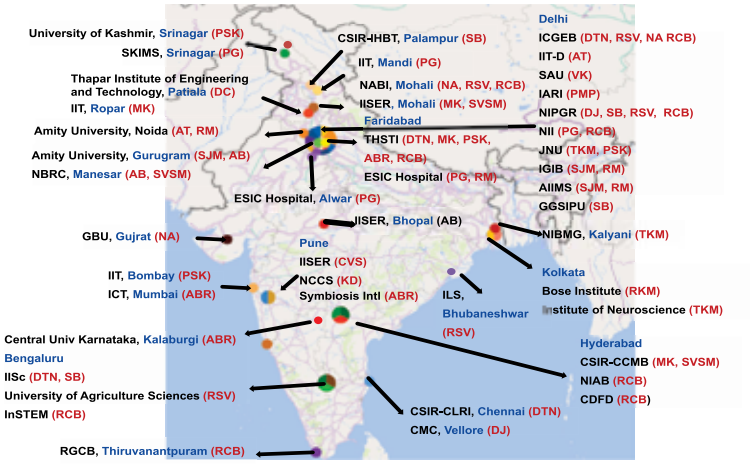
A cellular imaging-based high-content screening of natural compounds identified withaferin A (WFA), a steroidal lactone isolated from the plant Withania somnifera, as a potent antiviral against Chikungua virus virus both in vitro and in the animal model.

Virtual screening of the natural compound library identified N-[2-(5-methoxy-1H-indol-3-yl) ethyl]-2-oxo-1,2-dihydroquinoline-4-carboxamide, which exhibited potent anti-Chikungunya virus activity both in vitro and in vivo.

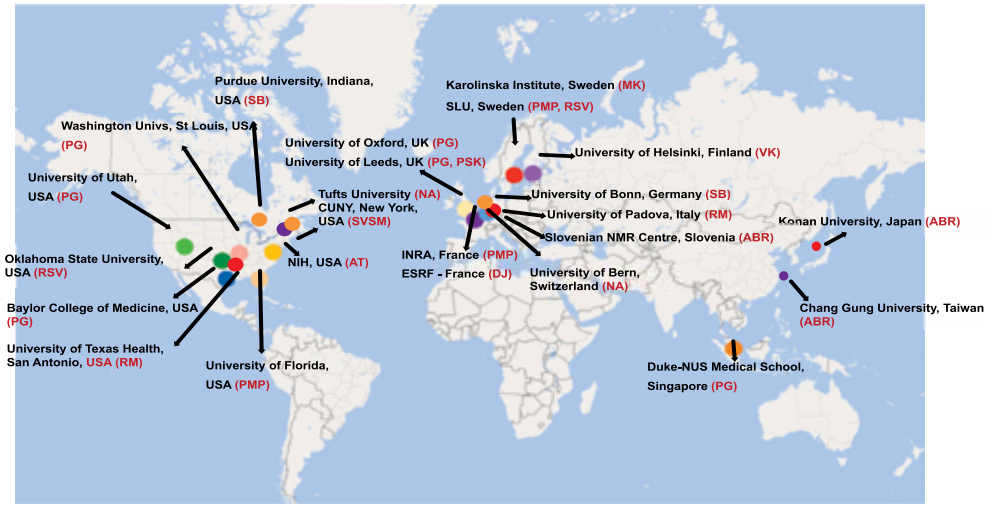
The mechanistic target of rapamycin (mTOR) regulates cell growth, metabolism, and survival through mTORC1 and mTORC2, both of which can drive cancer progression. Next-generation inhibitors, especially RapaLinks, overcome resistance and provide stronger, more durable anti-tumor effects. A thorough understanding of the mTOR pathway and its crosstalk with other cellular processes is crucial for advancing innovative and effective therapies against cancers and other mTOR-driven diseases.

The prevalence of antibiotic resistance makes treating polymicrobial wound infections caused by Gram-negative bacteria highly challenging. To address this, a niacin–cholic acid–peptide conjugate (amphiphile 1) has been created which disrupts the bacterial membranes and enables the entry of erythromycin (ERY) and thus can rejuvenate the therapeutic efficacy of macrolide antibiotics. The amphiphile–ERY combination can eliminate both mono- and polymicrobial biofilms, and effectively treat Gram-negative wound infections, and hence can revitalize ERY's efficacy against resistant pathogens.

National Collaborations



International Collaborations



Infrastructure and Support Services

Advanced Technology Platform Centre

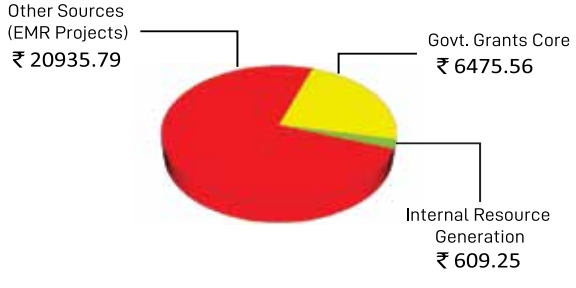
Biosafety Support Unit

BSC BioNEST BioIncubator

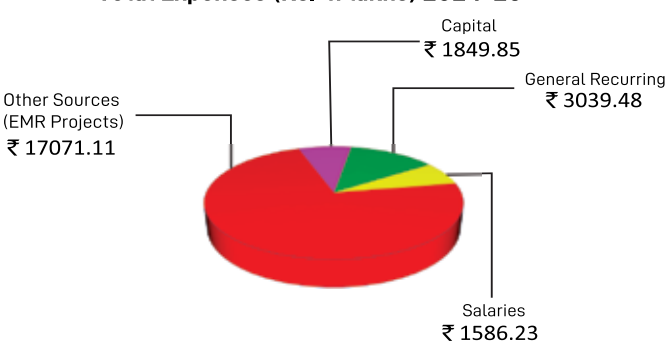
IBDC & DBT HRD-PMU

Financial Figures

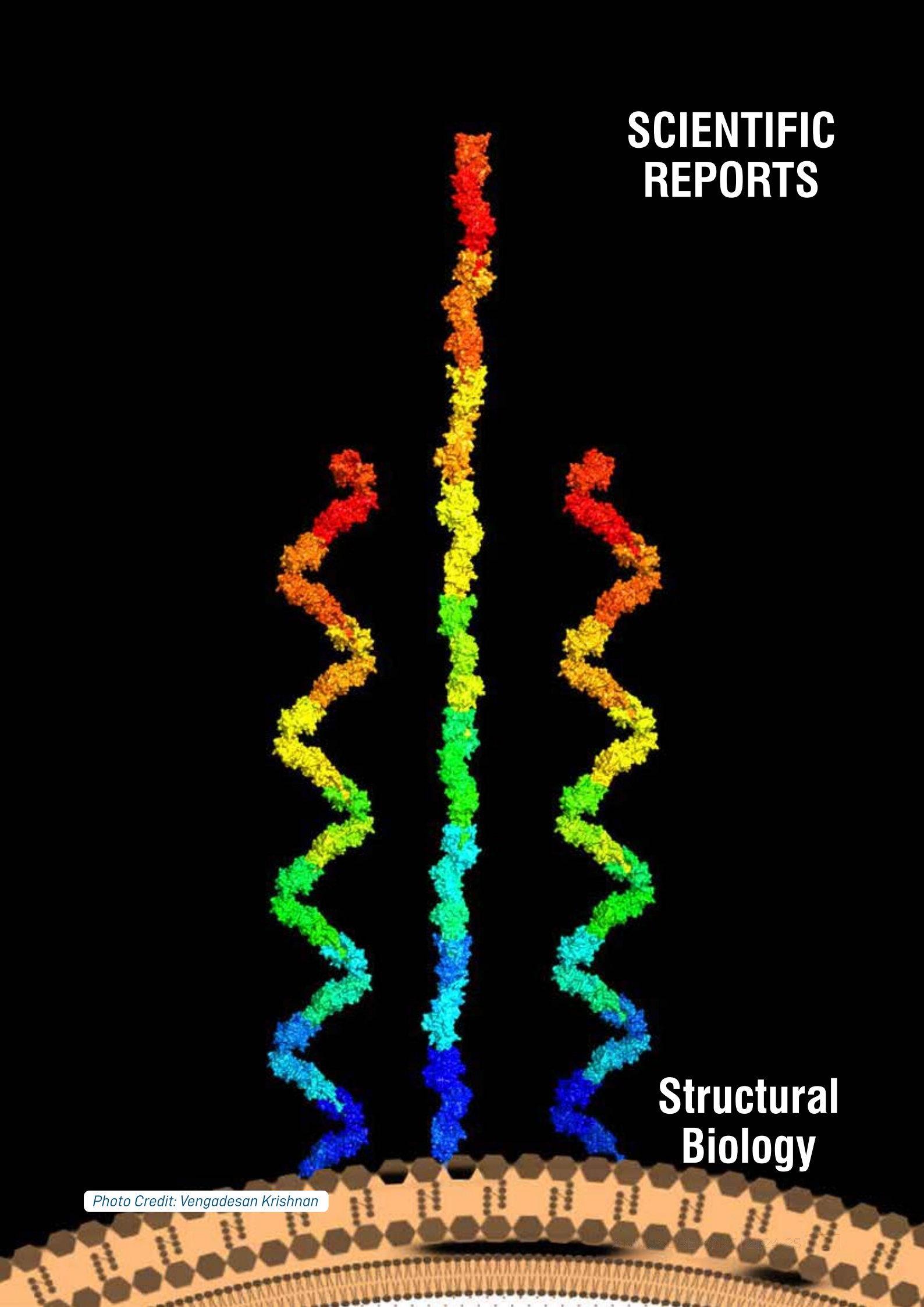
Total Income (Rs. In lakhs) 2024-25



Total Expenses (Rs. In lakhs) 2024-25



SCIENTIFIC REPORTS



Structural Biology

Photo Credit: Vengadesan Krishnan

Molecular determinants of genomic integrity and plasticity

Deepak T Nair
Principal Investigator

For all cellular processes to function optimally, the integrity of the genome must be maintained. Conversely, plasticity in the genome can relieve selection pressures imposed by an adverse environment. These two conflicting requirements have led to the presence of molecules and pathways that either prevent or facilitate changes in the genome. In the case of pathogenic bacteria and viruses, genomic plasticity is implicated in the onset of drug resistance and reduction in vaccine efficacy. We aim to elucidate the structural mechanisms utilised by different molecular determinants of genomic integrity and plasticity to achieve function. Within this broad aim, the biological processes under scrutiny in our laboratory are DNA Mismatch Repair, high-fidelity DNA replication, Stress-Induced Mutagenesis, RNA virus genome replication and Transposition (Fig.1). The insight from our studies sheds light on how organisms evolve and provides a robust platform for developing novel therapeutic strategies against pathogenic bacteria and viruses.

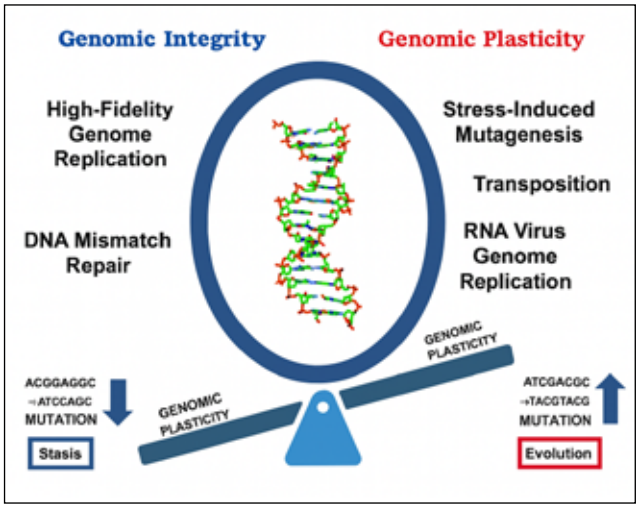


Figure 1: Molecular Determinants of Genomic Integrity & Plasticity: *A schematic of the research questions addressed at the Laboratory of Genomic Integrity & Evolution is shown.*

DNA Mismatch Repair

The Mismatch Repair (MMR) Pathway maintains genomic integrity by correcting errors that appear during replication. In *E. coli*, the specific components of MMR are MutS, MutL, and MutH. Most bacteria and all eukaryotes lack a homolog of MutH. These organisms show significant differences in MMR, especially in strand discrimination and nick-creation mechanisms. In these organisms, the endonuclease activity responsible for creating a nick in the daughter strand is present in the C-terminal

Lab Members

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Dhiraj Kumar
Subhasis Roy
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Dr. Namadurai Sivakumar

domain (CTD) of MutL. Using the pathway from *Neisseria gonorrhoeae* as a model system, we aim to elucidate the mechanism of MMR in organisms that do not follow the *E. coli* paradigm. The MutS and MutL homologs in *Neisseria* are named NgoS and NgoL, respectively.

The β-subunit of the DNA polymerase III holoenzyme functions as a processivity clamp during replication and is known to interact with the C-terminal domain of MutL. We have obtained a structure of the complex of NgoL-CTD and the β-subunit from *Neisseria* (named Nβclamp). Based on this structure, site-specific mutants were prepared and tested for their ability to disrupt the association using gel filtration analysis. The X-ray structure, along with MultiAngle-Light-Scattering and Small-Angle-Xray-Scattering experiments showed that the NgoL-CTD dimer sits transversely across the Nβ-clamp toroid, like a spoke on the bicycle wheel (Fig. 2). Since MMR genes in *Pseudomonas aeruginosa* (Psa) bear high homology to that in *Neisseria*, a complementation assay was developed with MutL-deleted strains of Psa. These assays, conducted with wt- and mutant versions of NgoL, validated the elucidated structure of the NgoL-CTD:Nβ-clamp complex.

The comparison of the complex structure with that of the partial prokaryotic replisome suggests that the observed orientation of the endonuclease domain and the clamp may help orient the newly synthesised daughter strand towards the active site of one of the monomers. Nicking assays conducted with wt- and mutant NgoL-CTD in the presence and absence of Nβ-Clamp support this inference. Overall, our studies posit that strand discrimination in non-methyl-directed MMR is achieved through a structural strategy involving the β-Clamp, which is distinct from the chemical strategy employed in prokaryotes like *E. coli* (Nirwal et al., 2025, *Nuc. Acids Res.* 53:gkaf094). Also, the structure of the NgoL-CTD:Nβ-clamp complex obtained from this study can be used to identify molecules that bind to the clamp and perturb DNA Repair and Replication in pathogenic bacteria such as *Neisseria.*

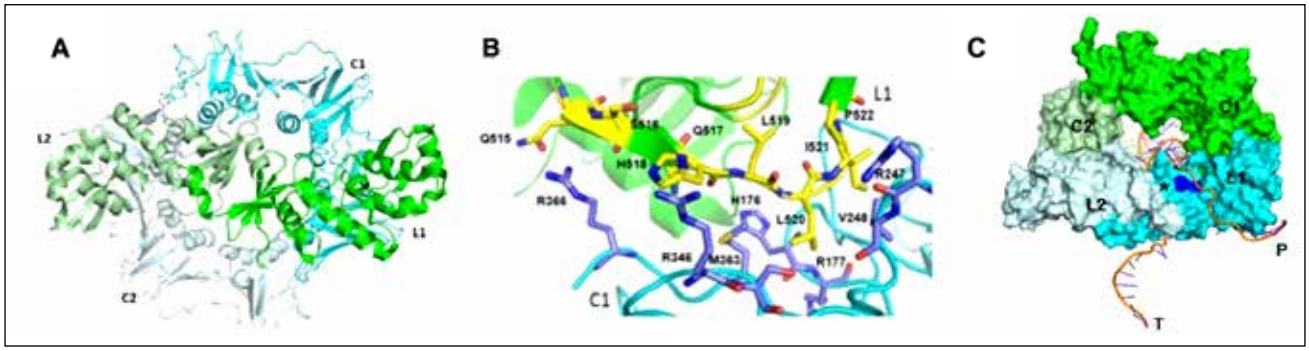

Figure 2: Structure of the NgoL-CTD*: Nβclamp complex. (A) The structure of the NgoL-CTD: Nβclamp is displayed. (B) The interactions between residues of the clamp and the clamp binding (^{517}QHLLIP^{522}) motif of NgoL-CTD are displayed, and the L520 residue is present in a hydrophobic cavity. (C) The computational model of DNA bound to the NgoL-CTD is shown and the predicted arrangement will lead to a nick in the newly synthesised strand to initiate the MMR reaction.*

A database of experimental-derived cellular toxicity information for potential drug molecules

In the last five years, we have started using computational drug discovery tools to identify candidate lead molecules that inhibit target proteins in pathogens to develop novel therapeutic strategies. However, we observed that many drug discovery exercises fail because small molecules that are effective inhibitors of target proteins exhibit high cellular toxicity. Early and effective assessment of toxicity and pharmacokinetics is essential to accelerate the drug discovery process. Conventional methods for toxicity profiling, including *in vitro* and *in vivo* assays, are laborious and resource-intensive. In response, we developed the Small Molecule Cell Viability Database (SMCVdb), a comprehensive resource containing toxicity data for over 24,000 compounds obtained through high-content imaging (HCI). SMCVdb seamlessly integrates chemical descriptions and molecular weight data, offering researchers a holistic platform for toxicity data and aiding compound prioritisation and selection based on biological and economic considerations (Pandey et al, 2024, *Database,* 2024:baae100). Data collection for SMCVdb involved a systematic approach combining HCI toxicity profiling with chemical information and quality control measures to ensure data accuracy and consistency. The user-friendly web interface of SMCVdb provides multiple search and filter options, allowing users to query the database based on compound name, molecular weight range, or viability percentage. SMCVdb empowers users to access toxicity profiles, molecular weights, compound names, and chemical descriptions, facilitating the exploration of relationships between compound properties and their effects on cell viability. The database provides experimentally derived cellular toxicity information for over 24000 drug candidate molecules to academic researchers and pharmaceutical companies. The SMCVdb will keep growing and will be a pivotal resource to expedite drug discovery and compound evaluation research. Database URL: http://smcvdb.rcb.ac.in:4321/

Structural biology of host-microbial interactions in health and diseases

Vengadesan Krishnan
Principal Investigator

Microbial attachment to host surfaces is the first step in colonization. Subsequent events in pathogenesis or probiosis are highly dependent on these initial interactions. Targeting the host-microbial interface is an attractive approach for improving health and combating infections. As this approach does not directly kill bacteria, it may serve as an alternative to antibiotics, which often result in the development of resistance. However, such an anti-adhesive approach requires detailed knowledge of how microbes attach to the host and how adhesive strategies differ among microbes. To provide the essential foundations for this approach and understand how microbes adhere to and interact with host surfaces, we aim to generate structural knowledge by studying key molecules that establish initial contact between the host and microbes. We currently focus on hair-like surface organelles (pili) that mediate initial contact with host surfaces for colonization and biofilm formation.
Our ongoing structural investigation programme covers beneficial and pathogenic strains to obtain insights into tissue tropism and microbial interaction strategies in health and disease.

Beneficial strains from gut microbiota

The most common probiotics are lactic acid bacteria (e.g., *Ligilactobacillus, Lactococcus,* and *Bifidobacterium* spp.). Pili from these beneficial strains play vital roles in adherence, persistence, and health benefits. We selected representative beneficial strains to understand pilus structures, assembly, and pili-mediated interactions with the host. Our previous work on *L. rhamnosus* GG revealed new insights into pilus shaft formation and pili-mediated lectin-type interactions with mucins. We have now purified the pili to visualize their entire architecture.

L. ruminis, an autochthonous member of the indigenous microbiota present in the gut of humans and animals, assembles a pilus with three pilins (LrpA, LrpB, and LrpC). *L. ruminis* pilus binds to various intestinal surface components such as collagen and fibronectin but lacks mucus binding. We obtained the crystal structures of *L. ruminis* pilins. Interestingly, the LrpA structure consists of three Ig-like domains with a unique bent conformation (Fig. 1), which differs from previously known shaft pilin

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structures. Interestingly, the snapshots of the two bent conformations captured for the LrpA backbone pilin facilitate pilus-like structures in the crystal lattice by docking a C-terminal tail into the hydrophobic groove in the N-terminal domain, but with a previously unobserved compressed zigzag-like shape. Small-angle X-ray scattering and structural analyses revealed that LrpA adopts a typical linear conformation, resulting in an elongated pilus morphology. The bending movement of the N-domain provides a dynamic nature to the LrpCBA pilus, allowing it to switch between elongated and compressed, zigzag-like structures. Ultimately, N-domain motion enables *L. ruminis* to adjust its pilus length and direction to project the adhesive tip pilin LrpC towards host cell receptor-binding sites for attachment and colonization (Fig. 2). Using various conformational analyses and biophysical experiments, including domain motion analysis, intrinsic fluorescence spectroscopy, and dynamic light scattering, we showed that a hinge region located at the end of the flexible N-terminal domain of LrpA facilitates a new closure-and-twist motion for assembling dynamic pili. Such dynamic properties and actions might be representative of other sortase-dependent pili as a common strategy for reaching surface receptor sites and withstanding shear forces during gut colonization. Our ongoing structural analysis of LrpB and LrpC will shed light on LrpCBA pilus anchoring and receptor binding.

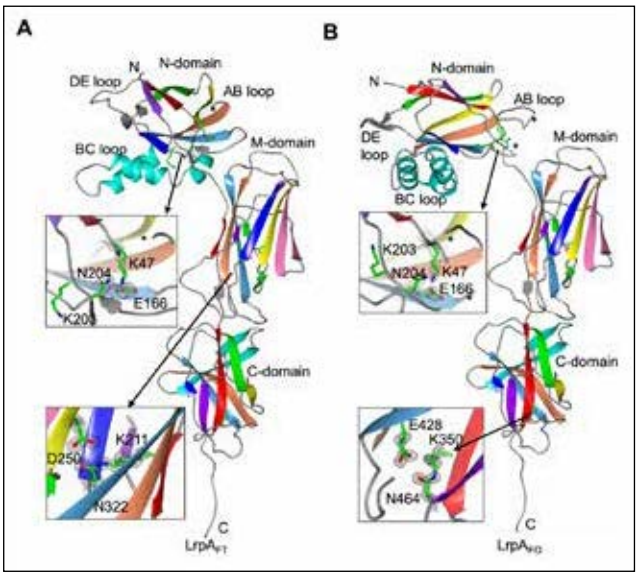

Figure 1: Crystal structures of LrpA in the bent conformations. *(A) LrpA Structure from a trigonal crystal (LrpA^{FT}) highlighting the core β-strands of the N-, M-, and C-domains in a rainbow color scheme. The residues of the intra- and inter-isopeptide bonds (sticks) are shown in enlarged views (arrows) in the electron density maps (2Fo-Fc). (B) LrpA Structure from orthorhombic crystal (LrpAFO), represented as shown in Figure 1A. Disordered loops are indicated by dashed lines and asterisks (*).*

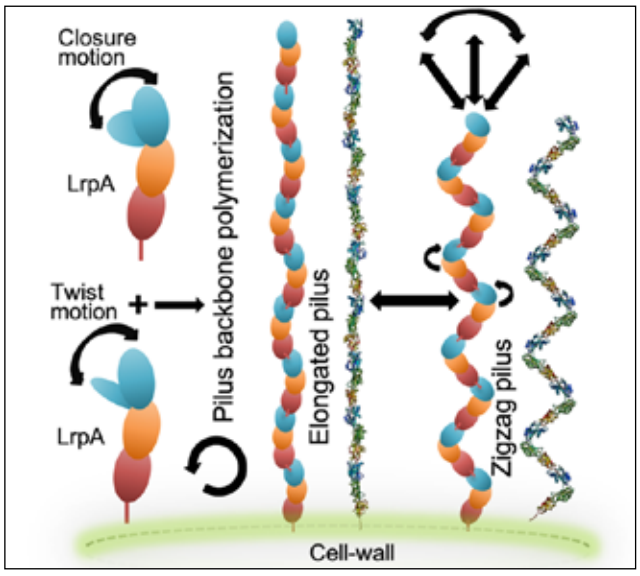

Figure 2: Schematic representation showing how closure and twist motion in LrpA enables L. ruminis to assemble an elongated and compressed zigzag-pilus shaft. *The arrows indicate the dynamic properties of the pili from the motion of the N-terminal domain of LrpA. The ribbon representation of LrpA structures in bent and linear conformations, showing their head-to-tail stacking in the crystal lattice, allows pilus assembly in two different conformations and switching between them.*

L. lactis, the best-characterized and most widely used LAB strain in dairy fermentation and biotechnological applications (e.g., delivery of oral vaccines), uses pilus-specific and housekeeping sortases to catalyze and anchor pili, respectively, as we demonstrated previously. The visualization of the entire structure of *L. lactis* pilus is currently in progress.

Pathogenic strains from the oral cavity

Primary colonizers adhere to the surface of the oral cavity through pili and provide attachment sites for secondary colonizers to develop oral biofilms or plaques. The attachment of primary colonizers and their coaggregation promote biofilm growth. Plaque can lead to several oral diseases and infective endocarditis. Our work on the PI-2 heterodimeric pilus from *S. oralis* provided insights into pilus assembly and pili-mediated coaggregation with *A. oris.* We also characterized the pilus-specific sortase from *S. sanguinis* and demonstrated how its activity can be inhibited to prevent pilus polymerization. We recently obtained the structures of the basal and shaft pilins and are in the process of obtaining the entire pilus architecture by determining the structure of the tip pilin.

Collaborative projects

Mycobacterium tuberculosis is the causative agent of tuberculosis (TB), one of the deadliest infectious diseases. To enhance our current knowledge of the complex host-pathogen interactions in TB, we obtained the structures of critical molecules (VapB12 and MMAR_2190) from the Mycobacterium genus, and their analysis is currently in progress. Molecular docking and analysis were performed to understand the interaction between the Japanese encephalitis virus NS5 protein and human nucleolin. Crystal structure determination and analysis of E-type sortase from *Thermobifida fusca* are ongoing.

Transcription Regulation: Structure and Mechanism

Deepti Jain
Principal Investigator

Pseudomonas aeruginosa is a gram-negative, opportunistic human pathogen, which is listed as a "critical" category pathogen in the DBT-WHO priority list of antibiotic-resistant bacteria. A significant contribution to the persistence of *P. aeruginosa* is due to its ability to transition from a motile flagellated form to a sessile biofilm mode of life. This phenotypic transition is regulated at the transcription level, the pivotal regulatory checkpoint for gene expression in bacteria. We employ an integrated approach involving structural tools, biophysical techniques, biochemical methods, and functional *in vivo* assays to investigate the molecular mechanisms of transcription regulation of flagellar and biofilm genes in *P. aeruginosa.* The mechanistic insights obtained are exploited to discover novel therapeutic agents against *P. aeruginosa.*

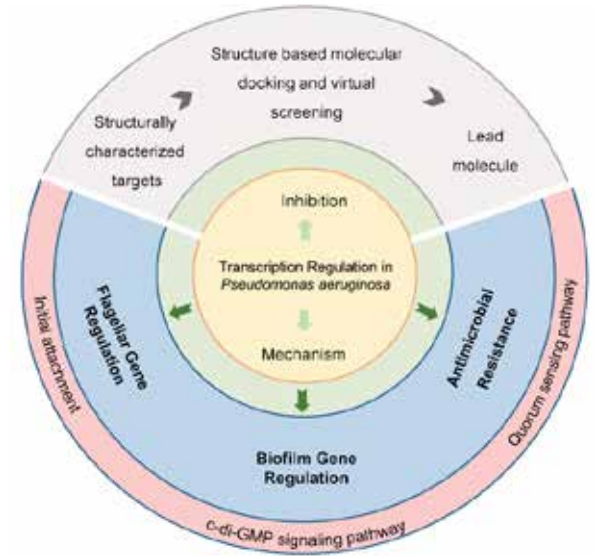

Figure 1: Transcription Regulation: Structure and Mechanism.

Structural Insights into Polarity of the Flagellar Machinery

The pathogenic bacteria *P. aeruginosa* utilize external appendages, such as flagella, for motility to move towards favorable environments and away from unfavorable ones. Additionally, adhesion and invasion of the lung epithelial cells by *P. aeruginosa* during infection depends on its flagella. Loss of flagella results in reduction in motility with a consequent decline in adhesion and invasion by this organism. Therefore, understanding the intricate regulatory mechanisms governing bacterial flagellar assembly is pivotal in unravelling the details of bacterial motility and pathogenesis (Fig. 1).

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The assembly of the bacterial flagella is regulated through a four-tiered transcriptional hierarchy. Central to the regulation of polar flagellar assembly is the protein FlhF, a GTPase, which belongs to the signal recognition particle (SRP) family. FlhF functions as a molecular switch and co-localizes with the flagellum at the bacterial cell poles in several monotrichous bacteria, including *P. aeruginosa.* FlhF is a multidomain protein and comprises three domains, B, N, and G or the GTPase domain. However, the role of different domains in the assembly and maintenance of the flagellum in clinically important pathogen remains unclear. FlhF is essential for maintaining swimming and swarming motilities. Overexpression of *flhF* leads to an increase in the number of polar flagella, while loss of *flhF* results in non-motile aflagellate cells. We have determined the X-ray crystal structure of FlhF from *Pseudomonas aeruginosa* in its apo, GDP- and GMPPNP-bound states. The structures reveal that FlhF crystallizes as a monomer in all three states, a finding validated through bacterial two-hybrid assay. A comparison of the structures also reveals that there is a drastic conformational change in the apo structure compared to the nucleotide-bound forms. Further, the nucleotide-bound form of FlhF preferentially localizes to the cell pole through the C-terminal GTPase domain. Complementation assays using truncated constructs show that both B and N domains are required for flagellar assembly. Additionally, we demonstrate that the structured N-terminus part of the B domain interacts with the C-ring protein, and this interaction is indispensable for flagellar formation. We have thus deciphered the molecular mechanisms underpinning the polar flagellar assembly, paving the way for the development of novel antimicrobial strategies targeting bacterial motility and pathogenesis. We also demonstrate that the mutants of FlhF that affect GTP hydrolysis are defective in biofilm formation, establishing FlhF as a good target for development of anti-biofilm therapeutics.

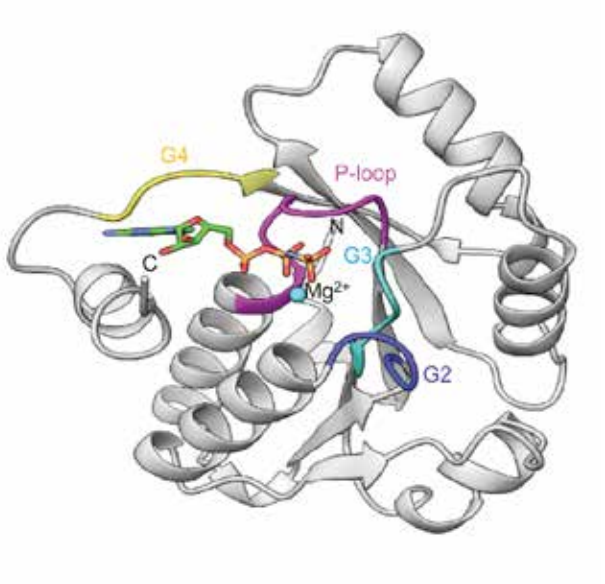

Figure 2: Crystal structure of the SRP-like GTPase bound to GMPPNP from P. aeruginosa.

Inhibition of *Pseudomonas aeruginosa* Biofilms

Pseudomonas aeruginosa causes acute and chronic infections that are hard to treat. The persistence of *P. aeruginosa* is due to its ability to develop into biofilms, which are sessile bacterial communities attached to substratum and encapsulated in matrix consisting of layers of self-produced exopolysaccharides. The biofilms provide enhanced protection from the host immune system and resilience towards antibiotics, which poses a challenge for treatment. The current remediation approaches offer some hope for clinical usage. However, the treatment and eradication of pre-formed biofilms is still challenging. Thus, identifying novel targets and understanding the detailed mechanism of biofilm regulation becomes imperative.

We have identified small-molecule inhibitors of transcription factor FleQ, a master regulator of biofilm formation in *P. aeruginosa.* We have performed *in-silico* screening of small molecule libraries using the crystal structure of FleQ, which was determined in our lab as the target. Amongst the selected compounds, five molecules have been identified that inhibit the ATPase activity of FleQ and demonstrate better than 50% reduction in biofilm formation. Additionally, we have determined the crystal structure of one of the inhibitors in a complex with the transcription factor. The inhibitors bind to a cavity very close to the ATP binding site, interacting with residues common to ATP binding. Simultaneously, we have also screened commercially available chemical compound libraries of small molecules against FleQ for biofilm inhibition. 8 molecules have been identified that demonstrate 50% reduction in biofilm formation. Further validation of these compounds is in progress.

Protein synthesis in pathogenic microbes and drug design

Prem S. Kaushal
Principal Investigator

Protein synthesis or translation is a crucial cellular process that occurs on the ribosome in all cells. This process is one of the most energy-consuming processes and consumes nearly half of the cell's energy. The ribosome is a target of nearly 40% of known antibiotics. Our research focuses on protein synthesis and ribosome assembly in pathogenic microbes, mainly *Mycobacterium tuberculosis,* which causes the deadliest disease, tuberculosis, and *Entamoeba histolytica,* which causes bloody diarrhea and liver abscess. We have been applying structural biology tools, mainly cryo- electron microscopy (cryo- EM), with molecular biology and biochemistry techniques to illustrate the ribosomal functional complexes in atomic detail (Fig. 1) and using the structure-based drug design platform for inhibitor design.

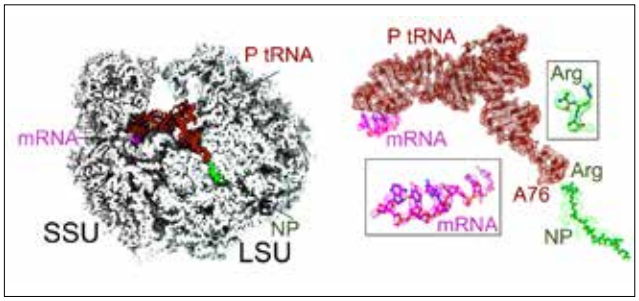

Figure 1: Our laboratory's overall research theme. *The cryo- EM is used to decipher the structure of the ribosome functional complexes and identify the species-specific unique features of its translation machinery. Left panel, the 3 Å resolution cryo- EM map of 75S ribosome. The 70S ribosome is sliced passing through roughly the core. Right panel, translation factors P- tRNA, mRNA, NP are shown in sticks with cryo- EM density at 90% transparency. The mRNA and arginine of NP are zoomed and reoriented in the box to give a better view.*

Protein synthesis in the pathogenic protozoan *Entamoeba histolytica*

Entamoeba histolytica (Eth) is an anaerobic parasite responsible for amebiasis, an intestinal infection that results in bloody diarrhea and liver abscesses. Amoebiasis is more predominant in tropical areas with poor sanitation, including India. Amoebiasis puts a huge economic burden on our country. One of the first-line drugs used to treat amoebiasis, 'paromomycin,' targets the ribosome. However, currently used drugs have their side effects and cell toxicity, and the drug resistance strains of Eth are also emerging. We aim to determine the high-resolution cryo- EM structure of the Eth ribosome and identify its protozoan-specific unique features. This project is being carried out in collaboration with Prof. S. Gourinath's laboratory at JNU, New Delhi.

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In achieving our goal, we have reported the first cryo- EM structures of the 53S ribosome large subunit (LSU) and 75S associated ribosomes, with P-tRNA, A/P, and P/E tRNAs, and with paromomycin antibiotic, between 2.8 Å and 3.4 Å resolution. The 75S ribosome paromomycin complex structure provided the atomic details of its interactions (Fig. 2). The base stacking interaction between ring I of PAR with G1901 (G1491 in *E. coli*) appears to be the major stabilizing interaction, where G1901 makes Watson Crick base pair with C1812 (C1409 in *E. coli*) and provides a stable platform for base stacking interaction with the ring I of PAR (Fig. 2E). In contrast, in humans, the corresponding residue A1823 adopts slightly different confirmation and does not base pair with the opposite strand nucleotide, which is C1710. Therefore, in humans, the base stacking interaction would be disfavored upon PAR binding; consequently, PAR would bind with a higher affinity to the *E. histolytica* ribosomes than human ribosomes.

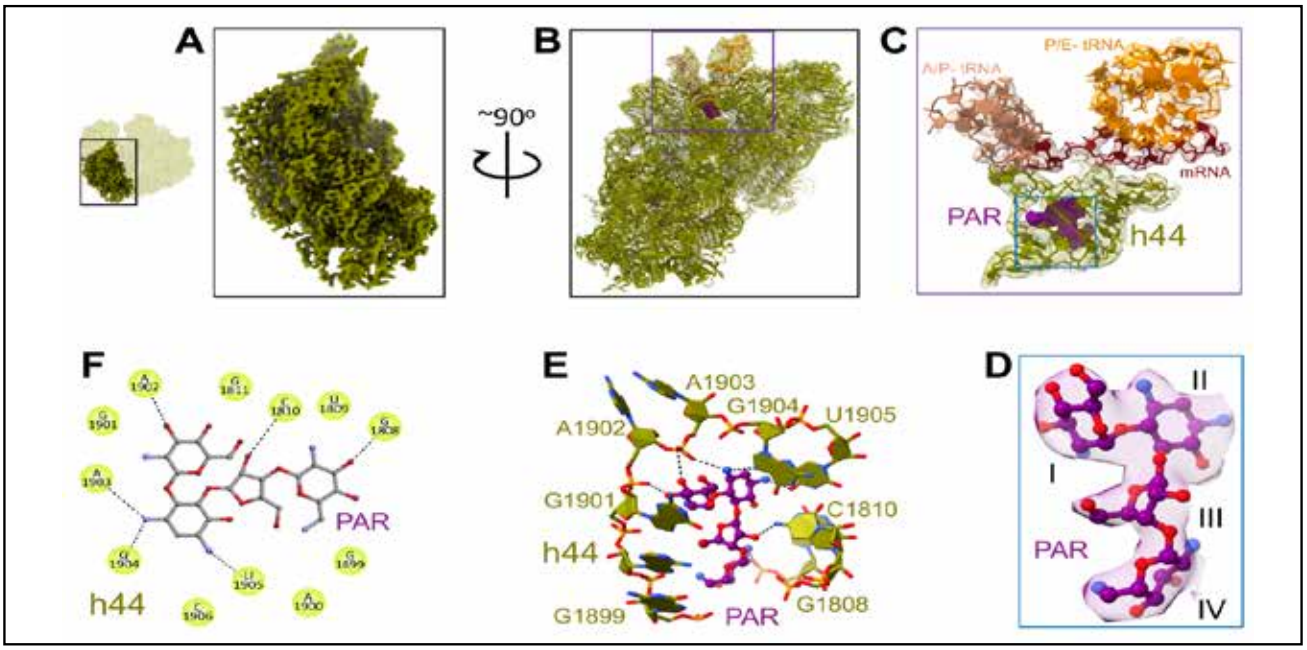


Figure 2: Cryo- EM structure of E. histolytica 75S ribosome with bound antibiotic, paromomycin. *(A) cryo- EM maps of 3D focus refinement of SSU body (olive). (B) the map of the panel a rotated by ~90° along the Y axis, and atomic models of SSU body (olive), mRNA (red), anticodon stem-loop of A/P- tRNA (salmon), P/E- tRNA (orange) and paromomycin cryo- EM density (magenta) are s hown. (C) a zoomed paromomycin binding pocket. (D) paromomycin coordinates fitted in cryo- EM density. (E) paromomycin binding pocket residues. (F) A 2D diagram of the paromomycin binding pocket residues.*

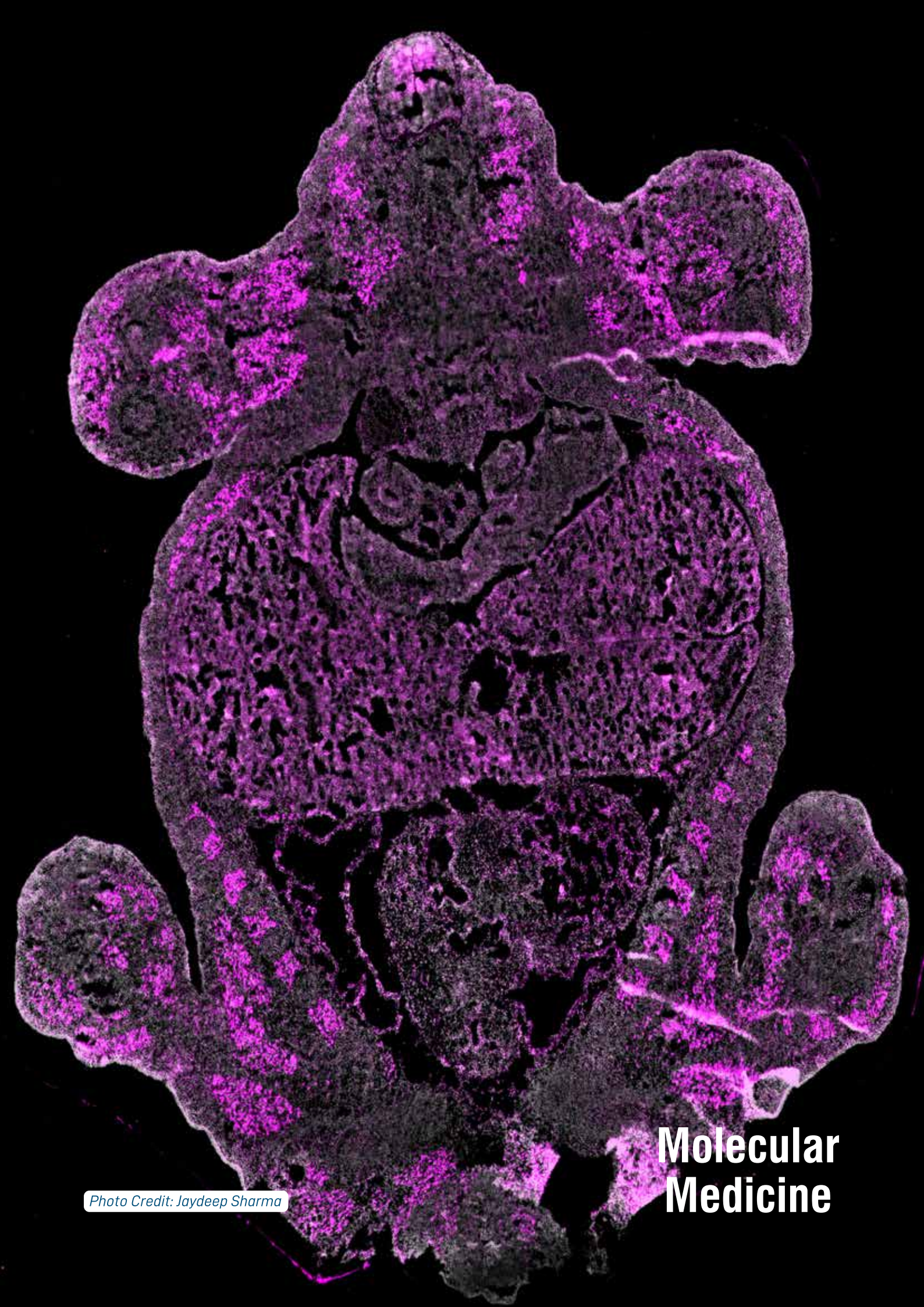
This study opens a new avenue to thoroughly investigate protein synthesis in *Entamoeba*, which is vaguely understood, and to design novel amoebicidal drugs. In the near future, we plan to determine the cryo- EM structure of ribosomal functional complexes with other aminoglycoside antibiotics such as azithromycin, telithromycin, etc.

Understanding the translational strategy Mycobacterium tuberculosis adopts under different stresses

Mycobacterium tuberculosis (Mtb) is the etiological agent of one of the most deadly bacterial diseases, tuberculosis (TB), remains a major health threat to the human race. The Mtb becomes dormant, non-replicating, and phenotypically drug-resistant while encountering multiple stresses within the host macrophages. This condition is known as latent tuberculosis infection (LTBI) or dormancy. LTBI affects about one-third of the world's population, with ~10% of those infected developing acute TB infection. Therefore, the latent Mtb infection serves as a reservoir for TB spread.

Ribosome hibernation is a key survival strategy bacteria adopt under environmental stress, where a protein, hibernation promotion factor (HPF), temporarily inactivates the ribosome and slows its overall protein synthesis. We have grown *M. smegmatis* cells under normal growth conditions (normoxic cells) and under prolonged hypoxia stress (hypoxic cells). Isolated the ribosome for structural studies. The cryo- EM structures of the 70S and 50S ribosomes from normoxic and hypoxic cells were reported between 3.1 Å and 3.6 Å resolution. A comparative analysis showed that RafH bound to 20% of 70S ribosomes of hypoxic cells. The RafH is a hypoxia induced ribosome hibernation factor. The RafH binds to the same pocket reported earlier for the lab, in the in vitro reconstituted 70S ribosome RafH complex. 15 % showed tRNA bound to the P-site of the 70S ribosome, 10% of the 70S ribosomes were empty, and the remaining 55% contained tRNA at the E-site of the ribosome. On the contrary, all the 70S ribosomes of the normoxic cells contain tRNA bound to the P- and E-sites of the ribosome. We believe that the different states of ribosomes in hypoxic cells represent snapshots of ribosomes exiting from hypoxic stress as the cell replenishes oxygen during harvesting.

Besides hypoxia stress, our lab has isolated ribosomes from different stress and nutrition starvation, H_2O_2, low pH, and heat shock. Further, we would like to get the atomic details of ribosomes in different stress conditions and understand how ribosomes are protected under different stresses.



Molecular Medicine

Photo Credit: Jaydeep Sharma

Thrombosis, Inflammation and Immune Response in Human Health and Diseases

Prasenjit Guchhait
Principal Investigator

Our major research programme focuses on investigating the signaling pathways of thrombosis, inflammation and immune responses in human diseases, including viral infections and polymorphism-associated pathogenesis. We investigate viral pathogenesis and host immune response using *in vitro* experiments, mouse models, as well as samples collected from patients. Our goal is to identify biomarkers and molecular targets associated with the severity of viral pathogenesis, diabetes and polymorphism-associated disorders. Further, we are designing small molecule anti-viral and vaccine to develop potential therapeutics.

Dengue:

Dengue virus (DENV) is the causative agent of dengue fever. Previously, we reported the pro-viral role of the platelet factor 4 (PF4 or CXCL4) on DENV replication (Ojha *et al*, 2019, Singh *et al*. 2023 a,b). Recently, we developed a small-molecule antagonist to CXCR3 (receptor of CXCL4) and described that compound 7D potently rescued mice from DENV2 infection *in vivo* (Fig. 1A; Gaur *et al*. 2024). CXCL4-mediated activation of CXCR3:p38:IRF3 signaling leads to suppression of IRF3 and IFNα/β/λ in monocytes/macrophages. Conversely, 7D supplementation reverses the above suppression and improves the IFNα/β/λ synthesis. Besides, 7D increases acetylation and phosphorylation of STAT3, which in turn promotes the plasmablast proliferation and IgG synthesis via suppression of deacetylase activity of Sirt-1. Consolidated, 7D turns out to be a promising drug candidate against all subtypes of DENV. Currently, we are testing the anti-viral role of 7D in DENV2-infected non-human primate model Rhesus macaques at the NII, New Delhi.

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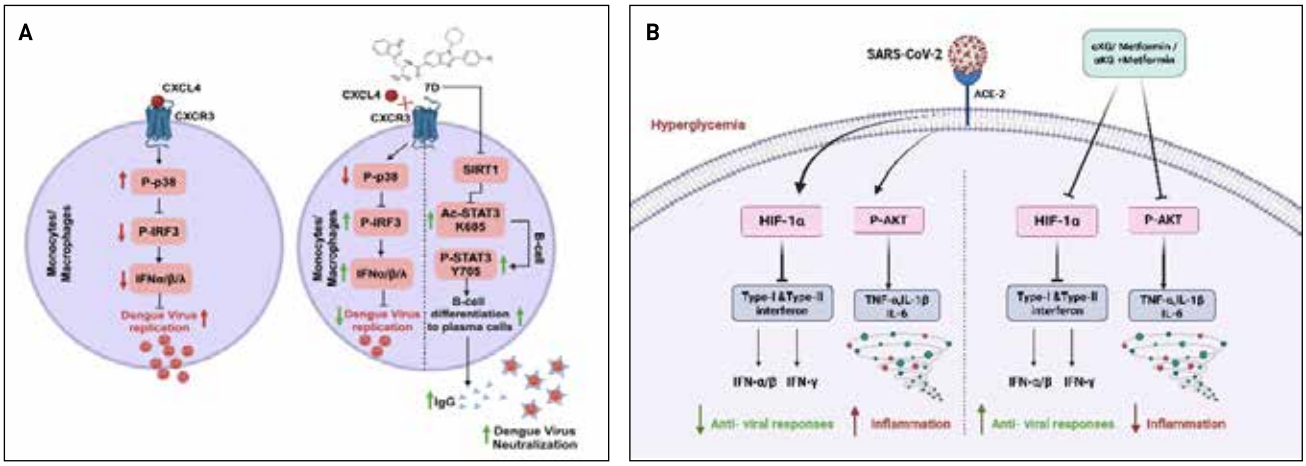

Figure 1: (A) Schematic representation of the CXCL4-mediated activation of CXCR3:p38:IRF3 signaling, which in turn leads to suppression of IRF3 and IFNα/β/λ in monocytes/macrophages and the inhibitory effect of 7D. (B) Supplementation with metformin and αKG rescues the IFNs and decreases viral infection in diabetic mice.

COVID-19

We investigated the mechanism of inflammation and clot formation in the lungs of SARS-CoV-2-infected mice/hamsters. The dietary supplementation with a common metabolite α-Ketoglutarate (αKG) significantly reduced the above-mentioned COVID-19 pathophysiology by suppressing the HIF1α – pAKT axis, and improved animal survivability (Shrimali *et al*, 2021; Agarwal *et al*, 2022). Recently, we described the mechanistic insights into the severity of COVID-19 in diabetes in mice and patients. The αKG supplementation with metformin (a commonly used anti-diabetic drug) significantly improved IFN synthesis by suppressing HIF1α axis, and decreased SARS-CoV-2 infection in both T1D/T2D mice. Patients with T2D showed an improved IFN synthesis and lesser COVID-19 severity, those who were taking higher doses of metformin (Fig. 1B). Metformin suppressed the inhibitory effects of HIF-1α on IFNs and improved IFN synthesis. Our study thus suggested the usage of metformin against COVID-19 in diabetic patients and has been accepted for publication (Joshi et al, 2025).

Gene polymorphisms and pathophysiology

Recently, we described that the Tibetan-specific mutations in prolyl hydroxylase-2 (PHD2, gene EGLN1), known as PHD2$^{D4E/C127S}$ protected these highlanders from hypoxia-triggered inflammatory response and related symptoms like high altitude pulmonary edema (HAPE; Bhattacharya *et al*, 2021). This polymorphism also showed protection against hypercoagulation in these Tibetan highlanders with PHD2$^{D4E/C127S}$ by regulating HIF1α- Protein-S axis (Fig. 2A).

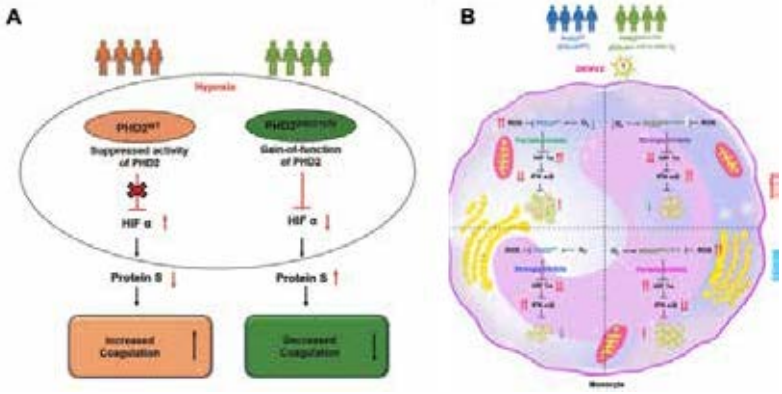

Figure 2: (A) The differential regulation of the coagulation process by HIF1α- Protein-S axis in Tibetan with PHD2$^{D4E;C127S}$ variant. (B) The crosstalk between the Tibetan PHD2$^{D4E;C127S}$ variant with pO_2 in regulating HIF:IFN axis in monocytes in dengue and COVID-19 infections.

Furthermore, the PHD2$^{D4E;C127S}$ monocytes displayed protection against DENV2 and COVID-19 infections in these Tibetan individuals by suppressing HIF1α, in turn promoting IRF-3/7/9 and IFNα/β expression under hypoxia. Study described a unique crosstalk of PHD2$^{D4E;C127S}$ variant with HIF1α-IFN axis under environmental pO2 in protecting or predisposing Tibetans to viral infections (Fig. 2B). Our data further confirmed the inverse correlation between HIF1α and IFN pathways. CAY10585, a HIF1α-inhibitor, decreased the DENV2 infection by increasing IFN-A/B and IRF-3/7/9 expression. HIF1α-depleted monocytes also showed a similar response to the infection. The observation in Tibetans serves as a model for us to appreciate the crucial role this gain-of-function mutation plays in the modulation of HIF1α-mediated IFN responses against viral infections. Hereafter, we are attempting to resolve HIF1α-associated viral pathogenesis *in vitro* by augmenting the synthesis of IFNs using a HIF1α inhibitor. This work has been accepted for publication in a high-repute journal (Ghosh et al, 2025).

Pregnancy complication: From molecular understanding to biomarker discovery

Tushar Kanti Maiti
Principal Investigator

Preterm birth stands as a significant global public health challenge, representing the primary cause of neonatal mortality. India accounts for approximately a quarter of global preterm births and related deaths. From a clinical standpoint, comprehending the molecular mechanisms underlying preterm birth is imperative for its early prediction and prevention. RCB collaborates with THSTI, NIBMG, Gurugram General Hospital, and several other institutions for the Inter-institutional Advanced Research on Birth Outcome-DBT India Initiative (GARBH-Ini), with our team taking the lead in the proteomics component. Moreover, our involvement in the global Multi-Omics for Mothers and Infants (MOMI) Consortium allows us to address diverse inquiries related to pregnancy complications. At the heart of our endeavors lies the overarching objective of pinpointing biomarkers crucial for the early detection of preterm birth (Fig.1).

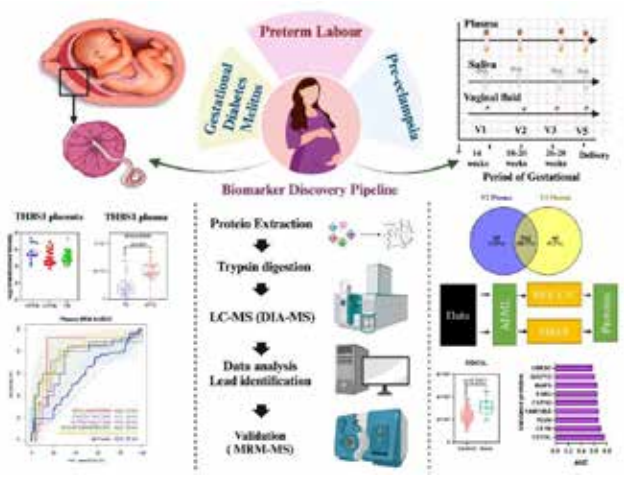

Figure 1: Schematic diagram of the proteomics biomarker discovery pipeline for pregnancy complications.

Plasma proteome profiling identifies predictive signatures for preterm birth risk

Preterm birth (PTB) is a significant cause of neonatal mortality and morbidity worldwide, with the Indian subcontinent contributing over 3 million preterm births annually. The GARBH-Ini cohort estimates the incidence of preterm births at approximately 13%. Early prediction of PTB can significantly reduce its incidence and associated burdens. More than 50% of PTB cases are spontaneous,

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with unknown underlying causes. Various proteomics studies have attempted to identify and validate protein markers in biofluids like plasma and high vaginal fluid, highlighting proteins such as fetal fibronectin, C-reactive protein (CRP), serum amyloid A, interleukins, insulin-like growth factor-binding protein 4 (IBP4), and sex hormone-binding globulin (SHBG). However, these studies are limited by low sensitivity, lack of external validation, small sample sizes, and relevance only to symptomatic pregnancies.

Our primary objective is to develop a comprehensive model for early (mid-trimester) risk stratification of mothers at risk of spontaneous preterm birth, facilitating timely medical intervention. To achieve this, we conducted a high-throughput comprehensive plasma proteomics study within the GARBH-Ini cohort. The plasma proteomics analysis on a nested case-control study identified ~620 protein groups with high data completeness. Approximately 16% of the plasma proteome showed expression changes in both early and late mid-trimester stages of pregnancy, deviating from normal trajectories. Functional enrichment analyses revealed disruptions in key developmental pathways (respiratory, brain, circulatory, skeletal systems) and molecular functions (calcium transport and growth factor activity). Using machine learning tools, 42 predictive proteins were validated in a case-cohort study design comprising 51 cases, with the remaining participants considered as non-cases. Among 42 proteins, MICAL2 and CAPS2 were selected based on feature selection criteria, and subsequent prediction models were built. MICAL2, linked to actin remodeling and aberrant ERK/AKT signaling that may contribute to adverse pregnancy outcomes. CAPS2, a calcium-binding protein, plays a role in uterine muscle contractions and was previously associated with sPTB through SNP analysis. Altered plasma levels of CAPS2 may reflect disrupted calcium homeostasis, a known risk factor for preterm labor. The final predictive model, based on CAPS2, demonstrated high sensitivity (>90%) and good specificity, particularly in identifying high-risk cases (delivery ≤32 weeks). The model remained effective across a broader cohort, including idiopathic sPTB, PPROM, and comorbidities like pre-eclampsia, making it clinically promising (Fig. 2). The study emphasizes CAPS2 as a strong biomarker candidate for mid-trimester screening, potentially enhanced by integration with clinical and multi-omics data. Validation efforts across diverse Indian regions are ongoing. This work lays a foundation for the early prediction of sPTB and informs future diagnostic strategies.

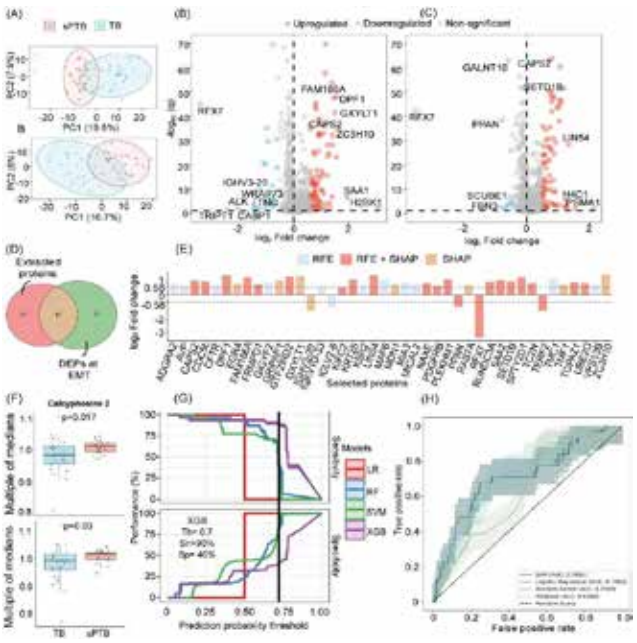

Figure 2. Plasma samples collected at EMT and LMT timepoints were subjected to global proteomics. *Differential analysis identified more than 100 plasma proteins differentially expressed in the sPTB condition. Machine learning based feature extraction and targeted MRM validation identified increased levels of plasma CAPS2 as an important predictor of high-risk sPTB. The prediction sensitivity of the model was more than 90% maintaining around 40% specificity.*

Research undertaken by DST- Inspire Faculty, Dr. Nitu Singh

Developing Proximity-Based Strategies to Revitalize Autophagy-Lysosomal Pathway in Parkinson's Disease

Dr. Nitu Singh

Neurodegenerative diseases such as Parkinson's disease (PD) are characterized by disrupted proteostasis, leading to the accumulation of toxic α-synuclein (α-Syn) aggregates that damage the dopaminergic neurons. Current therapies are limited to symptomatic relief and do not prevent disease progression, primarily due to the absence of effective strategies targeting α-Syn aggregates. A crucial mechanism for clearing these toxic aggregates is the autophagy-lysosomal pathway (ALP), which is often impaired in PD. Small GTPases of the Rab family regulate vesicular trafficking in ALP and require geranylgeranylation for their proper function. Recent studies suggest that modulating prenylated proteins can restore lysosomal activity and reduce α-Syn pathology. Therefore, we are currently developing a proximity-based strategy to selectively degrade Rab-geranylgeranyltransferase using PROTAC (PROteolysis Targeting Chimera) technology, offering a targeted, less toxic alternative to conventional inhibitors. Additionally, prenylomic profiling in wild-type and α-Syn mutant PD mouse models is underway to identify key therapeutic targets. By integrating targeted degradation strategies with molecular insights into Rab biology and prenylation, this approach seeks to restore.

Signals that regulate skeletal muscle structure and function

Sam J Mathew
Principal Investigator

The skeletal muscle is the largest tissue in our body, essential for vital functions such as locomotion, support, posture maintenance, and regulation of whole-body metabolism. We are investigating the mechanisms that regulate skeletal muscle formation and controls its function. Skeletal muscle damage or injury occurs in accidents, during physical activity such as sports, or due to congenital diseases such as muscular dystrophy. Muscle stem cells known as satellite cells, present in the skeletal muscle, help in its repair and regeneration. We are studying how skeletal muscle repair and maintenance occurs, identifying and characterizing the genes involved. We are also studying a cancer type called rhabdomyosarcoma, where the tumor cells exhibit properties of muscle cells, to identify signaling pathways that can be targeted for therapies to treat such tumors.

Myosin Heavy Chain-perinatal is required for proper myogenic differentiation

Mammalian adult skeletal muscle is crucial for locomotion, posture maintenance, support and metabolic regulation. Multinucleated, contractile myofibers are the major cell type making up the skeletal muscle. These myofibers form through a differentiation process called myogenesis, involving stage specific expression of transcription factors and regulatory proteins. The myofibers contain sarcomeres, which are functional contractile units, composed of thin and thick filaments. Myosins are the contractile proteins that constitute the thick filaments, composed of different subunits, of which Myosin heavy chains (MyHCs) are the major subunit. Several MyHC isoforms exist, among which one, MyHC-perinatal encoded by the *Myh*8 gene, is expressed during muscle development or during muscle injury and associated regeneration. Mutations in *MYH8* lead to human congenital musculoskeletal disorders such as Trismus-Pseudocamptodactyly Syndrome. It is therefore vital to understand the functions of MyHC-perinatal in muscle differentiation, which will help develop strategies to treat such muscle disorders.

MyHC-perinatal, encoded by the *Myh8* gene, exhibited transcript expression from day 3 of C2C12 mouse myogenic differentiation, peaking at days 5 and 7 (Fig. 1A). To decipher its role in myogenic differentiation, *Myh8* expression was depleted by siRNA treatment, which led to an increase in the number of myofibers and differentiation index (Fig. 1B-D).

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The proportion of cycling, undifferentiated cells within the differentiated C2C12 culture, known as reserve cells, exhibited a striking decrease in number upon *Myh8* depletion (Fig. 1F-H). Quantifying the transcript levels of the myogenic regulatory factors (MRFs) and *Pax7*, genes involved in myogenic differentiation, indicated increased expression of the late differentiation markers *MyoG* and *MRF4*, and a decrease in the early differentiation marker *Myf5* (Fig. 1E). At the protein level, a significant increase in MyoD (at days 3 and 5), and MyoG (at days 5 and 7) expression were observed upon *Myh8* knockdown (Fig. 1J, N, O). Compensatory effects on other MyHC isoforms, causing downregulation of MyHC-slow and upregulation of the fast MyHC-IIb was also observed upon Myh8 depletion (Fig. 1I, K-M).

Our findings indicate that loss of MyHC-perinatal function leads to enhanced differentiation, reduced reserve cell numbers, a switch from slow type I to fast type IIb fiber type and reduced mitochondrial numbers. Paracrine signals mediate the effect of loss of MyHC-perinatal function on myogenic differentiation, mediated by non-apoptotic Caspase-3 signaling. Thus, MyHC-perinatal is a crucial regulator of myogenic differentiation and myofiber oxidative phenotype (Fig. 2).

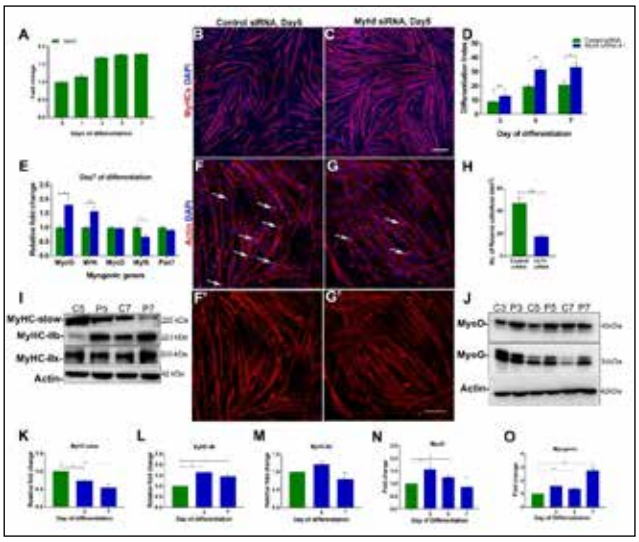


Figure 1: MyHC-perinatal regulates C2C12 differentiation. *(A) Myh8 transcript levels from day 0-7. (B-D) Control and Myh8 siRNA treated cells on day 5 (MyHCs-red; DAPI-blue), and differentiation index. (E) Myogenic gene transcript levels upon control and Myh8 siRNA treatment on day 7. (F-H) Control and Myh8 siRNA treated cells on day 5 (Actin-red; DAPI-blue; arrows-reserve cells); quantification of reserve cells. (I-O) Western blots for MyHCs and myogenic factors at days 3-7 and densitometry.*

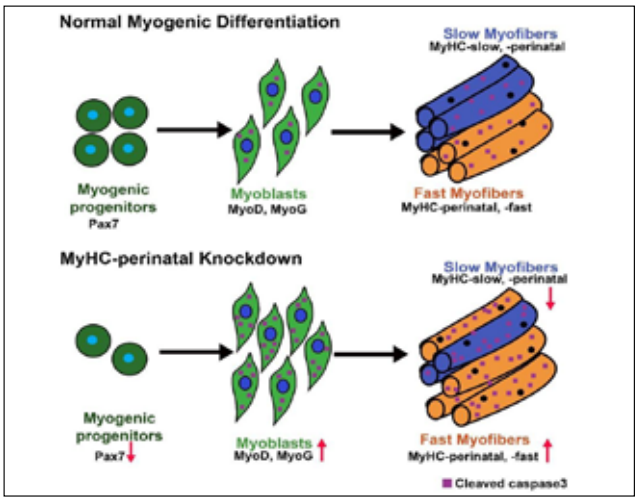


Figure 2: MyHC-perinatal is required for proper myogenic differentiation. *MyHC-perinatal is a predominantly developmentally expressed myosin protein, required to regulate the rate of differentiation and myofiber-type proportion during myogenesis. Depletion of MyHC-perinatal leads to enhanced differentiation characterized by a reduction in myogenic progenitor pool, increase in myoblasts, and a switch from slow to fast fiber type, mediated by non-apoptotic Caspase-3 signaling.*

Research undertaken by India Alliance Early Career Fellow Dr. Masum Saini

Modulation of MET signaling and its role in myogenesis

Dr. Masum Saini

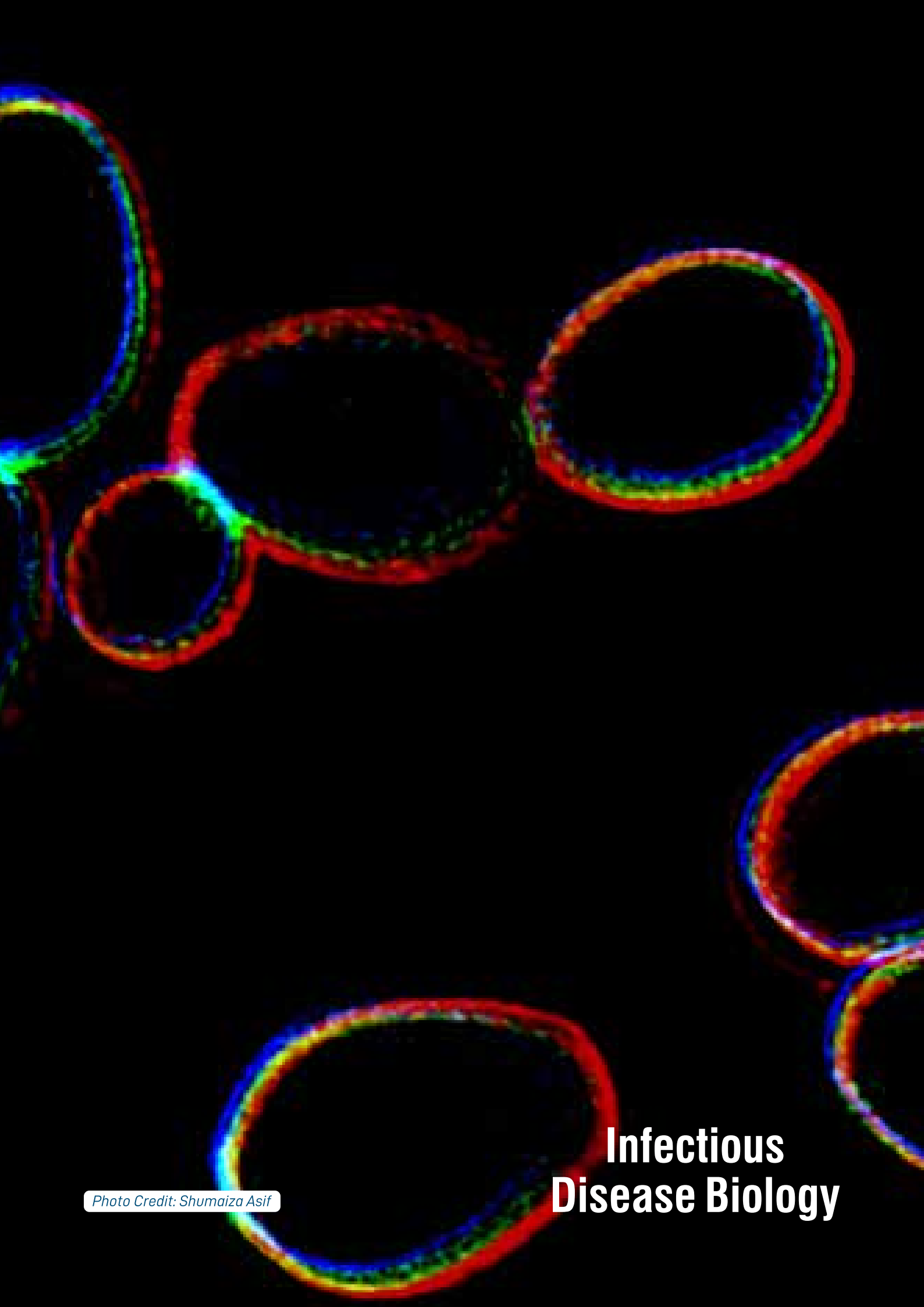
Receptor tyrosine kinases (RTKs) regulate vital processes such as embryonic development, postnatal tissue homeostasis, regeneration, and are implicated in diseases such as cancer. MET, a proto-oncogenic RTK, is crucial to embryonic morphogenesis, especially in muscle precursor migration during myogenesis and in postnatal muscle stem cells mediated skeletal muscle regeneration. To understand the role of MET in myogenesis, I use genetically engineered mice to ablate its function in the skeletal muscle progenitors. Loss of MET function did not impact embryonic survival, but its absence was lethal after birth. I am trying to identify the reasons underlying this postnatal lethality and characterize defects in skeletal muscle formation in the Met knockouts. This work contributes to understanding the role of MET signaling during development, regeneration and disease.

Research undertaken by DST Women Scientist A (WOS-A) Dr. Sanghamitra Mylavarapu

Deciphering the Role(s) of β-catenin in Cell Division

Dr. Sanghamitra Mylavarapu

Evolutionarily conserved β-catenin, the central regulator of the Wnt signaling pathway is well studied both in health and disease context. An exciting new role of β-catenin in directly controlling mitosis has recently been reported. The overall aim of the project is to understand the mechanism(s) through which β-catenin modulates cell division. The study has brought forth novel functions of β-catenin in directly modulating mitosis wherein, critical events ensuring fidelity of genome segregation are impacted upon perturbation of the protein. Mechanistic studies are underway to determine the molecular interplay between β-catenin and other cellular machineries that govern mitosis, including specific amino acids on β-catenin that are key determinants of these interactions.



Infectious Disease Biology

Photo Credit: Shumaiza Asif

Biology of Medically Important Viruses

Sudhanshu Vrati
Principal Investigator

Viruses pose an ever-increasing threat to the well-being of the human population at large, and this scenario is particularly ominous in the Indian context, where epidemics of various viral infections are reported at regular intervals. Understanding the biology of virus infection, replication, and pathogenesis will help in designing novel antivirals for effective therapeutic and prophylactic interventions. We are studying the biology of Chikungunya virus (CHIKV) and Japanese encephalitis virus (JEV) to understand their replication and pathogenesis with a view to designing novel antiviral strategies. Also, high-throughput platforms for screening small-molecule libraries for antiviral activity against CHIKV and JEV are being used. Provided below is a summary of some of the key projects under the program.

Assay development for image-based drug screening against JEV and its validation

To discover novel inhibitors against JEV replication, we established an EGFP-based infection assay using a high-content imaging platform (Fig. 1). A recombinant JEV was produced where the EGFP coding sequence was located under the JEV promoter. Therefore, EGFP is expressed every time with viral translation, and EGFP fluorescence indicates the replicating virus in the infected cells. Any reduction in EGFP expression would be an indication of reduced viral replication. This reduction could be due to the inhibition of viral entry, genome replication, or any other steps in the JEV life cycle. Therefore, compounds that inhibit CHIKV replication can be

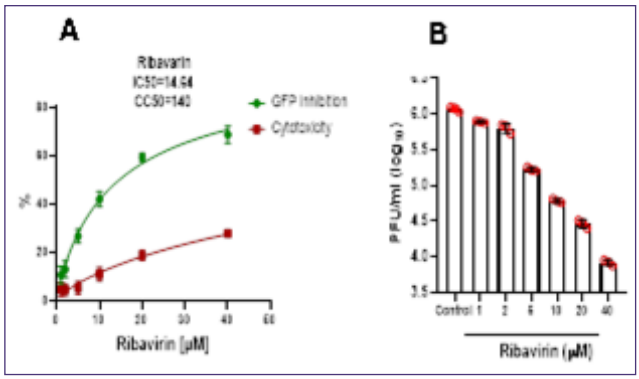


Figure 1: Validation of the antiviral assay. *(A) Graph demonstrating the per cent EGFP-JEV inhibition and per cent cytotoxicity in virus-infected (1 MOI, 24 h) and DMSO/Ribavirin-treated Vero cells at indicated concentrations. (B) Bar graph showing JEV titer in virus-infected (1 MOI, 24 h) and DMSO/Ribavirin-treated Vero cells at indicated concentrations.*

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identified by direct imaging and quantification of EGFP levels compared with controls.

A high-throughput screening assay was established in the 384-well plate format. The statistical/quality assessment was done to ensure robustness, sensitivity, accuracy and reproducibility of the assay using quality parameters such as signal to noise (S/N) ratio, coefficient of variation (CV% %) and Z' factor. The S/N ratio was 36.32, the CV was 1.94, and Z' was 0.63, demonstrating the quality of the high-throughput assay.

Identification of the host factors involved in CHIKV entry into human cells

Virus attachment to its specific receptor and entry through the endocytic portal are the initial critical steps of infection. This information is valuable for designing novel antivirals. Virus receptors are usually host membrane proteins that bind to the viral envelope/structural proteins. Purified CHIKV was used as a bait to identify the interacting membrane proteins from Huh7 cells using mass spectrometry. We identified Junction plakoglobin (JUP) and Flaggrin (FLG), Annexin 2 (ANXA2), Hornerin (HRNR), and 1-Acylglycerol-3-Phosphate O-Acyltransferase 1 (AGPAT1) as binding with CHIKV virions.

AGPAT1 is a transmembrane lipid-modifying enzyme. Using confocal microscopy, we demonstrated its presence on the cell membrane of Huh7, ERMS, and HAP1 cells (Fig. 2). CHIKV virions were found to interact with AGPAT1 on the plasma membrane of Huh7 cells. Additionally, CHIKV binding to Huh7 cells was inhibited by the AGAPT1 antibody. CHIKV uptake and replication were reduced in AGPAT1 siRNA-treated cells. CHIKV binding, uptake, and replication were significantly reduced in the AGPAT1 knockout (KO) HAP1 cells. Importantly, the ectopic expression of AGPAT1 rescued the reduced CHIKV uptake and replication in the AGPAT1 KO HAP1 cells. *In silico* studies showed that AGPAT1 interacted with the CHIKV E1 protein in Huh7 cells. We have identified the amino acid residues of CHIKV E1 and AGPAT1 involved in the virus-host interaction. Mutation of these residues caused reduced E1-AGPAT1 interaction resulting in retarded CHIKV uptake and replication in the cell.

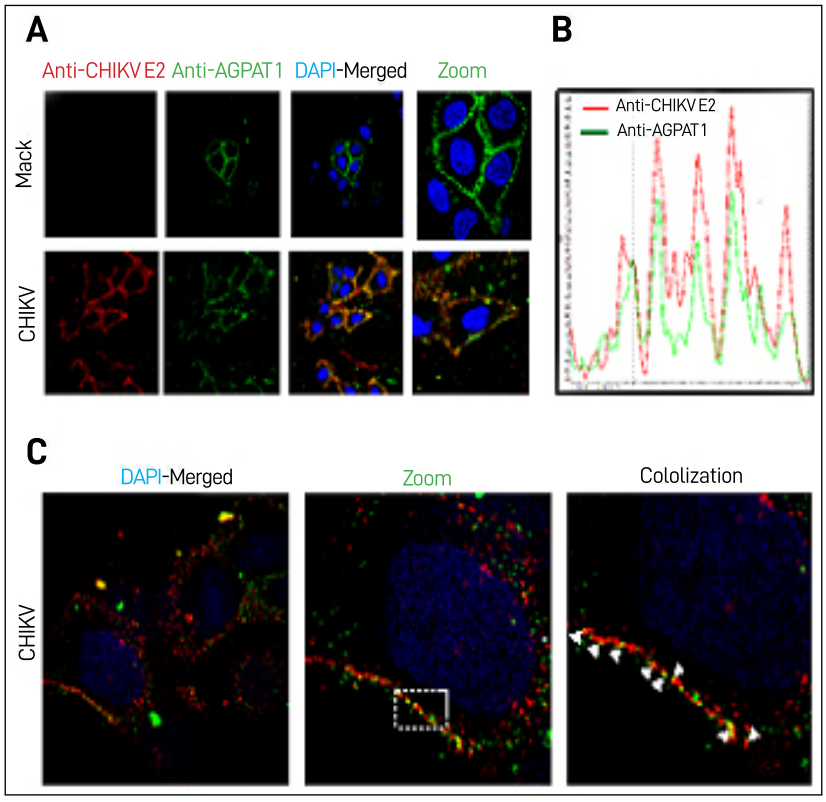

Figure 2: CHIKV interacts with AGPAT1 at the plasma membrane of Huh7 cell. *(A) Immunolocalization of CHIKV E2 and AGPAT1 in Huh7 cells. The nuclei were stained with DAPI. (B) Line plot showing the co-localization of the red (CHIKV) and green (AGPAT1) fluorescence signal. (C) Co-localization of CHIKV and AGPAT1 observed by super-resolution structured illumination microscopy (SIM). The white arrows show the co-localized puncta under 100X magnification and 10X zoom.*

Laboratory of Gut Inflammation and Infectious Biology

Chittur V. Srikanth
Principal Investigator

Inflammation, particularly chronic inflammation, is known to stimulate cancers of several kinds, including Gallbladder cancer (GBC) and colorectal cancer. Among the gastrointestinal cancers, GBC is one of the most aggressive types. Chronic inflammation in the gallbladder resulting from the presence of gallstones or *Salmonella* infections is considered to be a major factor contributing to GBC. However, the actual connection between *Salmonella* infection and GBC pathogenesis remains unexplored. Poor prognosis of GBC may be linked to delayed detection and a lack of understanding of cellular and molecular aspects. In the current study, we show a strong association between GBC and chronic *Salmonella* infection occurring through a novel host epigenetic mechanism. Our findings have significant potential to guide preventive strategies for GBC, particularly in chronic *Salmonella* carrier subjects.

Enteric Salmonella chronically colonizes the Gallbladder in a Gallstone mice model

GBC has a high prevalence in certain parts of the world, particularly in countries like India, Chile and South America. Notably, the Indo-Gangetic belt inhabitants, specifically women from this area, are most affected with an incidence of ~22 per 100000 population. Delayed diagnosis and unsatisfactory response to available chemotherapeutic drugs make this disease a significant health burden. Curative surgery is possible in only <10% of patients, typically those with incidental early diagnosis.

Prolonged inflammation in the gallbladder has been considered to be connected to GBC. Inflammation of the gallbladder (cholecystitis) arising from chronic *Salmonella* infections or the presence of gallstones (cholelithiasis) and genetic predispositions are some of the common risk factors for GBC. Loss of heterozygosity, mutations in *KRAS, PIK3CA* and *TP53* genes are most frequently reported genetic aberrations linked to GBC. A multi-step process ensues tumorigenesis in GBC, often taking several years before tumours become metastatic. During cancerous transformation, epithelial cells of the gallbladder undergo

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trans differentiation, losing differentiated markers and gaining mesenchymal properties, a process referred to as epithelial to mesenchymal transition (EMT). The cellular and molecular events that govern EMT in GBC are not fully understood.

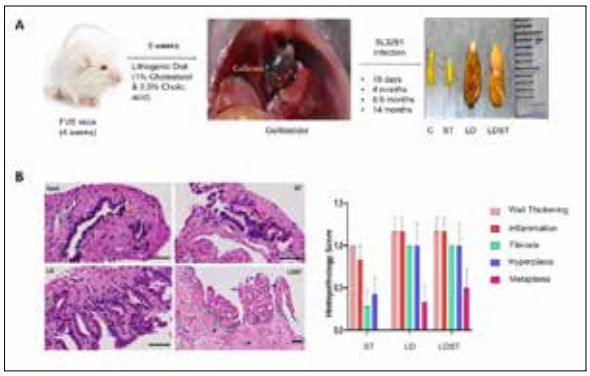

Figure 1. Development of a murine model of gallstone and chronic Salmonella infection. (A) *Schematic representation of the steps involved in the development of gallstones and the chronic Salmonella mice model. Mice were given a lithogenic diet for 9 weeks, followed by ST infection.* ***(B)*** *Detection of Histopathological alterations in the Gallstone mice model. Representative images of Haematoxylin & Eosin-stained gallbladder sections (left panels) and histopathology score plots (right panel).*

Using relevant mouse models, cell culture systems and human gallbladder samples, this current study aimed to investigate the possible connection between *Salmonella* infections and GBC. To understand the mechanism of GBC carcinogenesis, a murine model with gallstone disease and chronic *Salmonella* infection was established (hereafter referred to as gallstone-chronic *Salmonella* mice; Fig. 1A). The protocol for induction of gallstones in mice was a modification of a previously well-established protocol. This involved feeding of FVB/N mice with a lithogenic diet consisting of cholesterol and cholic acid for 9 weeks, followed by infection with a *Salmonella* Typhimurium ΔaroA mutant, suitable for chronic infections. At the end of the experiment, the presence of gallstones was observed in all the animals subjected to a lithogenic diet. In each case, the relevant tissue was examined for the presence of *Salmonella* as well as various markers of inflammation. The presence of viable *Salmonella* in gallstone-chronic *Salmonella* mice was also confirmed by culturing and 16S qRT-PCR-based specific assay (Fig. 1A). Notably, a detailed histopathological examination revealed clear signs of pre-malignant changes in the gallbladders of gallstone-chronic *Salmonella* mice (Fig. 1B). In line with this, resected gallbladders as well as faecal microbiome of GBC patients, but not healthy controls, showed the presence of *Salmonella*.

Chronic *Salmonella* infection induces epigenetic alterations in the murine gallbladder

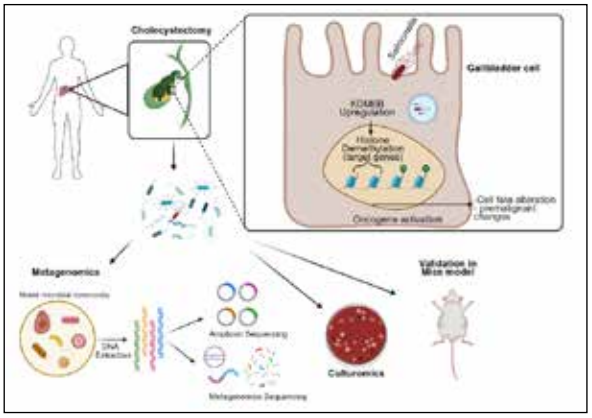

Figure 2. Schematic illustration showing Invasive Salmonella Typhimurium colonization in the gallbladder and its role in gallbladder carcinogenesis. *The figure depicts the key methodology involved in the study (top left and bottom panel) along with the study outcome (inset). Figure generated through BioRender.*

In a previous study from our lab, we reported that chronic *Salmonella* infection induces epigenetic changes in the host (Rana et al., 2021). The involvement of Kdm6B, a histone demethylase, was necessary for this mechanism, particularly during chronic *Salmonella* infections. The gallstone-chronic *Salmonella* mice were investigated for the possible role of Kdm6B in mediating the observed pre-malignant alterations. An upregulated expression of Kdm6B was observed in the gallbladder of gallstone-chronic *Salmonella* mice. Similar phenotypes were also observed in resected gallbladders of GBC patients. The observed changes were accompanied with elevated expression of drivers of tumorigenesis including ADAMTSL5. Among the differentially expressed genes, those with regulatory function, such as ADAMTSL5 and SPSB4, were significantly dysregulated in the gallbladder-derived NOZ cell line upon infection with *Salmonella*. Chromatin immunoprecipitation showed a 3-fold higher binding of Kdm6B on the promoter of ADAMTSL5 in NOZ cells infected with *Salmonella* compared to control cells. In line with this, a concomitant decrease in the H3K27me3 mark, i.e. histone-3 lysine 27 tri-methylation was also observed. The complete overview of the workflow and the outcome is represented in Fig. 2. Taken together, our data highlights, for the first time, the mechanism and direct involvement of *Salmonella* in GBC. These findings have important implications towards devising preventive strategies for GBC, particularly in chronic *Salmonella* carrier subjects.

Host-pathogen Interactions of flaviviruses and antiviral development

Manjula Kalia
Principal Investigator

Dengue virus (DENV) and Japanese Encephalitis Virus (JEV) are mosquito-borne flaviviruses, with a significant health burden in India. The treatment given to patients is mostly symptomatic, and there is an urgent need for the development of antiviral treatment. During virus infection, a constant battle between the host and the virus decides the course of the disease. We are trying to understand how these viruses invade the different cells of the human body, including the brain, and how they exploit the cellular machinery and metabolic pathways to grow and spread. We are actively engaged in testing and designing new broad-spectrum antiviral therapeutics that target essential host factors hijacked by viruses, rather than directly targeting the virus itself. This approach aims to circumvent the rapid emergence of drug resistance, a common limitation of traditional antiviral therapies. We aspire towards the identification and development of antiviral strategies and drugs.

Identification & characterization of endocytic targets for JEV: Endophilin-mediated endocytosis & Epidermal growth factor receptor

The focus of this study was to understand how the mosquito-borne *flavivirus*: JEV, enters the neuronal cells. JEV is the leading cause of virus-induced encephalitis in South and Southeast Asia, leading to approximately 50,000 to 175,000 cases per year with high morbidity and mortality.

Virus binding and entry into the host cell are the two key early determinants of infection. This involves virus interaction with attachment factors and specific receptors/co-receptors, followed by either fusion at the plasma membrane or endocytosis. Viruses can exploit multiple endocytic pathways and activate signaling pathways that favor infection. Clathrin-mediated endocytosis (CME), one of the best-studied and characterized pathways in diverse physiological and disease contexts, has also been described as an entry portal for several viruses. Over the past two decades, several studies have advanced our understanding of clathrin-independent endocytosis (CIE) both in terms of the molecular players and cargoes. Not surprisingly, viruses have also been shown to hijack these CIE pathways.

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The entry pathway for JEV is established to be cell-type dependent. Studies from our and other groups have shown that JEV entry in neuronal cells follows CIE, as opposed to CME in cell types such as fibroblasts and epithelial cells. The cell biology of JEV internalization through CIE in neuronal cells is still not completely understood.

Recently, a class of BAR domain (Bin, Amphiphysin, Rvs) family proteins have emerged to be essential for CIE pathways. One of the BAR domain family members, endophilin A, was shown to control an endocytic pathway independent of clathrin, named Fast endophilin-mediated endocytosis or FEME. Clathrin-independent and endophilin-mediated endocytosis have been described in neuronal cells, including synapses. Major molecular players of FEME, such as dynamin, cholesterol, actin, Rho, Rac and PAK1, are also involved in JEV entry in neuronal cells. JEV is also known to be associated with filopodia, an active site for FEME.

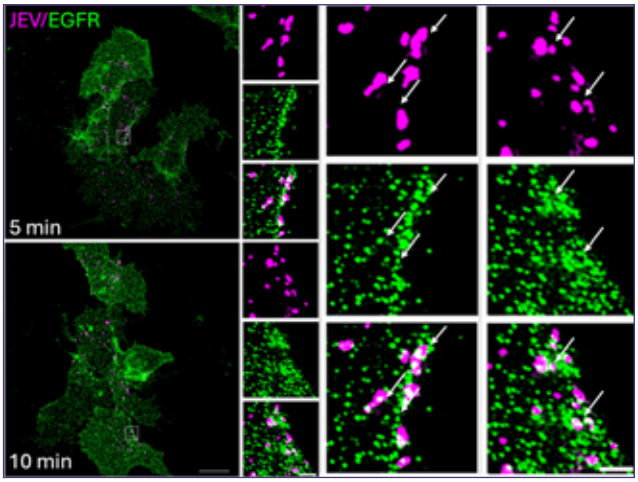

Figure 1. EGFR colocalizes with JEV particles. *Human neuronal SH-SY5Y cells were incubated with 100 MOI of virus for 1 h on ice and were subsequently fixed post at 5 and 10 min of virus internalization. Cells were immunostained with JEV capsid (magenta) and EGFR (green) antibodies. Insets show the zoomed image of capsid-positive structures colocalized with EGFR; scale: 10 µm, inset: 1 µm.*

This study further delineates the pathway exploited by JEV to enter its target neuronal cells. We observe that endophilin A is a major host factor for JEV entry in human neuronal cells. Genetic knockdown of endophilin A isoforms leads to a decrease in virus internalization, while specific activation of the FEME pathway using an inhibitor of GSK3β enhanced virus entry. Using dominant negative domain mutants of endophilin, the crucial role of membrane curvature sensor domain BAR, and the receptor binding domain SH_3 in JEV entry was established. JEV internalization also led to extensive remodeling of the actin cytoskeleton. High-resolution fluorescence imaging of virions showed overlap with Endophilin A2 puncta. Virus entry led to rearrangements of the actin cytoskeleton and was highly sensitive to any pharmacological actin perturbation.

Endophilin-mediated endocytosis has also been reported to be crucial for the uptake of many receptor tyrosine kinases (RTKs), such as epidermal growth factor receptor (EGFR). JEV internalization led to the phosphorylation of EGFR, and inhibition of EGFR kinase activity blocked virus entry. Treatment of cells with EGFR extracellular domain binding antibody, cetuximab, and EGF led to a decrease in JEV attachment and internalization, further supporting the hypothesis that EGFR could potentially be involved in the initial binding of JEV to the host cell surface. Virus particles showed strong colocalization with EGFR at early times of infection (Fig. 1). A specific interaction of the JEV-envelope domain (ED) III with EGFR was confirmed through BLI. Collectively, our study demonstrates the cellular trafficking and signaling pathways exploited by JEV (Fig. 2), further deepening the understanding of the molecular pathogenesis of JEV neuronal cell entry, which ultimately will be crucial for developing suitable antiviral therapies.

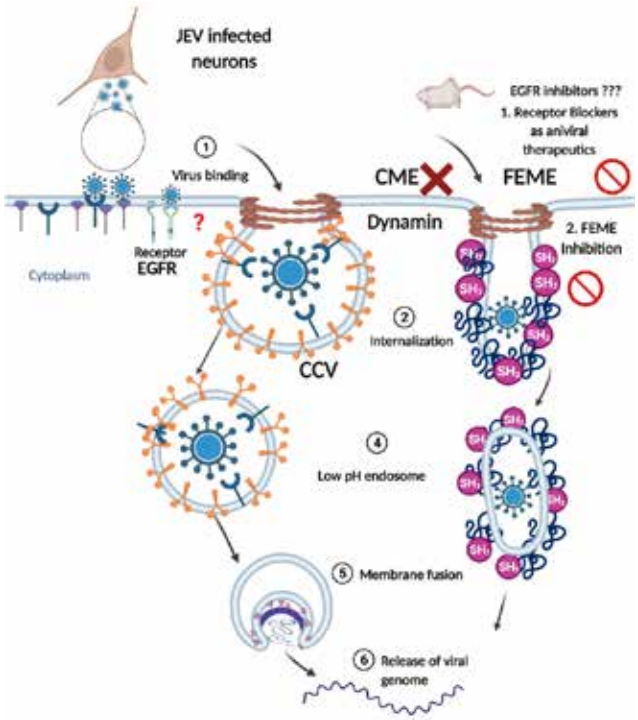

Figure 2: Schematic model of JEV infection in neuronal cells through EGFR as a potential receptor molecule and the clathrin-independent Fast-endophilin mediated endocytosis. *Created with BioRender.com.*

Understanding the Pathobiology of Flaviviruses Prevalent in India

Arup Banerjee
Principal Investigator

Neutrophils are primarily responsible for the body's first line of defence against infection and display phenotypic heterogeneity, with the ability to adapt to different inflammatory scenarios. However, it is unclear how these phenotypic changes are related to cell fate decisions in imparting adverse disease outcomes. Understanding mechanisms that fine-tune neutrophil biogenesis and responses is critical for disease intervention. In our lab, we aim to understand how neutrophil heterogeneity arises during dengue and Japanese encephalitis viral infection and use these insights to develop neutrophil-targeting therapies to control inflammation in viral infections. Our lab is also interested in using extracellular vesicles to understand disease biology and identify novel interventions for viral infections.

Contribution of plasma-derived extracellular vesicles to endothelial dysfunction in Dengue pathogenesis

Dengue is a mosquito-borne viral disease caused by the dengue virus, posing a significant global health challenge. These severe manifestations are primarily driven by uncontrolled immune cell activation and excessive inflammation, critical in disease progression. This response may involve direct cell-to-cell interactions or contact-independent mechanisms mediated by extracellular vesicles (EV) released from infected cells. EV are small, membrane-bound structures (30–200 nm) produced by most cells and found in various body fluids. EV cargo can modulate cellular functions, establishing EV as critical mediators in pathological processes. In this study, we isolated and characterized circulating EV from the plasma of mild (MD) and severe dengue (SD) patients and investigated their effects on naïve $CD4^+$ T cells and endothelial cells (EC) (Fig.1). Our findings revealed that platelets are the primary source of EV in the plasma of severe dengue patients. These SD-EV carried elevated levels of cytokines and immunoregulatory proteins (such as PD-L1 and CD44), which suppressed $CD4^+$ T cell proliferation. Additionally, we demonstrated that SD-EV-modulated $CD4^+$ T cells (SD-EV-CD4) and their secretome

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delayed EC migration, arrested ECs in the G1 phase, and increased the expression of PD-L1 and ICAM-1 on ECs via the Notch signalling pathway.

Further analysis revealed that ICAM-1 expression and hyaluronic acid (HA) release from ECs were mediated by CD44, which was elevated on SD-EV-CD4 cells, indicating a defect in endothelial permeability. Blocking CD44 on SD-EV-CD4 significantly reduced ICAM-1 expression on ECs and improved endothelial barrier function.

In conclusion, our findings highlight that SD-EV-CD4 cells, carrying PD-1 and CD44, significantly alter endothelial cell properties through their interaction (Fig. 1). These alterations likely play a crucial role in dengue-mediated endothelial dysfunction, providing novel insights into the mechanisms of severe dengue pathogenesis and highlighting the importance of circulating EV in the development of severity in viral infection.

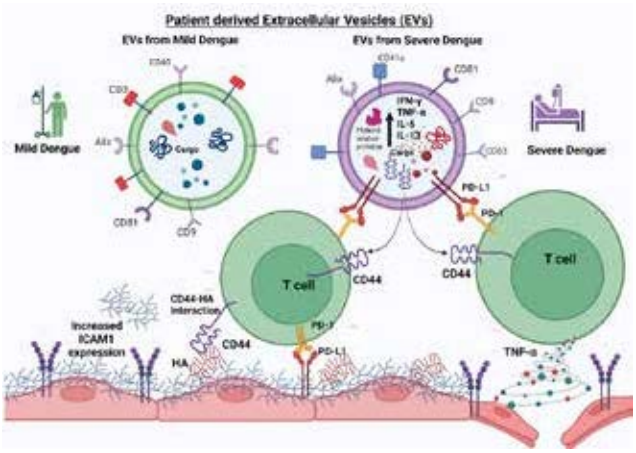

Figure 1: Graphical representation of the study, depicting SD-EV-CD4 interaction as well as EV-CD4-EC interaction leading to endothelial damage.

Integrated proteomics and connectivity map-based approach to identify potent antiviral compounds against Japanese Encephalitis virus (JEV) infection

The JEV infection continues as a significant public health threat and contributes to a substantial disease burden in Southeast-Asian countries, including India. The case fatality rate is as high as ~ 20–30%, and among the survivors, about 30-50% of cases continue to have severe neurological deficits. Vaccination is the most effective way to prevent JEV infection. However, due to its zoonotic cycle, the disease expanded to new areas and outbreaks occurred in unexpected regions, making vaccination planning challenging. To date, no antivirals have been clinically approved to treat JEV infection. Thus, finding a safe and effective treatment is essential and urgent.

Over the last decades, tremendous advancements have occurred in developing computational pipelines, integrating the high-throughput omics platform in virtual drug screening methods. These omics-based computational screenings enable us to repurpose drugs targeting viral or host proteins that participate in the pathogen infection process and limit disease progression. Repurposing or repositioning drugs was found to be more economical and practical in the current drug development scenario. The current study aimed to develop a host-directed strategy through a computational drug repurposing approach. As part of the strategy, we first generated a dynamic signature of differentially expressed JEV infection-associated proteins in mice brains through a semiquantitative proteomics approach. With the help of the Connectivity Map (CMap) analysis, we narrowed down the lists of drugs with a high negative CMap score (-70 or lower) (Fig. 2). Based on the CMap score, we chose the top three compounds (Tipifarnib, Ly303511, MDL11939) with CMap scores of -91.83, -88.18, and -91.15, respectively. The antiviral potential of these three compounds was further compared in both JEV-infected mouse neuroblastoma cells and C57BL/6 mice. Oral administration of Ly303511 and MDL11939, alone or in combination, showed improved outcomes, e.g., delayed death, increased survival, and less viral load than Tipifarnib alone or combined (Fig. 2). The JEV-infected mice survived upon drug treatment, effectively reducing viral load and reversing the antiviral signature. Our results highlight Ly303511 and MDL11939 as promising host-targeted inhibitors of JEV infection and pathogenesis. Moreover, our results favour the combination of Ly303511 and MDL11939 therapy to improve clinical symptoms and reduce JEV-induced damage, and thus could be included in clinical studies.

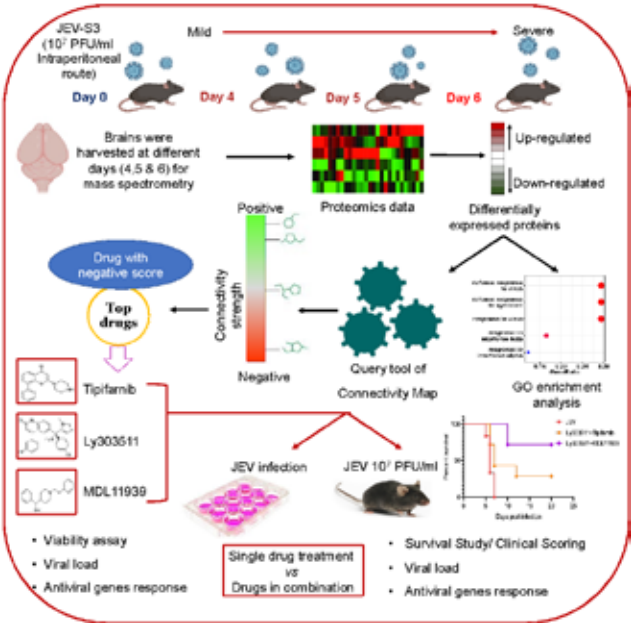

Figure 2: A schematic diagram depicting the pipeline used to identify drugs and their effects on JEV replication and pathogenesis.

Translational control of gene expression in yeast and fungal pathogens

Anil Thakur
Principal Investigator

Candida species present a growing concern due to their increasing drug resistance, making fungal infections challenging to treat. These pathogens infect millions worldwide, particularly immunocompromised individuals, with high mortality rates, emphasizing the urgency of developing effective antifungal strategies. To address this, we are understanding the intricate world of protein translation within *Candida species*, a fundamental cellular process crucial for fungal growth, development and virulence. Translational regulation that fine-tunes the translation of mRNA subgroups of pathogens required for host adaptation for virulence needs to be thoroughly investigated. Therefore, our broad objective is to unveil the molecular mechanisms that govern the synthesis of virulence factors, increasing the growth fitness of the fungus. By targeting key components of the fungal translation machinery, we aim to disrupt its growth and survival within hosts. This approach could potentially lead to the development of new antifungal agents that overcome the current limitations in treatment options.

Translation regulation promotes stress adaptation in the human fungal pathogen *Candida glabrata*

Invasive candidiasis presents a significant healthcare challenge. The Human opportunistic fungal pathogen *Candida glabrata*, a cause of mucosal and deep-seated infections, resists key antifungal drugs and rapidly proliferates within host macrophages, where it withstands high oxidative stress and amino acid starvation. Unlike *C. albicans, C. glabrata* lacks true hyphae and relies more on stress adaptation mechanisms than filamentation for virulence. This study explores the molecular mechanisms underlying stress adaptations in *C. glabrata* that contribute to its pathogenicity. Our findings revealed that *C. glabrata* survives oxidative stress and amino acid starvation more effectively than *S. cerevisiae, C. albicans*, and *C. auris*. We observed that amino acid starvation and oxidative stress downregulate global protein translation through Gcn2-mediated eIF2a phosphorylation, enabling adaptive recovery and activating the transcription factor Gcn4. The *gcn2*Δ and *gcn4Δ* mutants had impaired growth under stress conditions, highlighting the pivotal role of Gcn2-Gcn4 in regulating stress-specific transcripts and promoting fungal survival. Transcriptome sequencing under amino acid starvation conditions demonstrated that Gcn4 orchestrates the expression of a broad array of genes, primarily those involved in stress responses, which are essential for survival during nutrient deprivation. Notably, under oxidative stress,

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Gcn4 adopts unique adaptation strategies by upregulating a core set of oxidative stress-responsive genes by coordinating a more specialized transcriptional response tailored to oxidative stress. Additionally, gcn2Δ and gcn4Δ exhibited elevated levels of Reactive Oxygen Species (ROS) and defective replication within host macrophages, with Gcn4 being crucial in host survival and virulence (Fig. 1). This study underscores the importance of translational regulation in stress adaptation of C. glabrata.

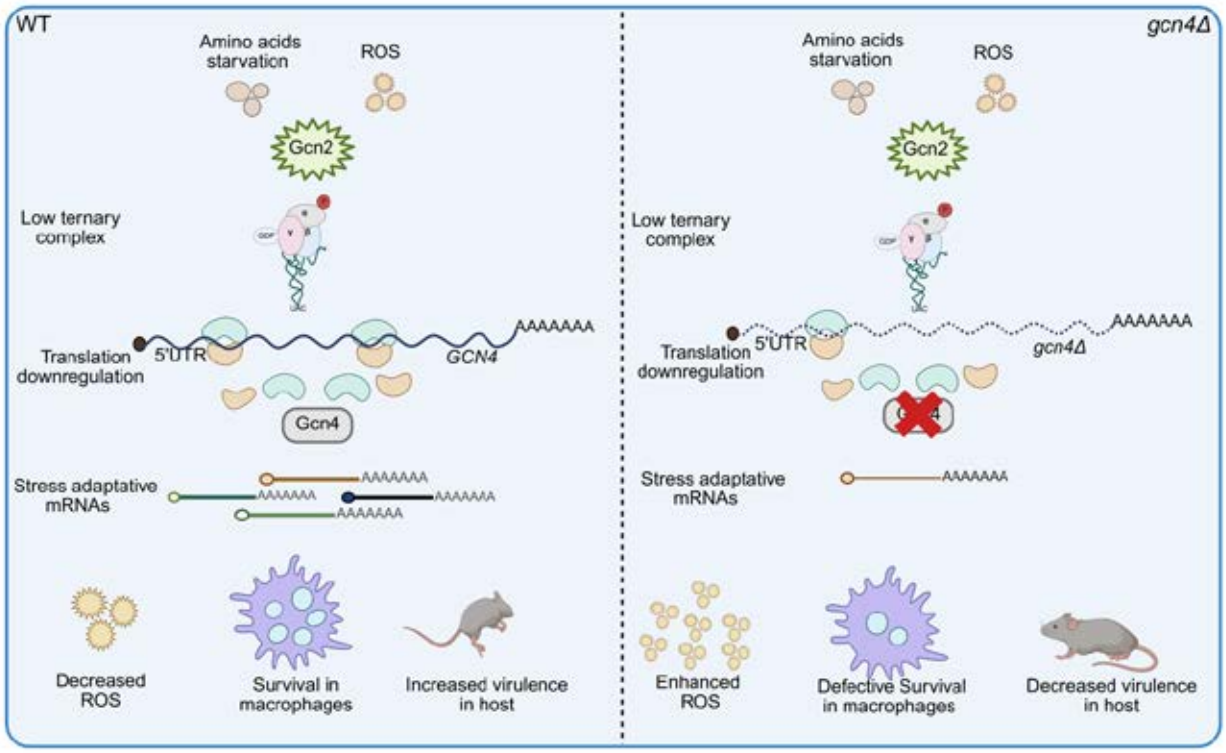


Figure 1: Translation regulation facilitates C. glabrata adaptation to amino acid starvation and oxidative stress. *Upon exposure to amino acid starvation and oxidative stress, C. glabrata downregulates global translation by phosphorylating eIF2α through the eIF2α kinase, which activates the transcription factor GCN4. GCN4 is crucial for C. glabrata's survival and for virulence in the host.*

Distinct uS11/Rps14 interactions with the translation preinitiation complex differentially alter the accuracy of start codon recognition

The eukaryotic 43S pre-initiation complex (PIC), containing Met-tRNA$_i^{Met}$ in a ternary complex (TC) with eIF2-GTP, scans the mRNA leader for an AUG start codon in a favorable "Kozak" context. Recognition of AUG triggers the rearrangement of the PIC from an open scanning conformation to a closed arrested state with more tightly bound Met-tRNA$_i^{Met}$. Cryo-EM reconstructions of yeast PICs suggest remodeling of the interaction between 40S protein uS11/Rps14 with rRNA and mRNA between open and closed states; however, its importance in start codon recognition was unknown. uS11/Rps14-L137 substitutions disrupting rRNA contacts favoured in the open complex increase initiation at suboptimal sites, and L137E stabilizes TC binding to PICs reconstituted *in vitro* with a UUG start codon, all indicating inappropriate rearrangement to the closed state at suboptimal initiation sites. Conversely, uS11/Rps14-R135 and -R136 substitutions perturbing interactions with rRNA exclusively in the closed state confer the opposite phenotypes of initiation hyperaccuracy, and for R135E, accelerated TC dissociation from reconstituted PICs (Fig. 2). Thus, distinct interactions of uS11/Rps14 with rRNA stabilize first the open and then the closed conformation of the PIC to influence the accuracy of initiation in vivo.

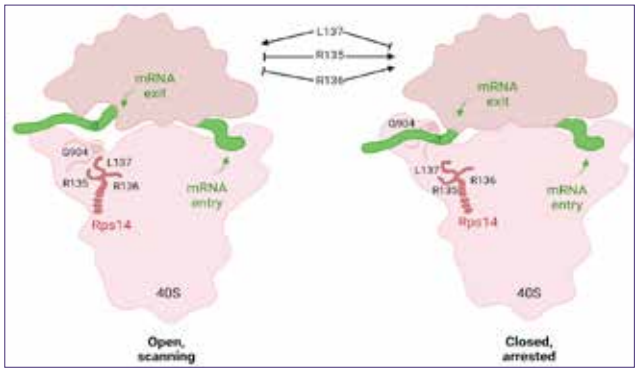
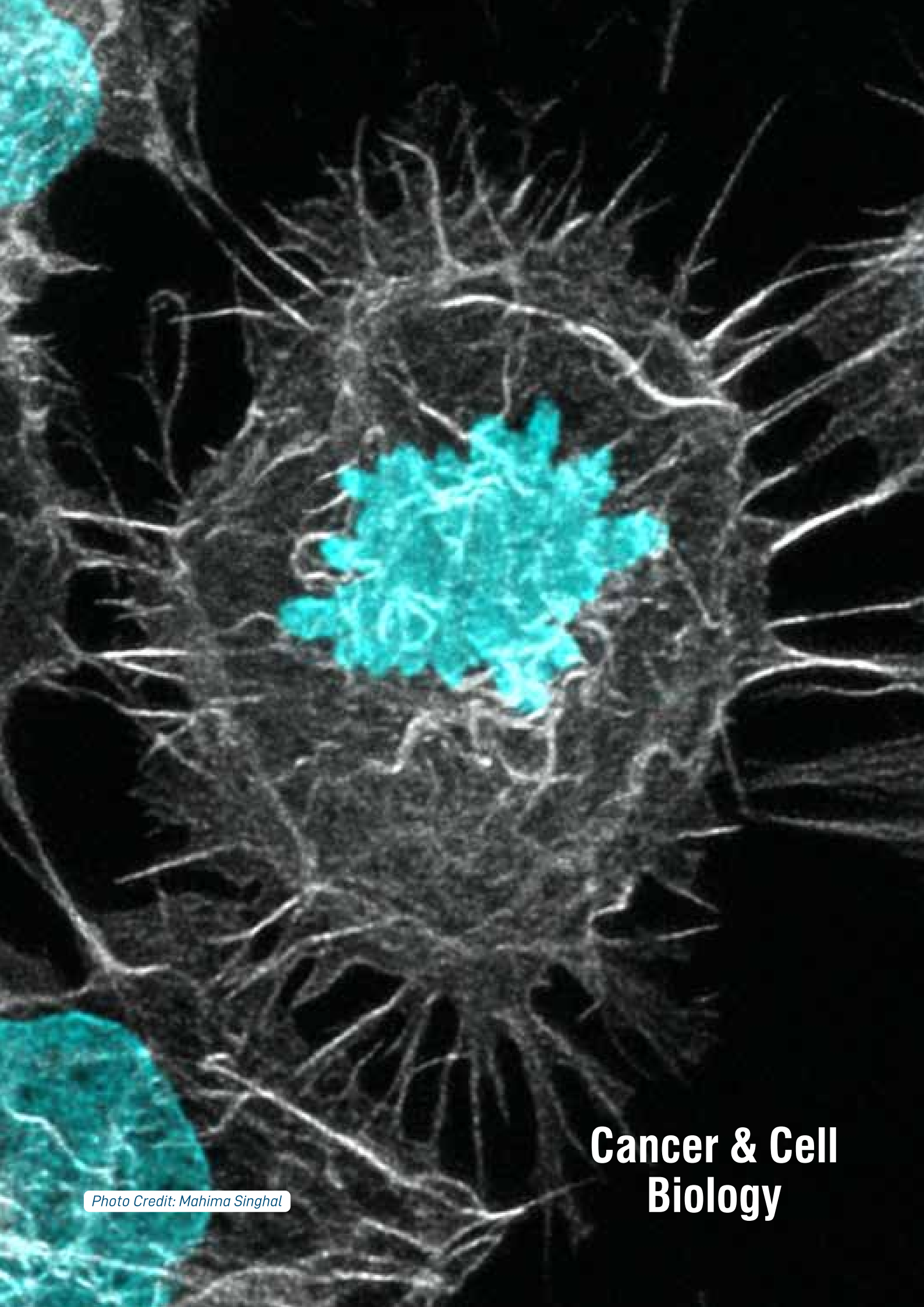
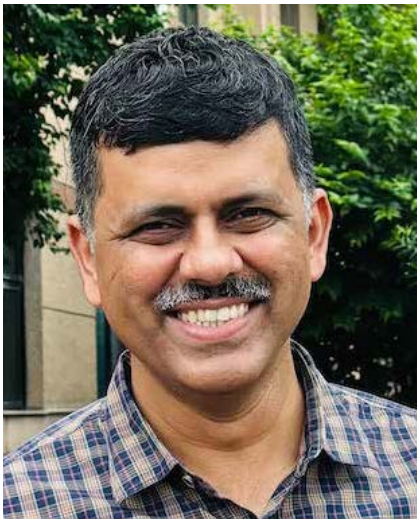


Figure 2: The role of Rps14 in the conformational switch in PIC between the open scanning and closed conformations upon start-codon recognition. *Residue L137 promote the open scanning conformation by anchoring the rRNA-G904 in open conformation. Closed complex engaging rRNA-G904 with mRNA context nucleotides, and L137 interacts with the backbone of mRNA. The interactions of R135 and R136 with rRNA, aid to fix the mRNA in the exit channel and stabilize the closed/^{PIN} state at the start codon.*



Cancer & Cell Biology

Photo Credit: Mahima Singhal



Engineering of Nanomaterials for Biomedical Applications

Avinash Bajaj
Principal Investigator

Our research investigates the intricate mechanisms of immune modulation within the tumor microenvironment, infectious diseases, and inflammatory disorders. We also aim to elucidate the cross-talk between immune cells and neurons in cancer progression; the role of lipid metabolism in shaping antimicrobial responses and curbing anticancer immunity. We seek to identify novel therapeutic targets and propose probable outcomes through integrative approaches.

Combination chemotherapy has demonstrated improved clinical outcomes by concurrently targeting multiple oncogenic pathways. However, non-specificity and organotoxicity pose major drawbacks to chemotherapy. In this work, we engineered a triple drug-loaded chimeric nanomicelles (TDC-NMs) that can simultaneously target three key hallmarks of cancer: proliferation, inflammation, and angiogenesis and enhance the therapeutic efficacy, covering the side effects of conventional chemotherapy by site-specific accumulation and esterase-based drug release at the tumor site. Firstly, we synthesized enzyme-sensitive prodrugs by conjugating anti-proliferating drugs like gemcitabine (GEM), an anti-inflammatory drug like dexamethasone (DEX) and an anti-angiogenic drug like combretastatin A4 (CA4) separately to PEGylated bile acid (Fig.1A). These prodrugs can self-assemble individually or in different combinations that result in mono or dual or triple drug-loaded chimeric (TDC) nanomicelles of sub-100 nm size. TDC-NMs effectively inhibited the tumor growth in comparison to their dual drug nanomicelles in the subcutaneous syngeneic CRC model (CT26 cells, BALB/C mice) (Fig. 1B). There was a >12-fold reduction in tumor growth upon treatment with TDC NMs compared to untreated control mice, while treatment with bimolecular NMs (GEM-DEX NMs GEM-CA4 NMs and DEX-CA4 NMs) showed only 2-5-fold reduction in comparison to untreated control mice.

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Flow cytometry revealed a >1.5 fold reduction in Ki67+ cells (Fig.1C) and a ~3 fold increase in the early apoptotic cells in TDC NMs treated tumor tissues (Fig.1D). These results validated the effectiveness of TDC NMs over dual drug-carrying NMs and untreated control. Further, our results demonstrated a >2.5-fold increase in the percentage of iNOS-expressing M1 macrophages, and a ~2-fold increase in the M1/M2 ratio in TDC NMs treated tumors compared to untreated tumors (Fig.1E). TDC NMs further resulted in >2-fold reduction in G-MDSCs and a 3-fold reduction in M-MDSCs in tumor tissues compared to untreated control mice (Fig.1F). The infiltration of both CD8 and CD4 effector T-cells found to be increased by >1.5 fold with the TDC NMs treatment (Fig.1G). Overall, our TDC NMs induced T-Cell immunity with the reduction of immunosuppressive MDSCs in the subcutaneous CRC microenvironment.

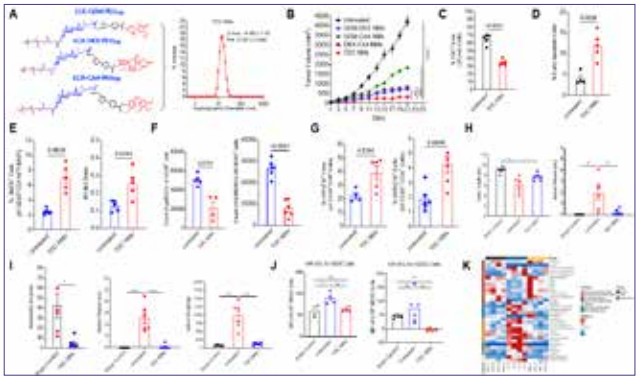


Figure 1: TDC NMs reshape to the tumor microenvironment and control metastasis. *(A) structure of drug conjugates and the size distribution of TDC NMs. (B)Effect of TDC NMs on CT26 tumor kinetics, proliferation (C), and apoptosis (D). (E) Effect of TDC NMs on macrophages, (F) MDSCs, and (G)T cells. In the orthotopic model, TDC NMs reduce CRC progression (H) and liver metastasis (I). TDC NMs inhibit the establishment of PMNs (J) and (K).*

We next evaluated the therapeutic efficacy of TDC NMs in an orthotopic colorectal cancer (CRC) model by inoculating CT26 cells into the cecum wall of BALB/c mice. TDC NMs, containing GEM (5 mg/kg), DEX (2.5 mg/kg), and CA4 (20 mg/kg), were administered intravenously every other day for a period of 20 days. Treatment with TDC NMs significantly restored colon length and markedly reduced tumor burden at the cecum wall. Furthermore, a greater than 10-fold reduction in ascites volume and an approximately 1.2-fold decrease in abdominal circumference were observed compared to the untreated control group (Fig.1H).

Liver metastasis remains a major challenge in colorectal cancer (CRC) treatment and is the leading cause of CRC-related mortality. To evaluate the anti-metastatic potential of TDC NMs, we established a liver metastasis model via intrasplenic injection of CT26 cells in BALB/c mice. Treatment with TDC NMs resulted in a >9-fold reduction in metastatic tumor burden in the liver and a >25-fold decrease in ascites volume compared to the untreated control group (Fig.1I). Additionally, spleen weight was reduced by >7-fold with TDC NMs treatment. Given these promising results, we next investigated the role of TDC NMs in pre-metastatic niche (PMN) formation. For this, we analyzed two early time points—Day 5 and Day 7—post-CT26 cell inoculation. TDC NMs treatment led to a ~1.5-fold reduction in inflammation at both time points relative to controls. Moreover, there was a ~2.7-fold and ~2.3-fold downregulation of IL10 MDSCs on Day 5 and Day 7, respectively, indicating restoration of immune homeostasis and inhibition of PMN establishment (Fig.1J). Untargeted metabolomics further revealed a shift in the liver metabolome toward a spleen-like, tumor-associated profile during PMN formation in untreated mice. In contrast, TDC NMs treatment primarily modulated amino acid and fatty acid metabolism, restoring distinct metabolic clustering in plasma, liver, and spleen comparable to that of the controls (Fig.1K). These findings underscore the capacity of TDC NMs to reprogram the dysregulated metabolic landscape and inhibit metastatic progression.

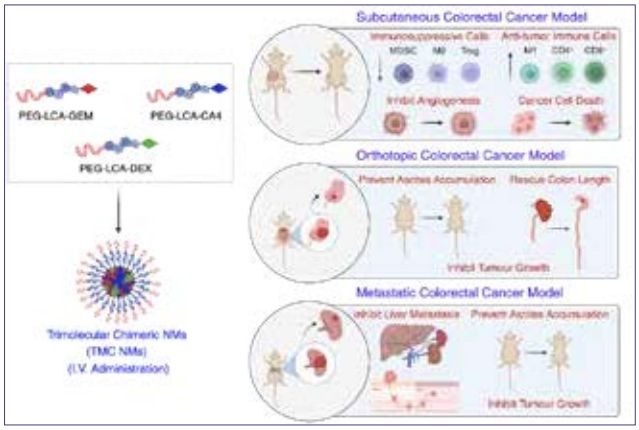


Figure 2. A schematic of the development of TDC NMs targeting cell proliferation, inflammation, and angiogenesis simultaneously to inhibit tumour progression and metastasis.

Overall, this work presented an effective delivery of a combination of chemotherapeutics against CRC, which could potentially regress both tumor progression and metastasis (Fig. 2). TDC NMs-mediated targeting of IL10 would be an effective strategy to prevent the formation of PMNs for inhibiting metastasis.

Molecular mechanisms of cell division, intercellular communication and cellular dynamics

Sivaram V S Mylavarapu
Principal Investigator

We study the molecular regulation of cell division and intercellular communication, two vital and dynamic cellular processes essential for cell survival and organism development that are subverted in both infectious and non-infectious diseases. We hope to exploit knowledge gained from our studies towards strategies for the understanding and/or amelioration of disease conditions.

Cellular protrusions called Tunneling Nanotubes (TNTs), discovered two decades ago, are thin, long and hollow plasma membrane tubes supported by a backbone of F-actin and microtubules/intermediate filaments. TNTs mediate the direct intercellular transfer of various cellular cargoes in different systems (Fig. 1). TNTs and TNT-like structures have been shown in various in vivo contexts, indicating the fundamental importance of these structures across biology. Despite their rapidly expanding importance in biology, there is an absence of a deep mechanistic understanding of their biogenesis and functions, which requires localized actin remodulation, membrane bending and membrane addition. MSec is an important protein required for TNT formation in several cell types. Determination of the MSec interactome from our lab has revealed various classes of interacting proteins. The actin-based motor myosin-X has been shown to be important for TNT formation and function. However, the microtubule-based motors, dyneins and kinesins, which also have cortically enriched pools, have not been implicated in TNT formation. Our present efforts are focused on investigating these molecules' involvement to address some of the molecular mechanisms

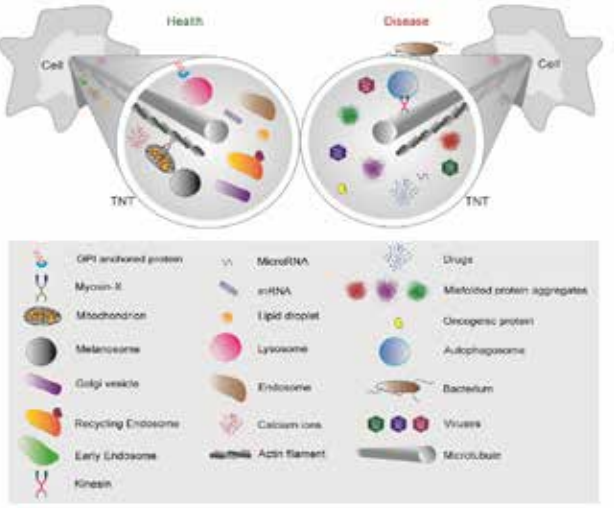
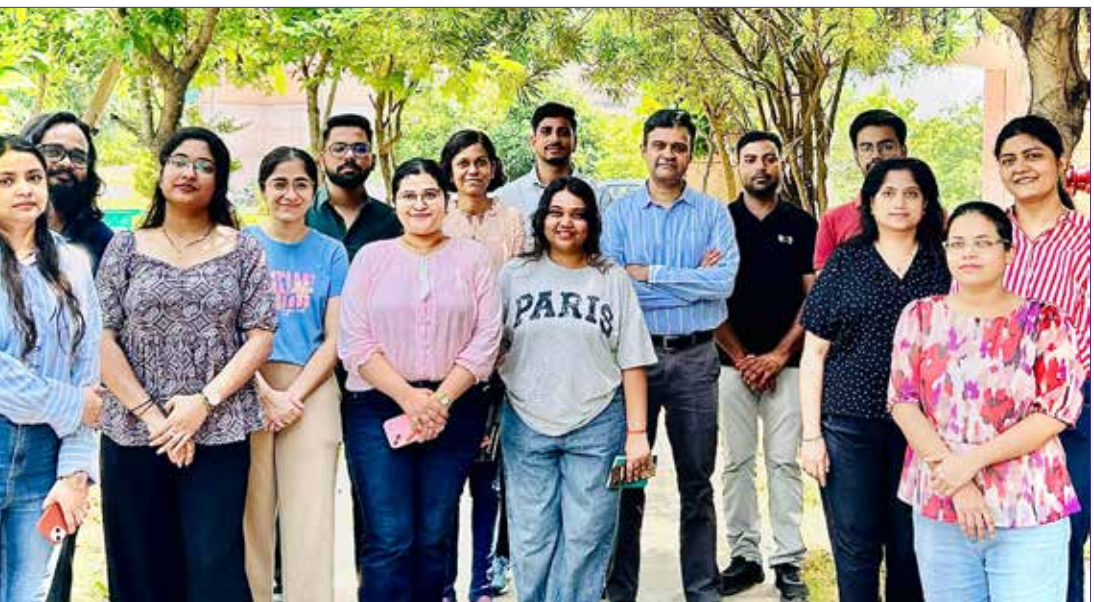


Figure. 1: Tunneling nanotubes are long, thin, hollow, plasma membrane-enclosed channels that connect distantly located animal cells. Various cargoes are transported through tunneling nanotubes in health and disease.



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underlying TNT formation, with a view to eventually devising potential strategies for modulating TNT-mediated intercellular cargo transfer.

Cytoplasmic dynein is required for TNT formation

We showed that dynein, a microtubule-based motor, is required for TNT formation, using siRNA-mediated depletion of dynein in multiple cell types (Fig. 2A), and using two specific dynein inhibitors followed by quantitative confocal imaging (Fig. 2B, C). Out of two subpopulations of dynein, i.e., LIC1-dynein and LIC2-dynein, our experiments revealed that LIC2 dynein is required for TNT formation. We also observed that MSec interacts with LIC2 dynein in immunoprecipitation experiments. Further, co-depletion experiments suggested that LIC2-dynein and MSec may work as part of a single biochemical pathway to induce TNT formation.

We proceeded to confirm that intact microtubules are required for TNT formation. The dynein motor usually requires the cofactors dynactin and LIS1 for optimal activation and processivity. Knockdown of p150 and LIS1 individually in U2OS cells revealed a significant reduction in TNT numbers, suggesting that active dynein is required for TNT formation. Having observed that MSec and dynein may function in the same biochemical pathway, we proceeded to examine their order of function. Our experiments revealed that LIC2 overexpression could not rescue the reduction in TNT numbers upon MSec depletion, while MSec overexpression was able to rescue the reduction in TNT numbers upon LIC2 depletion. These observations confirmed that LIC2-dynein plays a specific function upstream of MSec to induce TNTs.

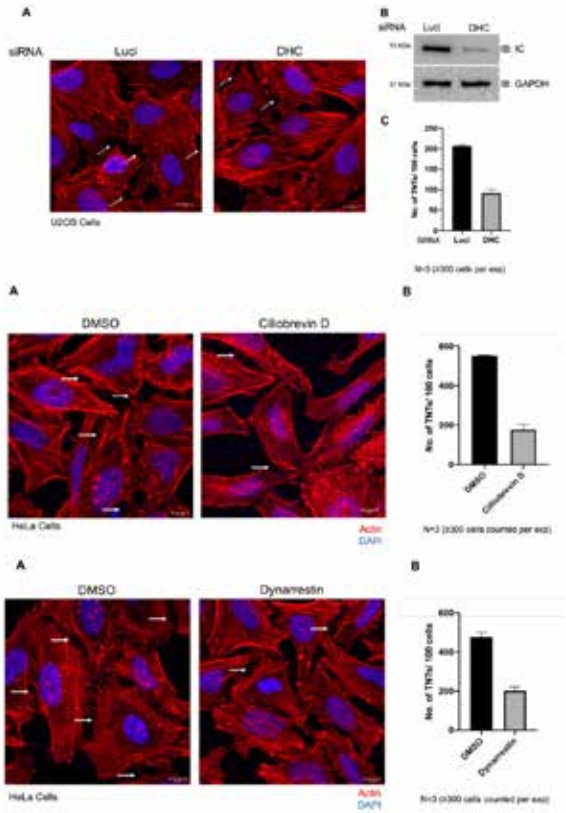

Figure 2: Dynein HC depletion reduces TNT numbers in U2OS cells. Dynein's ATPase activity inhibition reduces TNT numbers. Inhibiting Dynein-microtubule interaction reduces TNT numbers.

Quantitative confocal microscopy showed that LIC2-dynein could be vital for the proper cortical enrichment of MSec. In searching for factors that might couple dynein to the cell cortex, we investigated dynein's association with the polarity protein Par3. Co-depletion experiments suggested that LIC2 and Par3 may operate in a common pathway to induce TNT formation. Rescue experiments designed to validate whether MSec, LIC2-dynein, and Par3 operated through the same pathway suggested that Par3 could be the most downstream determinant for TNT formation.

We are testing whether cortically localised dynein is required for TNT formation and will examine potential interactions between these three molecules. We will identify the minimal region of MSec that interacts with LIC2. Overall, we will mechanistically study the involvement of dynein, Par3 and its interacting partners in TNT formation.


Dr. Deepu Sharma

Characterizing cell biological signatures driving cancer drug resistance *(PI: Dr. Deepu Sharma, MK Bhan Young Researcher Fellow)*. We aim to identify and characterize novel cell biological changes regulating survival and chemo-resistance in cancer cells, a globally confounding biomedical problem. In this study, we are integrating various cutting-edge methodologies including high-resolution quantitative imaging, proteomic, transcriptomic and biochemical methods to investigate reproducible cell biological changes that characterize chemoresistance in specific cancers. As a proof-of-concept for devising futuristic therapeutic strategies, we hope to genetically reverse chemoresistance based on knowledge gained from this study.

Integrative Approaches to Discover Novel Small Molecule Drugs against Mycobacterial Infection *(PI: Dr. Sunita S Shankaran, DHR Women Scientist Fellow)*. The global biomedical burden of tuberculosis (TB) has been compounded by the emergence of multidrug resistance, underscoring the urgent need for discovering new treatments. This study employs a zebrafish (Danio rerio) model of Mycobacterium infection, which offers significant conservation with human systems, to screen a panel of promising novel compounds for antimycobacterial activity. Transcriptomic profiling will be conducted to identify treatment-affected host pathways, followed by functional validation using CRISPR interference (CRISPRi) against candidate genes. We aim to uncover novel therapeutic compounds and deepen our understanding of host-Mycobacterium interactions, potentially informing future treatment strategies.


Dr. Sunita S Shankaran

Understanding the role of calcium signaling in human health and diseases

Rajender K Motiani
Principal Investigator

Ca^{2+} signaling regulates a plethora of cellular functions and thereby plays a critical role in maintaining tissue homeostasis and health. Perturbation in Ca^{2+} dynamics causes impairment of cellular physiology, eventually leading to diseases. The focus of our group is to understand the role of Ca^{2+} signaling in skin pigmentation, pancreatic cancer and metastasis. We are aiming to delineate the role of organelle Ca^{2+} dynamics in these pathophysiological conditions and elucidate detailed molecular mechanisms connecting dysregulated Ca^{2+} signaling to pancreatic cancer and pigmentary disorders. Eventually, we aim to utilize this knowledge for devising strategies for better management and treatment of these pathophysiological conditions.

Calciomics of Skin Pigmentation

Skin pigmentation plays a vital role in protection against UV-induced cancers. Perturbations in pigmentation pathways result in pigmentary disorders like solar lentigo, melasma, and vitiligo. These disorders are considered social stigma; impart long-term psychological trauma and are a huge economic burden. The current therapeutic regimes are not efficient in alleviating pigmentation defects. Therefore, it is critical to identify the novel molecular players regulating pigmentation and devise strategies for targeting them. For identifying novel regulators of pigmentation, we performed microarrays on hyperpigmented and hypopigmented human melanocytes. Interestingly, we observed significant deviations in the Ca^{2+} homeostasis in these cells. Notably, the significance of organelle Ca^{2+} signaling and the functional relevance of intracellular Ca^{2+} handling proteins in skin pigmentation remains unappreciated. Therefore, this program is focused on understanding the role of inter-organelle crosstalk, via Ca^{2+} dynamics, especially ER-Mitochondrial, mitochondrial-melanosome and ER-lysosome communication in regulating pigmentation.

Pigmentation is a result of melanosome biogenesis and melanosome degradation (melanophagy). An emerging concept in pigmentation biology is that defects in melanophagy process contribute to skin pigmentary disorders. However, the molecular

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mechanisms that drive melanophagy remain poorly appreciated. The key bottleneck in the progress of melanophagy field is the lack of robust and reliable live-cell imaging probes to study melanophagy. We developed and systematically characterized two *de novo* ratiometric probes to assess melanophagy flux in live cells. Using a multi-pronged approach employing these probes, biochemical assays, ultrastructural studies, confocal microscopy, molecular analyses and calcium imaging, we demonstrate that inositol 1,4,5-trisphosphate receptor 2 (IP_3R2) is a negative regulator of melanophagy. *In vivo* studies in the zebrafish model system further substantiate IP3R2's functional relevance in pigmentation. Mechanistically, IP_3R2 knockdown decreases mitochondrial Ca^{2+} uptake, augments ADP/ATP ratio and thereby activates melanophagy. Simultaneously, IP_3R2 knockdown increases ER-lysosome proximity, enhances lysosomal Ca^{2+} levels and decreases lysosomal pH. This in turn activates lysosomal TRPML1 channel and stimulates nuclear translocation of TFEB transcription factor, which facilitates transcription of the melanophagy receptor and E3-ligase. Taken together, we uncover that IP_3R2 selectively keeps melanophagy in check thereby it acts as a critical determinant of skin pigmentation (Fig. 1).

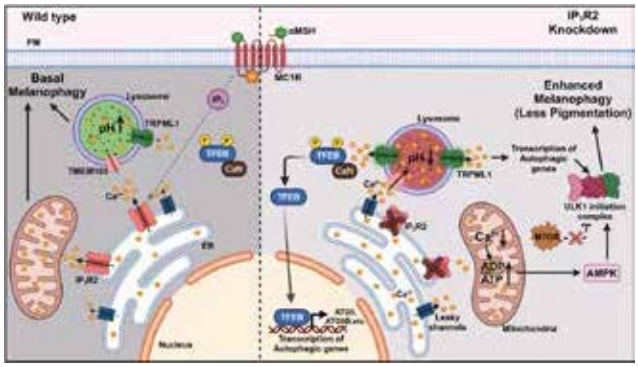

Figure 1: IP_3R2 is a novel melanophagy driver. *IP_3R2 silencing leads to proteasome inhibition of melanogenic proteins and thereby induces melanophagy by orchestrating perturbations in the Ca^{2+}-driven inter-organelle networking. Figure adopted from Saurav and Motiani, bioRxiv 2025.*

Targeting calcium signaling for curtailing tumor growth and metastasis

Pancreatic Cancer (PC) is one of the deadliest cancers and has a mean survival time of less than 5 years. Most of the PC deaths are associated with late diagnosis, secondary metastasis and chemoresistance. For developing effective treatment strategies, it is necessary to understand the molecular mechanisms that drive PC metastasis and chemoresistance. Ca^{2+} signaling plays a critical role in tumorigenesis by regulating the hallmarks of cancer progression such as cellular proliferation, invasion and metastasis. Cancer progression is often associated with altered cellular Ca^{2+} levels and dysregulated functioning of Ca^{2+} channels. We recently demonstrated that plasma-membrane localized Orai3 channel is overexpressed in PC tissue samples, and higher Orai3 levels are associated with metastasis, thereby leading to poor prognosis. However, the molecular mechanisms regulating Orai3 expression remain unappreciated.

We recently revealed that the same transcription factor, NFATc1 regulates both transcription and degradation of Orai3 in a context-dependent manner. We demonstrate that NFATc1 drives Orai3 transcription in non-metastatic pancreatic cancerous cells. Whereas in the invasive and metastatic pancreatic cancerous cells, NFATc1 induces Orai3 lysosomal degradation by transcriptionally enhancing MARCH8 E3-ubiquitin ligase. Our data show that MARCH8 physically interacts with Orai3, eventually resulting in its degradation. Mechanistically, the dichotomy in regulation of Orai3 expression emerges from the differences in epigenetic landscape of MARCH8. We uncover that MARCH8 promoter is hyper-methylated in non-metastatic cancerous cells. Importantly, we demonstrate that MARCH8 restricts pancreatic cancer metastasis by targeting Orai3 degradation thereby highlighting pathophysiological importance of this signaling module (Fig. 2).

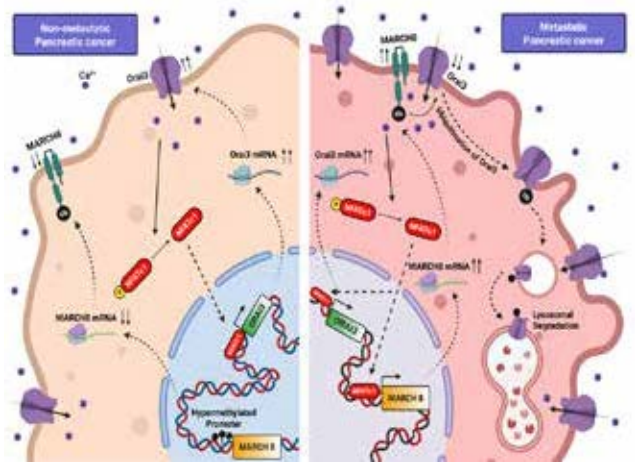

Figure 2: Dual role of NFATc1 in regulating Orai3 transcription and proteolysis*. In non-metastatic cells, NFATc1 drives Orai3 transcriptional upregulation, whereas in metastatic cells NFATc1 induces Orai3 lysosomal degradation via MARCH8 E3 ubiquitin ligase. The dichotomy in NFATc1's function in non-metastatic versus metastatic cells is an outcome of differences in the methylation status of MARCH8 promoter. Figure adopted from Raju et al. bioRxiv 2024.*


Dr. Jyoti Tanwar

Further, Dr. Jyoti Tanwar, a DST-INSPIRE Faculty fellow in our lab, is working on understanding the role of mitochondrial Ca^{2+} dynamics in PC progression, metastasis and chemoresistance. Her expertise is on mitochondrial Ca2+ signaling and her work would demonstrate functional significance of mitochondrial Ca2+ dynamics in PC.

Understanding the structure and function of Centriole based organelles

Karthigeyan Dhanasekaran
Principal Investigator

Centrosomes are microtubule-based membrane-less organelles studied for more than a century, and recently we understand their significance is no longer limited to cell division and the associated pathogenesis in aneuploidy and cancer after the recent developments in cell biology tools and techniques. Today we understand the biogenesis of centrosome and cilia largely, yet we fail to connect all possible events from nucleation to faithful segregation. Our research interests lie in understanding the perturbation of centriole-based organelles across varying disease states that contribute to the pathobiological manifestations and how best to intervene in them to restore the physiology by understanding the gaps in the field. We are trying to understand the centrosome and cilia using high-resolution imaging-based approaches and focusing on their signalling roles by means of biochemical and molecular cell biology approaches combined with modern proteomics, electron microscopy and super-resolution microscopy-based tools.

Viruses targeting microtubules and their organiser

The centrosome is a multifunctional organelle that consists of a pair of centrioles embedded in the pericentriolar matrix (PCM). They are involved in multiple cellular processes, and moreover, numerous structural and numerical defects in these organelles have been widely documented in human diseases, ranging from congenital defects, cancers, neurodegeneration, to various metabolic and infectious diseases. Our team is interested in understanding to what extent centriolar structures are hijacked during viral infections. Our screening of the RNA viral nonstructural proteins reveals multiple instances of such centriolar involvement. The proviral role is now appreciated across multiple such RNA viruses, and moreover, our studies reveal the common mechanisms that operate across multiple viral pathogenesis, which could serve as a potential point of intervention while treating such individuals where the existing regimes fail to protect them, especially in the long term or latent viral associations.

The preliminary work revealed the association of viral helicases like ZIKV, DENV, JEV, and CHIKV RNA helicases with centrosomes, and further mapping shows some of the common molecular signatures existing across these viral proteins

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that reside towards the C-terminus, and it aids in their targeting towards the centriolar structures. Proteomics also identified a healthy subset of centrosome, spindle and microtubule cytoskeletal components associated with these helicases (Fig. 1). Furthermore, the involvement of post-translational modification like phosphorylation seems to be involved in these dynamics of loading and unloading from the centrosomes, which is currently being explored *in vitro* and *in cellulo*.

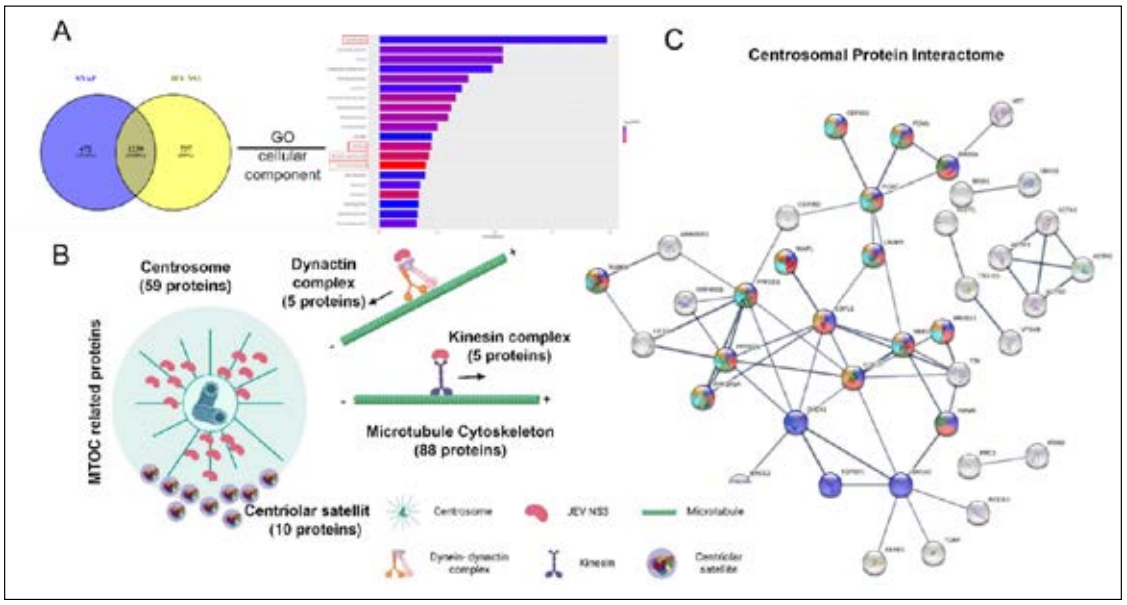

Figure 1. JEV NS3 Interactome: *AP-MS followed by the top 20 GO ontologies appearing unique to the NS3 interaction are listed as bar chart in panel A. Also, the centrosome/cytoskeletal element-related proteins are enumerated in the bottom left panel B. While the STRING network for just the centrosomal proteins are highlighted in panel C.*

CHIKV-infected host cell biology

Chikungunya virus (CHIKV), which is also a mosquito-borne alphavirus, causes a debilitating musculoskeletal disorder in infected humans. Understanding the molecular interactions between the virus and host cell is necessary in identifying more promising viral and/or host-directed therapeutic targets. Till today, the effect of CHIKV infection on the microtubule base structures is not well documented. Hence, exploring their involvement at the subcellular level upon infection in the cell line models, we have visualized various interesting centriolar phenotypes. So far, we have seen perturbations like the appearance of supernumerary centrosomes, ciliary defects and centriolar satellite redistribution, but for the first time beyond this, we have also seen another interesting phenotype with the microtubule network in the CHIKV infected cells. Having known that the microtubule-based cytoskeleton is important for the initial viral entry and its delivery to the site of uncoating but beyond that the dynamics were never understood. We, for the first time, have seen that the stability of the MT fibres is altered throughout infection, and moreover, there is a differential acetylation pattern (Fig. 2) that is strikingly correlated with infection. We also identified that perturbing this post-translational modification status could block the viral replication status significantly. Hence, in future the screening of drugs perturbing the cytoskeletal elements may be a promising strategy to identify disease modifying drugs to treat the chronic ailments associated with long term CHIKV infections.

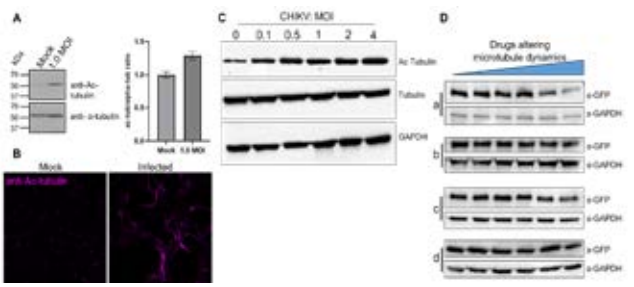

Figure 2. Cytoskeletal dynamics during viral infection. Acetylation levels of microtubules are enhanced upon infection *as shown by western blot analysis (A) and Imunocytochemistry (B). There dose dependent dynamics of this acetylation pattern in comparison to the total tubulin levels that are assessed by western blot analysis (C) and quantified below. While panel (D) shows the screening of various cytoskeletal drugs for their anti-viral effects using GFP tagged CHIKV replicon.*

Currently, we are trying to understand the centriolar and cytoskeletal mechanisms utilized by viruses to their own advantage for effective entry, replication and propagation events. Beyond this, the lab is also focused in deciphering the contributions of these organelles towards other non-infectious diseases like cancer, neurodegeneration and certain developmental disorders.

Plant Biotechnology

Photo Credit: Shubham Singh

Molecular mechanisms of signal transduction in innate immune responses of plants

Saikat Bhattacharjee
Principal Investigator

Intricate and interconnected signaling networks orchestrate both the regulation and elicitation of immunity in plants. These signals are then transduced by downstream modulators that include both metabolites and proteins. Pathogen effectors constantly evolve to evade this detection via multiple mechanisms. We are characterizing the virulence activities and immune-evasion strategies of a class of rapidly evolving effectors from *Pseudomonas syringae* (*Ps*). Further, we are surveying how the molecular functions of a key plant immune signaling hub are disrupted by various unrelated pathogen effectors. In a parallel effort, we are also elucidating the role of various inositol phosphates (InsPs), a class of versatile signaling metabolites, and the respective InsP-kinases in the maintenance of growth-defense balance in plants.

Kinase activities of IPK1 or ITPK1 affect their association with the CSN holo-complex

Soluble inositol polyphosphates (InsPs) regulate phytohormone perception and plant immunity. $InsP_6$ and $InsP_7$, the key players in these orchestrations, are synthesized by INOSITOL PENTAKISPHSPHATE 2-KINASE 1 (IPK1) and INOSITOL 1,3,4-TRISPHOSPHATE 5/6-KINASES (ITPK1/2), respectively. Previously, we identified intricate interactions between these InsP-kinases and subunits of the Cop9 signalosome (CSN), an evolutionarily conserved eight-subunit (CSN1-8) macromolecular complex that regulates the function of Cullin-RING ligases (CRLs). CRLs require covalent modification of a Nedd8 moiety on CULs (a process termed as neddylation) for activation and complex formation with specific co-receptors, adapters and with the ubiquitin E2 enzyme for subsequent degradation of targeted substrates. In the absence of cognate substrates, CRLs become vulnerable to self-ubiquitylation and are protected by the CSN. The CSN5 subunit in this holo-complex contains an MPN^{+}/JAMM metalloprotease motif that catalytically removes Nedd8 (deneddylation) from CULs, preventing their self-degradation. Previously, using yeast two-hybrid assays, we demonstrated that

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the interactions of CSN1/2/5 subunits with IPK1 and ITPK1 are conversely affected by their kinase activities. To validate these results *in planta*, we generated transgenic lines expressing either the wild-type or the kinase dead mutants in the corresponding mutant background. Expression of only wild-type transgene (*GFP-IPK1* or *GFP-ITPK1*), but not the kinase-dead version (*IPK1*^{KD}; harboring a K168A mutation or *ITPK1*^{KD}; harboring a D288A mutation), restored the growth defects previously known for these mutants (Fig. 1A, B). Immuno-enrichment of the GFP-tagged InsP-kinases validated that IPK1 and ITPK1 catalytic activities have a reverse effect in their association with CSN. While the kinase function of IPK1 promotes its interaction with the CSN2/4 subunits, the ITPK1 kinase activity hinders such equivalent associations (Fig. 1C, D).

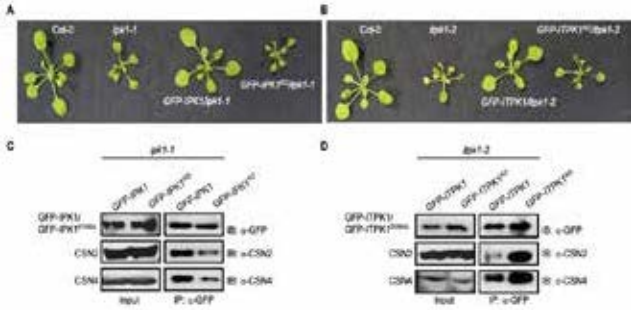

Figure 1: Kinase activities of the Arabidopsis IPK1 and ITPK1 conversely affect their interaction with the CSN holo-complex. *(A, B). Growth phenotypes of indicated plants. (C, D) Immuno-enrichments (IP) of IPK1 or ITPK1 from the corresponding complemented lines probed (IB) with anti-CSN2/4, or anti-GFP antibodies. IgG-agarose enrichments were used as negative controls. Respective protein amounts in the input extracts are indicated.*

$InsP_6$ potentiation on CSN deneddylase activity requires a kinase-active ITPK1

Previously, we reported that the basal ratio of neddylated: unneddylated CUL1 (CUL1^{Nedd8}: CUL1) are skewed in the *ipk1-1* and *itpk1-2* mutants. Higher CUL1^{Nedd8} levels than Col-0 are apparent in these mutants, implying deneddylation deficiencies. Further, we also identified that $InsP_6$ addition enhanced, in a dose-dependent manner, the deneddylation rate on the Nedd8-AML substrate by the Col-0 CSN holo-complex. Because ITPK1 is metabolically linked to IPK1 activity, we then tested whether supplemented $InsP_6$ required enzymatic conversion to $InsP_7$, and whether it is the latter metabolite that ultimately potentiated the deneddylation activity of the CSN holo-complex. We noted that exogenous supplementation of $InsP_6$ in the deneddylation reaction of *ipk1-1*, but not in *itpk1-2* mutant or in the transgenic line expressing GFP-ITPK1^{KD}, improved the deneddylation rate of the enriched CSN holo-complex significantly (Fig. 2A). These results implied that $InsP_7$ synthesis is essential to stimulate CSN deneddylation activity. The unavailability of commercial $InsP_7$ prevented a direct test of this metabolite in rescuing the deneddylation defects of the InsP-kinase mutants.

IPK1 rescues CSN-mediated suppression of ITPK1 activity

Mammalian CSN2 is known to bind $InsP_6$, and the critical residues involved in this coordination have been identified. Arabidopsis CSN2 retains these conserved residues and likely binds $InsP_6$. The interaction of Arabidopsis CSN2 with IPK1 supports this hypothesis. We speculated that CSN2, either as a direct competitor and/or allosterically, may limit $InsP_6$ substrate availability for the enzymatic activity of ITPK1 at the CSN platform. The kinase activity-dependent interaction of IPK1 with the holo-complex, which we identified earlier (Fig. 1D), may ameliorate this suppression either by allosteric interactions with CSN2 or by catalytically providing an increased local concentration of $InsP_6$ substrate to ITPK1. To test this hypothesis, we first optimized the $InsP_7$ synthesis by ITPK1 in an *in vitro* reaction, detected via PAGE. As anticipated, wild-type ITPK1, but not ITPK1^{KD}, was enzymatically competent to generate $InsP_7$ from $InsP_6$. Remarkably, recombinant CSN2 (His-rCSN2), added to the reaction, suppressed $InsP_7$ synthesis, whereas the $InsP_6$-binding deficient CSN2 (His-rCSN2^{K3A}, harboring alanine substitutions of conserved K64, K67, Q68 residues) did not. Most interestingly, recombinant ITPK1 (His-rIPK1) added to the reaction mitigated CSN2-mediated inhibition, increasing $InsP_7$ synthesis by ITPK1. Cumulatively, these results implied that metabolic coupling between the two InsP-kinases that leads to enzymatic activation of ITPK1 may define the rate-limiting step of deneddylation activity of the holo-complex. This activity, when consolidated with our earlier observations in turn, regulates the association-dissociation dynamics of the InsP-kinases through a feedback mechanism (Fig. 2).

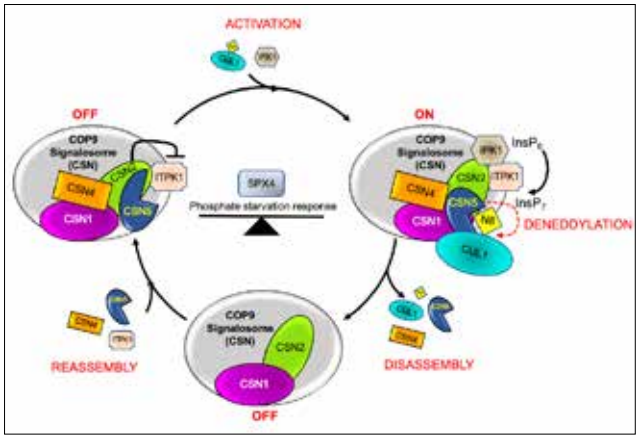

Figure 2: Schematic model of dynamics of CSN deneddylation cycles regulated by IPK1 and ITPK1. *CSN2 inhibits ITPK1 activity. Interaction of IPK1 with CSN2 increases the local synthesis of $InsP_6$, activating ITPK1 and enhancing subsequent $InsP_7$ production for deneddylation activity of the holo-complex on cullins (ON) and dissociation of deneddylated cullins, CSN4, CSN5 and the InsP-kinases from the holo-complex (OFF). The dynamics of these processes maintain the equilibrium of active CRLs.*

Investigations into the molecular mechanisms underlying legume-powdery mildew interactions

Divya Chandran
Principal Investigator

Powdery mildews (PM) are biotrophic fungal pathogens that cause substantial yield losses in grain and forage legumes. Our research program aims to identify molecular targets for powdery mildew disease management in legume crops. Specifically, we study the molecular interplay between the pea powdery mildew pathogen *Erysiphe pisi (Ep)* and legumes, including *Medicago truncatula*, pea, and mungbean, to identify plant resistance/susceptibility factors and pathogen virulence determinants that significantly impact disease development.

Advancing powdery mildew disease screening through the development of simple spray inoculation and image-based fungal quantification methods

Functional screening of antifungal compounds or resistance genes necessitates a reliable inoculation protocol that ensures precise control over spore concentration and consistent inoculum distribution within and across experimental replicates. Additionally, robust methods for the quantitative evaluation of disease severity are essential. We have developed a simple spray inoculation method using an airbrush that facilitates the uniform application of a defined concentration of *E. pisi* conidia on pea foliage. The homogeneity of spore distribution was assessed using a novel metric, the 'uniformity index'. Further, we developed a semi-automated image analysis pipeline using the ImageJ software to quantify powdery mildew disease symptoms. Lastly, we validated the reproducibility of the inoculation and symptom quantification methods via RT-qPCR analysis.

Our spray inoculation method represents a significant improvement over earlier methods in terms of simplicity, cost, speed, and application, as it does not require any specialized device and is suitable for the inoculation of excised leaf segments as well

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as intact plants (Ray and Chandran, 2024; Fig. 1). The images for the ImageJ-based powdery mildew disease quantification can be captured on a regular phone camera. In terms of time, the entire process, from conidia counting to spray inoculation, can be achieved in <1 hour, and by following the simple on-screen instructions, a relatively inexperienced ImageJ user will be able to perform the semi-automated disease symptom quantification method at the rate of ~1–2 min per leaf. Our quick and reproducible inoculation and quantification method can be easily extended to PMs infecting other plant species. These methodologies will enable high-resolution quantification of PM severity at phenotypic and molecular levels.

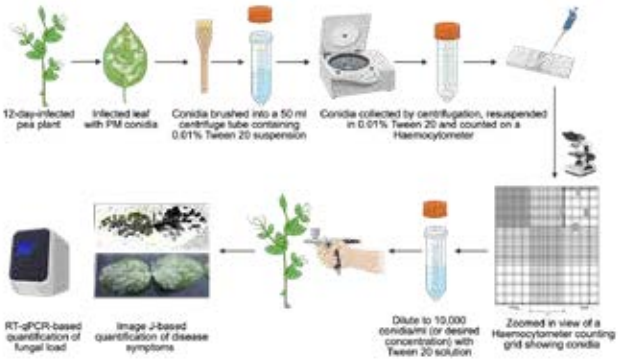

Figure 1: Overview of the powdery mildew spray inoculation and ImageJ-based disease symptom quantification methods. *The image is reproduced from the graphical abstract of Ray and Chandran, 2024.*

Evaluation of mungbean accessions for susceptibility to a non-adapted powdery mildew

Mungbean (*Vigna radiata*) is a legume that thrives in warm climates, but its yield is greatly affected by powdery mildew fungi, mainly *Erysiphe polygoni* and *Podosphaera xanthii*. While mungbean is not typically a host for *Erysiphe pisi*, the primary cause of powdery mildew disease in cool-season legumes like peas and Medicago, temperature changes that alter growing seasons could expose mungbean to this fungus. To assess mungbean's vulnerability to this non-adapted powdery mildew, we challenged 61 mungbean accessions with *E. pisi* in a controlled environment at 22°C, followed by a microscopic evaluation of fungal development. The results showed that 46 accessions were 'highly resistant' and 15 were 'resistant' to *E. pisi* based on the level of fungal growth (Fig. 2). Histological examination indicates that mungbean employs both penetration and post-penetration resistance strategies; however, a small fraction of *E. pisi* conidia formed primary and/or secondary hyphae on the resistant accessions at 22°C, a phenomenon not observed when some of these accessions were grown at 25°C. Our findings suggest initial signs of temperature-dependent resistance breakdown in mungbean against the non-adapted powdery mildew *E. pisi*.

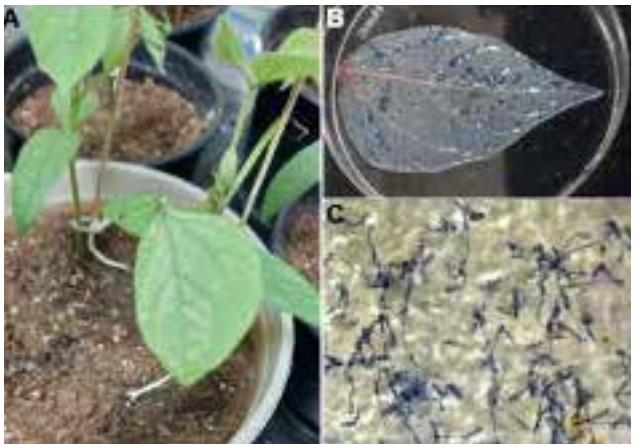

Figure 2: Mungbean is resistant to the non-adapted pea powdery mildew Erysiphe pisi. *Representative images of (A) mungbean plants grown under controlled environment conditions, (B) mungbean leaf stained with trypan blue, and (C) a microscopic image showing E. pisi conidia arrested at the primary hyphal stage on a resistant mungbean accession.*

Elucidating the metabolic signatures delineating symbiotic and pathogenic legume-microbe interactions


Dr. Ankita Alexander

To understand how plants distinguish between beneficial and harmful microbes, we are using the model legume *Medicago truncatula* (Mt) to investigate molecular and metabolic responses during interactions with the fungal pathogen *Erysiphe pisi* and arbuscular mycorrhizal fungi (AMF). We aim to uncover how plants reprogram their defense responses locally (leaf) and systemically (root) in these contrasting microbial interactions. Initial transcriptomic analysis revealed a significantly higher number of differentially expressed genes in *E. pisi*-infected leaf tissues than in root tissues at 3- and 7-day post-infection (dpi), suggesting a stronger or more localized defense response in aerial tissues. Gene Ontology (GO) enrichment analysis showed an over-representation of defense-related hormonal pathways, particularly those involving salicylic acid (SA) and abscisic acid (ABA), primarily in leaf tissues. These transcriptomic findings were supported by targeted metabolomic analysis, which confirmed elevated levels of SA and ABA in infected leaves. Interestingly, ABA levels were reduced in infected roots, indicating a tissue-specific hormonal rebalancing. Surprisingly, GO analysis revealed the downregulation of the terpenoid biosynthesis pathway in roots and leaves. In contrast, the phenylpropanoid and flavonoid pathways were upregulated, suggesting a shift toward flavonoid-mediated defenses and possible metabolic crosstalk. We are now establishing bipartite (plant-symbiont) and tripartite (plant-symbiont-pathogen) interaction systems involving AMF to explore how plants integrate signaling from beneficial and pathogenic microbes.

Translation mechanisms contributing to plant development and drought stress adaptation

Ramu S Vemanna
Principal Investigator

Plant adaptation to changing climatic conditions is crucial to improve the productivity of crops. Drought stress limits the growth and productivity of plants due to reduced availability of water. Under drought, oxidative stress is common due to reduced water potential increases the damage to proteins and warrants higher protein synthesis. As a survival mechanism, abscisic acid (ABA) accumulates to reduce water loss through stomatal closure; however, productivity is reduced due to a limitation in CO_2 uptake. Emphasis is on enhancing the CO_2 uptake without affecting the ABA accumulation in plants, which enhances the productivity of plants. Rice is infected with *Xanthomonas oryzae pv oryzae* that causes bacterial leaf blight, and there are no protective methods. From this context, we aim to identify genes involved in combined drought and pathogen stress. Emphasis is on developing strategies to enhance crop protection and productivity using genetic and chemical genomic approaches.

Modulation of stomatal aperture-regulating proteins to improve carbon gain

Higher stomatal conductance was shown to increase grain yield. Sustaining stomatal conductance has significant relevance in improving yield under moderate stress conditions. The stress-induced ABA activates cellular tolerance mechanisms and induces stomatal closure; however, it diminishes the growth and productivity. The hypothesis is that de-linking ABA-induced mechanisms may improve growth under moderate stress conditions. The stomatal aperture is regulated by the influx and efflux of osmotic ions through ion channels and E3 ligases associated with post-translational regulation of ABA signalling.

To identify the relevant E3 ligases, the guard cell-specific transcriptome from the ABA-treated and water control leaves of Arabidopsis was analysed. The ABA-treated samples showed a total of 3951 differentially expressed genes (DEGs), with

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1912 genes upregulated and 2039 genes downregulated compared to the control sample. The proteolysis group consisted of 54 upregulated genes and 37 downregulated genes, with majorly E3 ligases that consist of different families such as RING, F-Box, SKIP, and Cullin. Further, validation of two RING protein-encoding genes through the dsRNA approach showed the opening of stomata in ABA-treated conditions.

Malate-sensitive anion transporter (AMLT12) is permeable to chloride, nitrate, sulfate and malate, and is involved in dark-, CO_2-, ABA- and water-deficient-induced stomatal closure. Another transporter, slow, weak voltage-dependent S-type anion efflux channel (SLAC1), is involved in the maintenance of anion homeostasis. Cl- efflux through SLAC1 causes membrane depolarisation, which activates outward-rectifying K+ channels, leading to KCl and water efflux to reduce turgor further and cause stomatal closure, which reduces water loss and promotes leaf turgor (Fig.1). These channels are essential for stomatal closure in response to CO_2 and ABA. Downregulating genes encoding anion channels such as *ALMT12*, *SLAC1,* and specific E3 ligases may reduce stomatal closure and improve CO_2 exchange, carbon gain and increase yields.

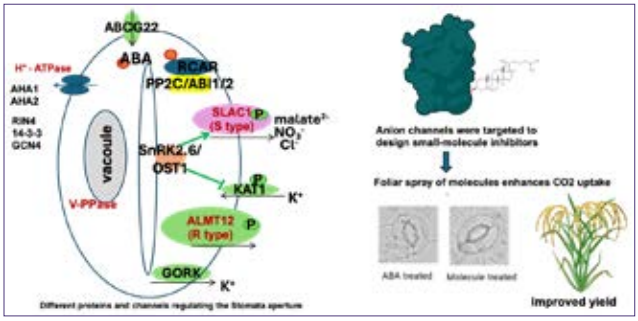

Figure 1. Different proteins and channels regulate the stomata aperture. *These Anion channels may be targeted by a chemical or genomics approach to enhance CO2 uptake and crop yield.*

Using structure-assisted drug designing, we identified two small molecules targeting these proteins from the Zinc library and custom-synthesized from MolPort. The bio-efficacy of these molecules was assessed in Arabidopsis, mungbean (green gram), cowpea, rice and wheat. The foliar application individually, or in combination, of these molecules on crops showed significantly enhanced CO_2 uptake, robust plant growth and higher yield (Fig. 2A).

Mitigating bacterial disease by a gene editing tool targeting virulent genes

The CRISPR–Cas9 mediated gene editing approaches have rapidly evolved to edit relevant genes for crop improvement. The conventional gene editing approach involves transformation of a plasmid containing Cas9 and guide RNA constructs along with a selectable marker gene, which is considered a genetically modified organism. We established a gRNA-Cas9 protein (RNPs) delivery system using cationic nanoparticles for editing the bacterial Type 3 secretory system master regulators. We have shown that the 160 kDa Cas9 protein was taken up by bacteria through an endocytosis mechanism. *Xoo* culture was incubated with Cas9-GFP protein and Cy3 or Cy7 labelled gRNAs, and fluorescence was detected using confocal microscopy and FACS. The *gRNAs* targeting *GFP* in bacteria successfully knocked out the gene and were confirmed by sequencing in *Xoo*.

We targeted the key bacterial virulence regulatory determinant genes in the *hrp* cluster, such as *HrpG* and *HrpX* using specific sgRNAs to knockout in *Xoo* bacteria. The rice plants infected with *Xoo,* after 24 h, were sprayed with or without polymer-RNP formulations. Bacterial disease symptoms and lesion length at 10 days post-spraying clearly suggest that RNP-sprayed plants develop less disease compared to untreated plants. Bacterial growth at 3 dps and 5 dps was reduced significantly compared to untreated plants. Similarly, the bacterial speck causing *Pseudomonas syringae pv. tomato* (DC3000) effector *HopP1*, and bacterial wilt-causing *Ralstonia Salanacearum* effectors *HrpG* and *HrpX* were targeted through polymer-mediated RNP complexes to inhibit bacterial virulence on Arabidopsis and potato, respectively (Fig. 2B-E). The RNPs are potential bio-agrochemicals which can be used against a broad spectrum of pathogens using specific gRNAs.

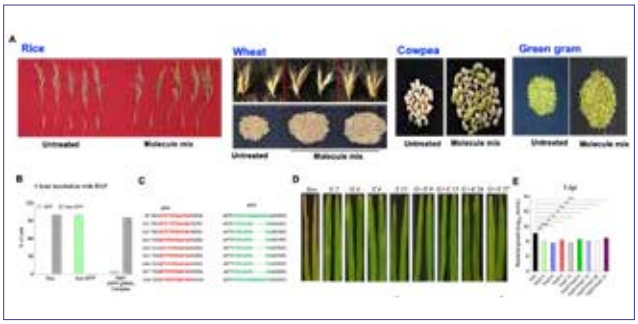

Figure 2. Enhancement of crop yield and delivery of RNP complexes to bacteria to improving disease resistance in plants. *(A) Improved yield in different crops after foliar spray of the small molecule mix targeting stomata channels. (B) uptake of RNP in Xoo cells detected by FACS. (C) Mutations in the GFP gene in RNP-targeted colonies of Xoo. (D-E) Disease phenotypes and bacterial growth in rice exogenously treated with polymer-RNP complexes targeting hrpG and hrpX of Xoo.*

Unravelling the plant cell wall biosynthesis and architecture for bioenergy applications

Prashant Mohan Pawar
Principal Investigator

The plant cell wall is the outermost layer of the cell, which has a complex and dynamic structure composed of energy-rich sugars and polymers. In our group, we are studying plant cell wall biosynthesis and fine-tuning its structure for efficient degradation of lignocellulosic biomass to produce biofuel.

Investigating the metabolic reprogramming in Arabidopsis *eskimo1* using OMICS-based approaches

The TBL family is a 46-member multigene family in Arabidopsis that primarily functions as polysaccharide acetyltransferases. Mutations in some of the *TBL* genes lead to a reduction in xylan acetylation. The *tbl29* or *eskimo1* shows a defect in xylan acetylation, resulting in a dwarf phenotype, and the mutant is also resistant to different kinds of stresses. To further understand the underlying cause for dwarfism, differential response in immunity, and possible cross-talks between xylan acetylation and metabolism, we performed comparative analysis of Arabidopsis *tbl29* and wild type (WT) plants.

The total cell wall acetyl content was reduced by 60% in *eskimo1* as compared to WT. However, leaf acetyl content was comparable to WT plants. Therefore, we performed most of the studies in the stem tissue of *eskimo1* and WT plants. Some earlier studies demonstrated that cytosolic acetic acid increases tolerance to drought stress by increasing jasmonate content while enriching histone H4 acetylation and stimulating the jasmonate signalling pathway in Arabidopsis. The loss of cell wall acetyl ester in *eskimo1* may lead to increased levels of soluble acetic acid or acetyl-CoA, affecting plant carbon metabolism and various processes. Therefore, we measured the endogenous soluble acetic acid content in the inflorescence stem of the xylan-hypoacetylated *eskimo1,* which was higher in the mutant as compared to WT. Further comparison of the RNA sequencing analysis revealed 2180 significantly differentially expressed genes (DEGs), of which 960 genes were downregulated, and 1220 were upregulated in *eskimo1*. The specific changes in glucosinolate (GSL) biosynthesis genes and genes involved in aliphatic GSL were upregulated in *eskimo1* as compared to WT plants. Further, *eskimo1* inflorescence stems had more accumulation of 4MSOB (aliphatic GSL) than Col-0, but the I3M (Indolic GSL) level was comparable to wild type. Consequently, *eskimo1* showed the decreased level of aliphatic GSLs catabolites iberin (3-methylsulfinylpropyl

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isothiocyanate), sulforaphane (4-methylsulfinylbutyl isothiocyanate), alyssin (1-isothiocyanate-5-(methylsulfinyl)-pentane). All these changes in GSL metabolism correlated with RNA sequencing data (Fig. 1)

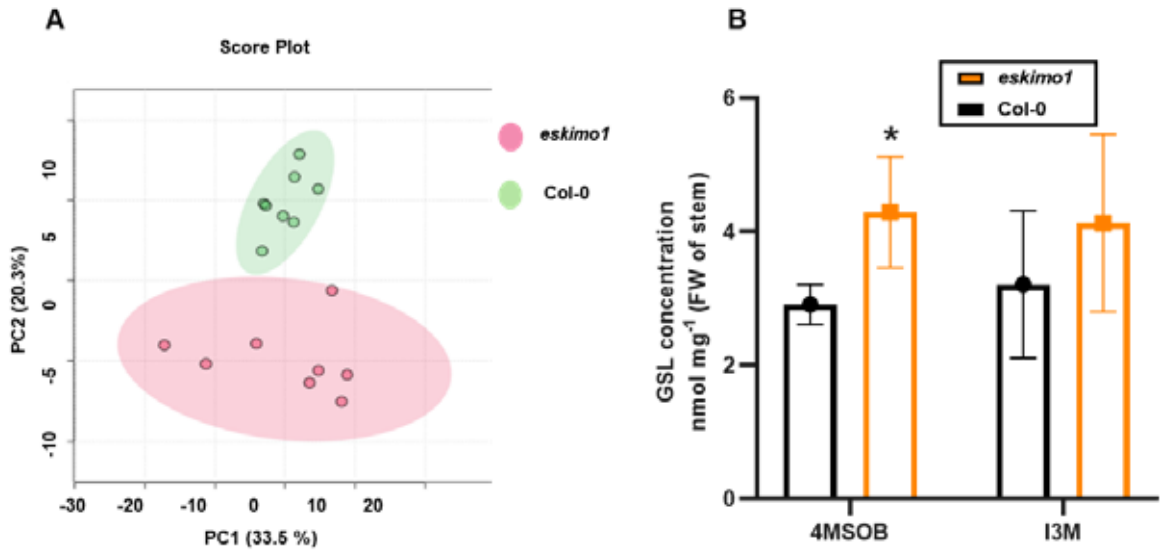


Figure 1. Comparison of untargeted and targeted metabolites analysis between eskimo1 and WT *(A) Soluble metabolites isolated in methanol and subjected to LC-MS. Plot generated using relative intensities by the principal component analysis, showing separation between Col-0 Vs eskimo1. (B) Comparing GSLs quantification in 6-week-old stem.*

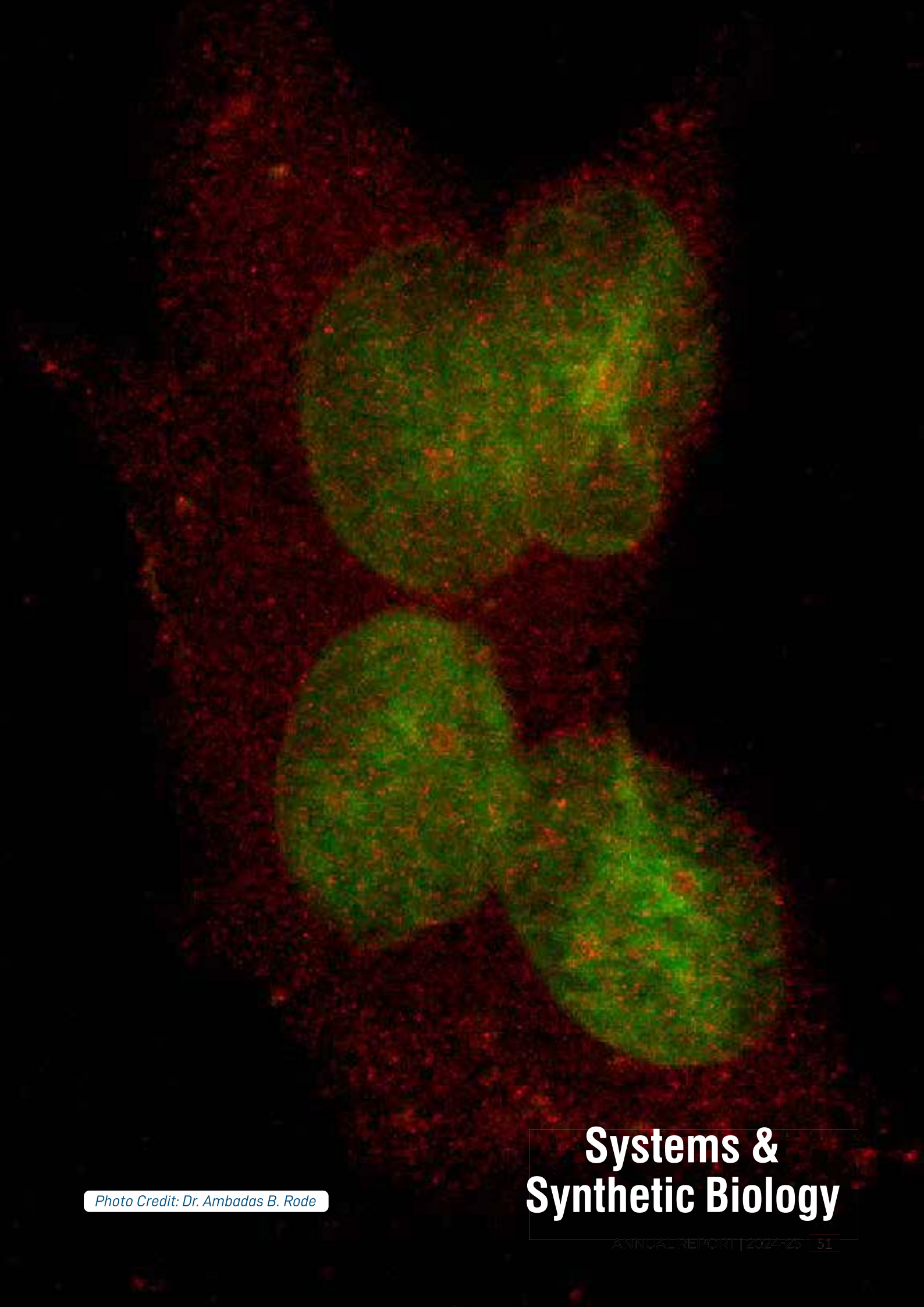
Both defence and growth hormones are involved in the GSL metabolism. And ABA and SA levels were upregulated in *eskimo1*. We also measured JA and its conjugate JA-Isoleucine and its biosynthetic precursor 12-oxyphytodienoic acid, and all were elevated levels in *eskimo1* as compared to WT plants. Assessment of genes involved in JA-related biosynthesis was also upregulated, further validating the results. The concentrations of transport activities of amino acids across membranes are the signatures of stress or the generation of secondary metabolites for defence, stress, or growth. Methionine is the precursor to the aliphatic GSLs in Arabidopsis, which go through a three-step chain-elongation cycle. Methionine was specifically downregulated. However, other amino acid levels were either up or comparable in *eskimo1* as compared to WT.

In conclusion, our research showed that xylan hypo-acetylation in the *eskimo1* inflorescence stem might be the reason for the elevated soluble acetate level, which can subsequently induce transcription regulation of JA biosynthesis, which can induce JA production. This has resulted in the upregulation of aliphatic GSL gene expressions and the cellular uptake of free Met to aliphatic GSL synthesis and formation of GSL catabolites, i.e., isothiocyanates (Fig. 2). This complex interplay between cell wall acetylation, GSLs, and hormone biosynthesis can be exploited further to generate plant varieties with distinct characteristics for biotechnological applications.

Figure 2: Proposed model explaining changes in different metabolites in eskimo1 as compared to WT. *The xylan hypo-acetylation in the eskimo1 inflorescence stem may cause increased soluble acetate that can induce the synthesis of the phytohormone JA. JA can further induce aliphatic GSL accumulation and reduce methionine levels (indirectly). Lower levels of isothiocyanates could be because of major reprogramming in GSL metabolism.*

FTIR based chemotyping of different mungbean accessions

Dissecting complex plant cell wall structures requires sensitive and quantitative methods. FTIR is commonly used to identify specific linkages in cell walls; however, quantification and spectral band assignment remain challenging, especially in crops. Our study addresses these challenges using ATR-FTIR spectroscopy, a high-throughput, cost-effective, and non-destructive approach to understand plant cell wall composition. We assigned wavenumbers 1050-1060 cm^{-1} and 1390-1420 cm^{-1} to quantify cellulose and lignin in Arabidopsis, *Populus*, rice, and mungbean. Using KBr as a diluent, we established a method to relatively quantify cellulose and lignin among different tissue types. This method was applied to field-grown mungbean genotypes, revealing cellulose content variation from 28% to 52% and lignin content variation from 14% to 32%. The ATR-FTIR-based method was cross-validated using canonical wet-chemistry methods, suggesting its utility for relative quantification of lignin and cellulose in different plant species.



Systems & Synthetic Biology

Photo Credit: Dr. Ambadas B. Rode

Peptide Ligation and Protein Semisynthesis

Rajendra P Roy
Principal Investigator

The housekeeping sortase enzymes, ubiquitously present in gram-positive bacteria, typically recognize a LPXTG type of pentapeptide motif in surface proteins for covalent surface anchoring of these proteins to the cell wall. The anchoring process involves a transpeptidation reaction in which sortase cleaves the T-G peptide bond of the motif in the surface protein and transfers the Protein-LPXT to the terminal Gly residue of the pentaglycine arm of the peptidoglycan. However, E-type sortases preferentially recognize sorting signals with alanine at P3 (LAXTG) instead of a pro that is present in most housekeeping sortases. We are interested in delineating the structural features of a class E enzyme (TfSrtE) with a view to engineer new sortases endowed with improved catalytic efficiency and enhanced stability for facile biotechnological applications.

Sequence analysis of all class E sortases reveal the conserved unique Tyr residue in the vicinity of the active site residue. Computational modelling indicates the potential interaction of the Tyr residue with Ala at the P3 position of the LAXTG peptide substrate. We have experimentally tracked the functional consequences of the above Tyr residue through mutation analyses by engineering chemically disparate residues at the Tyr position. The results have been described for TfSrtE in previous reports. The Tyr mutants (Tyr128) of TfSrtE show curious behaviour: while Tyr to Phe mutant prefers LPXTG substrate akin to a housekeeping sortase, Ala mutant behaves like a protease. Interestingly, Ala mutant of a truncated version of the enzyme behaves in much the same way as the Phe mutant. We have attempted elaborate structural elucidation to understand the curious behaviour of the mutants. Unfortunately, only the shorter mutant versions (90 residues deleted from the N-terminal) of the enzymatically competent catalytic domain were amenable to crystallization.

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The overall structure of the wild type TfSrtE exhibits conserved sortase □-barrel fold in which the active site occupied by a tripeptide (PLP, residues 92-94) from the N-terminal region of another molecule of the protein in the asymmetric unit which plays a crucial role in stabilizing the complex by interacting with active site pocket (Fig. 1). The active site Arg231 interacts with the carbonyl oxygen of Pro92 and Leu93 in the PLP tripeptide, likely mimicking the sorting motif. Computational modelling of the LAXTG and LPXTG peptdide substrates reveal that Tyr 128 interacts with Ala but not Pro containing pentapeptide substrate indicating a better fit of the LAXTG peptide in the active site of TfSrtE. Here Tyr128 stabilizes the LAXTG peptide through a hydrogen bond formed between the Tyr hyroxyl and backbone NH contributed by Ala. In Y128F mutant, the N-terminal tripeptide aligns similarly to the wild type but with a slight shift at P94 since both the hydrogen bond donor and acceptor are absent in TfuSrtE Y128F, the side chain of Phe128 cannot form a hydrogen bond with the backbone nitrogen of Pro94 (Fig. 1). The Ala128 mutant was recalcitrant to crystallization. Ala128 did crystallize if when the active site Cys 222 was also mutated (Cys222 to Ala). However, the electron density due to PLP was not observed in this mutant, likely due to an enlarged cavity (Fig. 1). The proteolysis of both LPXTG and LAXTG substrates by Ala mutant may arise perhaps because both the peptides could be freely accommodated in the expanded active site cleft.

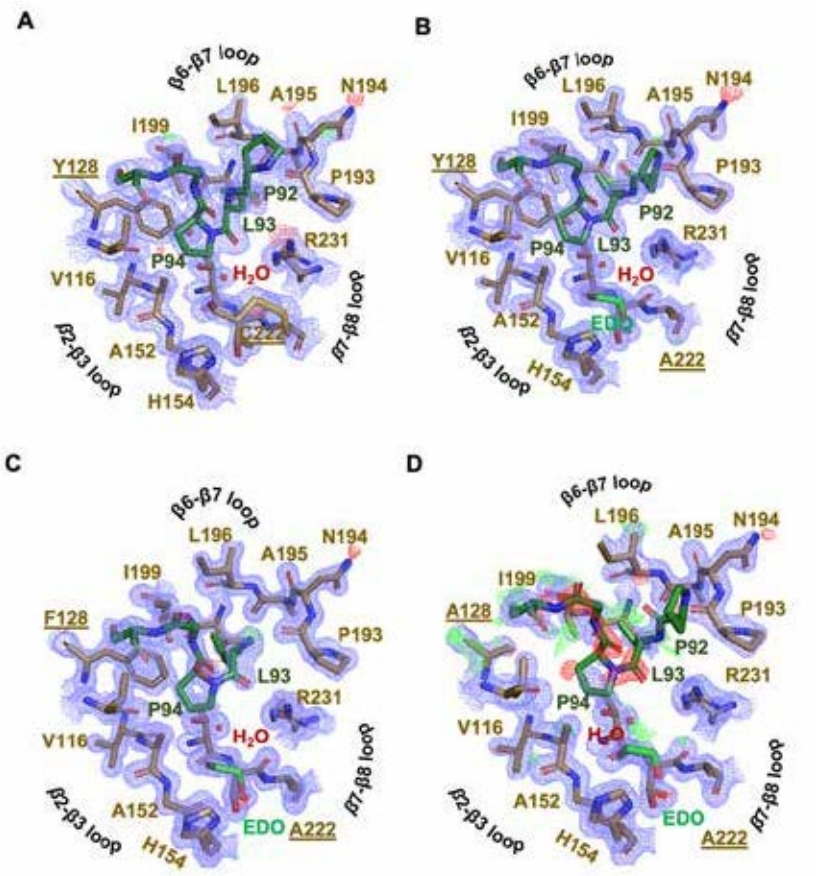

Figure 1: The interaction of the N-terminal PLP peptide of TfuSrtE at the active site of another molecule in the asymmetric unit. *The TfuSrtE protein (brown sticks) and the noncovalently bound N-terminal peptide (green sticks) are shown within the electron density maps, 2Fo-Fc (blue mesh) and Fo-Fc map (green and red mesh) contoured at 1.6 and 3 σ levels, respectively. A) Wild type (Y128, C222), B) Mutant (Y128, C222A), C) Mutant (Y128F, C222A), D) Mutant (Y128A, C222A).*

Molecular Engineering of Functional Nucleic Acids for Biomedical and Biotechnological Applications

Ambadas B. Rode
Principal Investigator

Our research focuses on harnessing nucleic acid structure-mediated gene regulation in humans, bacteria, and viruses for biomedical applications. The propensity of nucleic acids to control cellular processes relies not only on their base-pair identities but also on their inherent ability to form tertiary structures, such as triplexes, G-quadruplexes, pseudoknots, and riboswitches. These structures are diverse and are involved in a remarkably broad spectrum of biological processes, ranging from gene expression to genome maintenance. Thus, these structures have gained attention as therapeutic targets. In addition, the modular nature of nucleic acid structures makes them promising synthetic biology tools. We are developing synthetic riboswitches for conditional and spatiotemporal gene regulation for a variety of applications. We also aim to design and synthesize novel synthetic molecules to target functionally important conformations for therapeutic applications.

Targeting RNA G-Quadruplexes in SARS-CoV-2 with Tetraphenylethene Derivatives for Antiviral Therapy

Coronavirus disease (COVID-19) is an infectious disease caused by Severe Acute Respiratory Syndrome Coronavirus-2 (SARS-CoV-2), resulting in global health and economic crises. To date, the World Health Organization (WHO) has approved numerous vaccines. Despite their success, the produced COVID vaccines have several limitations, including the requirement for multi-dose vaccination, variations in efficiency based on the number of doses, and the type of SARS-CoV-2 variants. SARS-CoV-2 variants with certain mutations are of serious concern because they can evade the protection provided by previous infections or vaccines, which may make current vaccines and treatments less effective. This emphasizes the urgent need for the discovery of new antivirals. One alternative antiviral strategy is to develop small-molecule drugs to target key proteins and nucleic acids present in SARS-CoV-2 that are required for viral infection and progression.

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RNA targets in viruses offer promising features but are relatively underexplored compared to conventional protein targets. A key aspect of this potential lies in RNA's ability to adopt diverse secondary and tertiary structures within cells. Among the RNA structures, the G-quadruplex (RGQ) forming sequences have been predicted in all human viruses, and have been demonstrated to influence viral infectivity and pathogenesis by regulating various stages of the virus lifecycle. Given the RGQs' crucial role in the virus lifecycle, the development of RGQ stabilizing ligands to inhibit viral replication can be used as a novel antiviral strategy. Like other viruses, putative RGQ structures are conserved across beta coronavirus strains, including SARS-CoV-2, and could play an essential role in virus replication and pathogenesis. Due to these structural conservations, the GQ-targeting ligand is expected to be effective against mutant variants and show broad activity within the viral genus.

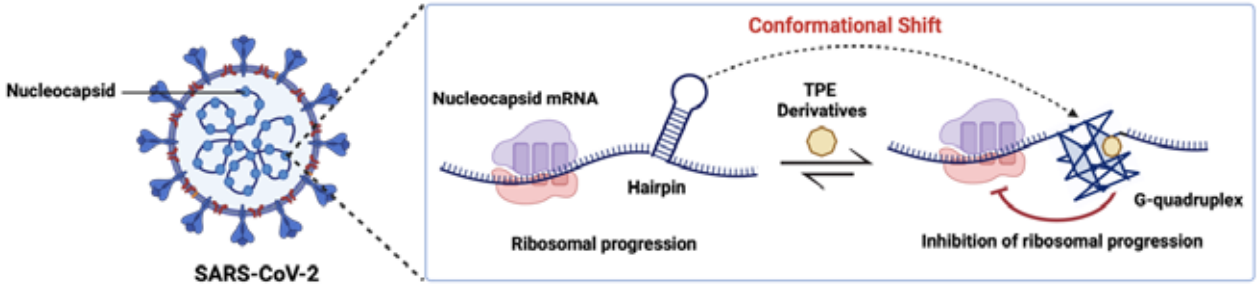

Figure 1: Graphical representation of Hairpin (Hp)-G-quadruplex (GQ) conformational equilibria in the SARS-CoV-2 nucleocapsid gene.

Nucleocapsid gene of SARS-CoV-2, important for viral packaging, contains four putative RGQ-forming sequences. Notably, the putative RGQ-1 derived from the SARS-CoV-2 nucleocapsid gene folds into an unstable intramolecular two-tetrad RGQ and exists in Hairpin (Hp)-G-quadruplex (GQ) conformational equilibria (Fig. 1). The CD spectrum of RGQ-1 indicates the presence of a hairpin conformation, along with both intra- and intermolecular G-quadruplex conformations. From this, we envision that developing small molecules capable of shifting the Hp-GQ equilibrium towards the GQ conformer could serve as a potential antiviral strategy against SARS-CoV-2.

We synthesized TPE derivatives targeting the intramolecular Hairpin (Hp)-G-quadruplex (GQ) equilibrium in RGQ-1 for potential antiviral therapy. Electrophoretic Mobility Shift Assay (EMSA), Fluorescence assays, and Isothermal Titration Calorimetry (ITC) studies show the specific interaction of TPE-MePy and TPE-Allyl Py with RGQ-1. CD thermal melting experiments demonstrated an increase in the thermal stability of RGQ-1 in the presence of TPE derivatives. Furthermore, our luciferase assay in A549 cells indicated the suppression of luciferase activity in the presence of TPE derivatives, which was further validated by western blot analysis and *in vitro* translation assay.

We used an immunofluorescence-based antiviral assay in SARS-CoV-2-infected Vero E6 cells to evaluate the impact of TPE derivatives. The results show that TPE-MePy and TPE-Allyl Py suppressed nucleocapsid gene expression (Fig. 2A). We further performed antiviral assays in SARS-CoV-2-infected human lung cancer A549 cells. Post-infection treatment with TPE derivatives inhibited viral RNA levels by suppressing nucleocapsid and spike protein, as determined by RT-qPCR and western blot data (Fig. 2B-2C). To determine the effect of TPE derivatives on viral entry, we performed pre-infection treatment with TPE derivatives. RT-qPCR and western blot data suggested that TPE derivatives did not suppress viral RNA and protein levels (Fig. 2D-2E). Notably, these results indicate that TPE derivatives do not prevent viral entry but act on the post-entry stages of viral replication by shifting the intramolecular Hp-GQ conformational equilibria towards the GQ conformation in the ORF of the SARS-CoV-2 nucleocapsid gene (Fig. 1A). These results highlight the promising use of TPE derivatives as an antiviral drug to alter the crucial gene expression in SARS-CoV-2.

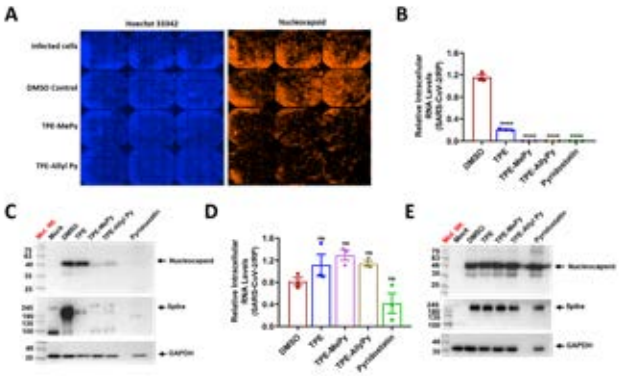

***Figure 2:** (A) Immunofluorescence-based antiviral assay in SARS-CoV-2-infected Vero E6 cells; (B) RT-qPCR and (C) Western blot representing change in viral RNA, Nucleocapsid and spike protein levels after treatment of SARS-CoV-2 infected A549 cells with TPE derivatives; (D) RT-qPCR and (E) Western blot depicting TPE derivatives do not affect viral entry.*

Synthetic biology to understand and improve the production of value-added products

Nidhi Adlakha
Principal Investigator

Our research focuses on understanding microbial strains for industrial and biomedical applications. The lab aims to optimize existing microbial cell factories and concentrate on improving the cost economics of enzyme or bioproduct synthesis. Another goal of our group is to understand the underlying mechanism that phytopathogens employ, with the aim of devising strategies to combat plant infections. Our initial efforts will be directed toward the following project.

Temporal proteome profiling of *Botrytis cinerea* reveals proteins involved in plant invasion and survival

Understanding the proteome dynamics of phytopathogens during infection can help combat plant diseases. However, most proteomic studies on phytopathogens face interference from abundant host proteins. Here, we optimized a solid media that better mimics in-planta conditions and used it to perform the temporal protein dynamics in *Botrytis cinerea*. Out of 3244 quantified proteins, 2045 showed differential regulation. Glycosyl hydrolases, pectin esterases, stress protein DDR48, RhoGEF and essential transcription factors were found to be upregulated during the early phase, highlighting their role in fungal virulence. These important leads will be further used to develop aptamer-based theranostics against this devastating phytopathogen. Overall, the study provides a comprehensive understanding of proteome dynamics during Botrytis infection.

Comparative evaluation of plant pathogenicity

Analyzing protein dynamics in phytopathogenic fungi is seen as an effective method for identifying targets for theragnostic development. However, the presence of plant host proteins in fungal samples complicates the identification of stage-specific virulence proteins. Therefore, it is essential to identify media conditions that closely mimic those of plant hosts. This will aid in conducting proteomics experiments in fungi by minimizing interference caused by an abundant host background.

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For our study, we considered *Botrytis* sp., a necrotrophic fungus whose proteome has shown a preponderance of pathogenic enzymes that mediate plant infection. However, different species of Botrytis vary in host plants, pathogenicity, and other relevant properties affecting disease control. Therefore, we screened virulent Botrytis species based on multi-dimensional analysis, including detached leaf assay, fruit inoculation and biochemical assays.

It was evident from *in planta* experiments that *Botrytis cinerea* NBRC5365 failed to colonize the fruit. In contrast, the other strains displayed comparable infection at three days post-inoculation (dpi), with *Botrytis cinerea* ITCC 6192 showing maximum pathogenicity (Fig. 1A). The estimated lesion diameters also indicated the highest colonization for the ITCC 6192 strain, with lesion diameters of 20 and 35 mm at 3 and 5 dpi, respectively (Fig. 1B). Apropos to our findings on ripe fruit, ITCC6192 demonstrated the highest virulence in the detached leaf assay (Fig. 1C). This is clearly illustrated in the bar graph depicting the highest lesion diameter in leaves infected with the ITCC6192 strain (Fig. 1D). Although all fungal strains exhibited similar growth patterns, *Botrytis cinerea* ITCC6192 demonstrated the highest levels of exo-glucanase (Fig. 1E) and endoglucanase activity (Fig. 1F) in vitro. Overall, the experiments demonstrated that *Botrytis cinerea* ITCC6192 exhibited the highest pathogenicity in tomato plants compared to other Botrytis strains. Therefore, it was selected for further study.

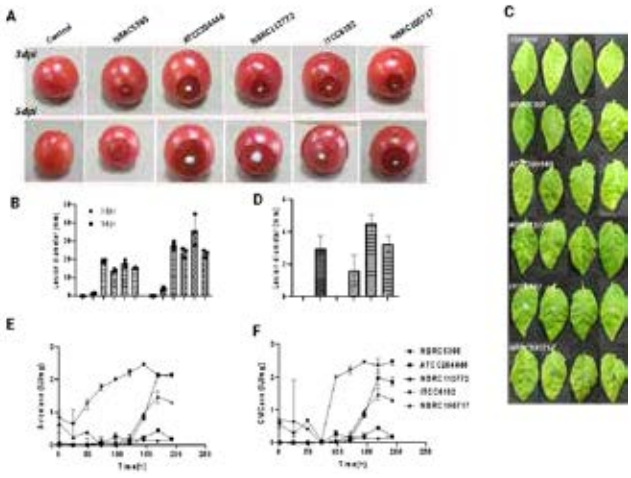

Figure 1. Selection of pathogenic Botrytis strain. *Five strains of Botrytis cinerea were evaluated for pathogenicity. A) 1X10⁶ spores were inoculated in tomato fruit and infection was monitored after 3dpi and 5dpi. B) Bar graph indicates lesion size in mm at 3dpi and 5dpi. C) Leaf infection experiment. D) Bar graph indicates lesion size in mm at 5dpi. E) Exo-glucanase activity measured in the culture supernatant. F) Endoglucanase activity measured in the culture supernatant.*

Stage-specific differential proteome expression in Botrytis cinerea

To gain insights into the regulation of pathogenesis in *Botrytis cinerea* and understand the early effector and late maintenance protein pool, protein isolates from different time points (12-, 36-, 72-, and 120-hours post-infection) were analyzed using label-free quantitative proteomics. The proteomics data obtained were analyzed using iDEP2.01 online. We quantified 3244 proteins across all time points at 1% FDR, and 2045 fungal proteins were observed to be differentially regulated. This represents a very high number of Botrytis proteins quantified/identified than the previously reported for this pathogen grown under in planta conditions.

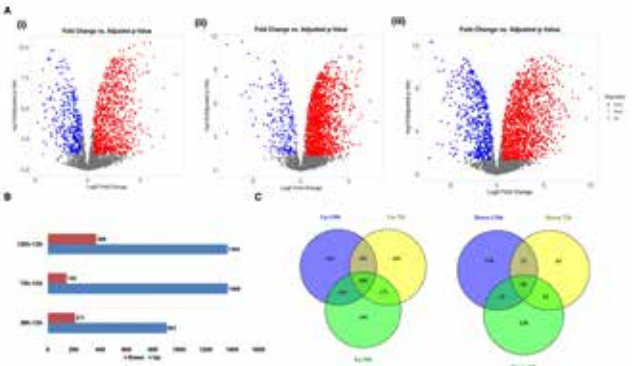

Figure 2. Identification and Label-Free Quantification of Proteins During Early and Late Growth Phase. *A) Volcano plots representing the results of the proteome analysis of proteins at 36 hpi (i), 72 hpi (ii), and 120 hpi (iii) compared to 12 hpi. B) Bar graph indicating exactly up and downregulated hits at various late growth phases. C) Venn diagram indicating the consistent upregulation of 563 proteins and downregulation of 62 proteins in late growth phase samples.*

The volcano plot distribution of differentially expressed proteins at late phases of growth displayed a higher number of significantly up-regulated proteins compared to down-regulated ones (Fig. 2A). The results of the quantitative proteome analysis suggested that 903 proteins were upregulated at 36 hours post-infection (hpi) compared to 12 hpi. This number increased to 1368 and 1365 proteins at 72 hpi and 120 hpi, respectively. In contrast, 211, 145, and 369 fungal proteins were found to be downregulated at 36 hpi, 72 hpi, and 120 hpi, respectively, compared to 12 hpi (Fig. 2B). Additionally, comparative analysis revealed that 388 proteins consistently showed upregulation throughout the infection, indicating their role in regular maintenance and cellular homeostasis (Fig. 2C). In contrast, only 36 proteins were consistently downregulated compared to 12 hpi at all time points analyzed. As the fungus *B. cinerea* progressed from early (12 hpi) to later stages (120 hpi), its proteome profile underwent substantial changes, with 278 unique proteins downregulated and 442 proteins upregulated only at 120 hpi. From this set, upregulated membrane proteins were identified, and the corresponding aptamers were selectively screened to facilitate the development of theragnostic kits targeting this phytopathogen.

Publications & Patents

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https://doi.org/10.1093/nar/gkaf163
RNA and RNA-protein complexes

OXFORD

Distinct uS11/Rps14 interactions with the translation preinitiation complex differentially alter the accuracy of start codon recognition

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ACS Chemical Neuroscience

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Glycation Produces Topologically Different α-Synuclein Oligomeric Strains and Modulates Microglia Response via the NLRP3-Inflammasome Pathway

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ELSEVIER

ROS and calcium signaling are critical determinant of skin pigmentation

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A conserved polar residue plays a critical role in mismatch detection in A-family DNA polymerases

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ORIGINAL RESEARCH

Physiologia Plantarum

Characterization of Arabidopsis *eskimo1* reveals a metabolic link between xylan O-acetylation and aliphatic glucosinolate metabolism

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Patent Applications

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1. Jha SK and Bajaj A. An oral formulation for treatment of gastrointestinal cancers. Indian Provisional Patent Application No. 202511012949, dated: 14 February 2025.
2. Pal G, Vemanna RS, Synthetic and natural molecules for crop protection against plant diseases caused by bacteria, nematodes, and viruses. 202411062781, dated: 20 August, 2024.
3. Shankar M, Bajaj A, Sneh Lata Pareekh, Vemanna RS. Transgene-free, *in planta*-mediated delivery of RNPs to edit genes in plants.202511006944 dated: 29 January 2025.

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1. Babitha KC, Veena HM and Ramu S Vemanna (07 February 2022). Pro-transpirants to increase crop productivity. Indian Patent Application No. 202211006352, Patent No. 550300, Granted date: 13 September 2024.
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Shreya Singh
Mrutyunjaya Parhi

Academic & Training Activities

Academic Programmes

1. PhD Programme in Biotechnology

RCB offers doctoral programme in Biotechnology to students holding a post-graduate degree (or an equivalent) in any field of science, medicine or technology and interested in pursuing research at the interface of multiple disciplines in the areas related (but not limited) to structural biology, molecular medicine, infectious disease biology, agricultural biotechnology, systems and synthetic biology, cancer & cell biology.

Currently, 123 students are pursuing PhD Programme in Biotechnology at RCB. During the period of this report, 12 students graduated with PhD degree.

2. PhD Programmes in Biostatistics & Bioinformatics

RCB offers an interdisciplinary doctoral programme in Biostatistics and Bioinformatics supported through a collaboration with the global pharmaceutical giant, GlaxoSmithKline Pharmaceuticals India Private Ltd. (GSK). These programmes are subject to RCB statutes, ordinances and regulations.

In addition to RCB faculty members, a virtual adjunct faculty pool created from partner institutions (IIT Delhi, NII New Delhi, ICGEB New Delhi, NIBMG Kalyani) act as mentors for the students admitted to these programme. Students receive a consolidated fellowship of Rs.45000 per month for the first two years and Rs.50000 for the next three years.

Currently, 07 students are pursuing PhD Programme in Biostatistics/Bioinformatics at RCB. During the period of this report, 03 student graduated with PhD degree.

3. MS-PhD Programme in Biotechnology

RCB introduced a MS-PhD Programme in Biotechnology in 2018-19 with focus on research-based learning. The programme provides extensive learning opportunities in the broad field of life sciences and biotechnology through rigorous classroom study and hands-on laboratory experiments. In the second year, the students work under the supervision of a faculty at RCB, in an area of mutual scientific interest, and submit a dissertation by the end of the fourth semester.

A student may exit the programme with a Master's degree or continue in the programme for pursuing PhD. The students admitted to the programme receive the RCB Ramachandran-DBT fellowship of Rs. 16000 per month for the first two years, after which, the Indian students continue in the PhD component with a fellowship from a national funding agency while the foreign students receive the RCB-DBT International Doctoral fellowship. At present, 68 students are registered in the programme. During the reporting period 08 students quit and graduated the programme with M.Sc. degree.

4. i3c BRIC-RCB PhD Programme in Biosciences

The i3c BRIC-RCB Ph.D Programme is a unique, nationally cohesive, inter-disciplinary programme in biosciences designed to develop highly skilled and globally competitive scholars with futuristic work capabilities.

The programme offers the chance for brilliant young minds to pursue doctoral studies in any of the 15 premier research institutions which are a part of this network across the country. The Institutes are Regional Centre for Biotechnology, International Centre for Genetic Engineering and Biotechnology (ICGEB), and 13 institutions of BRIC (iBRIC) i.e., National Institute of Immunology, National Centre for Cell Science, National Brain Research Centre, Center for DNA Fingerprinting and Diagnostics, National Institute of Plant Genome Research, Institute of Life Sciences, Institute of Bioresources and Sustainable Development, Rajiv Gandhi Centre for Biotechnology, Institute for Stem Cell Science and Regenerative Medicine, Translational Health Science and Technology Institute, National Institute of Biomedical Genomics, National Agri-Food Biotechnology Institute, National Institute of Animal Biotechnology

At present, 57 students are registered in the programme. Out of 57 students, 6 students are pursuing PhD at RCB and the remaining are pursuing PhD in iBRIC (institutions of BRIC) and ICGEB.

5. Post Graduate Diploma in Industrial Biotechnology (PGDIB)

The PG Diploma program focuses on generic skills while providing an overview of industrial processes. The program includes six months of generic training relevant to the industry, which comprises theory and practical-based laboratory sessions to help students acquire essential knowledge in areas such as Clinical Research Regulations, Quality Control and Quality Assurance, Research Methodology, Biostatistics, basics of Information Technology, Vaccine Technology, General Principles of Intellectual Property, Scale-Up and Validation, Analytical Techniques, Basic Concepts in Drug Discovery and Development, and sessions on Soft Skills. The generic training is followed by a three-month elective course, where students can choose specialized subjects from a pool of options. After the elective training, they undergo a three-month internship at selected biotechnology-related companies that have a Memorandum of Understanding (MoU) with the Regional Centre for Biotechnology.

At present, 18 students are registered in the programme.

6. Research & Training Programme at RCB

RCB offers research training to post-graduate students of biotechnology related areas from various universities/ institutions/ colleges of repute to carry out their project work towards partial fulfilment of their post-graduate degrees.

Short-term summer trainings/ internships are also offered to students interested in research areas of specialization in RCB. Selection is based on the strength of resume and evaluation of write-up on their research interests. Selected candidates undergo research training under the mentorship of RCB faculty. They learn to carry out their own research projects in collaboration with other group members. Trainees get a realistic experience of several facets of conducting modern biological research and embarking on a research career. The training programmes range from one to six months' duration. During the reporting period, 54 research trainees joined for research and training programme at RCB.

7. Academic Programmes at RCB's Recognized Centers

RCB has granted academic recognition to the various institutions of excellence, as per Clause 10(1) f of the RCB Act and RCB Ordinance, for their academic programmes. Students admitted to these programmes are registered at RCB for their degrees. At present, following 06 institutions and their academic programmes are recognized by RCB. The number of students registered under the various programmes are provided below:

Name of the Recognized Centre	Programme	Branch	Students	Adjunct Faculty
1. Biotechnology Research and Innovation Council (BRIC) (2024)				
i) BRIC -National Institute of Immunology (2024)	PhD	Biosciences	4	25
ii) BRIC - National Centre for Cell Science (2022)	PhD	Biotechnology	79	28
	PhD	Biosciences	5	
iii) BRIC - National Brain Research Centre (2024)	PhD	Biosciences	3	10
iv) BRIC - Center for DNA Fingerprinting and Diagnostics (2017)	PhD	Biotechnology	53	23
	PhD	Biosciences	4	
v) BRIC - National Institute of Plant Genome Research (2024)	PhD	Biosciences	3	29
vi) BRIC - Institute of Life Sciences (2018)	PhD	Biotechnology	119	30
	PhD	Biosciences	5	
vii) BRIC - Institute of Bioresources and Sustainable Development (2021)	PhD	Biotechnology	13	13
	PhD	Biosciences	1	
viii) BRIC - Rajiv Gandhi Centre for Biotechnology (2019)	PhD	Biotechnology	96	40
	PhD	Biosciences	4	
	MSc	Biotechnology	39	

ix) BRIC - Institute for Stem Cell Science and Regenerative Medicine (2022)	PhD	Life Sciences	37	13
	PhD	Biosciences	4	
x) BRIC - Translational Health Science and Technology Institute (2018)	PhD	Biosciences	3	15
	MSc	Clinical Research (Clinical Trials)	28	
xi) BRIC - National Institute of Biomedical Genomics (2019)	PhD	Biotechnology (Biomedical Genomics)	47	21
	PhD	Biosciences	4	
	MS-PhD	Biotechnology (Biomedical Genomics)	34	
xii) BRIC - National Agri-Food and Bio-Manufacturing Institute (NABI) (2017)	PhD	Biotechnology	66	34
	PhD	Biosciences	5	
xiii) BRIC - National Institute of Animal Biotechnology (2017)	PhD	Biotechnology	95	22
	PhD	Biosciences	1	
2. International Centre for Genetic Engineering and Biotechnology (ICGEB), New Delhi (2024)	PhD	Biosciences	5	5
3. Christian Medical College, Vellore (2020)	PhD	Medical Biotechnology (Haematology)	17	10
	PhD	Medical Biotechnology (Biomedical Genetics)	4	
4. ESIC, Faridabad (2021)	PhD	Biomedical Sciences	15	32
5. IAV, Thiruvananthapuram (2023)	PhD	Virology	3	11
6. Max Society of Medical Academics Innovation and Research, New Delhi (2023)	MSc	Clinical Research	27	0
	PG Diploma	Clinical Research	0	
Total			**823**	**361**

Webinars/ Seminars

Date	Title	Speaker
24 March, 2025	Candida glabrata: The odd fungal pathogen with very little Superpower!	Dr. Rupinder Kaur, BRIC-CDFD, Hyderabad
24 February 2025	Stem Cells in mammary gland biology & breast cancer	Dr. Anu Rangarajan, Indian Institute of Science, Bengaluru
11 February 2025	Exploring biologically relevant DNA structures for drug development	Dr. Roshan Satange Assistant Professor, Chang Gung University, Taoyuan, Taiwan
10 February 2025	Is Al the new language of biology?	Dr. Anurag Agrawal, Dean, BioSciences and Health Research Ashoka University
3 February 2025	Probing Metabolic Questions through Genetics	Prof. Anand K Bachhawat, IISER Mohali
23 January 2025	Population-Based Approaches in Translational Cancer Research.	Prof. Upender Manne, Director, Translational Anatomic Pathology, School of Medicine, University of Alabama Birmingham
18 December, 2024	Improve your manuscript writing skills by dissecting its anatomy	Prof. Kalai Mathee Former Editor-in-Chief J. Med. Microbiol., Council Member & Trustee, Microbiology Society, and Editor, mBIO
18 December, 2024	Title - Uncovering the essential function of thymidylate kinase in *Pseudomonas putida* using synthetic biology tools	Dr. Pablo I. Nikel *Professor & Chair of Synthetic Bacteria Metabolism DTU Biosustain, Denmark*
4 December, 2024	Role of small RNAs in development and disease	Dr. Manish Kumar,NIH *USA*
2 December 2024	Nucleoporins Regulate ER-Mitochondria Contact Sites and their Functions	Dr. Jomon Joseph, NCCS Pune (RCB Seminar Series)
28 November 2024	Learning to do better: Unfinished immunological stories	Dr. Satyajit Rath, IISER Pune
20 November 2024	ADAMTS13/VWF axis in thrombosis and stroke	Prof. Anil Chauhan, Iowa University
18 November 2024	Long-distance signalling governs tuber development in potato: The 4th most important food crop on the planet	Dr. Anjan Banerjee, IISER Pune (RCB Seminar Series)
23 October 2024	Celiac Disease: A Model for Integrating Clinical and Fundamental Science	Dr. Govind Makharia, AIIMS New Delhi
22 October 2024	A Glimpse into Molecular Pathways Governing Stem Cell Pluripotency and Differentiation in planarians	Dr. Dasaradhi Palakodeti, InStem, Bangalore (RCB Seminar Series)
21 October 2024	Beta 2-glycoprotein 1 and the clearance of circulating mitochondria	Prof. Perumal Thiagarajan, Baylor College of Medicine, TX, USA
18 October 2024	Recent Advances in Bio-Imaging	Mr. Mahavir Tanwar, Nikon-India

17 September 2024	Decoding Ionotropic Glutamate Receptors: Bridging the Gap Between Structure, Function, and Therapeutics	Talk by Dr. Janesh Kumar, CCMB Hyderabad (RCB Seminar Series)
2 September 2024	Chemical Biology Approach for Solving Unmet Clinical Needs	Dr. Praveen Vemula, InStem Bangalore
8 August 2024	Evolution of a Cancer Biologist.	Dr. Sorab Dalal, TMC ACTREC & HBNI (RCB Seminar Series)
15 July 2024	HIV-1 Transcriptional _ silence:~ The Symphony of the Silent. Virus	Dr. Udaykumar Ranga, JNCASR, Bangalore (RCB Seminar Series)
09 July, 2024	"Democratizing drug discovery: Al-enabled virtual vs traditional high-throughput drug screening methods (case study in cardiac therapeutics)"	Dr. Priyanka Parijat *King's College London, UK and The Write Source MSC, USA.*
26 June, 2024	"Exploiting Metabolic Adaptations in Pancreatic Cancer: Novel Therapeutic Strategies Targeting the Tumor Microenvironment"	Dr. Divya Murthy *Baylor College of Medicine, USA*
21 Jun, 2024	"Bacterial transcription terminator, Rho:mechanism of action, physiology and inhibition"	Prof. Ranjan Sen *BRIC-CDFD, Hyderabad*
14 June, 2024	Population Genomics for Public Health.	K. Thangaraj *Centre for Cellular and Molecular Biology, Hyderabad*
20 May 2024	"Cryo-EM structure of the switched-off state of myosin II and its relation to hypertrophic cardiomyoapathy."	Dr.Prince Tiwari *IIT Roorkee*
10 May 2024	Chromatin Readers as molecular architects in shaping extracellular matrix and metabolic landscape in breast cancer.	Dr. Chandrima Das Saha Institute of NuclearPhysics, Kolkata
3 May 2024	Mechanisms of DNA Repair in Bacteria	Prof. Marcin Nowotny (International Institute of Molecular and Cell Biology, Poland)
19 April, 2024	Genetic Control of Growth and Geometry - Shaping up a leaf.	Dr. Utpal Nath *Indian Institute of Science, Banglore*
10 April, 2024	THSTI-RCB Seminar	Dr. Anil Thakur, RCB Dr. Srikanth Sadhu, THSTI

Events Organized

Summer Research Internship Programme Facilitated by Gujarat State Biotechnology Mission (GSBTM)

Regional Centre for Biotechnology organised a Summer Research Internship Programme facilitated by Gujarat State Biotechnology Mission (GSBTM), Department of Science and Technology, Govt. of Gujarat was from June 03 to July 01, 2024.

The main objective of the Programme was to provide early exposure to the students pursuing MSc/BE (Biotech) in Biotechnology and allied areas of Biotechnology about the research environment and mechanism that can help them take better career decisions.

A total number of 20 interns were allotted for the Programme who successfully completed their internship with hands-on exposure in the areas of Biotechnology like Cell Biology, Stem Cells, Agricultural Biotechnology, Industrial Biotechnology, Structural Biology, Virology, Animal Models and Cancer Biology in order to help them build an interest and enthusiasm to pursue higher education and instill a sense of aspiration to do future research in places of repute like RCB.

A Biotechnology Career Counselling session was also setup to help them decide on their future career path in the biotechnology industry/research. A visit to the Advanced Technology Platform Centre (ATPC) and BSc BioNEST Bioincubator (BBB) was also organised to enable them to understand the nuances of biotechnology research, and the research possibilities available at RCB.

Events organised for Swachhata Campaign 4.0 at RCB on account of the 'Swachhata Hi Seva'-2024 (SHS-2024)

As a part of Swachhata Campaign 4.0 and on account of the 'Swachhata Hi Seva'-2024 (SHS-2024), RCB organized the following events during September 2024:

S. No.	Date	Topic	Speaker
1	23rd Sep 2024	Air Pollution	Avikal Somvanshi Centre for Science & Environment
2	24th Sep 2024	Micro Plastic	Siddharth Singh Centre for Science & Environment

RCB also organised sensitization workshops for health & well-being nature awareness and Ayurveda on 26th September 2024

Day	Doctors	Activities
26 Sep 2024	Yogacharya Antarang	Yoga Session
26 Sep 2024	Dr. Arsha MU	Health Talk
26 Sep 2024	Dr. Arsha MU	Complimentary Health Consultation

Hindi Pakhwada 2024

Hindi Pakhwada (Fortnight) is celebrated every year during the month of September and Hindi Diwas on 14th September to promote the progressive use of official language, Hindi, in government offices in compliance with the Official Language Policy of the Government of India. In this sequence, Hindi Pakhwada was organized from 14 to 30 September 2024 at the Regional Centre for Biotechnology.

The closing ceremony of the fortnight was held on 30 September under the chairmanship of the Executive Director, RCB at M. K. Bhan Auditorium. On this occasion Dr. Arvind Sahu (Executive Director, RCB), Dr. R.P. Roy (Dean Academics, RCB) and Dr. Nidhi Sharma (Hindi Nodal Officer, RCB), apprised the personnel about the importance of Hindi and its history. A total of eight competitions were organized during the fortnight in which the personnel and research students participated enthusiastically. The Executive Director and the Dean (Academics) jointly gave awards and certificates to the winning employees during the event.

Vigilance Awareness Week 2024

As per the directives of the Central Vigilance Commission and DBT, the Vigilance Awareness Week 2024 was observed at RCB during 28th October to 3rd November 2024. The official theme for Vigilance Awareness Week 2024 was "सत्यनिष्ठा की संस्कृति से राष्ट्र

की समृद्धि" "Culture of Integrity for Nation's Prosperity". Accordingly, pledge taking ceremony was organised on 30 October 2024.

Design Thinking Workshop

The Design Thinking workshop was coordinated by Dr. Deepti Jain and Dr. Divya Chandran at RCB. The workshop was conducted by Dr. Anbu Rathinavel and V. Ramakrishnan, from the School of Design Thinking, Intellect Design Arena on 25th-27th October 2024. The workshop was attended by 58 i3C-BRIC-RCB PhD students. The program featured a well-structured blend of dynamic learning experiences that fostered a focused problem-solving mindset among students and highlighted the importance of aligning individual skills with broader societal needs. Through a combination of hands-on activities, real-world simulations, and collaborative exercises, students engaged in immersive learning experiences centered on Design Thinking concepts and frameworks. The application of these concepts and tools will bring about a positive and meaningful impact on the research initiative that the students will embark on in the future.

Science Communication Workshop

RCB organized a Science Communication Workshop during 21-25 November 2024 under i3c BRIC-RCB PhD programme in Biosciences. The event was attended by more than 100 students. The experts of this workshop were Dr. Gaurav Das, Dr. Vasudevan Seshadri, & Dr. Jomon Joseph (all from NCCS Pune) trained the participants in basics of science communications, writing a manuscript, presentation skills, writing grants, preparing CVs etc.

3rd Convocation Ceremony 2024

Regional Centre for Biotechnology organised its 3rd Convocation Ceremony on December 16, 2024, at the M K Bhan Auditorium.

The degrees were conferred to the students of PhD and Master's programmes, by the Chief guest Prof. Ajay K. Sood (Principal Scientific Advisor, GoI).

The Convocation began with a grand academic procession followed by Saraswati Vandana sung by the students of RCB. The Convocation was declared 'Open' by Dr. Rajesh Gokhale, the Secretary, DBT and Chairperson, Board of Governors, RCB. The Director's Report was presented by Dr. Arvind Sahu, the Executive Director, RCB.

A total of 93 students graduated. 56 PhD in Biotechnology and 37 Master of Science in Biotechnology degrees were awarded to the students.

Prof. Ajay K. Sood (Principal Scientific Advisor, GoI) addressed the Convocation. The Convocation was declared 'Closed' by Dr. Rajesh Gokhale, Secretary, Department of Biotechnology and Chairperson, Board of Governors, RCB.

'Genomics Data Conclave' and release of Genome Data by Hon'ble PM and other releases and announcements by Hon'ble Minister (S&T)

The Indian Biological Data Centre (IBDC) has achieved a remarkable milestone by collaborating with the GenomeIndia consortium to archive 1 Petabyte of genomic data from 10,000 human genomes. This monumental achievement was inaugurated by the Honourable Prime Minister, Shri Narendra Modi, on January 9, 2025, at the Genomics Data Conclave. Additionally, IBDC, in partnership with the Data Management Group, developed the FeED protocols by DBT and a Data Access Portal for controlled-access data sharing, unveiled by the Honourable Minister of S&T, Dr. Jitendra Singh. These initiatives underscore IBDC's leadership in advancing data accessibility and driving innovation in life sciences.

1st Computational Biology Conference 2025

RCB organised the 1st Computational Biology Conference from February 19-21, 2025. It was a resounding success featuring 19 distinguished speakers from five countries - India, USA, UK, Israel and Australia- who presented cutting-edge developments in computational biology and data sciences. The conference gathered 200 participants and featured 67 poster presentations by researchers from 50 organisations across 20 states of India. The event also nucleated a dialogue with EBI-EMBL (UK) for potential collaboration on data hosting, curation and visualisation.

National Science Day 2025

The National Science Day was celebrated at Regional Centre for Biotechnology on February 28, 2024. On the occasion of National Science Day, the Regional Centre for Biotechnology (RCB) organized an Open Day exhibition for the public, wherein various activities highlighting RCB's research programs, games, quizzes, hands-on experiments, live demos, a nukkad natak competition etc were organized.

RCB Foundation Day 2025

In 2016, RCB was ordained with the status of an "Institution of National Importance" through an Act of the Parliament. It was brought into effect by a Gazette notification on March 01, 2017. To commemorate this momentous occasion, March 01 has been adopted as the RCB Day.

The Foundation Day started out with mini-symposium presentations made before the panel of judges by the final year PhD students and the award for the best scientific presentation was distributed to the winners. Dr. Arvind Sahu, the Executive Director of the Regional Centre for Biotechnology, gave a welcome speech to start off the programme. The day's guest of honour Prof. Mewa Singh (INSA Distinguished Professor, University of Mysore) visited RCB and delivered the RCB Day Oration followed by a splendid Santoor Recital by Maestro Pt. Abhay Rustum Sopori (Bharat Sanskriti, Dhrupad Samman Awardee).

Manuscript writing workshop

A three-day manuscript writing workshop was organized from 5 - 7 March 2025 for our research scholars in collaboration with Editage. Dr Sunaina Singh and Dr Vihang Ghalsasi - the experts -introduced the basics of scientific writing through extensive exercises and discussions. The event received an overwhelming response from the scientific community of RCB.

International Women's Day 2025

This time RCB celebrated International Women's Day at Sariska Tiger Reserve in Rajasthan along with RCB's annual scientific retreat. A panel discussion on 'Women in Science' was conducted to understand the challenges women face. Faculty & staff

engaged in conversations around the need for sensitization, equity & inclusion in the scientific community to achieve our full potential in advancing science.

i3c BRIC-RCB Leadership Talk Series

A series of talks, titled i3c BRIC-RCB Leadership Talks, were organised to hone soft skills of the scholars enrolled in the i3c BRIC-RCB PhD programme in Biosciences. Leaders included scientists like Prof. Vijay Raghavan and Dr. Apurva Sarin, who have led public and private institutions & scientific organisations to expand & strengthen the scope of scientific research in the country as well as entrepreneurs like Dr. Anand Deshpande & Mr. Subramani Ramachandrappa, who successfully led a team in building AI, Big Data (Persistent Systems) & Biotech (Fermbox Bio) ventures. The leaders visited RCB to engage with students and inspire a spirit of ambition toward achieving great heights while making a positive impact on society.

Details of the talks scheduled in the FY 2024-25:

S. No.	Speaker	Date
1	Prof. K VijayRaghavan, Emeritus Professor & Former Director NCBS, Former Principal Scientific Adviser to the GoI & Former Secretary DBT	10 August 2024
2	Mr. Subramani Ramachandrappa, Founder Fermbox Bio	31 August 2024
3	Dr. Apurva Sarin, CEO, DBT Wellcome Trust India Alliance	21 September 2024
4	Prof. Nikhil Tandon, Head, Dept. of Endocrinology and Metabolism, AIIMS New Delhi	18 October 2024
5	Dr. Anand Deshpande, Persistent Systems	8 November 2024
6	Ms. Rouble Nagi, Rouble Nagi Art Foundation	26 November 2024

Sports Month 2025

Sports at RCB is a month-long activity which includes outdoor and indoor sports competitions like badminton, table tennis, chess, carrom, volley ball, football, cricket, basket ball, shot put, Discus throw, Tug of war and running, signifying that physical and mental health are as important as intellectual health. The prize distribution for the winners of all the events was done on 1st March 2025 on the occasion of RCB foundation day.

Outreach Programmes

Regional Centre for Biotechnology organised various outreach programmes as a part of the Scientific Social Responsibility (SSR) activity under SERB to imbibe a culture of social commitment among SERB Grantees. The following Programmes were organised:

27 November 2024 - MVN University students' visit (Outreach activity)
18 November 2024 - Manav Rachna University B.Sc B.Ed students' visit to RCB (Outreach activity)
14 November 2024 - Vigyan Jyoti scholars (Jawahar Navodaya Vidyalaya Faridabad) visit to RCB (Outreach activity)
17 October 2024 - Vigyan Jyoti scholars (Jawahar Navodaya Vidyalaya Palwal) students' visit to RCB (Outreach activity)
22 August 2024 - DAV Public School (Gurugram) students' visit to RCB (Outreach activity)

Scientific and Other Events Conducted

Prof. Deepak T Nair

1. Organized 1st Computational Biology Conference (CBC2025) at the Regional Centre for Biotechnology, Faridabad, held from 19th-21st February, 2025.

Prof. Vengadesan Krishnan

1. Co-organized RCB day mini-symposium at the Regional Centre for Biotechnology, Faridabad, on March 1st, 2025.
2. Conducted a Three-dimensional (3D) demonstration of biomolecules to students during National Science Day organized at RCB, NCR Biotech Science Cluster, Faridabad on February 28th, 2025.
3. Organized an online workshop and training on Empowering research and Academic writing using Grammarly on February 7th, 2025.
4. Organized an online workshop and training session on Plagiarism-checking on August 8th, 2024.

Dr. Karthigeyan Dhanasekaran

1. Organized a Two-day ZOYC workshop on Fluorescence Microscopy along with Zeiss, India team on 10th-11th April, 2024.
2. Organized a Two-day training on 3D-SIM microscopy along with Nikon, India team in our ATPC facility on 2nd-4th April, 2024.
3. Open day of the CCB lab for the BRIDGE-SIP GSBTM students on 4th June, 2024.
4. Organised the Scientific Manuscript Writing workshop at RCB, 5th – 7th March, 2025.

Dr. Saikat Bhattacharjee

1. Conducted the online Webinar on the i3C BRIC-RCB PhD programme in Biosciences on 23rd March, 2024.
2. Organized the Cultural events for RCB Convocation Day, 2024 and RCB Foundation Day, 2025.

Dr. Divya Chandran

1. Co-organized an HFSP Master Class event (a grant writing workshop) and a Frontier HFSP Workshop on "Driving Innovation in the Life Sciences: A role for AI?" at NII, New Delhi, between 27th-29th November, 2024.

Dr. Ramu S Vemanna

1. Organized the i3C BRIC-RCB PhD program interaction session at RCB, Faridabad, 3rd-5th July, 2024.
2. Co-ordinated and organized the "National Science Day (Open day)", 28th February 2024, at RCB, NCR Biotech Science Cluster.

Dr. Nidhi Adlakha

1. Co-organised International Women's Day.
2. Co-organised RCB Day.
3. Co-organised a scientific visit for Delhi University students.

Membership of Professional/Academic bodies/Editorial boards

Prof. Deepak T Nair

1. Member of Expert Committee to review proposals submitted under the Niche Creating High Science and Focused Basic Research schemes for the Healthcare theme of CSIR.
2. Co-Member Secretary (*ex officio* as IBDC Head), Data Management Group (DMG) of DBT for implementation of BIOTECH PRIDE guidelines.
3. Member, Working Group 2: Structural Data in the DMG of DBT.
4. Co-Member Secretary (*ex officio* as IBDC Head), Expert Advisory Committee of the IBDC, 2024.
5. DBT Nominee for the "Beamline Review Panel for Indus-3" constituted to review technical specifications of first 12 beamlines in the proposed 4th generation High Brilliance Synchrotron Radiation Source (HBSRS) at RRCAT in Indore, India.
6. Member of the National Committee for the International Union of Crystallography (IUCr) of the Indian National Science Academy.
7. Acting Head, Indian Biological Data Centre of the Department of Biotechnology.
8. Life Member, Indian Crystallographic Association.
9. Life Member, Indian Biophysical Society.
10. Life Member, Society of Biological Chemists.

Prof. Vengadesan Krishnan

1. Member, Indian Crystallographic Association (ICA).
2. Member, Indian Biophysical Society (IBS).
3. Member, International Union of Crystallography (IUCr).
4. Member, Electron Microscopy Society of India (EMSI).
5. Member, Probiotic Association of India (PAI).
6. Member, Association of Microbiologists of India (AMI).

Prof. Deepti Jain

1. Biofilm Society of India – President.
2. Deputy Council member from India of the Asia Pacific Protein Association.
3. Member of the selection committee for MK Bhan Post-Doctoral program, DBT.
4. Indian Crystallography Association – Life Membership.
5. Electron Microscope Society of India – Life Membership.
6. Society of Biological Chemists – Life Membership.
7. Review Editor of Frontiers in Bioengineering and Biotechnology.
8. Protein Society of India – Member.

Dr. Prem Singh Kaushal

1. Life Member, Indian Crystallography Association (ICA).
2. Life Member, Electron Microscopy Society of India (EMSI).

Prof. Prasenjit Guchhait

1. Member, Reviewer board for DBT-ICMR joint program, 2025.
2. Member, Molecular Immunology Forum meeting, IISER, Bhopal.
3. Member, International Society for Thrombosis and Hemostasis Congress, Bangkok.

Prof. Tushar Kaniti Maiti

1. General Secretary, Proteomics Society of India.
2. Member, American Society for Biochemistry and Molecular Biology.

Prof. Sam J Mathew

1. Member, Expert Committee for National Biological Reference Standards and in vitro diagnostic QC panels, National Institute of Biologicals, NOIDA, 2024.
2. Member, Indian Society for Developmental Biology (InSDB).

Prof. Sudhanshu Vrati

1. Life Member, Indian Society for Cell Biology.
2. Life Member, Society of Biological Chemists, India.
3. Life Member, Association of Microbiologists of India.
4. Life Member, Indian Immunology Society.
5. Life Member, Indian Virology Society.
6. Editorial Board Member, Therapeutic Advances in Vaccines (SAGE, UK).
7. Independent Director and Chairman, BIBCOL, Bulandshahar.
8. Member, Covid-19 Solidarity vaccine Trial - WHO Candidate Vaccine Prioritization Working Group.
9. Coordinator, INSACOG.

Prof. Chittur V Srikanth

1. Member, Molecular Immunology Forum.
2. Member, Domain Expert Group, CSIR.
3. Member, Project Screening expert committee, ICMR.
4. Member, TEC of DBT (Infectious Disease Biology).
5. Member, American Society for Microbiology.
6. Member, Research Council, IGNO University.
7. Member, Khorana Program for Scholars (DBT-IUSSTF).
8. Member, Incubator Seed Management Committee.
9. Editorial advisory board member, Journal of Gastrointestinal Infections.

Prof. Arup Banerjee

1. Editorial Board member, *Journal of Leukocyte Biology.*
2. Contributing member of the F1000 Faculty Infectious Diseases of the Nervous System Section in F1000Prime (https://f1000.com/prime).
3. Editorial Board member (Infectious Diseases) of *Scientific Reports.*
4. Review editor, Virology section, *Frontiers in Microbiology.*

Dr. Anil Thakur

1. Member, American Society of Microbiology.

Prof. Avinash Bajaj

1. Fellow National Academy of Sciences (FNASc) Allahabad, India.
2. Member, TEC, Biomedical Science, DBT, Govt. of India.
3. Elected Member, Guha Research Conference, India.
4. Member, Molecular Immunology Forum, India.
5. Co-Member: Program Advisory Committee, Biomedical and Health Sciences, SERB.
6. Member, Travel Grant and Symposia Management (TGSM) Unit of CSIR-HRDG, India.
7. Member, TEC, BIRAC, DBT, India.
8. Member, TEC, ICMR, New Delhi, India.

Prof. Sivaram VS Mylavarapu

1. Life Member, Indian Society for Cell Biology (ISCB).
2. Member, Board of Studies, Faculty of Life Sciences and Biotechnology (FLSB), South Asian University (SAU), New Delhi.

Dr. Rajender K Motiani

1. Member, Veterinary Council of India, New Delhi.
2. Member, Rajasthan State Veterinary Council, Jaipur.

Dr. Karthigeyan Dhanasekaran

1. Member, Indian Society of Cell Biology.
2. Member, Indian Society of Chemical Biology.
3. Member, Indian Veterinary Council.

4. Member, Tamil Nadu State Veterinary Council.
5. Member, Veterinary Council of India.

Dr. Saikat Bhattacharjee

1. Member, International Society- Molecular Plant-Microbe Interactions (IS-MPMI).
2. Editorial Board member, Discover Immunity Journal.
3. Review Editor, Frontiers in Plant Science Journal.

Dr. Divya Chandran

1. Member, DBT Technical Expert Committee (TEC) of Plant Biotechnology.
2. Member, ANRF Subject Expert Committee for Life Sciences - II: Plant Sciences, Biochemistry, Biophysics and Molecular Biology.
3. Associate Editor, Plant Molecular Biology Reporter.
4. Member, International Society for Molecular Plant-Microbe Interactions.
5. Member, British Society for Plant Pathology.

Dr. Ramu S Vemanna

1. Life member – Indian Society of Plant Physiology (ISPP).
2. Life member – Indian Society for Plant Biochemistry and Biotechnology (ISPBB).

Prof. Rajendra P Roy

1. Member, Governing Body, NCCS, Pune.
2. Member, Research Area Panel - Scientific Advisory Committee, NCCS, Pune.
3. Member, Research and Academic Advisory Committee, IISER Berhampur.
4. Member, American Peptide Society.
5. Member, Guha Research Conference.
6. Member, Association of Microbiologists of India.

Dr. Manjula Kalia

1. Editorial board member, Journal of Virology (ASM)
2. Immunology Associate Editor, Autophagy Reports
3. Editor, Microbiology Spectrum (ASM).

Dr. Ambadas Rode

1. Member, Indian Biophysical Society.
2. Member, Society of Biological Chemists.
3. Member, Indian JSPS Alumni Association.

Dr. Nidhi Adlakha

1. Review Editor, Frontiers in Bioengineering and Biotechnology.
2. Member, American Society of Microbiology.

Distinctions, Honours and Awards

Prof. Deepak T Nair

1. Invited to attend the "at home reception" hosted by the Honorable President of India, Shrimati Droupadi Murmu, at Rashtrapati Bhavan on 15th August 2024.
2. Elected Member, Guha Research Conference.
3. Elected Fellow, Indian National Science Academy.

Prof. Deepti Jain

1. Power fellowship, SERB.

Dr. Prem Singh Kaushal

1. EMSI Excellence in Microscopy Award, 2023.
2. EMBO Global Investigator Fellow 2025

Prof. Sam J Mathew

1. Elected as a Fellow of the National Academy of Sciences (NASI), India, in 2024.
2. Elected as a member of the Guha Research Conference (GRC), in 2024.

Prof. Sudhanshu Vrati

1. Elected Fellow, National Academy of Sciences, India.
2. Elected Fellow, Indian Academy of Science, Bangalore.
3. Elected Fellow, Indian National Science Academy, New Delhi.
4. Elected Member, Guha Research Conference.
5. J C Bose National Fellow, SERB.

Dr. Anil Thakur

1. Ramalingaswami Fellowship from DBT, India

Dr. Karthigeyan Dhanasekaran

1. Ramalingaswami Fellowship from DBT, India

Prof. Avinash Bajaj

1. Elected Fellow, National Academy of Sciences, India.

Prof. Sivaram VS Mylavarapu

1. Elected Fellow, Indian National Science Academy (INSA), New Delhi, India.
2. Elected Fellow, National Academy of Sciences (NASI), Prayagraj, India.
3. Elected member, Guha Research Conference (GRC), India.
4. Distinguished Alumnus Award, Deshbandhu College, University of Delhi.

Dr. Rajender K Motiani

1. EMBO Global Investigator Network (GIN) Fellowship (2025-2028).
2. DBT/Wellcome Trust India Alliance Intermediate Fellowship (2020-2026).
3. INSPIRE Faculty Fellowship to Jyoti Tanwar, Post-Doctoral fellow in the lab (2022-2027).

Dr. Saikat Bhattacharjee

1. Bonn International Fellowship (2025).

Dr. Prashant Pawar

1. DST - INSPIRE Faculty.
2. DBT - Energy Bioscience Overseas Fellowship (Relinquish).

Prof. Rajendra P Roy

1. Elected Fellow, National Academy of Sciences, India.
2. Elected Fellow, Indian National Science Academy.
3. Elected Fellow, Indian Academy of Science.
4. JC Bose National Fellowship

Dr. Ambadas Rode

1. JSPS Bridge Fellowship (2025) from Japan Society for the Promotion of Science (JSPS).

Dr. Nidhi Adlakha

1. Har Govind Khurana-Innovative Young Biotechnology Award (2024).
2. Elected Fellow, Indian National Young Academy of Sciences (2024).

Lectures delivered/ Conferences attended/ Visits abroad/Outreach

Prof. Deepak T Nair

1. Attended the "AlphaFold Education Summit" organized by EMBL-EBI & Google DeepMind held from January 14-16, 2025 at the Wellcome Genome Campus in Hinxton, UK.
2. Participated in the Panel Discussion on "Global Ethics of Data Sharing" during the Genomics Data Conclave held at Vigyan Bhawan, New Delhi on 9th January, 2025.
3. Delivered the talk titled "New answers for old questions regarding DNA synthesis by DNA polymerases" at the 7th DNA polymerase meeting held in Warsaw, Poland, from 28th August to 1st September, 2024.
4. Delivered a talk titled "New answers for old questions regarding DNA synthesis by DNA polymerases" at the National Symposium on Advances in Biosciences held at Kannur University, Kerala, on 16th August, 2024.
5. Delivered an invited talk titled "Structural studies on P4A2 mAb and ApPol1" on 24th May, 2024 at IIT-Delhi, New Delhi.

Prof. Vengadesan Krishnan

1. Attended Computational Biology Conference (CBC2025) held at the Regional Centre for Biotechnology, Faridabad, during 19th-21st February, 2025.
2. Delivered an invited talk on 'Protein Crystallization' in the Hands-on Training course and workshop as part of Prof M Vijayan School of Macromolecular X-ray Crystallography and Protein Structure Prediction, conducted at the National Institute of Immunology (NII) during 20th-22nd January, 2025.
3. Attended the Genomics Data Conclave organized by the DBT at Vigyan Bhawan, New Delhi, on 9th January, 2025.
4. Delivered a plenary talk on 'Targeting bacterial attachment to control oral biofilm formation and combat infections' and participated in the International Conference on Recent Developments in Biofilms and Biofouling Control (BBC2024) held at Bhabha Atomic Research Centre (BARC), Kalpakkam, during 12th-14th December, 2024.
5. Attended Navigating the Publishing Landscape: From Submission to Publication and DeLCON Nodal officers meeting held at the National Institute of Immunology, New Delhi, on 10th December, 2024.
6. Delivered an invited talk on 'New structural insights into the mechanism of sortase-mediated pili extension and compression' and participated in the National Seminar on Crystallography (NSC51) held at Visvesvaraya National Institute of Technology (VNIT), Nagpur, during 27th-29th November, 2024.
7. Delivered a plenary talk on 'New structural insights into the assembly of dynamic pili in gut-dwelling Ligilactobacillus ruminis' and participated in the Conference on Structural Biology and Drug Discovery (CSBDD2024) held at SRM Institute of Science and Technology (SRMIST), Kattankulathur, during 8th-10th October, 2024.

Prof. Deepti Jain

1. Delivered an invited talk titled "Structural Insights into Transcription Regulation of Late Flagellar Genes" at the Transcription Assembly meeting held at the unified academic campus, Bose Institute on 19th-21st March, 2025.
2. Invited mentor talk titled "Seeing is believing: My Journey in Structural Biology" at the Young Investigator meeting in Agra from 3rd-5th March, 2025.
3. Delivered a talk titled "Transcription Regulation: Structure and Mechanism" at the MiniPAC held at RCB on 18th February, 2025.
4. Delivered an invited talk titled "Structural basis of transcription regulation of late flagellar genes by FliA in *P. aeruginosa"* at the National Seminars in Crystallography 51, held at VNIT Nagpur from 27th-29th November, 2024.
5. Delivered an invited talk titled "Functional Insights from 3D Structures of Proteins" at JC Bose University of Science and Technology, YMCA on 13th August, 2024.
6. Delivered an invited talk titled "Structural Insights into Flagellar Gene Regulation in *Pseudomonas aeruginosa*" at IISER Mohali on 17th April, 2024.
7. Delivered an invited talk titled "Structure-Based drug Discovery for mitigation of *Pseudomonas aeruginosa* Biofilms" at the DFG-sponsored workshop on 11th-13th April, 2024.
8. Delivered an invited talk titled "Structural Insights into Flagellar Gene Hierarchy in *Pseudomonas aeruginosa*" at the "SATHI Summit: Single Particle CryoEM & Cellular Tomography," the 4th annual symposium of the CEM3DIP Society of India at IITD on 5th April, 2024.

Dr. Prem Singh Kaushal

1. Delivered an invited talk titled 'Structural studies of ribosomes from pathogenic protozoa Entamoeba histolytica, revealed

unique features of its architecture' at the 'Horizons in Structural and Computational Biology (HSCB-2025)' organized by IIT Hyderabad & University of Hyderabad, on February 28th – March 1st, 2025.

2. Delivered an invited talk titled 'Structural studies of ribosomes from pathogenic protozoa Entamoeba histolytica, revealed unique features of its architecture' at the '51st National Seminar on Crystallography (NSC-51)' organized by VNIT Nagpur, on 27th-29th November, 2024.
3. Delivered an invited talk titled 'Microbial diversity in protein synthesis as a potential target for therapeutic interventions' at the 'National Conference on Mountain Ecosystem: Biodiversity Focus' organized by Govt Degree College Kullu, HP, on 21st-22nd October, 2024.
4. Delivered an invited talk titled 'Cryo-EM: a tool for understanding the structures of biomolecules in the atomic details' at the Department of Biochemistry, University of Delhi, South Campus, on 20th August, 2024.
5. Delivered an invited talk titled 'Cryo- EM studies of ribosomes from pathogenic protozoa Entamoeba histolytica, reveal unique features of its architecture' at the 'inaugural symposium of the SERB National Facility for Cryo-Electron Microscopy (Cryo-EM)' organized by IIT, Madras, on 9th-10th August, 2024.
6. Delivered an invited talk titled 'Ribosome structure of pathogenic protozoan *Entamoeba histolytica*' at the '12th RNA group meeting' organized by IIT Guwahati, on 22nd-24th May, 2024.
7. Delivered an invited talk titled 'Cryo- EM structure of ribosome from pathogenic protozoan; Entamoeba histolytica' at the 'International Conference on Electron Microscopy' organised by IIT Bombay, on 16th-18th May, 2024.
8. Delivered an invited talk titled 'Cryo- EM structure of ribosome from pathogenic protozoan *Entamoeba histolytica*' at the 'SATHI Summit: Single Particle CryoEM and Cellular Tomography – 4th Annual Symposium of CEM3DIP Society of India' organized by SATHI, IIT Delhi, on 5th April, 2024.

Prof. Prasenjit Guchhait

1. Attended the Molecular Immunology Forum meeting, IISER, Bhopal, October 2024.
2. Attended the International Society for Thrombosis and Hemostasis Congress, Bangkok, June, 2024.

Prof. Tushar Kanti Maiti

1. Delivered an invited talk titled "Delivered an invited talk titled "Ubiquitination and deubiquitination crosstalk in palmitic acid-induced death of human hepatoma cells" at the National Symposium and Workshop on Clinical Proteomics (NSWCP) organized by the Institute of Life Sciences, Bhubaneswar, India, 20nd-23rd August, 2024.
2. Delivered an invited talk titled "Unraveling post-translational modifications with mass Spectrometry: Implications for cellular signaling and disease mechanisms" at the Education Day program of 16th Annual Meeting of Proteomics Society, India (PSI) and International Conference on International Conference on Integrated Omics Approaches for Decoding Biological Research" organized by National Chemical Laboratory and National Centre for Cell Science Pune, India, 19th-22nd November, 2024.
3. Delivered an invited talk titled "Mechanistic insights and biomarker discovery in spontaneous preterm birth" at the Society of Animal Physiologists of India (SAPI) and International Symposium on Advances in Physiological Research in the Omics Era for Sustainable Animal Production and Livelihood Security under the Changing Climatic Scenario, organized by ICAR-Central Institute for Research on Cattle, Meerut, India, 19th-22nd November, 2024.
4. Delivered an invited talk titled "Biomarker discovery in pregnancy complications" at the APT-2025 organized by the Indian Institute of Technology, Bombay, India, February, 2025.
5. Delivered an invited talk titled "Mechanistic insights and biomarker discovery in spontaneous preterm birth" at the EZACBICON 2025: The Eastern Zone ACBI Conference, organized by the Department of Biochemistry, AIIMS Kalyani and the Department of Biochemistry, College of Medicine & JNM Hospital, Kalyani, India, February 27th-March 1st, 2025.
6. Delivered an invited talk titled "Mechanistic understanding of OTUB1 aggregation and potential role in Parkinson's disease pathogenesis" at International Conference entitled "From Proteostasis to Pathology: Exploring Protein Aggregation and Amyloid Formation in Health and Disease." organized by the Department of Biotechnology, Central University of Rajasthan, Rajasthan, 11th-12th March, 2025.
7. Delivered an invited talk titled "N-linked Glycoproteomic and Proteomic Signatures as Potential Markers for Gestational Diabetes at Multi-Omics of Mother and Infant (MOMI) Consortium Convening," organized by the Gates Foundation, Seattle, USA, 8th-10th April, 2025.
8. Delivered an invited talk titled "Proteomics in Biomedical Research and Clinical Applications" at the National Institute for Research in Bacterial Infections, Kolkata, 17th April, 2025.

Prof. Sam J Mathew

1. Delivered the invited talk "A Myosin view of muscle development and homeostasis" as the keynote speaker at the Bioworld Retreat organized by the Kusuma School of Biological Sciences, Indian Institute of Technology (IIT) Delhi, at the Lake Resort, Naukuchiatal, Uttarakhand, from 26th-29th November, 2024.
2. Invited participant at the Guha Research Conference (GRC) 2024 at Kaziranga, Assam, presenting the talk "A Myosin view of muscle development and homeostasis" on 6th November, 2024.
3. Participated as an instructor in the "Muscling through species to treating diseases" workshop at the Centre for Cellular and Molecular Biology (CCMB), Hyderabad, from 4-7 November, presenting the talk "Skeletal muscle fiber type and disease" on 4th November, 2024.
4. Invited speaker at the 10th Annual National Conference of Federation of Physiological Societies and the Association of Physiologists of India (FIPS-ASSOPICON 2024) meeting where a talk titled "Development to disease: Recent advances in skeletal muscle physiology with special focus on an Indian scenario" was delivered at the Department of Physiology, All India Institute of Medical Sciences, Patna, on 24th October, 2024.

Prof. Sudhanshu Vrati

1. Delivered an invited talk on "Development of antivirals against Chikungunya virus" at the 9th International Symposium on "Current trends in drug discovery research (CTDDR-2025), at CDRI, Lucknow, on February 20th, 2025.
2. Delivered the Foundation Day lecture at the National Institute of Animal Biotechnology, Hyderabad, on December 17t, 2024.

Prof. Chittur V Srikanth

1. Delivered an invited talk titled 'Beyond the gut- the evolving strains of Salmonella and their unexpected outcomes' at ALARM SYMPOSIUM organized by Amritapuri, Kerala, during 22nd-23rd November, 2024.
2. Delivered an invited talk titled 'Eavesdropping goblet cell-microbiota crosstalk to decode secrets of mucus health' at the CCMB, Hyderabad, organized by AIN during 20th-22nd January, 2025.
3. Delivered an invited online lecture 'Communicating research Findings Through Poster Presentation' as a part of a workshop organised by Hansraj College, Delhi on 21st March 2025.
4. Participated in the Molecular Immunology Forum Meet 2024 at IISER Bhopal during 26th-28th September, 2024.
5. Delivered an invited talk titled 'Biotechnology as a means to combat health challenges' at ISTIC, Malaysia organized by UNESCO, duration of the 15th-17th May, 2024
6. Attended the 2nd HFSP Frontier workshop in 'Driving Innovation in Life Sciences: A role for AI' at the National Institute of Immunology, Delhi on 26th November, 2024.
7. Attended the Masterclass Course organised by HFSP at the National Institute of Immunology, Delhi during 27th-28th November, 2024.
8. Attended the Computational Biology Conference 2025 held at the Regional Centre for Biotechnology, Faridabad during 19th-21st February, 2025.

Prof. Manjula Kalia

1. Delivered an invited talk titled 'Mouse model in COMBAT' at Advancing Pandemic Preparedness: Innovative Multidisciplinary Strategies for COMBATing Severe Dengue, at the Karolinska Institute, Sweden, 3rd-4th February, 2025.
2. Delivered an invited talk titled 'STING generates a neuroprotective inflammatory response during JEV infection' at 6th Autophagy India Network meeting, Biology Across Scales: Insights from Microbes to Mice, at CSIR-CCMB, Hyderabad, 20th-22nd January, 2025.

Prof. Arup Banerjee

1. Delivered an invited talk titled 'Extracellular vesicles in viral infection: Insights into cargo and their role in disease progression and antiviral response' on the Workshop: Extracellular Vesicles: Isolation, Characterization, and Applications, at the Aravind Medical Research Foundation, Madurai, TN, on 24th -25th October, 2024.
2. Delivered talk titled 'Functional Diversity of Neutrophils in Dengue Virus Infection: A New Paradigm in Immune Modulation' on Molecular Immunology Forum meeting organised by IISER Bhopal 2024 (MIF 2024) on 26th-28th September, 2024.

Dr. Anil Thakur

1. Delivered a talk titled "Translation regulation of amino acid metabolism: A novel determinant of *Candida glabrata* pathogenesis." as a part of the RCB-THSTI seminar series on April 10th, 2024.
2. Participated in "Global Bio-India (GBI) at Pragati Maidan, New Delhi, with a focus on 'Biotech Innovation Ecosystem' and 'Bio-manufacturing" from September 12th-14th, 2024.

Prof. Avinash Bajaj

1. Delivered an invited talk entitled "Targeting of Triangular Neuron-Cancer Cell-Immune Cell Cross-talk as a Potential Cancer Immunotherapy Strategy" at the EMBO global lectures series at Shiv Nadar Institution of Eminence on 8th March, 2025.
2. Delivered an invited talk at National Conference-cum-Workshop on 'Sustainable Biotech Solutions for Global Challenges,' held at Jamia Hamdard, New Delhi, from 19th-21st February, 2025.
3. Delivered an invited talk at "Drug Discovery 2025: Emerging Trends and Future Prospects," held at the Centre for Interdisciplinary Research in Basic Sciences, Jamia Millia Islamia, New Delhi, on 24th-26th February, 2025.
4. Delivered an invited talk at the International Symposium on "Mitochondria, Apoptosis and Cell Death: Frontiers in Cancer Research" held at Jawaharlal Nehru University (JNU), New Delhi, on 17th-18th February, 2025
5. Delivered an invited talk entitled "Targeting of Triangular Neuron-Cancer Cell-Immune Cell Cross-talk as a Potential Cancer Immunotherapy Strategy" at Bose Institute, Kolkata on 14th Fenruary, 2025.
6. Delivered an invited talk at 5th International Global Cancer Conference on "Advances in Cancer and Cancer Immunotherapy" held at Amity University Noida, India from 29th-31st January, 2025.
7. Delivered an invited talk entitled "Localised Targeting of Nerve-Cancer Cell-Immune Cell Crosstalk for Mitigating Tumor Progression. at The Pan-IIT Meeting and Conference on Engineering in Medicine held at Indian Institute of Technology, Kanpur from 6th-8th December, 2024.
8. Delivered an invited talk entitled "Engineered Chimeric Nanomicelles Target the Tumor Microenvironment and Activate the T Cell Immunity." At 1st NIBMG Cancer Research Symposium, held on 24th September, 2024.
9. Delivered an invited talk entitled "Developing Strategies to Generate Systemic Immune Response against Tumour Microenvironment Using Engineered Biomaterials." at symposium entitled "Emerging Technologies and Materials in Medicine" held at Indian Institute of Technology, Kanpur from 3rd-4th May, 2024.
10. Delivered an invited talk entitled "Nanoparticle-mediated Gene Therapy Strategies for Mitigating Inflammatory Bowel Disease." at the National Conference on "RNA Based Therapeutics: Discovery to Clinic" held at Shiva Ji College, New Delhi from 25th-26th April, 2024.

Prof. Sivaram VS Mylavarapu

1. Delivered an invited lecture titled "A Deep-Dive into the Fascinating World of Tunneling Nanotubes" at Synapse '25, the Annual Life Sciences festival, organized by Synergia, the Life Science Society of Deshbandhu College, University of Delhi, on March 25th, 2025.
2. Organized and participated in several scientific and educational outreach events as part of the National Science Day celebrations at RCB, Faridabad, on February 28th, 2025.
3. Delivered an invited lecture titled "Preventing Illicit Traffic in our Cells: The Many Functions of Dynein" as a Resource Person in the 29th Refresher Course in Life Sciences & Biotechnology (Residential), organized by UGC-MMTTC, JNU on November 14th, 2024.

Dr. Rajender K Motiani

1. Delivered an invited talk titled 'Orai3 oncochannel: The master regulator of pancreatic cancer progression and chemoresistance' on the occasion of National Science Day at AIIMS, New Delhi, on 28th February, 2025.
2. Delivered an invited talk titled 'Calcium driven inter-organelle crosstalk: a master regulator of melanophagy' at the 6th Autophagy India Network (AIN) Meeting held at CSIR-Centre for Cellular and Molecular Biology (CCMB), Hyderabad, on 21st January, 2025.
3. Delivered an invited talk titled 'Zebrafish as an alternative animal model system for biomedical research' at the 6th Workshop on Basic Training in Animal Handling and Experimentation, Institute of Liver and Biliary Sciences (ILBS), New Delhi, on 17th December, 2024.
4. Delivered an invited talk titled 'Calcium driven inter-organelle crosstalk: a master regulator of skin pigmentation' at the 17th International Meeting of European Calcium Society at Cambridge University, Cambridge, UK, on 1st September, 2024.
5. Attended 17th International Meeting of European Calcium Society at Cambridge University, Cambridge, UK, 31st August to 4th September 2024.
6. Hosted B.Sc. and B.Ed. Students from Manav Rachna University for one day in our Lab, 18th November, 2024.

Dr. Karthigeyan Dhanasekaran

1. Delivered an invited talk titled "Centrosome and Cilia in Disease" in the Cilia ney Adda meeting held at IHS, Kolkata, April 2024.
2. Represented RCB in IISF-2024 held at IIT-Guwahati between 30th November-3rd December, 2024.

Dr. Saikat Bhattacharjee

1. Delivered an invited Seminar titled 'Inositol polyphosphate kinase activities regulate COP9 signalosome functions in Phosphate homeostasis' at the 'Interfaculty Plant Science Colloquium', organized by the Univ. of Bonn, Germany, on 30th January, 2025.
2. Delivered an invited Seminar titled 'Dynamics of a Plant Immune System: Intricate interplay between Immune Modulators and Signaling Messengers' at the '8th India Biodiversity Meeting (IBM)' at the 'Indian Statistical Institute (ISI), Kolkata', on 24th March, 2025.

Dr. Divya Chandran

1. Delivered an invited lecture entitled "The Remarkable World of Microbes: harnessing their power for sustainable living" as a part of the STEAM session at Shiv Nadar School, Faridabad, on 18th Novemver, 2024.
2. Delivered an invited lecture entitled "Decoding the molecular interplay between plants and a biotrophic fungal pathogen" as part of the New Phytologist Workshop organized by the New Phytologist Foundation and IISc Bengaluru on 17th October, 2024.
3. Delivered a motivational talk on Biotechnology at the Pre-orientation Program for BSc and MSc Biotechnology and Microbiology students at IMS Ghaziabad on 13th August, 2024.

Dr. Ramu S Vemanna

1. Attended the EMBO Lab Leadership Course at the National Centre for Biological Sciences-TIFR, Bangalore, organized by EMBO–excellence in life sciences, Germany, in coordination with India Biosciences from 21st- 24th October 2024.
2. Represented and coordinated RCB scientific activities at the "India International Science Festival (IISF), 2024, held at IIT Guwahati, Assam, from November 30th -December 3rd, 2024.
3. Delivered an invited talk titled "Gene editing technologies to create genetic variability to improve agronomic traits and crop protection" in a workshop on genome editing conducted at the National Genome Editing and Training Centre (NGETC)" organized by National Agri-Food Biotechnology Institute (NABI), Mohali, Punjab, from April 23rd-26th, 2024.

Dr. Prashant Mohan Pawar

1. Delivered an Invited talk titled "Enhancement of lignocellulosic biomass by finetuning plant cell wall structure" at Jaipur, organized by Manipal University, April 1st-3rd, 2024.
2. Delivered an invited talk titled "Improvement in plant cell wall properties through genetic engineering" at the Central University of Rajasthan, April 4th, 2024

Dr. Ambadas Rode

1. Delivered an invited talk entitled "Molecular engineering of functional nucleic acids for Biomedical applications at the RNA technology meeting, organised by IISC Bangalore, from 25th-26th October, 2024.
2. Delivered an invited talk entitled "Can targeting the viral genome RNA conformational ensemble lead to effective antiviral therapies? A case study of SARS-CoV-2" at the B or Not to B meeting at Kobe Portopia, organised by FIBER institute, Kobe, Japan, on 7th March, 2025.

Dr. Nidhi Adlakha

1. Delivered an invited talk titled "Biomanufacturing of specialty chemicals-a synthetic biology approach" organized by School of Biotechnology, JNU, held on 24th May, 2024.

Reviewer of proposals/thesis/research articles

Prof. Deepak T Nair

1. Reviewer for *Nucleic Acids Research, FEBS journal, Journal of Structural Biology & Protein Science.*
2. Examiner for PhD theses from IIT, TIFR, JNU, Manipal University, IISc, IISER and ACSIR.
3. Reviewed the performance of faculty/dean in other universities/institutes for promotion/continuation.

Prof. Vengadesan Krishnan

1. Reviewer for PhD thesis from the Indian Institute of Technology (IIT), New Delhi.
2. Reviewer for DBT grants.
3. Reviewer for *Archives of Microbiology, International Microbiology, International Journal of Biological Macromolecules, Frontiers in Cellular and Infection Microbiology, Vaccines, Acta Cryst F Structural Biology Communications, Biofouling, and Biophysical Chemistry.*

Dr. Prem Singh Kaushal

1. Reviewer for research manuscripts of *Nature Communications*, PhD thesis, and grants of DST-SERB & DBT.

Prof. Prasenjit Guchhait

1. Reviewer for R&D Proposals of DBT, BIRAC, DST, CSIR and ICMR, since 2015.
2. Reviewer for scientific journals: *Blood*, *eLife, Frontiers in Immunology, Emerging Microbes and Infections; Antioxidants and Redox Signaling; Frontier in Bioscience; Journal of Thrombosis and Thrombolysis; British Journal of Hematology; Haematologica; PLoS One; Journal of Immigrant and Minority Health; Scientific Reports*, since 2011.
3. Reviewer for PhD theses of 3 students of various Universities in India.

Prof. Tushar Kanti Maiti

1. Reviewers for *Biochemical J, Biomacromolecules, J. Proteomics, Bioscience Report, Int. J. Biol. Macromol., J. Proteome Research, ACS Chemical Neuroscience.*
2. Reviewer, ICMR and DBT grant proposal.
3. Reviewer PhD theses from JNU, AcSIR, IIT Delhi, NIPER Ahmedabad, and BITS Pilani.

Prof. Sam J Mathew

1. Reviewer for research proposals for DBT, CSIR, SERB, CEFIPRA, French Muscular Dystrophy Association (AFM-Telethon), Israel Science Foundation, Medical Research Council (UK), United Kingdom Research and Innovation (UKRI) and INSERM-CNRS (France).
2. Reviewer for PhD theses from AcSIR, IISc, JNU, and ILS.
3. Reviewer for *Nature Communications, Acta Physiologica, Cell Death and Disease, Developmental Biology, EMBO Molecular Medicine, FASEB Journal, Journal of Cell Science, FEBS Letters, Molecular Therapy, IUBMB Life, and Zoology.*

Prof. Chittur V Srikanth

1. Reviewer of PhD theses from IISc, JNU, NII, IIT-R and CDFD.
2. Reviewer for research grants of DBT, ICMR, DRDO, DST and HFSP.
3. Reviewer for Journals *mSpectrum, Communication Biology, Cell Reports.*

Prof. Manjula Kalia

1. Reviewer for *Nat. Comm, Autophagy, mBio, Journal of Virology, Science Signalling, Virus Research, Virology, Virus Disease.*

Prof. Arup Banerjee

1. Reviewer for Ph.D. Thesis from BHU, Calcutta University and IIT, Roorkee.

Dr. Anil Thakur

1. Reviewer of *Scientific Report* and *Journal of Pharmaceutical Research International.*
2. Reviewer for research proposal/grants for SERB-DST, DBT.

Prof. Avinash Bajaj

1. Reviewer, *American Chemical Society, Royal Chemical Society.*

Prof. Sivaram VS Mylavarapu

1. PhD thesis reviewer for theses from IISc Bengaluru, IISER Pune, University of Delhi, IACS Kolkata, CSIR-CCMB.

Dr. Rajender K Motiani

1. Reviewer of research proposals submitted to ICMR, DBT and Swiss National Science Foundation (SNSF).
2. Reviewer for the Journals: *iScience, Cell Calcium, Communication Biology, BBA-Molecular Cell Research and Cell Death & Differentiation.*
3. Ph.D. Thesis Examiner of Mr. Dayanidhi Singh and Ms. Vandana Singh, Institute of Genomics and Integrative Biology (IGIB), New Delhi.
4. Ph.D. Viva Examiner of Ms. Vandana Singh, Institute of Genomics and Integrative Biology (IGIB), New Delhi.

Dr. Karthigeyan Dhanasekaran

1. Reviewer for *IEEE Access, Cytoskeleton, Chem Comm, Academia Oncology.*
2. Screening committee member for Khorana Program for Scholars, November 2024.
3. Member of Question Paper Setting Committee for DBT GAT-B, January 2024.

Dr. Saikat Bhattacharjee

1. Reviewer for *Plant Mol. Biol., Physiol. Mol. Biol. Plants, Plant Cell Environ., Plant Cell Rep.*
2. Expert Reviewer for multiple DBT proposals.
3. Invited Member in the Fulbright-Nehru Doctoral Research Fellowships (STEM I) selection committee.
4. Reviewer of PhD theses from NIPGR (JNU), New Delhi and CSIR-IHBT, Palampur.

Dr. Divya Chandran

1. Invited Member, Screening Committee for Fulbright-Nehru Doctoral Research applications in Agricultural Sciences.
2. *Ad hoc Reviewer for Plant Physiology, World Journal of Microbiology and Biotechnology, Frontiers in Plant Science.*
3. Reviewer for Ph.D. thesis for BITS Pilani.

Dr. Ramu S Vemanna

1. Proposal reviewer- SERB, CRG Scheme, DBT.
2. Thesis evaluation titled "Understanding the molecular basis of essential oil biosynthesis in aromatic grasses (*Cymbopogon sp.*)" by Priyanka Gupta, CSIR-Central Institute of Medicinal and Aromatic Plants (CIMAP), Lucknow at AcSIR.
3. Manuscript Reviewer for *Plant Cell, Plant Biotechnology, Plant Physiology, Plant Molecular Biology Reporter, Tissue and Organ Culture, Plant Physiology Reports, Molecular Biotechnology, Frontiers in Plant Biology.*
4. Mentoring six (6) i3C-RCB PhD students in the immersion program at ATREE, Bengaluru.

Dr. Prashant Mohan Pawar

1. Reviewer for *Frontiers in Bioengineering and Biotechnology, Frontiers in Energy Research, Plant Physiology and Biochemistry, Physiologia Plantarum.*

Dr. Ambadas Rode

1. Reviewer for DBT- BioCARe, DST research grant proposals.
2. Reviewer for *Nature Communications, ChemBioChem, ACS Omega.*
3. Reviewer for PhD theses from IIT Bombay, BITS Pilani, and Mumbai University.

Dr. Nidhi Adlakha

1. Reviewer for research grants of DBT and CSIR.
2. Reviewer for *Applied and Microbial Technology and Infections and Biotechnology for Biofuels and Bioproducts.*


BRAHM

Extramural Activities & Networking

Indian Biological Data Centre (IBDC)

The Indian Biological Data Centre (IBDC) (URL: https://ibdc.dbtindia.gov.in) is the first national digital data repository mandated to archive all life science data generated from publicly funded research in India. It is supported by the Government of India (GoI) through the Department of Biotechnology (DBT). At present, IBDC is a joint collaboration between the Regional Centre for Biotechnology (RCB), the National Institute of Immunology (NII), the International Centre for Genetic Engineering & Biotechnology (ICGEB), and the National Informatics Centre (NIC). The Executive Director of RCB, Dr. Arvind Sahu, is the designated lead coordinator of the IBDC project, and the Director of NII, Dr. Debasisa Mohanty, is the co-coordinator. Dr. Dinesh Gupta from ICGEB and Prof. Deepak T. Nair from RCB are the other PIs in the project with the latter also serving as acting Head of IBDC.

The IBDC enables the implementation of the "Biotech-Pride Guidelines" (Promotion of Research and Innovation through Data Exchange). The computational infrastructure, including a High-Performance Computing (HPC) facility and archival data storage, is hosted at RCB and NIC, Bhubaneswar. RCB houses a computing power of about 961 Tera Flops (GPU+CPU) along with a 4.5 petaByte (PB) of storage, while NIC (Bhubaneswar) has a data storage capacity of about 1 PB. The two sites are connected by high-bandwidth internet connectivity through NKN. The biological data generated by researchers in India is being archived and curated at IBDC. The measures for routine and scheduled maintenance to ensure the proper functioning of the HPCC facility have been carried out on a timely basis. The centre was conceptualized by the DBT in 2019, the grant was approved in 2020, the first portal became online in 2021 and after complete installation of the sanctioned hardware, the centre was formally launched by the Honourable Minister for Science & Technology, Dr Jitendra Singh in November 2022.

Owing to the magnitude and complexity of the expected data, IBDC is being developed in a modular manner. Currently, IBDC operates through eight specialized data portals dedicated to the archival and sharing of diverse types of biological data (Figure 1).

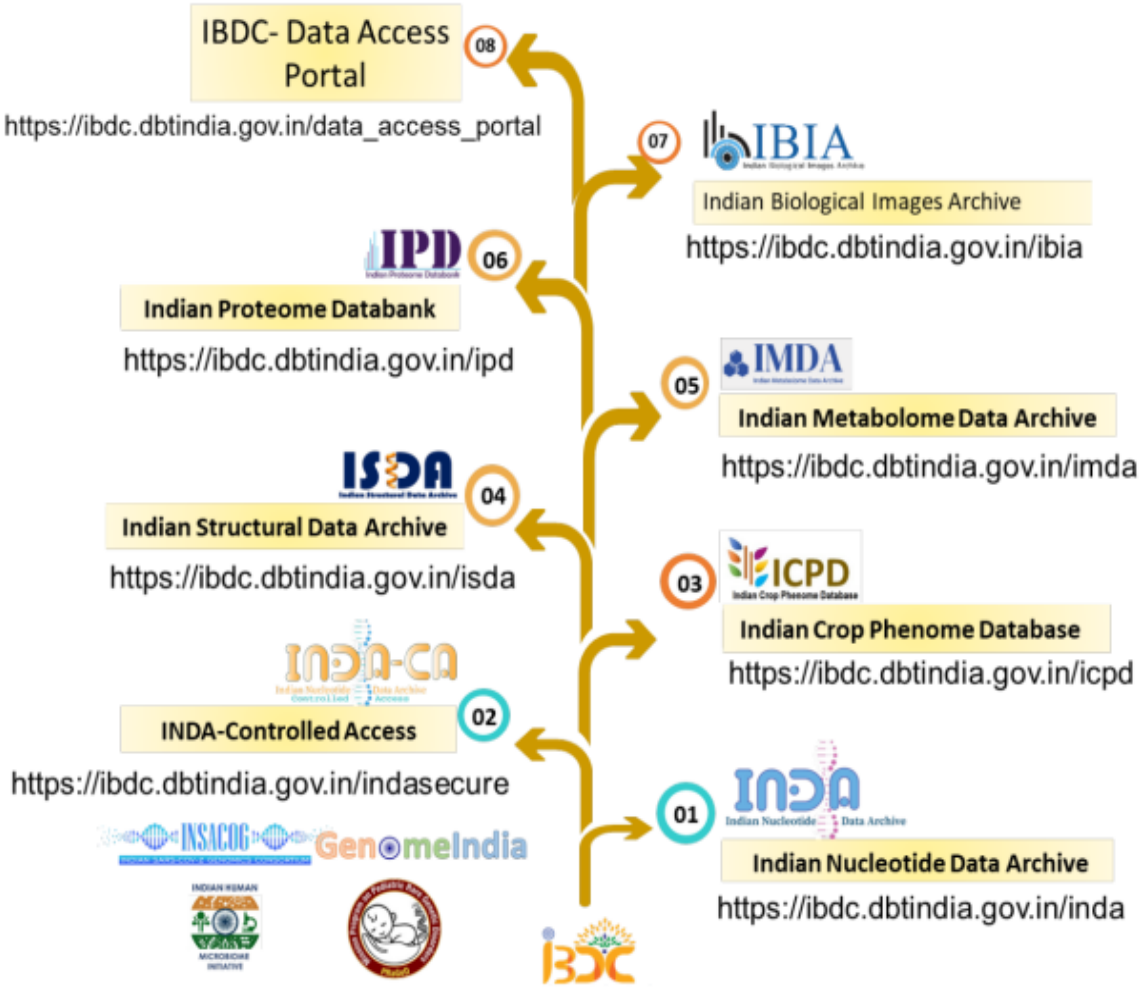

Figure 1. *Active portals of the Indian Biological Data Centre (IBDC)*

IBDC Statistics

Currently, IBDC has 6 Data submission portals, 1 data knowledge resource and 1 common data access portal for controlled/managed access submitted to IBDC. Total submissions of 545898 amounting to 1010 TB (~1 Petabyte), and the growth plot for submitted data is given in Figure 2. There are about 500 registered users of IBDC from different institutes/companies/organisations from 235 different locations spread across India (Figure 3).

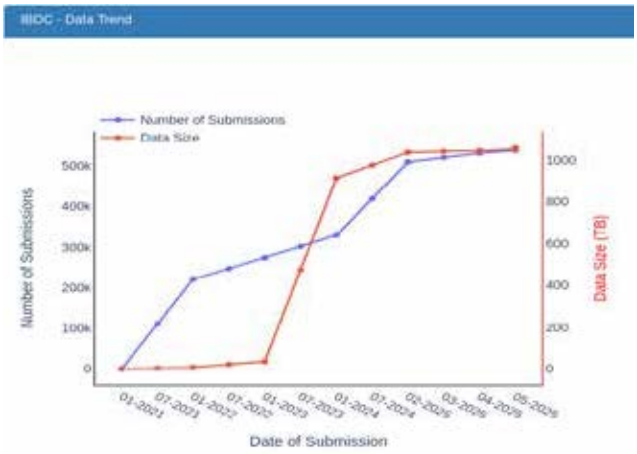

Figure 2: *Plot of cumulative number of submissions and size of data in IBDC since inception*

Indian Nucleotide Data Archive (INDA) (URL:https://ibdc.dbtindia.gov.in/inda/home): INDA is an open-access (Time-released) platform for archiving, managing, and sharing diverse types of nucleotide sequencing data generated across India. Data is synced with INSDC (The International Nucleotide Sequence Database Collaboration) repositories like GenBank-NCBI, ENA, and DDBJ. Submission to IBDC automatically generates both IBDC and INSDC (NCBI, ENA-EMBL, and DDBJ) accessions, and thus, there is no need to resubmit the data to international repositories (Figure. 4).

A total of 17643 Raw Data submissions, 162 Assembly submissions, and 741 annotated sequences have been submitted to IBDC from 278 different organisms, accounting for 57491760 million bases and 45 TB. Also, data from mission mode projects of Safflower, linseed, wheat and sesame have been submitted to INDA.

Figure 3: *Distribution of registered users in India. The dots specify locations of the registered users.*

Indian Nucleotide Data Archive-Controlled Access (INDA-CA) (URL:https://ibdc.dbtindia.gov.in/indasecure/home): INDA-CA is a controlled access platform for archiving and managing diverse types of nucleotide sequencing data (similar to INDA) generated across India. In contrast to INDA, data submitted to INDA-CA is not shared with any international repository and resides securely on servers in India (IBDC) only. Data accessibility in INDA-CA is defined as per Biotech PRIDE guidelines and FeED protocols. IBDC has also developed special submission tracks for projects of national relevance, such as INSACOG, INSACOG Sewage Surveillance, GenomeIndia and Indian Human Microbiome Initiative. Data from crop mission mode projects of Rice, Chickpea, Cow pea and Linseed have been submitted to INDA-CA. INDA-CA is also serving as a data hub for the Mission project on Paediatric Rare Genetic Disorders *(PraGeD)* data.

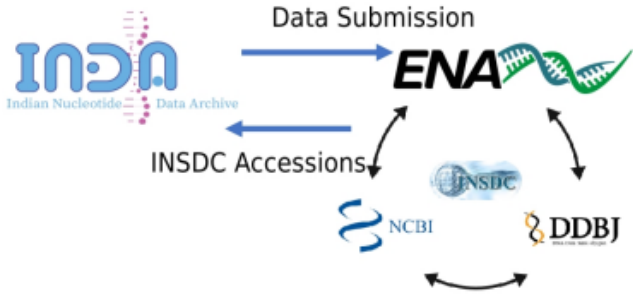

Figure 4. *Nucleotide data submission cycle at IBDC-INDA*

On the INDA-CA portal, 14341 submissions from 17 organisms have been received. A total of 259210 SARS-CoV-2 genomes from 60 different institutes have been submitted via the INSACOG portal, with a total of 1358 variants identified (Figure 5). The FASTA files from the INSACOG portal can be accessed by signing up to the portal. A total of 1180 SARS-CoV-2 sewage surveillance samples from five different institutes have been submitted via the INSACOG sewage surveillance portal. A total of 9768 GenomeIndia samples have been submitted to IBDC, which include VCF, UBAM, FASTQ files and phenotype data with a size amount around 900 TB (0.9 Petabytes). The data from the Indian Human Microbiome Initiative has also been deposited with 9833 samples.

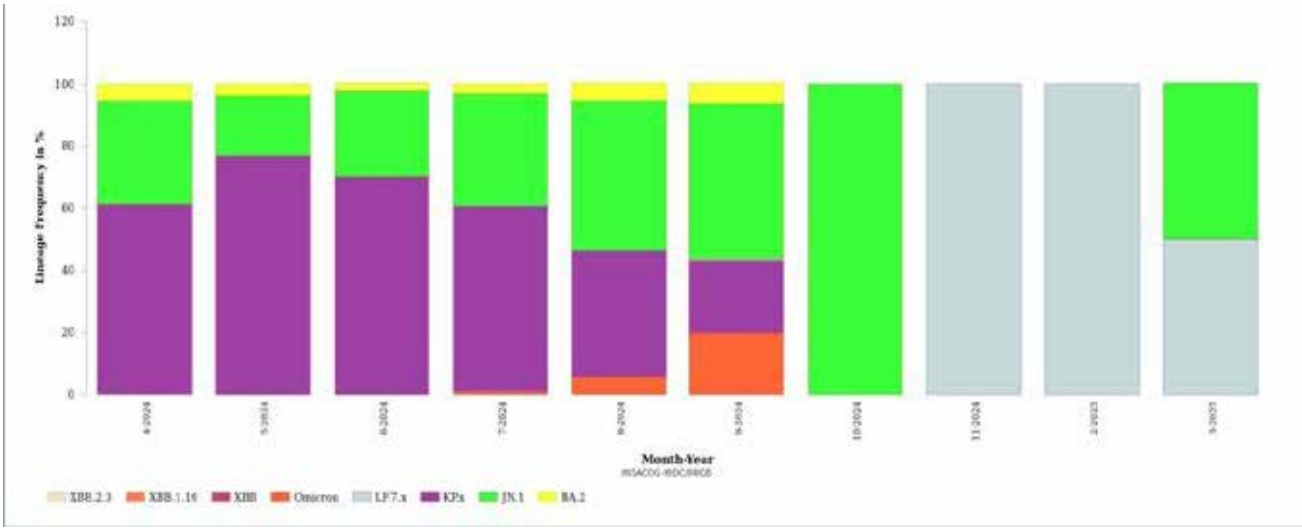

Figure 5: *Analysis of the data generated in the INSACOG project provides information of the prevailing SARS-CoV-2 variant in India. The month wise distribution of the lineage frequency of the virus for FY2024-25 is shown here.*

Indian Crop Phenome Database (ICPD) (URL:https://ibdc.dbtindia.gov.in/icpd/): ICPD is a dedicated domain of the IBDC to sustainably archive, manage, and share the diverse crop phenome data generated across India. In alignment with global standards, all data submissions to ICPD adhere to the Minimum Information About a Plant Phenotyping Experiment (MIAPPE) guidelines and follow the FAIR principles—ensuring data is Findable, Accessible, Interoperable, and Reusable. To support data standardization and semantic interoperability, ICPD uses well-established ontologies for traits, tissues, growth stages, and measurement methods. These ontologies enable consistent annotation, efficient search, and integration across diverse datasets. Each dataset receives a unique and persistent IBDC accession, enabling traceability and citation. ICPD supports both open and managed access submission modes and operates under a structured Creative Commons license (CC BY-NC-SA), which promotes ethical, non-commercial data reuse while ensuring proper attribution. Currently, ICPD has 71 registered users from 40 different organisations. At present, ICPD has 38 projects, 361 studies and 321 data files, including 38,26,746 genotype samples from 7 crops. This includes the data from 6 mission mode projects funded by DBT (Rice, Wheat, Safflower, Linseed, Chickpea and Sesame). 53 studies are under open access, and 331 are under managed access in ICPD. Data at ICPD consists of 70 different meta traits, including 325 traits, 66 tissues, 199 methods and 80 developmental stages. The data portal also provides personalised desktops for the users where they can view and download their studies. ICPD is routinely accessed by the research community (visitor count 1633) to browse and download (number of downloads = 2547) crop phenotype.

Indian Structural Data Archive (ISDA: https://ibdc.dbtindia.gov.in/isda/): ISDA is a highly integrated Structure-Function knowledge mining resource which connects experimental 3D structures of macromolecules (Proteins, Nucleic acids, and Complex Assemblies) and theoretical models with multiple resources of genetic mutations, functional annotations, and protein-ligand association network mapping. ISDA also contains curated structural data records of Indian origin with respective meta-information. At present, ISDA contains **237423** experimental structures (MX, NMR, and Cryo-EM, etc) and **871240** computational models (Alphafold models). To provide an interactive environment to the user, a JS-based visualizer is embedded to explore the structural features and polypharmacological bio-active molecules. The archive mirrors the data files present in the wwPDB and is updated on a weekly basis.

Indian Metabolome Data Achieve (IMDA: https://ibdc.dbtindia.gov.in/imda/) is an open-access platform for archiving, managing, and sharing metabolomics data and associated experimental metadata generated through analytical techniques such as Mass Spectrometer (MS) and Nuclear Magnetic Resonance (NMR). IMDA accepts targeted and untargeted data and metabolite structures identified in metabolomics experiments. IMDA database supports raw (d, raw, idb, netcdf, wiff, scan, dat, etc.) as well as derived (mzml, nmrml, mztab, mzxml, mzdat) file formats of metabolomics studies. The raw data can be uploaded in the form of binary files and processed data in the form of quantitated metabolite concentrations, MS peak height/area values, LC retention time, NMR binned areas, etc. A unique and persistent IBDC accession will be assigned on data submission to IMDA. At present, 55 users from 36 different Institutes/Universities are registered on the portal, 18 projects, 11136 samples and 2900 metabolites have been submitted from users across the country and with one international submission from Nepal.

Indian Proteome Databank (IPD: https://ibdc.dbtindia.gov.in/ipd/) is an open-access web portal to facilitate the submission, management, and dissemination of Mass Spectrometry-based proteomic data generated across experimental labs. The

Indian Proteome Databank (IPD) web portal was released in July 2024 and accepts both Complete and Partial submissions as mentioned in the Framework for Exchange of Data (FeED) protocol guideline for easy data submission and sharing. IPD supports different file formats, such as machine-generated raw files as well as processed identification result data files, such as mzIden/mztab. The user can submit the data either using the web-based protocol or the FTP-based protocol. The final submitted project will get a stable accession ID after submission validation. At present, 52 users from 25 different Institutes/ Universities are registered at the portal, and 103 projects have been submitted across the country.

Indian Biological Images Archive (IBIA: https://ibdc.dbtindia.gov.in/ibia/) is an open-access repository of biological images (generated at biological research institutes and hospitals). The IBIA aims to collect, store and disseminate all types of biological images including but not limited to multispectral and hyperspectral imaging, thermal imaging, microscopy images, agricultural images, unmanned aerial vehicle (UAV) images, digital X-ray, computed tomography (CT), magnetic resonance imaging (MRI), positron emission tomography (PET), ultrasound, histopathology and the associated metadata. The archive was released for public use in August 2024, since its launch, it has been widely used for biological image data submission and use. All types of biological image data submission can be done and shared with the IBIA users according to DBT's Framework for Exchange of Data (FeED) protocol guidelines.

At present, a total of 60 users from 40 different organizations [belonging to 12 states and a union territory (UT) of India], are registered at the IBIA portal. A total of 11 Projects containing 231751 images (Clinical Images: 177041; Plant Images: 54710; from 30 different organisms) in 11 Studies are deposited by 9 users from 9 different organizations. Of 231751 images, 230059 are publicly available with an "Open Access" license, whereas, 1692 images possess a "Managed Access" license type. The currently deposited five different types of imaging technologies data include image types such as histopathology, mammography, dry fruits, spices, plant diseases, etc. At present, the portal archives images from thirty different organisms including humans. To enhance the image visualization potential of the archive, an open-source image visualizer named "TissUUmaps", is integrated with IBIA for the visualization of image formats that are not supported by the browsers.

Data Access Portal (https://ibdc.dbtindia.gov.in/data_access_portal/): The Data Access Portal at IBDC provides a seamless platform for accessing managed access datasets by adhering to the Biotech-PRIDE guidelines for data access levels. With clearly defined access levels, the portal ensures secure and compliant data sharing. Featuring a user-friendly graphical interface, users can easily track the progress of their data access requests in real time. To ensure accountability, users are required to accept and comply with the terms and conditions outlined in the Biotech-PRIDE guidelines and the FeED Protocols before gaining access.

BIONODE (https://ibdc.dbtindia.gov.in/bionode/): A dashboard to analyse biological data termed as "BIONODE" was created to enable data-driven discovery and support the life science community across India with tools for genomics and structural bioinformatics. Soon, the platform will also house tools for biomanufacturing. The structural bioinformatics portal was utilized to conduct part of the Data Science practical module for the students of the RCB-BRIC-PhD and Post-Graduate Diploma in Industrial Biotechnology (PGDIB).

Upcoming Data Portals: Portals that archive phenome data (Indian Phenome Repository) and microarray-based data (Indian Array Data Archive) are currently under development.

Integration with DBT-CDAC integrated computing environment (ICE): DBT-CDAC has developed an integrated platform for online software development and analysis called ICE, which is hosted by IBDC (Figure 6). Through this platform, researchers can directly access the installed computing environment, open access data in IBDC, and other applications available under IBDC computing resources. At present, users of ICE use a separate entry point, and it has been proposed that ICE users may also have access to IBDC data sets through a seamless mount point. In this regard, ICE and IBDC will aim to come up with an authorisation protocol that will avoid multiple levels of entry and usage of IBDC datasets and aim to unify the licensing conditions wherever possible. Users of these platforms will be provided an API-based access through ICE with the same conditions as other IBDC users.

Figure 6: *CDAC developed the ICE-FLAKES module which is hosted at IBDC.*

The ICE platform was used to conduct part of the Data Science practical module for the students of the RCB-BRIC-PhD and Post-Graduate Diploma in Industrial Biotechnology (PGDIB). The practical module included basics of Linux, and hands on training of tools used for structural bioinformatics and genomics data analysis.

Data Analysis Service

In addition to data archiving services, IBDC also provides bioinformatics data analysis and access to 'BRAHM-HPC' to the research community upon request. Several research groups are already availing of the HPC storage service and analysis support. IBDC provided data analysis services (In-depth Whole whole-genome variant call and phylogenetic analysis, RNA-seq analysis, *de novo* genome assembly, MiRNA microarray data analysis, SARS-CoV-2 variant analysis, etc.) to 11 different research groups affiliated with 8 institutions. Now, IBDC is in the process of offering payment-based analysis services for users across India.

BRAHM HPC Access

A total of 68 principal investigators from 40 different organisations are using the IBDC HPCC (Table 1). On average, about 1900 jobs per month have been executed on BRAHM HPC by the users. IBDC is working on the implementation of a paid service model for HPC access to researchers across India.

Table 1. List of institutions of BRAHM HPC users.

1. AIIMS, Bibinagar, Telangana
2. AIIMS, New Delhi
3. B. R. Ambedkar Centre for Biomedical Research (ACBR), Delhi
4. Babasaheb Bhimrao Ambedkar University, Lucknow
5. Benette University, Noida
6. BRIC-Institute of Life Sciences (ILS), Bhubaneswar
7. BRIC-National Institute of Immunology (NII), New Delhi
8. BRIC-National Institute of Plant Genome Research (NIPGR), New Delhi
9. BRIC-Translational Health Science and Technology Institute, Faridabad
10. Central University of Himachal Pradesh, Kangra, Himachal Pradesh
11. Chaudhary Devi Lal University, Sirsa, Haryana
12. Chaudhary Ranbir Singh University, Jind, Haryana
13. CSIR-Centre for Cellular and Molecular Biology, Hyderabad
14. CSIR-Institute of Genomics and Integrative Biology, New Delhi
15. Department of Science and Technology, New Delhi
16. Govind Ballabh Pant Hospital (GIPMER), Delhi
17. Gujarat Biotechnology University (GBU), Gandhinagar, Gujarat
18. ICAR-Indian Agricultural Statistics Research Institute, New Delhi
19. ICAR-Research Complex for Eastern Region (RCER), Patna
20. ICMR-National Institute for One Health (NIOH), Nagpur
21. ICMR-National Institute of Virology (NIV), Pune
22. ICMR-Rajendra Memorial Research Institute of Medical Sciences (RMRIMS), Patna
23. ICMR-RMRC, Dibrugarh (Northeast Region), Assam
24. ICMR-RMRC, Sri Vijaya Puram (Andaman and Nicobar Islands)
25. Indian Institute of Engineering Science and Technology (IIEST), Shibpur, Howrah
26. Indian Institute of Science (IISc), Bengaluru
27. Indian Institute of Technology Delhi (IIT Delhi), New Delhi
28. International Centre for Genetic Engineering and Biotechnology (ICGEB), New Delhi
29. Jamia Islamia, New Delhi
30. Jawaharlal Nehru University (JNU), New Delhi
31. Jaypee Institute of Information Technology, Noida
32. King George's Medical University (KGMU), Lucknow
33. Madurai Kamraj University, Madurai
34. National Institute of Pharmaceutical Education and Research (NIPER), Kolkata

35. Regional Centre for Biotechnology (RCB), Faridabad
36. St. Xavier's College, Kolkata
37. University of Delhi, Delhi
38. University of Jammu, Jammu
39. University of Madras, Chennai
40. Vellore Institute of Technology, Vellore

To guide and explain to the users the submission process of data to IBDC portals database-specific SOPs, the HPC request form and BRAHM-HPC access guide and video tutorials are made available on the IBDC website under tutorials-SOP section (https://ibdc.dbtindia.gov.in/tutorial-sop/). Further, IBDC support (support@ibdc.rcb.res.in) dedicatedly handles all user-specific queries and service requests.

Workshops and Webinars

To spread the word about the activities of IBDC, training and workshops are conducted on a regular basis for data submission (nucleotide data, phenome data, INSACOG data, and GenomeIndia data); IBDC BRAHM HPC Usage and data analysis discussions. As of now, a total of 123 workshops with more than 1111 participants associated with 92 institutions have been successfully conducted. The map showing the distribution of institutions is shown in Figure 7. Apart from the workshops, the monthly webinar series has been successfully completed with 7 online webinars on IBDC and its different data portals, joined by 1324 participants from institutions across India. All the webinars are available at the IBDC website and its YouTube account (https://www.youtube.com/@IBDC-RCB)

Figure 7: *Location of institutions that participated in IBDC workshops.*

Conferences

The 1st Computational Biology Conference (CBC 2025), conducted by the Indian Biological Data Centre (IBDC) of the Regional Centre for Biotechnology (RCB), Faridabad, took place from February 19–21, 2025. This inaugural conference served as an interdisciplinary forum for computational biologists, bioinformaticians, researchers, and industry experts to discuss emerging trends, exchange innovations, and foster collaborations in computational biology and bioinformatics. The conference gathered 200 participants from 5 countries, including India, USA, Australia, UK and Israel (Figure 8). There were seminars by 19 world-renowned computational biologists, representatives of the Department of Biotechnology, and industry partners. The conference also included 67 poster presentations by researchers from 50 organisations across 20 states of India. The four best posters have been awarded the Best Poster Award after the evaluation by the jury. This event was supported by the generous grants from the CTEP Program of the Department of Biotechnology, Anusandhan National Research Foundation (ANRF) and Council of Scientific & Industrial Research (CSIR-HRDG). Furthermore, the event was supported by sponsorship from AWS, Netweb, DDN, Locuz, IRTech, RGInformatics and Schrodinger. The next edition of the conference- Computational Biology Conference 2.0 (CBC2.0) is planned for December, 2025.

Figure 8: *Group photograph of all the participants of the CBC2025 conference.*

IBDC Team

Team IBDC comprises experts from diverse disciplines, including different domains of biological sciences, bioinformatics, information technology, etc (Table 2). A total of 29 personnel are currently working in IBDC and trained extensively in various IBDC activities (Figure 9).

Figure 9: *Group photograph of all the IBDC personnel*

Collaborators of Faculty Members

RCB Principal Investigator	Collaborators
Prof. Deepak T Nair	Prof. D. N. Rao (IISc, Bangalore), Dr. Arvind Sahu (RCB) Dr. Dinakar M. Salunke (ICGEB, New Delhi), Prof. Sudhanshu Vrati (RCB), Dr. VG Vaidyanathan (CSIR-CLRI, Chennai), Dr Sangeeta Sawant (SPPU, Pune) and Dr. Shailendra Asthana (THSTI, Faridabad).
Prof. Vengadesan Krishnan	Dr. Priti Saxena (SAU, New Delhi), Dr. Amit Kumar Pandey (THSTI, Faridabad), Dr. Airi Palva's group (University of Helsinki, Finland), Dr. RP Roy (RCB, Faridabad).
Prof. Deepti Jain	Prof. Sudhanshu Vrati, Prof. Deepak T Nair, Dr. Divya Chandran, Ambadas Rode (RCB), Niranjan Chakraborty (NIPGR).
Dr. Prem Singh Kaushal	Prof. Ruchi Anand (IIT Bombay), Prof Ajay Saxena (JNU), Prof. Nisheeth Agarwal (THSTI), Prof. N. Gourinath (JNU) and Dr. Javid Yusuf Bhat (Kashmir University).
Prof. Prasenjit Guchhait	Prof. Mortimer Poncz (Children's Hospital of Philadelphia, USA), Dr. Niluka Goonawardane (University of Leeds, UK), Dr. Asley St. John (Duke-NUS Medical School, Singapore), Dr. Sumana Sanyal (University of Oxford, UK), Prof. Josef T Prchal (Univs of Utah, USA), Prof. Perumal Thiagarajan, Prof. Miguel M Cruz (Baylor College of Medicine, USA), Prof. Jorge Di Paola (Washington Univs, St Louis, USA), Prof. Anil Chauhan (Iowa University, USA), Prof. Tulika Seth, Prof. Aashish Choudhary, Dr. Megha Brijwal (AIIMS, New Delhi), Prof. Parvaiz Kaul (SKIMS, Srinagar), Prof. Tashi Thinlas, Dr. Tsewang Chorol, (SNM Hospital, Leh), Prof. Anil K Pandey, Dr. Nikhil Verma, Dr. Priyanka Sharma, Dr. Pooja Pandey (ESIC Hospital, Faridabad), Prof. Asim Das (ESIC Hospital, Alwar), Dr. Shailendra Asthana, Dr. Milan Surjit, Dr. Sailendra Mani, Prof. Amit Awasthi, Prof. Bhabatosh Das (THSTI, Faridabad), Dr. Soumen Basak (NII, New Delhi), Dr. Garima Agarwal (IIT, Mandi).
Prof. Tushar K Maiti	Dr. Shinjini Bhatnagar, Dr. Bhabatosh Das, Dr. Nitya Wadhwa, Dr. Pallavi Kshetrapal (THSTI, Faridabad); Dr. Partha P Majumder, Dr. Arindam Maitra (NIBMG, Kalyani, West Bengal); Dr. Dinakar M Salunke and Dr. Neel Sarovar Bhavesh (ICGEB, New Delhi); Dr. Prasenjit Guchhait, Dr. Sam Mathew, Dr. Sivaram Mylavarapu, Dr. Manjula Kalia, Dr. Prem Kaushal, Dr. Karthigeyan Dhanasekaran (RCB); Dr. Sobhan Sen (JNU, New Delhi); Dr. Hrishikesh Kumar and Dr. Supriyo Choudhury (Institute of Neuroscience Kolkata); Dr. Matthias Mann, Max Planck Institute of Biochemistry, Martinsried, Germany.
Prof. Sam J Mathew	Dr. Tushar Maiti (RCB, Faridabad), Dr. Manoj Menon (IIT, New Delhi), Dr. Munia Ganguli (IGIB, New Delhi), Dr. Janvie Manhas (AIIMS, New Delhi), Dr. Jayanth Kumar (AIIMS, New Delhi), Dr. V. Y. Vishnu (AIIMS, New Delhi), Dr. Gargi Bagchi (Amity University, Gurugram), Dr. Vivek Natarajan (IGIB, New Delhi), Dr. Samarendra Singh (Banaras Hindu University, Varanasi), Dr. Richa Shrivastava (BITS, Pilani)
Prof. Sudhanshu Vrati	Dr. Renu Wadhwa (AIST, Japan), Dr. Sanjay Batra (CDRI, Lucknow).
Prof. Chittur V. Srikanth	Dr. Vineet Ahuja, Gastroenterology, AIIMS, Delhi, Dr. Girish Ratnaparkhi, IISER, Pune, Dr. Pramod Garg, THSTI, Faridabad, Dr. Sujoy Paul, Gastroenterology, AIIMS, Delhi, Dr. Prasenjit Das, Gastroenterology, AIIMS, Delhi, Dr. Rashna Bhandari, CDFD, Hyderabad, Dr. Ramandeep Singh, THSTI, Faridabad.
Prof. Manjula Kalia	Dr. Dinesh Mahajan (THSTI), Dr. Santosh Chauhan (CSIR-CCMB), Dr. Krishnan H. Harshan (CSIR-CCMB), Dr. Shailendra Asthana (THSTI).

Prof. Arup Banerjee	Dr. Sujata Mohanty (AIIMS, New Delhi), Dr. Anirban Basu (NBRC, Manesar), Dr. Sweety Samal (THSTI, Faridabad), Tushar K Maiti (RCB), Samrat Chatterjee (THSTI).
Dr. Anil Thakur	Dr. Alan G. Hinnebusch (NIH, USA), Dr. Ishaan Gupta (IIT – Delhi), Dr. Rekha Puria (GBU Greater Noida).
Prof. Avinash Bajaj	Dr. Sagar Sengupta, Dr. Vinay Nandicoori, Dr. Arnab Mukhopadhyay, Dr. Santiswarup Singha, and Dr. Veena S Patil (NII, New Delhi), Dr. Ujjaini Dasgupta and Dr. Rajendra Prasad (Amity University Haryana), Dr. Aasheesh Srivastava (IISER Bhopal), Dr. Prasenjit Das, Dr. Vineet Ahuja, Dr. Shalimar and Dr. Sunil Kumar (AIIMS, New Delhi), Dr. C. V. Srikanth and Dr. Ramu Vemanna (RCB, Faridabad).
Prof. Sivaram VS Mylavarapu	Dr. Sourav Banerjee, NBRC Manesar; Dr. Anjana Saxena, CUNY USA; Dr. Megha Kumar, CSIR-CCMB Hyderabad; Dr. Amitabha Mukhopadhyay, IIT Delhi, New Delhi; Dr. Tushar K Maiti, Dr. Sam J Mathew, Dr. Prasenjit Guchhait, Dr. Manjula Kalia, Dr. Karthigeyan Dhanasekaran, Dr. Prem S Kaushal (all RCB Faridabad).
Dr. Rajender K Motiani	Dr. Manjula Kalia (RCB, Faridabad), Dr. Tushar K Maiti (RCB, Faridabad), Dr. Prasenjit Guchhait (RCB, Faridabad), Dr. Mahesh Kappanayil (Amrita Institute of Medical Sciences, Kochi) Dr. Subhragshu Chatterjee (Bose Institute, Kolkata), Dr. Shantanu Chowdhury (IGIB, New Delhi), Dr. Pramod Garg (AIIMS, New Delhi), Dr. Deepika Uikey (ESIC Hospital, Faridabad), Dr. Sumit Pal Singh (Shiv Nadar University) and Dr. Santosh Chouhan (CCMB, Hyderabad).
Dr. Karthigeyan Dhanasekaran	Dr. Soumik Siddhanta (IIT-Delhi), Prof. Sudhanshu Vrati (RCB, Faridabad), Prof. Tushar K Maiti (RCB, Faridabad), Dr. Santosh Kumar (NCCS, Pune), Dr. Madhuri Subbiah (NIAB, Hyderabad).
Dr. Saikat Bhattacharjee	Dr. Girish TR & Sailaja Nori (Sea6 Energy Pvt. Ltd., Bengaluru), Dr. Souvik Bhattacharjee (JNU, New Delhi), Dr. Nimisha Sharma (GGSIPU, New Delhi), Dr. Ramu Vemanna (RCB, Faridabad), Dr. Prashant Pawar (RCB, Faridabad), Dr. Debabrata Laha (IISc, Bengaluru), Dr. Vipin Hallan (CSIR-IHBT, Palampur), Dr. Subhra Chakraborty (NIPGR, New Delhi), Dr. Gabriel Schaaf (University of Bonn, Germany), Prof. Stan Gelvin (Purdue University, USA).
Dr. Divya Chandran	Dr. Senjuti Sinharoy, Dr. Senthil Kumar Muthappa (NIPGR, New Delhi), Dr. Bonamali Pal (Thapar Institute of Engineering and Technology, Patiala), Dr. Archana Chugh (IIT Delhi), Dr. Deepti Jain (RCB, Faridabad).
Dr. Ramu S Vemanna	Dr. Kiran Mysore, (Oklahoma state university, USA), Dr. Prasanna Kumar M (University of Agricultural Sciences, Bangalore), Dr. Avinash Bajaj, Dr. Saikat Bhattacharjee (RCB), Dr Tushar Maiti (RCB).
Dr. Prashant Mohan Pawar	Dr Yashwant Kumar (THSTI), Dr New Delhi), Dr Ewa Mellerowicz (SLU Sweden), Dr Jeongim Kim (University of Florida, USA).
Prof. Rajendra P Roy	Dr. Vengadesan Krishnan (RCB, Faridabad)
Dr. Ambadas B Rode	Prof. Sheshnath Bhosale (Central University of Karnataka), Dr. Milan Surjit (THSTI, Faridabad).
Dr. Nidhi Adlakha	Dr. Syed Shams Yazdani (ICGEB, New Delhi), Dr. Charanpreet (NABI, Mohali), Dr. Tarun Sharma (GBU, Gujarat), Prof. Rakesh Bhatnagar (JNU, New Delhi)

Extramural Funding

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Ministry of Science & Technology
Government of India

EMBO

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Extramural Funding

S.No.	Investigator	Project title	Funding Agency	Grant Amount (Rs.)	Duration
1.	Prof. Deepak T Nair	Renewal of access to Structural Biology Facilities at ESRF, France.	DBT	2639.8 lakhs	2021-24
2.	Prof. Deepak T Nair	Identification of lead molecules for the development of novel therapeutic strategies against viruses.	DBT	242.7 lakhs	2022-27
3.	Prof. Deepak T Nair	Chemical synthesis of adducts induced by 3-nitrobenzanthrone and evaluation of the effect of these adducts on natural DNA synthesis.	ANRF	15 lakhs	2022-25
4.	Prof. Deepak T Nair	Structural Insight regarding the interaction between the processivity clamp and DNA polymerase I in prokaryotes.	ANRF	47 lakhs	2023-26
5.	Prof. Vengadesan Krishnan	Elucidating the Structural characteristics of pilus components from *Enterococcus faecalis*, an opportunistic pathogen of the Urinary tract .	DBT	49.7 lakhs	2022-25
6.	Prof. Deepti Jain	Structural and functional Analysis of FlhF: A signal recognition particle (SRP) type GTPase involved in flagellar localization in *Pseudomonas aeruginosa.*	ANRF	53.6 lakhs	2024-27
7.	Prof. Deepti Jain	Investigating the mechanism of regulation of flagellar gene expression by FliA-FlgM and FliA-RNAP complex from *Pseudomonas aeruginosa:* Implication in pathogenesis and virulence.	ANRF-Power fellowship	35 lakhs	2023-26
8.	Prof. Deepti Jain	Antibiotic tolerance And Resistance In Biofilm-Associated Infections: A Belgian-Indian Networking Approach to Address a Worldwide Problem - A joint Indo-Belgian Network.	Indo-Belgian Networking Grant, DBT	35 lakhs	2022-26
9.	Prof. Deepti Jain	Targeting Bacterial Motility and Adherence for Inhibition of Biofilms from *Pseudomonas aeruginosa.*	DBT	84.6 lakhs	2022-25
10.	Dr. Prem S Kaushal	EMBO Global Investigator Network Fellowship	EMBO	2800 euros	2025-28
11.	Dr. Prem S Kaushal	Understanding the role of HspX protein from *Mycobacterium tuberculosis* in translation regulation: its implication in structure-based drug design.	ANRF	42.61 lakhs	2023-26
12.	Dr. Prem S Kaushal	Exploring the *Entamoeba histolytica* ribosome as a potential drug target to treat amoebiasis.	DBT	94.17 lakhs	2023-26

13.	Dr. Prem S Kaushal	Identification of small molecule inhibitors of SARS-CoV-2 non-structural protein 1 (Nsp1) for the treatment of COVID-19.	CSIR	24 lakhs	2023-26
14.	Prof. Prasenjit Guchhait	Dietary Alpha-ketoglutarate as a potential therapeutic against acute respiratory distress syndrome (ARDS) and pulmonary fibrosis in Covid-19 infection.	BIRAC, DBT	49.5 lakhs	2023-25
15.	Prof. Prasenjit Guchhait	Investigating the severity of dengue infection in diabetes	ICMR	149.5 lakhs	2023-26
16.	Prof. Prasenjit Guchhait (Co-PI)	Lethal Aortopathy syndrome associated with novel FBLN4D203A Mutation among Mappila Children of Malabar, Kerala - seeking novel clinical, molecular genetics and anthropological insights.	ICMR	149.5 lakhs	2023-26
17.	Prof. Prasenjit Guchhait	Investigating the role of platelet factor 4 and CXCR3 in dengue infection in mice with/without diabetes.	DBT	62 lakhs	2024-27
18.	Prof. Prasenjit Guchhait (organizer)	To host the India EMBO Lecture Course at RCB, Faridabad on "RNA viruses and host immune response"	EMBO	45000 euros	For 2026
19.	Prof. Tushar K Maiti	Inter-Institutional Program for Maternal, Neonatal and Infant Sciences: A translational approach–Interdisciplinary Group for Advanced Research on BirtH outcomes-DBT INdia Initiative (GARBH-Ini Phase II).	DBT	138.4 lakhs	2021-26
20.	Prof. Tushar K Maiti	MOMI Ideas Fund 2021: N-linked glycosylation in gestational diabetes mellitus.	BMGF	57.9 lakhs	2022-25
21.	Prof. Tushar K Maiti	MOMI scale up nutritional and multi-omics analysis (Phase III)	BMGF	226.5 lakhs	2025-27
22.	Prof. Tushar K Maiti	Generation of a reference database for total proteome analysis of selected bacterial pathogens and validation studies using the LC-HRMS platform	DRDE	48.8 lakhs	2024-26
23.	Prof. Sam J Mathew	Functional characterization of skeletal muscle myosin heavy chain-embryonic in adult muscle regeneration and disease.	DBT	77 lakhs	2020-24
24.	Prof. Sam J Mathew	The Wnt signaling pathway and its repressor Transducin-like Enhancer of Split 3 (TLE3) as therapeutic targets to treat Rhabdomyosarcoma tumors	ICMR	54 lakhs	2021-24
25.	Prof. Sam J Mathew	Regulation of mammalian growth, homeostasis and differentiation by Transducin-like Enhancer of Split (TLE) proteins.	ANRF	53 lakhs	2022-25

26.	Prof. Sam J Mathew	Generation and characterization of a pre-clinical model for the India-specific Agarwal founder mutations in Limb Girdle Muscular Dystrophy Type 2A	ICMR	125 lakhs	2025-28
27.	Prof. Sam J Mathew and Dr. Manoj Menon	Sensitizing cells to the chemotherapeutic SMAC mimetics and investigating the dependence on cellular differentiation	RCB-IIT Delhi collaborative project proposal scheme	10 lakhs per year (5 lakhs per year for RCB)	2023-24
28.	Dr. Masum Saini (Mentor: Prof. Sam J Mathew)	Role of Sprouty2 as a modulator of MET signaling during mammalian skeletal muscle development, regeneration and disease.	Wellcome Trust/DBT India Alliance Early Career Fellowship	167 lakhs	2018-24
29.	Prof. Sudhanshu Vrati	Development of small molecule antivirals against Chikungunya and Japanese encephalitis virus.	DBT	480.7 lakhs	2020-25
30.	Prof. Sudhanshu Vrati	Genomic Surveillance for SARS-CoV-2 in India: INSACOG - Phase II	DBT	628 lakhs	2022-24
31.	Prof. Chittur V. Srikanth & Dr. Girish Ratnaparkhi	From the gut SUMO cycles its way into gastrointestinal disorders.	MHRD	93 lakhs	2020-24
32.	Prof. Chittur V. Srikanth & Dr Vineet Ahuja	Studying the mechanism of Rab7 based regulation of Goblet cell function in Ulcerative colitis.	DBT	87 lakhs	2023-26
33.	Prof. Chittur V. Srikanth	Studying the crosstalk between microbiota and intestinal goblet cells in ulcerative colitis.	ICMR	120 lakhs	2025-28
34.	Prof. Chittur V. Srikanth (i3C BRIC-RCB PhD collaborative project)	Polyphosphate signaling in regulation of microbial pathogenesis, inflammation and immunity.	DBT	50 lakhs	2025-28
35.	Dr. Chittur V. Srikanth (PI), Dr. Tushar Maiti (Co-PI)	Mechanistic studies on SUMOylation and Salmonella intracellular pathogenesis.	DBT	73.5 lakhs	2024-27
36.	Prof. Manjula Kalia	Role of Guanylate-binding proteins and Gasdermin D in the inflammatory response to Japanese encephalitis virus infection and link to pyroptotic cell death.	ANRF	48.8 lakhs	2021- 25
37.	Prof. Manjula Kalia	Establishment of Centre for Advanced Research for Rapid Development of Host-directed broad Antivirals (Multi-Institutional).	ICMR	140 lakhs	2024- 29
38.	Prof. Arup Banerjee	Assessing the efficacy of engineered extracellular vesicles targeting NLRP3 inflammasome in the neuroinflammatory disease model.	ICMR	55 lakhs	2024-27

39.	Prof. Arup Banerjee	Understanding the impact of dengue virus infection on myeloid cell differentiation in bone marrow and its implications in disease outcome.	ANRF	61 lakhs	2024-27
40.	Dr. Anil Thakur	Translation dynamics govern fungal virulence and drug resistance in Candida species	DBT	42.5 lakhs	2020-25
41.	Dr. Anil Thakur	"Genetic and translational landscape of Candida glabrata pathogenesis for identification of novel antifungal drug targets	ANRF	44.9 lakhs	2023-26
42.	Dr. Anil Thakur	Deciphering the drug sensing pathway/s for the development of a therapeutic regime against multidrug-resistant fungus *Candida auris*	ANRF	59.8 lakhs	2024-27
43.	Prof. Avinash Bajaj	Engineering of Long-lasting Breast Hydrogel Implants for Cancer Immunochemotherapy.	DBT	95.5 lakhs	2023-26
44.	Prof. Avinash Bajaj	Synthesis and Identification of Antibiotic Adjuvants for Mitigation of Pan-resistant Gram-negative Bacterial Infections.	DBT	80.5 lakhs	23-26
45.	Prof. Avinash Bajaj	Developing Repertoire of Orally Deliverable Phospholipid-Drug Conjugates (PDCs) for Targeting Colorectal and Hepatocellular Carcinoma.	ANRF	67.8 lakhs	23-26
46.	Prof. Avinash Bajaj	Repurposing and Validating the FDA-approved UDP-Glucose Ceramide Glucosyltransferase (UGCG) Inhibitor "Eliglustat" as a Potential Intervention for Breast and Oral Cancer Immunotherapy.	ICMR	103 lakhs	25-28
47.	Prof. Avinash Bajaj	Elucidating the Role of Ceramide Kinase in Cancer Cell-Macrophage Cross-talk in Tumor Microenvironment and Build New Therapeutic Strategies for Breast and Oral Cancer Treatment.	ICMR	55.2 lakhs	25-28
48.	Prof. Sivaram VS Mylavarapu	Understanding the role of transgelin-2 in cell division.	ANRF	57.3 lakhs	2022-25
49.	Dr. Rajender K Motiani	Role of ER and Mitochondria in Pigmentation: Organellar Calcium signaling perspective.	DBT/ Wellcome Trust India Alliance	360 lakhs	2020-25
50.	Dr. Rajender K Motiani	Demystifying the mystery of Orai3 function in pancreatic cancer: Elucidating role of Orai3 in partial EMT and chemoresistance.	SERB	64 lakhs	2024-27

51.	Dr. Rajender K Motiani (PI), Dr. Mahesh Kappanayil (Amrita Institute of Medical Sciences, Kochi; PI) and Prasenjit Guchhait, RCB (Co-PI)	Lethal Aortopathy syndrome associated with novel FBLN4D203A Mutation among Mappila Children of Malabar, Kerala - seeking novel clinical, molecular genetics and anthropological insights.	ICMR (In collaboration)	150 lakhs (RCB share 56 lakhs)	2024-27
52.	Dr. Rajender K Motiani	Deciphering the molecular mechanisms that drive Orai3 expression and regulate Orai3 mediated pancreatic cancer progression.	DBT	82 lakhs	2025-28
53.	Dr. Karthigeyan Dhanasekaran	Centrosome as a target for viral pathogenesis intervention.	DBT-RLF	42.5 lakhs	2021-26
54.	Dr. Karthigeyan Dhanasekaran (Co-PI) Dr. Soumik S (Co-PI)	Tracking protein dynamics in cells using clusteroluminescence.	IITD-RCB	10 lakhs	2023-25
55.	Dr. Karthigeyan Dhanasekaran (Co-PI) Dr. Soumik S (PI)	Tracking protein dynamics in cells using clusteroluminescence.	ANRF	12 lakhs	2024-27
56.	Dr. Saikat Bhattacharjee (Co-PI) Dr. Souvik Bhattacharjee, JNU (PI)	Translating the Phylogenetic affinities between a plant pathogenic oomycete *Phytophthora infestans* and a human pathogen *Plasmodium falciparum* to reveal evolutionary convergence in virulence secretion using *In-silico*, proteomic and metabolomics approaches.	ANRF	9.9 lakhs (RCB)	2021-24
57.	Dr. Saikat Bhattacharjee (PI)	Characterization of a novel post-transcriptional/translational mode of plant immune surveillance and evasive strategies deployed by a class of rapidly evolving and economically threatening pathogen effector.	ANRF	44.9 lakhs	2023-26
58.	Dr. Saikat Bhattacharjee (PI) Dr. Souvik Bhattacharjee, JNU (Co-PI)	Deciphering Inositol polyphosphate roles as crosstalk modulators of (a)biotic stress adaptation and biotechnological application of underlying signaling routes to improve defense response and nutritional uptake in plants.	DBT	80 lakhs	2024-27
59.	Dr. Divya Chandran (PI, RCB) (PI and Project Coordinator: Dr. Senjuti Sinharoy; Co-PI: Dr. Senthil-Kumar Muthappa, NIPGR)	Generation of a retrotransposon-based mutant population of chickpea for functional genomics studies.	DBT	128 lakhs (RCB share 39.10 lakhs)	2022-25

60.	Dr. Divya Chandran (PI, RCB) (PI: Dr. Bonamali Pal, Thapar Institute of Engineering and Technology)	Nanocarriers for topical delivery of pathogen-specific RNAi molecules for sustained protection of pea crop against powdery mildew.	DBT	63.5 lakhs (RCB share 38.3 lakhs)	2021-25
61.	Dr. Divya Chandran (Co-PI: Dr. Deepti Jain, RCB)	Elucidation of the functional interactome of legumes with the fungal pathogen Erysiphe pisi as keys to powdery mildew disease resistance.	ANRF	44 lakhs	2020-24
62.	Dr. Divya Chandran (PI, RCB) (PI: Dr. Archana Chugh, IIT Delhi)	Latarcin-derived membrane-active peptides for powdery mildew disease management in leguminous crops.	RCB-IITD	20 lakhs (RCB share 10 lakhs)	2023-25
63.	Dr. Ankita Alexander (mentor Dr. Divya Chandran)	Elucidating the metabolic signatures delineating symbiotic and pathogenic legume-microbe interactions.	MK Bhan Fellowship	87 lakhs	2023-26
64.	Dr. Ramu S Vemanna (PI), Dr Avinash Bajaj, Dr Saikat Bhattacharjee, Dr Prashant Pawar (Co-PIs)	Nanogel-mediated Gene Editing (CRISPR/Cas9) Technologies to Improve Crop Protection against Bacterial Leaf Blight in Rice.	DBT	118 lakhs	2022-25
65.	Dr. Ramu S Vemanna (PI), Dr Saikat Bhattacharjee (Co-PI)	Studying the ribosomal RNA (rRNA) diversity, functional relevance of rRNA processing factor 2 (RPF2) in ribosome biogenesis, root, shoot development and drought stress tolerance in rice.	DBT	89 lakhs	2024-27
66.	Dr. Shouvik Das (mentor Dr. Prashant Pawar)	An integrated molecular genomics approach to unveil genomic and epigenetic complexity of adaptive traits, like flowering time, seeds size and plant cell wall.	MK Bhan Fellowship	87 lakhs	2021-25
67.	Dr. Ambadas B Rode	Targeting riboswitches with synthetic small molecules for development of anti-tubercular drugs.	ANRF	46.12 lakhs	2023-26
68.	Dr. Ambadas B Rode	Rationally Targeting and Tuning Riboswitch Mediated Gene Regulation for Therapeutic applications.	DBT	54.42 lakhs	2024-27
69.	Dr. Ambadas B Rode	Regulation of miRNA expression and maturation via targeting G-quadruplex conformations using small molecules for glioma therapy.	RCB-IITD	Rs.10 lakhs	2023-25
70.	Dr. Nidhi Adlakha	Development of low phenylalanine diet for phenylketonuria patients using immobilized enzymes.	DBT	85 lakhs	2024-27
71.	Dr. Nidhi Adlakha	Rational Engineering of Talaromyces sp. to augment cellulase production.	ANRF	55 lakhs	2024-27

72.	Dr. Nidhi Adlakha	Aptamer-nanoparticles conjugate: a next generation theranostic agent for phytopathogenic fungi.	DBT-NanoAgri Call	Total Grant: 57 lakhs Grant for RCB: 19 lakhs	2022-25
73.	Dr. Arvind Sahu (Coordinator) Prof. Deepak T Nair (PI)	Setting up of the Indian biological Data Centre- Phase 1.	DBT	7578.8 lakhs	2020-26
74.	Prof. Deepak T Nair Prof. Vengadesan Krishnan Prof. Deepti Jain Dr. Prem Singh Kaushal	Bioinformatics Centre for Computational Drug Discovery- BIC at Regional Centre for Biotechnology, Faridabad.	DBT	197.3 lakhs	2021-26

Research & Innovation Infrastructure

Photo Credit: Shubham Singh

BSC BioNEST Bio-Incubator (BBB)

BSC BioNEST Bio-Incubator (BBB), a BIRAC's Associate Partner, continues to foster bio-entrepreneurship as a leading startup ecosystem enabler in the National Capital Region. The year was marked by significant milestones and strategic partnerships, further strengthening BBB's position as a catalyst for innovation and translational research. Operating from its expansive **35,000 sq. ft.** incubation space, BBB on boarded new startups and provided continued support to existing incubatees working on innovative, indigenous products aligned with the national priorities of **'Make in India'** and **Atmanirbhar Bharat**. The incubator's thrust areas include **Biopharmaceuticals, Nutraceuticals, Diagnostics, Medical Devices, Industrial Biotechnology, and Anti-Infectives**.

Key Highlights of BBB

1. **Recognition and Accreditations**
   BBB received prestigious acknowledgments at both national and state levels, reinforcing its position as a leading biotech incubator.
   - **National Recognition:** BBB was awarded the title of ***'Best Incubation Centre* (Tier-1 City category)'** at Global Bio-India 2024, recognizing its significant contributions to the bio-innovation ecosystem.
   - **State-Level Accreditation:** BBB, RCB was officially registered as a **Government Incubator under Startup Haryana**, Department of Industries & Commerce, Government of Haryana. This accreditation strengthens BBB's capacity to support biotech startups through state-linked initiatives and programs.

2. **Establishment of Early Translation Accelerator (ETA) Centre**
   The establishment of the ETA Centre at BBB was approved by BIARC. Focused on Industrial Biotechnology, the Centre is designed to bridge the gap between academic research and market-ready solutions by supporting proof-of-concept and validation. It aims to nurture high-potential innovations, foster collaboration between academia and industry, and engage with global translational ecosystems to drive impactful biotech ventures.

3. **Employment & IP Generation**
   To date, BBB has facilitated the creation of over **380 jobs** and enabled the filing of approximately **80 IP applications**, highlighting the ecosystem's innovation capacity and economic contribution.

4. **Funding Support under SISFS**
   Under the **Startup India Seed Fund Scheme (SISFS)**, a total of **₹3 crore** was approved for disbursal to support high-potential startups. To date, **11 startups** are receiving support under this initiative.
5. **Strategic Collaborations**
   BBB entered into strategic partnerships aimed at fostering entrepreneurship, co-developing programs, and promoting knowledge exchange with the following institutions:
   - FITT – IIT Delhi
   - Redcliffe Lifetech Pvt. Ltd.
   - PIEDS – BITS Pilani
   - SGT University

6. **Support under Government Schemes**
   - **MSME Innovative Scheme:** As a recognized Host Institute (HI), BBB conducted the **MSME Idea Hackathon 4.0**, forwarding **six shortlisted proposals** for final evaluation.
   - **BIRAC E-Yuva Initiative:** BBB was nominated as a **Knowledge Partner** for three new E-Yuva incubators, expanding its mentoring outreach to student-led innovations.

7. **Participation in National Events**
   BBB, along with its incubated startups, actively participated in **Global Bio-India 2024**, organized by BIRAC. The showcase attracted strong interest from academia, industry stakeholders, and the startup community.

Noteworthy Startup Achievements

- **Dharaksha Ecosolutions Pvt. Ltd.** raised **₹24.8 Cr** in funding and received national spotlight through an **all-shark deal** on **Shark Tank India**.

- **East Ocyon Bio Pvt. Ltd.** secured **₹36 Cr** to advance cutting-edge **Cell & Gene Therapy** programs.
- **Inte-e-labs Pvt. Ltd.** earned multiple accolades including the **Best Startup (Women Entrepreneur Category)** at Global Bio-India 2024 and recognition in **NASSCOM EMERGE 50**.

Outreach and Capacity Building

- BBB continued to disseminate its activities through **quarterly newsletters**, **social media**, and **awareness programs.**
- Several training workshops were organized to upskill **UG/PG students** in core biotech techniques and entrepreneurship.
- The **SPARK 2024 Innovation Challenge**, a flagship Ideathon, was conducted to promote early-stage entrepreneurial thinking among students.

With a revenue of **₹1.8 Cr in 2024**, BBB continues to scale its impact by equipping startups with world-class infrastructure, expert mentorship, and funding opportunities to address real-world challenges in healthcare, agriculture, and sustainability.

BBB Team

Awards & Recognition of BBB:

"Best Incubator" award among Tier1 category at Global Bio India 2024

Registered as a Government Incubator under Startup Haryana

Startups Supported since inception

S.No	Company Name	Area	Incubation Type
1	SHC Shine Biotech Pvt. Ltd.	Diagnostic	Residential
2	QbD BioSciences Pvt. Ltd.	Bio-Pharma	Residential
3	Bioheaven 360 Genotec Pvt. Ltd.	Molecular Diagnostic	Residential
4	NextGen InVitro Diagnostics Pvt. Ltd.	Diagnostic	Residential
5	VaxFarm Life Sciences LLP	Bio-Pharma	Residential
6	AIGen Therapeutics Pvt. Ltd.	Anti-infective	Residential
7	InnoDx Solutions Pvt. Ltd.	Diagnostic	Residential
8	BioDva Life Sciences Pvt. Ltd.	Bio-Pharma	Residential
9	Stellar Diagnostics India Pvt. Ltd.	Diagnostic	Residential
10	Vanguard Diagnostics Pvt. Ltd.	Diagnostic	Residential
11	Incredible Devices Pvt. Ltd.	Medical Device	Residential
12	BioCredence	Nutraceuticals	Residential
13	AptaBharat Innovation Pvt. Ltd.	Diagnostic	Residential
14	Sunny Corporation Pvt. Ltd.	Diagnostic	Residential
15	Biotide Solutions LLP	Anti-infective	Residential
16	Organic 121 Scientific Pvt. Ltd.	Industrial Biotechnology	Residential
17	Dharaksha Ecosolutions Pvt. Ltd.	Environmental Biotech	Residential
18	Peptomer Therapeutics Pvt. Ltd.	Anti-infective	Residential
19	Sleepiz India Pvt. Ltd.	Medical Device	Residential
20	Inte-e-Labs Pvt. Ltd.	Bio-Pharma	Residential
21	Genvynn Biologics Pvt. Ltd.	Bio-Pharma	Residential
22	Kantech Research Solutions	Anti-infective	Residential
23	3CR Bioscience Ltd.	Diagnostic	Non-Residential
24	TechInvention Lifecare Pvt. Ltd.	Bio-Pharma	Residential
25	Anziam Bio Pvt. Ltd.	Bio-Pharma	Residential
26	Celleome Biosciences LLP	Diagnostic	Residential
27	PriDignity Pvt. Ltd.	Sanitation	Residential
28	Valetude Primus Healthcare Pvt. Ltd.	Diagnostic	Residential
29	Ruhvenile Biomedical OPC Pvt. Ltd.	Anti-infective	Residential
30	Mr. Sharad Rai	Nutraceuticals	Residential
31	Advinogen Innovations Pvt. Ltd.	Diagnostic	Residential
32	Biotrends India Pvt. Ltd.	Industrial Biotech	Residential

S.No	Company Name	Area	Incubation Type
33	Micronic Analytical Device Pvt. Ltd.	Diagnostic	Residential
34	Meraki Herbzz	Nutraceutical	Non-Residential
35	Florecer Services Pvt. Ltd.	Industrial Biotech	Residential
36	Tritek Innovation Pvt. Ltd.	Diagnostic	Residential
37	Translational Research Innovations Pvt. Ltd.	Industrial Biotech	Residential
38	Biolytics Research & Innovation Pvt. Ltd.	Diagnostic	Residential
39	Dr. Suman Das	Diagnostic	Residential
40	Mr. Nidhin Murali	Bio-Pharma	Residential
41	Tropical Animal Genetics Pvt. Ltd.	Bio-Pharma	Residential
42	East Ocyon Bio Pvt. Ltd.	Bio-Pharma	Residential
43	Cellogen Therapeutics Pvt. Ltd.	Bio-Pharma	Residential
44	I2 Cure Pvt. Ltd.	Bio-Pharma	Residential
45	Third AI Platforms Pvt. Ltd.	Digital Health	Non-Residential
46	Vegen Labs LLP	Bio-Pharma	Non-Residential
47	Innovationsatss Pvt. Ltd.	Social Impact	Non-Residential
48	Pro Ortho Perfect India Pvt. Ltd.	Healthcare	Non-Residential
49	Grailmaker Innovations Pvt. Ltd.	Healthcare	Non-Residential
50	Biopan Scientific Pvt. Ltd.	Industrial Biotech	Non-Residential
51	Jivanu Therapeutics Pvt. Ltd.	Bio-Pharma	Residential
52	Success Arrow Superfoods Pvt. Ltd.	Nutraceuticals	Residential
53	Thrafford Lifescience Pvt. Ltd.	Bio-Pharma	Residential
54	PrecizionIQ Data Pvt. Ltd.	Diagnostic	Residential
55	Naturohabit Pvt. Ltd.	Ayurvedic & Wellness	Residential
56	DKS Incorporate	Bio-Pharma	Residential
57	Kumar Nishchay	Bio-Pharma	Non-Residential
58	Deepak Sharma	Industrial Biotech	Non-Residential
59	Vanshika	Industrial Biotech	Non-Residential
60	Jayanti Kumari	Bio-Pharma	Non-Residential
61	Rohit	Plastic Industry	Non-Residential
62	Kriash Medtech Pvt. Ltd. / Sneh	Med Tech Device	Non-Residential
63	Ethnobio Deeptech Innovations Pvt. Ltd.	Bio-Pharma	Non-Residential
64	Kapardi Pharma Pvt. Ltd.	Bio-Pharma	Residential
65	Zoencure Therapeutics Pvt. Ltd.	Bio-Pharma	Residential
66	Proteogenixx Lifescience Pvt. Ltd.	Bio-Pharma	Residential

Grants/Awards secured by startups in FY 2024-25

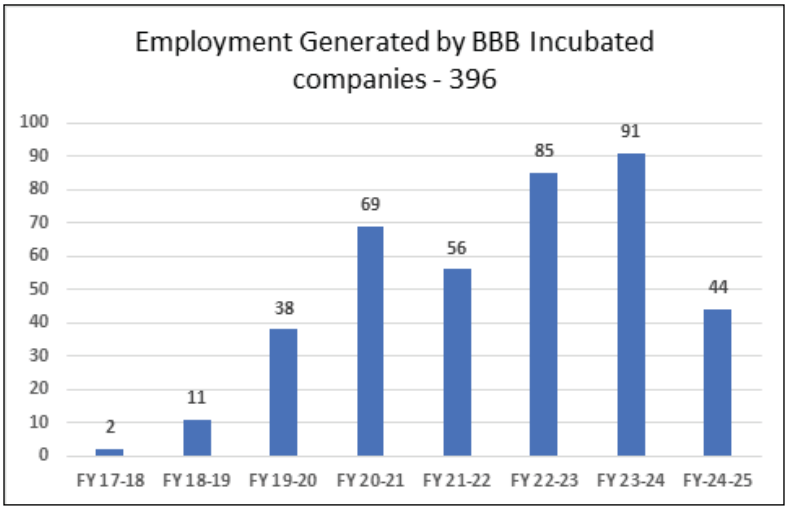
S.No	Name of Incubatee Company	Grant & Awards
1	Dharaksha Ecosolutions Pvt. Ltd.	Startup Grand Challenge 2.0; Seed Fund by Avaana Capital
2	Vegen Labs LLP	BIRAC SIBRI
3	East Ocyon Bio Pvt. Ltd	Seed Fund by Aeravti Ventures & Micro Labs
4	Techinvention Lifecare Pvt. Ltd.	Coveted Startup 50: The Trailblazers Award from Dun & Bradstreet
5	Inte-e-labs Pvt. Ltd.	NASSCOM EMERGE 50 Awards 2024; India5000 Best MSME Award 202 ; Best startup award in the Women category at GBI 2024 by BIRAC; India SME 100 Awards

Startups on boarded during FY 2024-25

BBB has incubated 10 new startups during FY 2024-25

S.No	Company	Area
1	DKS Incorporate	Bio-Pharma
2	Thrafford Lifescience Pvt. Ltd	Bio-Pharma
3	PrecizionIQ Data Pvt. Ltd.	Diagnostic
4	Naturohabit Pvt. Ltd.	Ayurvedic & wellness
5	Kriash Medtech Pvt. Ltd.	Med Tech Device
6	Kumar Nishchay.	Healthcare
7	Deepak Sharma	Industrial Biotech
8	Vanshika	Industrial Biotech
9	Jayanti Kumari	Bio-Pharma
10	Rohit	Plastic Industry

Employment generated by BBB Incubatees



Events Conducted During FY 2024–25

BBB has been actively fostering entrepreneurial spirit among young innovators through a range of strategic programs and outreach initiatives. Throughout FY 2024-25, BBB organized 50 events including workshops, seminars, and networking sessions to promote knowledge exchange and facilitate meaningful interactions between entrepreneurs, mentors, and industry experts.

S.No	Event Title (Shortened)	Category	Month
1	Go-to-Market Strategies – Awareness Session	Awareness Session	April '24
2	BIRAC BIG Call 24 – Awareness Sessions	Awareness Sessions (BIG)	Apr–May '24
3			
4			
5			
6			
7			
8	BioNEST & E-YUVA Conclave – Panel Participation	Networking	May '24
9	Webinar: Product Market Fit - Addressing the unmet need	Awareness Session	May '24
10	Talks on Entrepreneurship & IPR + Facility Tour	Awareness Session	May '24
11	SPARK Program: APAR Health- Facility Visit	Networking	June '24
12	Trinity Gets the Money – Funding Session	Awareness Session	June '24
13	SuFI Inaugural – Talk on Entrepreneurial Ecosystem	Networking	June '24
14	Webinar – Fundraising Fundas	Awareness Session	July '24
15	SiB Fellow Visit to BBB	Networking	July '24
16	Talk on Startup Ecosystem – Mr. Arpit Dhupar	Awareness Session	Aug '24
17	National Biopharma Mission Conclave Participation	Networking	Aug '24
18	Recombinant DNA Technology – Workshop	Workshop	Aug '24
19	GBI 2024 Roadshow	Networking & Awareness	Aug '24
20	Prof. VijayRaghavan Visit	Networking	Aug '24

S.No	Event Title (Shortened)	Category	Month
21	GD Goenka University Students Visit	Awareness Session	Aug '24
22	Speaker – Deeksharambh Program at SGT University	Networking	Aug '24
23	Rawal Public School – Facility Visit	Awareness Session	Aug '24
24	Talk – AI & Startups by Dr. Vanila Sharma	Awareness Session	Sep '24
25	Talk – Startup Ecosystem by Dr. Dinesh Kundu	Awareness Session	Sep '24
26	Talk – Value Proposition Canvas by Dr. Shriram Raghavan	Awareness Session	Sep '24
27	Global Bio India – Outreach Booth	Networking	Sep '24
28	Talk – Women's Safety & Innovation by Ms. Srishti Sharma	Awareness Session	Sep '24
29	Workshop with Hi-Media Laboratories	Workshop	Sep '24
30	Career Counselling Session on Science Communication	Awareness Session	Sep '24
31	ISBA Annual Conference 2024	Networking	Oct '24
32	Talk – Business Development by Mr. Chand Das	Awareness Session	Oct '24
33	Talk – Fundraising Fundas by Mr. Sachin Karnik	Awareness Session	Oct '24
34	Talk – Cell Therapy Innovations by Dr. K. Krishnan	Awareness Session	Oct '24
35	Talk – Biotech Entrepreneurship by Mr. Srayance Jain	Awareness Session	Nov '24
36	Talk – Healthcare Revolution by Mr. Abir Satsangee	Awareness Session	Nov '24
37	Talk – Is Biotech Entrepreneurship Worth It? by Ms. Sonia Madan	Awareness Session	Nov '24
38	Talk – Nerves of Steel by Mr. Syed Ahmed	Awareness Session	Nov '24
39	Workshop – In-Vitro Diagnostics (ELISA Technique)	Workshop	Nov '24
40	Talk – Startups & Entrepreneurship at SGT University	Networking	Nov '24
41	Talk – Food Ecosystem in India by Dr. Dinesh (FSSAI)	Awareness Session	Nov '24
42	Connect & Collaborate Founders Meet 2024	Networking	Dec '24
43	IPR Session & Facility Visit – SGT University	Awareness Session	Dec '24
44	SPARK 2024 Grand Finale – Ideathon Competition	Innovation Challenge	Dec '24
45	DBT-ILS Hackathon – Evaluator Participation	Awareness Session	Feb '25
46	Knowledge Sharing & Product Launch – with Thermo Fisher	Networking & Awareness	Feb '25
47	Investor Showcase – In partnership with FITT, IIT Delhi	Investor Meet	Feb '25
48	National Science Day – Participation	Networking	Feb '25
49	Talk – Pharma Startups at KR Mangalam University	Awareness Session	March '25
50	FCDO & BIRAC – Train the Trainers Workshop & Facility Tour	Networking	March '25

Pictures of Events @ BBB

BIONEST & E-YUVA CONCLAVE

"Connect & Collaborate: Founder's Meet 2024"

Workshop on "Recombinant DNA Technology"

Workshop on "*In-Vitro* Diagnostics Using the ELISA Technique"

Global Bio India 2024

Investor's Meet

UK Delegation Visit & FCDO-BIRAC-African Engagement at BBB

BIOSAFETY SUPPORT UNIT (BSU)

Biosafety Support unit (BSU) is a unit established by Department of Biotechnology, Government of India as a part of the reforms to strengthen biosafety regulatory system in partnership with Regional Centre for Biotechnology (RCB).

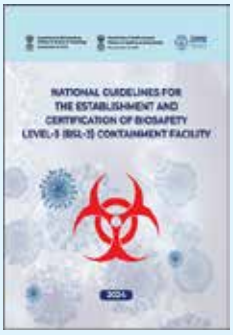
A. Major activities undertaken by BSU during the year 2024-25 include:

- Provided assistance to RCGM/GEAC (Statutory bodies established under Rules 1989 of EPA 1986) in the scrutiny of all the applications received for conducting research in biotechnology, product development and monitoring field trials. The activities of BSU includes desk review of all applications to ensure the completeness of the data requirements, compliance of the approved protocols/procedures to be followed at the time of field trials (Event selection, BRL-I and BRL-II) and preclinical toxicology (PCT) data and other regulatory compliances.
- Developed and updated a number of Guidelines, Standard Operating Procedures and Policy documents.
- Assisted the RCGM Secretariat in developing revised guidelines and protocols for generating biosafety data to address the challenges raised by the emerging new areas of Biotechnology such as Genome Editing.
- BSU team is also fulfilling the training needs of the personnel engaged in Biosafety regulations and developing e-learning modules for IBSCs and other stakeholders working in the regulatory science.
- BSU is fully engaged in providing a communication platform for scientific community and other stakeholders through Indian Biosafety Knowledge Portal, an online portal for all transaction and submission and tracking of applications.
- BSU provided all necessary services to RCGM and assisted RCGM Secretariat in organizing scheduled meetings of the RCGM, various sub-committees and monitoring teams, etc.

B. Major accomplishments:

B.1 RCGM/GEAC Related Activities:

- ***Review of applications:*** BSU evaluated a total of **3832** (2644 Biopharma and 1188 Agri-Biotechnology) new and revised applications submitted to Review Committee on Genetic Manipulation (RCGM), of which 1115 (833 Biopharma and 282 Agri-Biotechnology) applications were considered in RCGM meetings (**281st – 306th**) during year 2024-2025. BSU extended its support towards conducting all the meetings of RCGM by preparing Agenda notes and draft Recommendations. Further, in-depth desk review was carried out for each of the application/reports submitted by the applicants on Import/Export/Transfer/Receive of GE material/hazardous microbes, Information items to carry out R&D, Application to conduct Pre-clinical toxicity studies and Report of Pre-clinical toxicity studies for Biopharma while Import/Export/Transfer/Receive of GE plant material/hazardous microbes, Information items to carry out R&D, Confined field trials, and relevant compliance reports for Agriculture.
- ***Biosafety Protocols and Guidelines:*** BSU has undertaken a major activity of drafting/revising/updating of various guidelines related to biosafety of recombinant DNA research.
  The following guidelines have been **notified**:

DBT notified the "National Guidelines for the establishment and certification of Biosafety Level-3 (BSL-3) Containment Facility, 2024", vide OM dated 27.09.2024.	
DBT notified the Entry of Banana Bunchy Top Virus in "List of Infective Microorganisms corresponding to different Risk Groups, 2021" superseding the Annexure I of "Regulations & Guidelines for Recombinant DNA Research and Biocontainment, 2017", vide OM dated 07.05.2024.	

Standard Risk Assessment and Risk Management Plan for Environmental Safety for: 1. Undertaking Commercial Production of Ethanol Using Genetically Modified Organisms at the Distilleries. 2. Import of Genetically engineered organism for the purpose of commercial production.	

In addition, the following guidelines are ***under preparation***:

- Guidelines on Similar Biologics, 2025.
- Guidelines on Genetically Engineered plants containing stacked events, 2025.
- Handbook for Institutional Biosafety Committees (IBSCs), 2025.
- Checklist for CAR-T trials for NOC by RCGM (till preclinical stage).

Further the revision/drafting of following guidelines is ***under consideration***:

- Updation of Regulations & Guidelines for Recombinant DNA Research and Biocontainment.
- Revision of List of infective Microorganisms corresponding to different Risk Groups.

- ***Certification of BSL-3 facilities Nation-wide***: To ensure compliance with biosafety for high containment facilities, 'Guidelines for the Establishment of containment facilities: Biosafety Level 2 (BSL-2) & -3 (BSL-3) and certification of BSL-3 facility, 2020' defining specifications and SOPs for these facilities have been notified. Further, a mechanism for certification of such facility based on review of documents was also devised and now being followed with ongoing review of the applications. BSU assists in preliminary examination of applications for Certification of BSL-3 facility, Annual revalidation of certified BSL-3 facilities and Renewal of Certification of BSL-3 facility. During this period, 03 BSL-3 facilities were recommended by the Interministerial committee for BSL-3 certification and approved by RCGM for Certification. Further, 01 BSL-3 facility was approved for Renewal of Certification of BSL-3 facility. RCGM, DBT notified the *National Guidelines for the establishment and certification of Biosafety Level-3 (BSL-3) Containment Facility, 2024*, vide OM dated **27.09.2024. In view of the same,** a mechanism for certification of is being devised for review of the applications. BSU also facilitates site visit to BSL-3 facilities, to understand the design, procedures and engineering controls in the facility, and provide suggestions so that the facility meets to the specific requirements. During this period, 01 BSL-3 facility was visited, wherein the committee made several observations/recommendations.

- ***Risk Assessment and Risk Management (RARM)***: BSU continued its support to RCGM by providing RARM documents for each confined field trial application considered in the RCGM Meetings. During the period April, 2024 - March 2025, BSU has prepared 05 RARM documents for applications to conduct confined field trials of GE lines and assessed 01 revised RARMP for application to conduct environmental release of GE line.

- ***Risk Assessment and Risk Management Plan (RARMP)***: As per recommendation of GEAC, Risk Assessment and Risk Management Plan for Import of Genetically engineered microorganisms and for Environmental Safety for Undertaking Commercial Production of Ethanol, BSU has Assessed 12 RARMP forwarded by GEAC for RCGM consideration. Of these, 05 RARMP were recommended by RCGM are forwarded to GEAC.

- ***Commissioning of Indian Biosafety Knowledge Portal (IBKP)***: The Portal facilitates registration of Institutional biosafety committees and uploading of new applications through portal. It is the nodal point for IBSC registration and monitoring, in addition to submission of respective applications for RCGM consideration and notification of the appropriate decision to the applicant. BSU evaluated the following, since commencement of the Portal:

Number of organization registrations approved	1292
Number of IBSCs registered	864

- ***Monitoring of IBSCs and Assessment of compliance documents***: DBT-RCGM has taken several reforms including empowering of IBSCs, hence stringent mechanism to monitoring the IBSCs through their Minutes, Annual Compliance Reports and Medical Surveillance Reports has been started with IBKP portal. BSU is facilitating RCGM in the monitoring of IBSCs and assessment of compliance documents.

- ***Biological Research Regulatory Approval Portal (BioRRAP)***: BioRRAP tracks the regulatory approvals for a research proposal on a single portal and provides more credibility and recognition to such biological researches. BSU facilitates the functioning of BioRRAP.

- ***Interactive sessions for awareness raising of Researchers***: BSU Scientists provided training sessions to Researchers (Principal Investigators, Scientists, Post-doctoral researchers) from Academia, Start-ups and Industry. 21 sessions were conducted during this financial year, which were attended by approximately 1000 participants. 01 Special session was conducted at the University of Delhi (North Campus), Delhi.

Training and Capacity Building:

- ***BSL-3 facility visit***

◆ BSU facilitated the site visit of BSL-3 facility at Association for Bio-inspired Leaders & Entrepreneurs at SASTRA Deemed University-Technology Business Incubator, Thanjavur, by sub-committee constituted by DBT, held on 06.04.2024, to understand the design, procedures and engineering controls in the facility, and provide suggestions so that the facility meets to the specific requirements.

- ***Central Compliance Committee (CCC) visits***

A total of 43 visits by CCCs to monitor 17 different confined field trials, were conducted at 28 trial sites across various locations in India, of various genetically engineered plants at reproductive as well as harvest/termination stages of plant growth and post-harvest restriction period of completed confined field trials.

- ***Conference/Workshop/Training/Consultation***

◆ Dr. Pranjali Vishwakarma, Project Scientist - III, was Nominated from RCGM secretariat, DBT for discussion on the agenda items of **CBD CoP-16 on "Synthetic Biology" and "Risk Assessment and Risk Management"**, held in MoEF&CC, New Delhi, on August 30, 2024.

◆ Dr. Poonam Vishwakarma, Project Scientist – III, delivered presentation on "**Approval Process for Research Involving GMOs: RCGM Guidelines**", for the Biosimilar Regulatory Framework, Approval Pathway and Role of Key Stakeholders in India, module in the Annual training event: "**CBT Course Series 2024**", organized by DBT Center of Excellence for Biopharmaceutical Technology (COE-CBT), held in IIT-Delhi, New Delhi, on December 10, 2024.

◆ Dr. Poonam Vishwakarma, Project Scientist – III, Moderated the Panel Discussion on "**Compliance and Industry Perspective in Biotech sector and Strategic Trade**", for the **National Conference on Strategic Trade Controls (NCSTC) 2025**, organized by the Directorate General of Foreign Trade (DGFT) and the Ministry of External Affairs (MEA), at Hotel Conrad, Bengaluru, held on January 16, 2025.

- Dr. Manpreet Kaur, Project Scientist – III, delivered Presentations on "**Indian Bio-Safety Regulatory Frameworks**" and "**National System of Certification of High Containment Facility (BSL-3 Facility)**" during Session on Bio-Safety and Security for "**India-UNODA Capacity Building Program on Implementation of UNSCR 1540 and STC for the Asia-Pacific States in 2025**", held on 25-27 February 2025 at NACIN, Palasamudram.



- Dr. Govind Kumar Rai, Coordinator & Project Scientist - III, BSU represented RCGM Secretariat in the panel discussion on **Genome Editing: Future Technologies, Regulation & FTO (Freedom to Operate)**, during **Training on Genome Editing in Plants-Advance tools and techniques**, organized by ICAR and Gates Foundation at ICAR-IARI on 07.02.2025.



- Dr. Pranjali Vishwakarma, Project Scientist – III, attended the online, short course on "**Key Essentials: The Global Biodiversity Framework, Sustainable Development and the Law**", organized by Lucy Cavendish College, University of Cambridge, held on May 06-19, 2024.
- Dr. Poonam Vishwakarma, Project Scientist - III and Dr. Manpreet Kaur Project Scientist – III attended the **National Consultation on Legal Framework for One Health Implementation**, organized by National Centre for Disease Control, Directorate General of Health Services, MoHFW, at Hotel Ambassador, New Delhi held on June 27 – 28, 2024.
- Dr. Govind Kumar Rai, Coordinator & Project Scientist – III, and Dr. Shipra Shahi, Project Scientist – III, visited the trial site to observe the ongoing **BRL-I trial of GE Rubber** at Rubber Research Station, Saraturi, Guwahati on July 01, 2024.
- Dr. Bhawna Yadav, Project Scientist – II, attended the "**One-day National Conference on Environmental Impact Assessment: Resource Management & Policy Making (ERPM-2024)**", organized by CSIR-National Environmental Engineering Research Institute, Hyderabad, held on July 19, 2024.
- Dr. Poonam Vishwakarma, Project Scientist - III and Dr. Renu Arora, Project Scientist - II attended the "**9th Annual Cell and Gene Therapy Symposium**", organized by Centre for Stem Cell Research (a unit of inStem, Bengaluru), Christian Medical College Campus, Vellore, held on August 01-03, 2024.
- Dr. Govind Kumar Rai, Coordinator & Project Scientist – III, Dr. Pranjali Vishwakarma, Project Scientist – III, Dr. Shipra Shahi, Project Scientist – III, Dr. Manpreet Kaur, Project Scientist – III, Dr. Renu Arora, Project Scientist – II, Dr. Bhawna Yadav, Project Scientist – II, Dr. Subhasish Dutta, Project Scientist – II, Dr. Naveen Kumar, Project Scientist – II, Ms. Shubhi Sharma, Project Associate – II, Ms. Shalini Gupta, Project Associate – II, Dr. Surbhi Prithiani, Project Associate – I, and Ms. Pravritti, Project Associate – I, attended the **National Biopharma Mission Conclave**, organised by National Biopharma Mission, New Delhi, held on August 08, 2024.
- Dr. Pranjali Vishwakarma, Project Scientist - III and Dr. Subhasish Dutta, Project Scientist – II, attended the "**Global Bio-India 2024, Transforming Lives: Biosciences to Bioeconomy**", organized by DBT and BIRAC, held in Pragati Maidan, New Delhi, on September 12-14, 2024.
- Dr. Poonam Vishwakarma, Project Scientist - III and Dr. Bhawna Yadav, Project Scientist – II, attended the **19th International Conference of Drug Regulatory Authorities (ICDRA), INDIA-2024**, organized by Central Drugs Standard Control Organization (CDSCO), held in Yashobhoomi, IICC, Dwarka, New Delhi, on October 14-15, 2024.
- Dr. Naveen Kumar, Project Scientist – II, attended the 5th National Workshop on "**Genome Editing Mediated by CRISPR/**

Cas9: tools, experimental design, and applications", organized by National Genome Editing & Training Centre, National Agri-Food Biotechnology Institute (NABI), Mohali, held in NABI Campus, on October 21-24, 2024.

- Dr. Manpreet Kaur, Project Scientist – III, attended the Annual training event: "**CBT Course Series, 2024**", organized by DBT Center of Excellence for Biopharmaceutical Technology (COE-CBT), held in IIT-Delhi, New Delhi, on December 10-12, 2024.
- Dr. Renu Arora, Project Scientist – II, attended the 5-day Intensive Course on "**Pre-clinical Toxicology & Risk Assessment**", organized by Federation of Asian Biotech Associations (FABA), University of Hyderabad and Aspire BioNEST, held at University of Hyderabad, Hyderabad, on December 09-13, 2024
- Dr. Subhasish Dutta, Project Scientist – II, attended the **3-day Workshop on Biomanufacturing 1.0**, organized by National Agri-Food Biomanufacturing Institute (NABI), Mohali, held on December 16-18, 2024.
- Dr. Poonam Vishwakarma, Project Scientist – III, attended the discussion Meeting on "**Biopharma applications process flow in RCGM and steps towards streamlining of regulatory approval process**" organized under Chairmanship of Secretary, DBT, at DBT, New Delhi, held on February 04, 2025.
- Dr. Poonam Vishwakarma, Project Scientist – III, facilitated **Stakeholder Consultation** with 01 organization for addressing Cell and Gene Therapy product development related queries, on March 11, 2025.
- Dr. Manpreet Kaur, Project Scientist – III, facilitated Meeting with **World Bank Team,** for a discussion on establishment and certification of BSL-3 labs, in the Nation, on March 11, 2025.
- Dr. Govind Kumar Rai, Coordinator & Project Scientist – III, attended the **National Conference on Emerging Innovations in Biochemistry and Biotechnology for Holistic Development of Agriculture**, Organized by SKUAST-JAMMU & SPBB, Division of Biochemistry, ICAR-IARI, New Delhi; at SKUAST, Jammu, on March 06-07, 2025.

B.2. Other activities:

- BSU supports RCGM/GEAC for drafting affidavits/ replies for biosafety related matters for Parliamentary Standing Committee, Court Cases, Parliament questions etc.
- BSU provides background information to various Sub-committees (eg. GE Mosquito, BGIII RRF, Risk group updation, engineering controls, Gene therapy).
- BSU addresses queries submitted by stakeholders on biosafety related matters.

BSU Team (Coordinator, Scientists & Admin staff)

High Performance Computing Cluster & IT Infrastructure

In terms of IT Infrastructure & Computing Facilities hosted and managed by RCB, a high-performance computing (HPC) cluster and workstations with a Schrodinger suite server are placed at the **Graphics Lab** for research in computational biology and structure-based drug design. The Information and Communication facilities at RCB are continuously evolving with state-of-the-art facilities. All the computers at RCB are provided with the latest updated software and hardware. An impressive array of information technologies and resources has been deployed with a harmonious blend of old and new, notable among these are:

Computing Facilities

The Institute has state-of-the-art Computer facilities. All the computer facilities in the institute are provided with the latest updated software and hardware. Internet, printing, and scanning facilities are also available through the network. Desktops/ Laptops, multifunction printers have been provided to the staff with internet connectivity. There are about 300+ client machines with windows 10, Linux (CentOS, Red Hat Enterprise Linux) and Mac OS X. There are common Personal Computer in each research lab and MSc lab for students to access various commercial off-the-shelf software such as Antivirus, Adobe Premium & Standard Suite, Systat, Sigma Plot, PyMol, Graphpad Prism, SPSS, Turnitin, Endnote, Grammerly, and Corel Draw Graphics Suite for preparing manuscripts, various reports and presentations. Face Recognition Biometric Attendance System has also been enabled for the staff to register attendance by simply presenting his/her biometric. In addition, online resources are available for scholars for research, case studies, and the preparation of their projects.

Internet Connectivity

RCB has a 1 Gbps shared internet leased line from National Knowledge Network, offering high-speed Internet connectivity on the campus. Additionally, a 125 Mbps fiber connectivity has been provisioned from an alternate service provider as a backup. The internet connection is distributed to users and facilities through RCB's network infrastructure comprises about 1000 metres of fibre, with a 10Gbps backbone, 115+ wireless access points, and 45+ network switches that provide on-campus wireless and wired connectivity. The RCB has implemented a security policy to ensure the highest levels of network health and security. The Centre has been functioning in conformity with the guidelines of the Government of India with regard to guidelines on IPV6 implementation and has also been an active participant in the Government initiatives of the "Digital India Campaign". The campus is fully covered by Wi-Fi in all the administrative buildings, labs, the advanced platform technology centre (ATPC), associated centres, and hostels. Wi-Fi access is provided to internal users by Captive portal & media access control (MAC) address authentication, and to visitors by separate guest accounts.

E-mail and Website

The e-mail system at RCB offers a user-friendly web-based e-mail allowing users to access mail, both from inside the campus and outside. A very competent and experienced IT service support team has been put in place, and the centre has recently developed and implemented a highly attractive, user-friendly and dynamic website. All major information about the institute, academic research, infrastructure, people, job portal, news, and announcements is being regularly updated on the website.

Internet Security

The Campus Network is protected using Shopos XG3300 - where Unified Threat Management as a primary network gateway defense solution has been implemented with traditional firewall built into an all-inclusive security product able to perform multiple security functions: network firewalling, network intrusion detection/prevention (IDS/IPS), gateway antivirus (AV), gateway anti-spam, content filtering, load balancing, data loss prevention, and on-appliance reporting. Quick Heal Seqrite Endpoint Security Total Edition 18.0 has been implemented as protection from viruses, adware, spyware, etc.

Telephone Connectivity

The Campus has a PRI connectivity from Bharat Sanchar Nigam Limited and a distribution of about 300+ extensions for ease of communication within the campus and connecting with the outside world.

Audio Visual and Video Conferencing Facility

Auditorium, conference, and seminar halls are equipped with a hi-tech sound and projection system, digital podium,

and Internet connectivity. These facilities are actively used for regular seminar series, colloquia, distinguished lectures, hands-on workshops, and symposiums/ conferences. In addition, a projection facility has been set up in classrooms and discussion rooms for regular teaching, lab meetings, and scientific discussions. RCB has an Internet-based Video Conferencing Facility set up in the Seminar Hall. In addition to this, RCB has enrolled subscriptions for various virtual conference meeting rooms for holding virtual seminars or conferences. Classrooms, meeting rooms, and conference halls are furnished with the latest digital technology, i.e., digital podium, LCD projection system with audio/ video facility, and video conferencing systems in the Institute.

CCTV Surveillance and Biometric Attendance System

To enhance workplace security, streamline attendance monitoring, and ensure accountability, RCB Faridabad has implemented an integrated CCTV Surveillance System and an Online Biometric Attendance System across its premises. These systems are designed to improve institutional governance, staff management, and the safety of personnel and assets.

Digital Library

RCB has a small but fully functional library with several copies of standard international textbooks spanning various areas of biotechnology practiced by its researchers and taught in its coursework. The RCB library houses over 1400 books, including scientific textbooks, administrative, engineering, and Hindi books in multiple copies. Web-based Online Public Access Catalogue (WebOPAC) has been set up through KOHA Open Source Library Management Software at RCB Library to provide online access to RCB library catalogues. In addition, an electronic library provides access to a vast range of primary literature in the form of peer-reviewed journals and reviews, through the DBT electronic library consortium (DeLCON) and One Nation and One subscription (ONOS). The RCB library provides access to online resources to users 24/7 via the Intranet/Internet. The library also contains common Personal Computer systems for browsing online resources (e.g., journals and books) and checking for plagiarism.

Office Automation

RCB is moving towards adapting a paperless work environment in which the use of paper is eliminated or greatly reduced. This is done by converting documents and other papers into digital form and developing various online applications (services or facilities) through the intranet portal named eRCB. All the faculty and students have access to this customised online software package being used for administrative applications. The major modules in eRCB are online leave management, user management, vehicle booking, vendor management, HR, visitor management, bill claim portal, purchase workflow, etc. In continuation of the paperless work environment using office automation, IT has to implement the ERP System in the upcoming year. This system will provide a paperless centralised automation mechanism to complete any task faster with better traceability and reporting. This system will have the centralized cover of all the major activities for five sections, i.e., Finance, HR, Purchase, Academics and General Administration. In addition to this, many other online services are available over the internet and accessible from outside the institute. The majors are:

- GeM for all kinds of purchases at RCB
- An online system of APAR (Annual Performance Appraisal System) has been implemented.
- Central e-Procurement Portal (eWizard) for online tendering of any value.
- PhD and MS-PhD Admission portals with integration of payment gateway has been generated.
- Job portals with integration of a payment gateway is functional.
- Google forms are being used for various online applications to reduce paper usage
- Online Class Attendance for all programs
- Google Classroom / Zoom Meeting is available for conducting online classes
- Micro websites for various research workshops and conferences, with a facility for online registrations.
- Online Payment Gateway for collecting student fees, any conference registration fees, etc.
- Alumni portal for establishing closed relations with the RCB alumni
- Vendor registration portal, etc.

Further, the RCB uses an Online Payroll system for RCB officials and students for their online leave approval workflow and other payroll features like TDS declaration, leave records, daily IN/OUT punching details, salary slip, etc.

In addition to above core activities, the IT division of RCB extends appropriate technical support for smooth functioning and management of IBDC.

DBT-HRD Project Management Unit (DBT-HRD PMU) at RCB

Human resource development in Biotechnology and its allied areas is of utmost importance to the Department of Biotechnology (DBT), Ministry of Science & Technology, Government of India. Recognizing the need for nurturing large pool of skilled and dynamic human capital which are critical for success of the Indian Biotechnology sector, DBT supports several human resource development programmes for the capacity building as well as competency-building of students, research scholars, faculty scientists and entrepreneurs etc.

Since the year 2020, DBT has initially entrusted RCB as the Nodal Implementation Agency for management of three (3) key human resource development programmes through establishment of DBT-HRD Project Management Unit (DBT-HRD PMU) at RCB. Thereafter, DBT has assigned four (4) additional HRD programs to RCB for implementation on a national scale.

Currently, the programmes being managed by the DBT-HRD PMU are as follows:

1. Ramalingaswamy Re-entry Fellowship (RRF) Programme
2. Biotechnology Career Advancement and Re-orientation (BioCARe) Programme
3. Junior Research Fellowship (JRF) Programme
4. DBT Research Associateship (RA) Programme
5. Post-Graduate Teaching (PG) Programme
6. Biotech Industrial Training Programme (BITP)
7. DBT-TWAS Fellowship Programme (TWAS)

Summary of the activities undertaken and the progress made in the year 2024-25 are given below:

(A) Career Fellowship Programmes:

1. Ramalingaswami Re-entry Fellowship (RRF) Programme

The Ramalingaswami Re-entry Fellowship (RRF) programme, instituted by the Department of Biotechnology (DBT), Government of India, aims to attract Indian nationals working overseas in frontier areas of life sciences and biotechnology—including bioengineering, healthcare (human and animal), agriculture and veterinary biotechnology, bio-energy, and other allied fields—who are keen to return to India and contribute to research and development in Indian institutions. Launched in 2006–07, the programme has successfully facilitated over 600 fellowships, playing a pivotal role in the repatriation and reintegration of highly skilled scientists into the Indian research and innovation ecosystem.

In an effort to reverse brain drain and strengthen India's research ecosystem, the programme has made provisions to bring back up to 75 outstanding Indian scientists from overseas each year. The fellowship is open to Indian nationals born and educated in India who hold a M.D./ Ph.D. degree (or equivalent) in life sciences, agriculture, bioinformatics, biotechnology, medicine, or allied disciplines, and have acquired a minimum of three years of post-doctoral research experience in internationally reputed research laboratories abroad. Awardees of this prestigious fellowship are eligible to join any recognized scientific institution or university in India. Each fellow receives a consolidated fellowship of ₹1,35,000 per month, a research/contingency grant of ₹13,00,000 per annum, and an institutional overhead of ₹50,000 per annum for a period of three years. In addition, fellows are eligible to apply for regular research grants under extramural and other funding schemes of various Science & Technology (S&T) agencies of the Government of India, provided a regular faculty member serves as the Co-Principal Investigator (Co-PI).

During the year 2024–25, a total of 164 applications were received in response to advertisement under RRF Call 2023–24. Following a rigorous evaluation process, the Round I screening meeting, conducted in online mode on 18–19 April 2024, shortlisted 75 applicants for the next stage of evaluation. The Round II selection committee meeting, held on 25–26 July 2024 at the National Institute of Immunology (NII), New Delhi, reviewed these shortlisted candidates and recommended 36 applicants for the award of the fellowship. As of now, 12 researchers working overseas have joined the fellowship programme under the RRF Call 2023–24 at their respective host institutions in India.

Additionally, a review committee meeting was held at NII, New Delhi, on 29–30 January 2024, to assess the progress of 117 ongoing projects supported under the fellowship programme. Later the call for applications for the RRF 2024-25 session was announced via the Common Fellowship Portal (https://fellowships.gov.in/auth/login). To enhance programme visibility and guide prospective applicants on documentation and the application process, a Zoom webinar was conducted

on 14 February 2025. In response to the advertisement, a total of **282 applications** were received under the RRF Call 2024–25, which are currently undergoing preliminary screening.

In the financial year 2024–25, the DBT-HRD Project Management Unit at RCB disbursed a total of ₹26.28 crores to support 164 fellows under the DBT-RRF programme towards the implementation of their research projects.

2. Biotechnology Career Advancement & Re-orientation Programme (BioCARe)

BioCARe is a unique programme which aims to enhance the participation of women researchers in India towards research in Biotechnology and allied areas. It provides a special opportunity to women researchers who had a break in their career to help them re-enter into the mainstream research and to provide a launch pad for further forays into the field of Biotechnology and allied areas and hence, support in their overall career development.

Under this programme, unemployed/not in regular position Indian Women Researchers/ Scientists of age upto 55 years & having a qualification of Ph.D. in any discipline of Life Sciences or allied areas/ interdisciplinary sciences/ MD/ MDS/ M.V.Sc ***(Category-I)*** or M.Tech in Biotechnology or in allied areas/M.Pharma degree holders ***(Category-II)*** are supported with a consolidated fellowship and a Research Grant upto ₹ 40 - 60 lakhs to carry out their research endeavours in Indian universities, research institutions and laboratories.

During the year 2024-2025, the Seventh Call for Application was announced in October, 2024. The applications were invited on the newly introduced Common Fellowship Portal (CFP). A total of 624 applications were received under the Call which were evaluated by a Screening Committee on 22-24 January, 2025 at NII, Delhi in which 236 applications were shortlisted for Call for presentation and further evaluation. The shortlisted applicants made a brief presentation before the BioCARe Expert Committee meeting held on 20-22 March, 2025 at NII, Delhi in which a total of 75 candidates were selected under the Call. The result of the 7th call was announced in March 2025. An annual progress review was also conducted for 54 ongoing projects supported under various disciplines of Biotechnology and Life Sciences under the BioCARe program. Further, an Orientation Session was also organized to impart knowledge about the overall process including joining, project implementation, documentation, evaluation/review etc to the newly selected fellows.

During FY 2024-25, DBT HRD PMU established at RCB Faridabad has disbursed an amount of ₹ 5.705 Crores to support the ongoing fellows under the program.

(B) Student Fellowship & Skill Development Programmes:

3. Junior Research Fellowship (JRF) Programme

The Department of Biotechnology (DBT-JRF), under the Ministry of Science & Technology, Government of India, administers the prestigious "DBT-Junior Research Fellowship" (DBT-JRF) Programme to foster advanced research in biotechnology and life sciences. Launched in 2004, the programme has reached a significant milestone of 20 years in April 2024, marking more than two decades of significant contributions towards building a robust ecosystem for research and innovation and promoting research in frontier areas of biotechnology. Since inception, the programme has supported total 500 Ph.D fellowships annually enabling young scientists to pursue doctoral research at leading universities and institutions across India.

The DBT-JRF Programme selects candidates through the Biotechnology Eligibility Test (BET), a national-level computer-based examination conducted annually. The BET assesses candidates' aptitude and knowledge in biotechnology, shortlisting them into two merit categories—Category-I and Category-II—in accordance with the Government of India's reservation policies. Candidates selected under Category-I are eligible to receive fellowships to pursue Ph.D. research at any recognized university or institution in India, with emoluments aligned with the norms specified by the Department of Science and Technology (DST) Office Memorandum (OM).

In 2024, the Regional Centre for Biotechnology (RCB) conducted the BET examination through the National Testing Agency on 20th April across 91 centres in 54 cities nationwide. A total of 15,589 candidates registered for BET 2024, of which 12,691 candidates appeared for the exam. The result finalization committee meeting for BET 2024 conducted on May 21st 2024, and shortlisted a total of 507 candidates under Category I and 168 candidates under Category II.

In the year 2024-25, the DBT-JRF Programme has supported 1200 ongoing fellows receiving funding to pursue their Ph.D. studies. Additionally, 258 new fellows from Category-I have joined the program. The DBT-Human Resource Development Project Management Unit (DBT-HRD PMU), in collaboration with the Regional Centre for Biotechnology (RCB), has efficiently managed the programme, disbursed approximately ₹66 crores during 2024-25 to cover fellowships and arrears for eligible fellows.

4. DBT Research Associateship (RA) Programme

DBT- RA programme aims at training and nurturing young researchers, scientists and generate a critical mass of trained manpower in the area of Biotechnology. It lays the foundation for building a robust postdoctoral base for the growth of Biotechnology sector in the country. DBT Research Associateship programme provides fellowship for post-doctoral research in frontier areas of Biotechnology and Life Sciences at premier institutions in India. There is a provision for 100 fellowships per year.

During the year 2024-25, two Call for Applications were announced in the month of June, 2024 and November, 2024 respectively. 1140 applications were received under Call-I and 1118 applications were received under Call-II. RCB had organized the meetings of Screening and Selection Committees of DBT-RA program in which these applications were reviewed and a total of 100 candidates (including 25 candidates from NER) were selected during the year. A total of 87 new fellows have joined in their respective host institutes in the year 2024-25 under the program. RCB had also organized three evaluation meetings to review the progress of ongoing fellows in which 88 RAs seeking extension in their fellowship tenure had presented their progress on the research work carried out.

During FY 2024-25, DBT HRD PMU at RCB Faridabad disbursed an amount of ₹ 15.489 Crores to support the new and ongoing RAs under the program.

5. Post-Graduate Teaching Programme (DBT PG Program)

The DBT Post Graduate Teaching Program in Biotechnology aims to ensure high-quality teaching standards and provide state-of-the-art facilities to universities and institutions across India. The objective is to foster an ecosystem of a skilled workforce in the field of Biotechnology, which is essential for both academic and industrial advancement in the country. This program is under implementation in 21 states, 4 UTs across the country. The program provides financial aid for various needs, including equipment, consumables, studentship, and thesis grants, with selection through the National GAT-B Exam.

In 2024, the Regional Centre for Biotechnology (RCB) conducted the GAT-B examination through the National Testing Agency on 20th April 2024 at 81 centers across 54 cities in India. A total of 9,957 candidates appeared for the exam. Based on the results of GAT-B 2024, 670 candidates were admitted to DBT-supported postgraduate programmes in Biotechnology, offered across 76 programmes in 69 participating universities and institutes. During the academic year 2024–25, a total of 1,397 DBT-supported postgraduate students are enrolled in the first and second year of these programmes.

During FY 2024-25, DBT HRD PMU established at RCB Faridabad has disbursed ₹19.41 crores to 76 ongoing programs under recurring and non-recurring heads to host universities/institutions under the DBT PG program. To review the progress of the PG programs, Annual Advisory Committee meetings for 52 programs have been conducted during FY 2024-25.

6. Biotech Industrial Training Programme (BITP)

Biotech Industrial Training program is aiming to provide six months industry-specific training to Biotech students (B.E. / B.Tech. / M.Sc. / M.Tech Biotechnology) for skill development and enhancing their job opportunities in biotech industry.

Through this program, the Department has envisioned to facilitate both students and industries in order to build and nurture future skilled workforce in the area of Biotechnology as well as close the knowledge gap between the academic course and the real world of work. The program gives students a first-hand look at what it's like to work in an industrial setting, as well as an opportunity to evaluate their future employees.

DBT has adopted apprenticeship model for implementation of DBT-BITP Programme, and linkages has been established with Life Science Sector Skill Development Council (LSSSDC), New Delhi for selection of partnering industries. Stipend of ₹ 10,000/- per month is paid to the selected candidates by DBT and 9000/- per months by industry for six months' period.

During the year 2024-25, 247 candidates were qualified through 2023-24 call. As per candidate's preferences, matchmaking was done by DBT HRD PMU and total 82 candidates have been placed in companies associated with the program like Wockhardt, Biocon, Sun Pharma, Lyfius Pharma, Jubilant Biosys & Hetero Biopharma etc. 72 candidates have successfully completed their training, of which 33 have been absorbed by the companies.

7. DBT TWAS Programme

With the world's largest South-South PhD and postdoctoral research fellowship program, DBT-TWAS helps early-career researchers from developing countries (https://twas.org/66-countries) to gain education and experience at top science institutions in India.

The program provides fellowship under the categories: a) Full-Time Postgraduate Fellowship to pursue a PhD research program in India for 5 years for full time fellows & for 12 to 18 months for Sandwich Fellowships (for those registered for a PhD in their home country); b) DBT-TWAS Postdoctoral Fellowship to pursue a postdoctoral research program in India for 12-18 months to students of the developing Countries to promote capacity building and training in the field of Biotechnology. Foreign scholars from S&T lagging countries who wish to pursue research in emerging areas in Biotechnology in India apply under this program. The programme extends support to selected candidates through Fellowship/Stipend, HRA, medical insurance and contingency for research during the tenure of the award.

The programme aims to address societal challenges through S&T applications in emerging areas of biotechnology such as agriculture sciences, biological systems and organisms, chemical sciences, medical and health sciences, structural and molecular biology for scientists from developing countries who wish to pursue research in India.

Under this joint collaboration, through DBT TWAS joint Fellowship Call 2023 for 15th Batch, 73 applications were received from young researchers and scientists of the least developing countries through the UNESCO TWAS online portal. The DBT comprised Selection Committee met in July 2024 and identified 23 suitable candidates from different countries for Post Graduate to pursue PhD and Post-doctoral fellowship award at various DBT autonomous institutes, ICAR, CSIR labs, IITs, agricultural, medical and veterinary institutes in India.

Currently, the program is supporting 27 PhD and post-doctoral researchers. 10 researchers have completed their PhD (Full time/sandwich) research in India and 2 have completed their post-doctoral research in India.

During FY 2024-25, the DBT HRD PMU made significant progress in program development through proactive management, effective coordination with program partners and fellows, and timely disbursement of funds to both ongoing and newly inducted fellows via their respective Indian host institutions. During FY 2024-25, ₹ 1.276 Crores have been disbursed to 28 TWAS fellows under the program.

8. Alignment of HRD Programs and the engagement of relevant industries

DBT-HRD PMU Team

To explore the potential alignments between existing Human Resources Development programs in Biotechnology and the engagement of relevant industries with these programs, DBT convened a meeting at RCB Faridabad on June 4, 2024.The meeting saw the participation of industry stakeholders from Confederation of Indian Industry (CII), Federation of Indian Chambers of Commerce & Industry (FICCI), Association of Biotechnology Led Enterprises (ABLE), Association of Indian Medical Device Industry (AiMeD), academia, and Sector Skill Councils, including the Life Sciences Sector Skill Development Council (LSSSDC), Food Industry Capacity & Skill Initiative (FICSI), Agriculture Skill Council of India (ASCI), Healthcare Sector Skill Council (HSSC), and Biotechnology Industry Research Assistance Council (BIRAC). The meeting underscored the importance of fostering close collaboration and creating synergy between industries, Sector Skill Councils, and various DBT initiatives. Specific programs highlighted included the DBT-Biotechnology Industrial Training Program (BITP), Skill Vigyan, and the Biotechnology Research and Innovation Council (BRIC), which encompasses 13 autonomous DBT institutes, along with their PhD programs and other new initiatives.

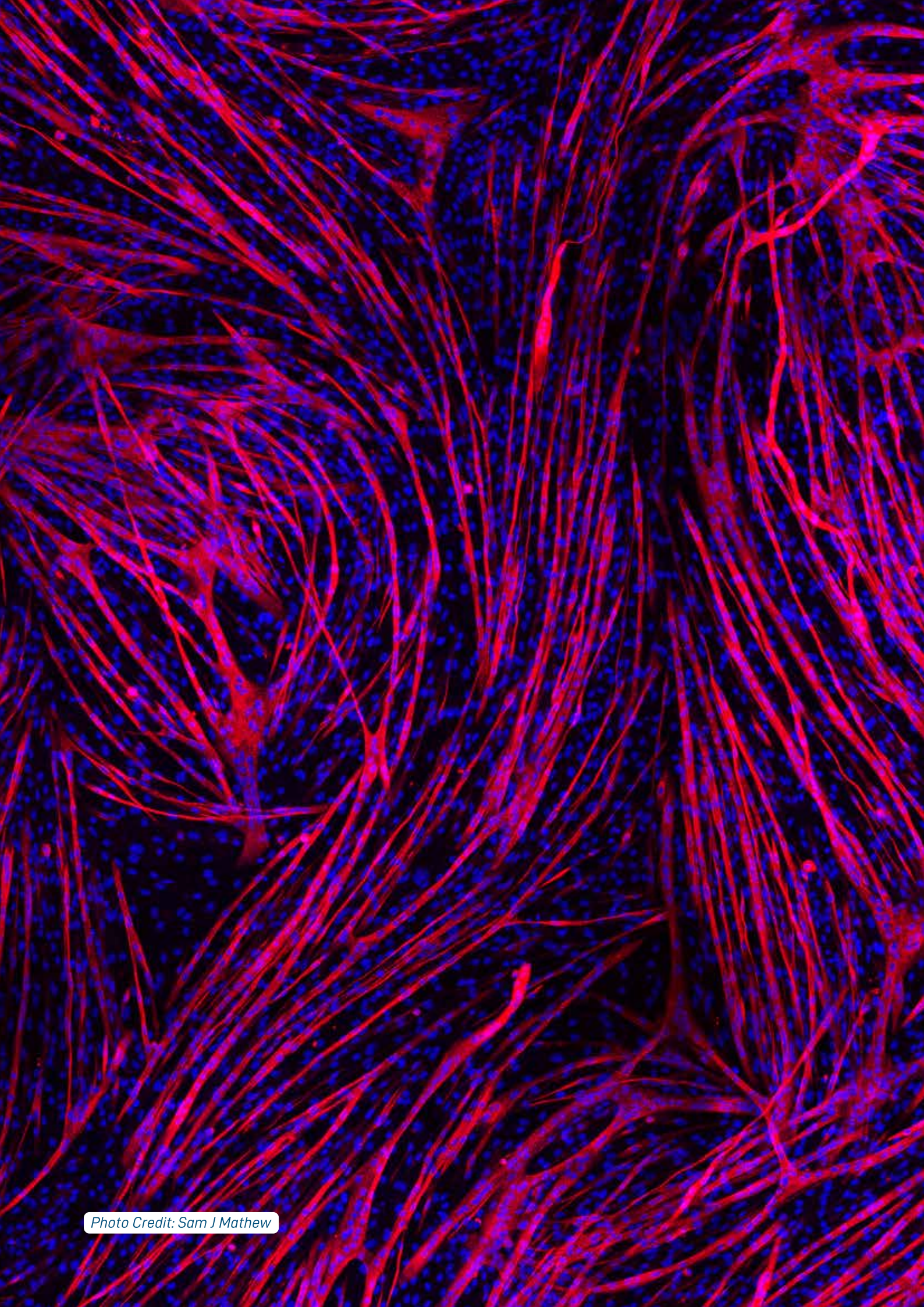
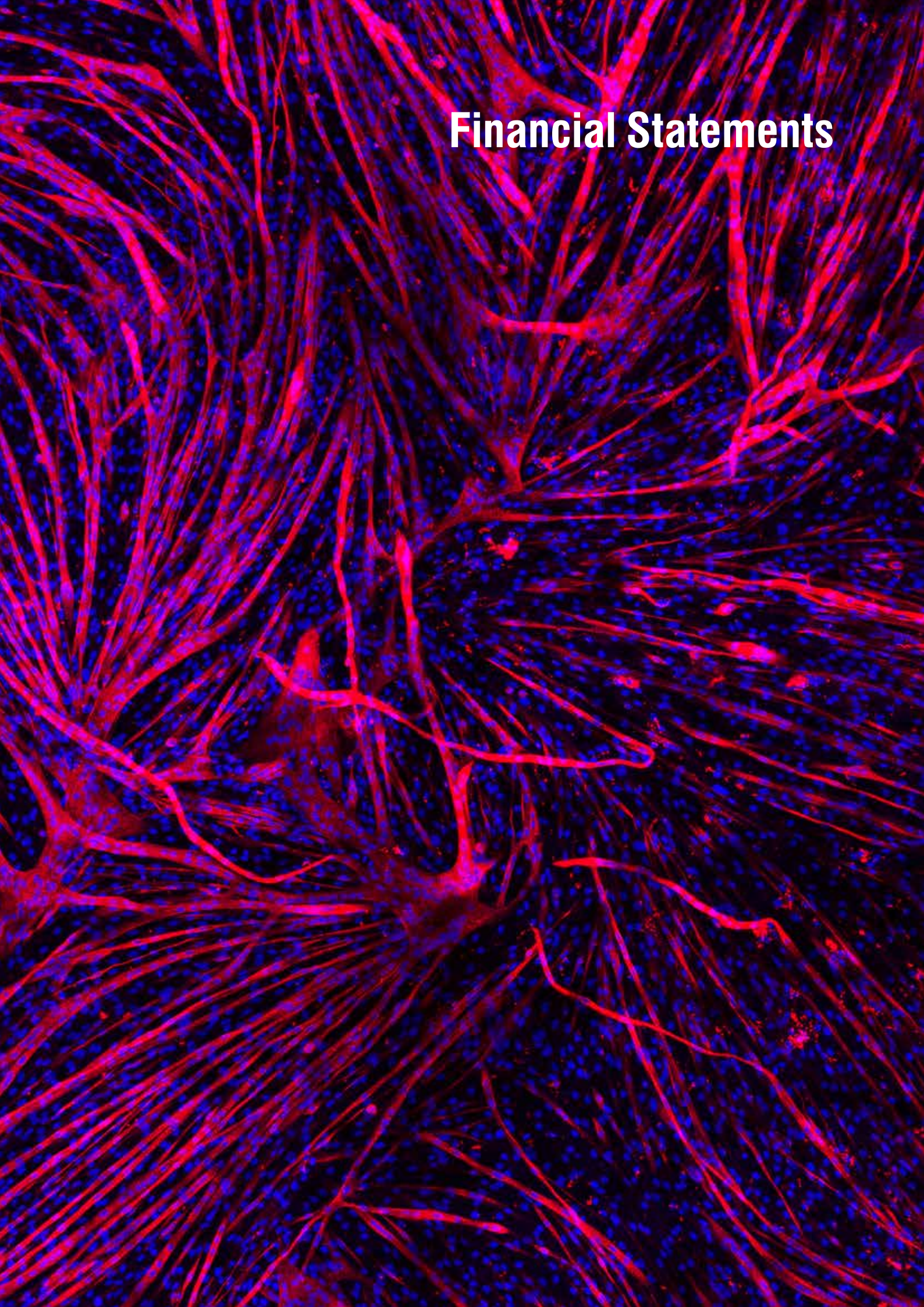


Photo Credit: Sam J Mathew



Financial Statements

REGIONAL CENTRE FOR BIOTECHNOLOGY, FARIDABAD

BALANCE SHEET AS AT 31st MARCH, 2025

Amount (₹)

LIABILITIES	Schedule	31.03.2025	31.03.2024
Corpus / Capital Fund	1	14,95,16,078	11,55,46,595
Reserves and Surplus	2	1,24,86,54,247	1,19,91,85,248
Earmarked/Endowment Funds	3	40,00,000	-
Secured Loans and Borrowings	4	-	-
Unsecured Loans and Borrowings	5	-	-
Deferred Credit Liabilities	6	-	-
Current Liabilities and Provisions	7	29,11,38,513	27,60,46,354
TOTAL		**1,69,33,08,838**	**1,59,07,78,197**
ASSETS			
Fixed Assets	8	95,47,50,561	99,73,68,711
Investment From Earmarked/Endowment Funds	9	-	
Investment-Others	10	30,82,41,762	29,61,37,261
Current Assets, Loans, Advances etc.	11	24,25,76,358	15,87,19,225
Capital Work In Progress	8	18,77,40,157	13,85,53,000
TOTAL		**1,69,33,08,838**	**1,59,07,78,197**
Significant Accounting Policies and Notes on Accounts	24		
Contingent Liabilities	25		

Schedules 1 to 25 form an integral parts of Accounts

(C.B. YADAV)
ADMINISTRATIVE OFFICER (F)

सी. बी. यादव, प्रशासनिक अधिकारी (वित्त एवं लेखा)
C.B. YADAV, Administartive Officer (F &A)
क्षेत्रीय जैवप्रौद्योगिकी केन्द्र
Regional Centre for Biotechnology
फरीदाबाद, हरियाणा/Faridabad, Haryana

(Dr. SUDEEP BHAR)
CONTROLLER of ADMINISTRATION

डॉ. सुदीप भार, प्रशासन नियंत्रक
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फरीदाबाद, हरियाणा

(PROF. ARVIND K. SAHU)
EXECUTIVE DIRECTOR

प्रो. अरविंद के. साहू / Dr. Arvind K. Sahu
कार्यकारी निदेशक / Executive Director
क्षेत्रीय जैवप्रौद्योगिकी केन्द्र / Regional Centre for Biotechnology
फरीदाबाद - 121 001 (हरियाणा) भारत / Faridabad 121 001 (Haryana) India

REGIONAL CENTRE FOR BIOTECHNOLOGY,FARIDABAD

INCOME & EXPENDITURE ACCOUNT FOR YEAR ENDED 31st MARCH, 25

Amount (₹)

INCOME	Schedule	31.03.2025	31.03.2024
Income from Sales/ Services	12	1,63,44,464	2,38,15,614
Grants/Subsides	13	46,25,70,981	39,66,66,808
Fees/Subscriptions	14	1,60,97,420	68,29,710
Income from Investments	15	-	-
Income from Royalty, Publication etc.	16	-	-
Interest Earned	17	2,42,93,890	2,40,99,292
Other Income	18	41,89,614	32,63,707
Increase/(Decrease) in stock of Finished goods and works in progress	19	-	-
Deferred Income-Fixed Assets		13,92,35,289	11,41,82,615
TOTAL (A)		**66,27,31,658**	**56,88,57,746**
EXPENDITURE			
Establishment Expenses	20	17,27,25,877	15,01,17,641
Other Administrative Expenses etc.	21	31,68,01,009	26,67,65,473
Expenditure on Grants , Subsidies etc.	22	-	-
Interest	23	-	-
Depreciation (Net Total at the year-end-corresponding to Schedule 8)		13,92,35,289	11,41,82,615
Prior period Adjustment A/c (ANN-A)			
TOTAL(B)		**62,87,62,175**	**53,10,65,729**
Balance being excess of Income Over Expenditure (A-B)		**3,39,69,483**	**3,77,92,017**
Transfer to special Reserve(Specify each)			-
Transfer to /from General Reserve		3,39,69,483	3,77,92,017
BALANCE BEING SURPLUS /DEFICIT CARRIED TO CORPUS/CAPITAL FUND		-	-
Significant Accounting Policies and Notes on Accounts	24		
Contingent Liabilities	25		

Schedules 1 to 25 form an integral parts of Accounts

(C.B. YADAV)
ADMINISTRATIVE OFFICER (F)

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क्षेत्रीय जैवप्रौद्योगिकी केन्द्र / Regional Centre for Biotechno
फरीदाबाद - 121001 (हरियाणा), भारत / Faridabad-121 001 (Haryana

Regional Centre for Biotechnology

Schedule 24: Accounting Policies and Notes Forming Parts of the Balance Sheet and Income & Expenditure Account for the Year Ended at 31st March 2025.

1. The annual accounts have been broadly prepared in the revised format of accrual system of accounting, **except for extramural funds and other project grants.**

2. The liability on account of terminal benefits to employees like leave encashment & gratuity have been accounted for in accordance with Accounting Stanbdard-15 on actuarial valuation basis.

3. (a) Recurring Grants have been recognised in the Income & Expenditure account and Non-Recurring Grants have been shown as part of Capital reserve.

(b) Grant of core funds relating to depreciable fixed assets are treated as deferred income and recognised in the Income and Expenditure Account on a systematic and rational basis over the useful life of such assets i.e. such grants are allocated to income over the periods and in the proportions in which depreciation in charged (As per Accounting Standard-12 title Accounting for Government Grants). During the year income recognised in respect of such Grants amounts to **Rs.13.92 crores.**

4. (a) The depreciation has been provided w.e.f. the date of installation/put to use of fixed assets as per the rates prescribed as per section 32 of Income Tax Act 1961.

(b) Depreciation has been charged during the year of acquisition, and no depreciation is provided during the year of assets sold / discarded. In respect of additions to/deductions from fixed assets during the year, depreciation is considered on pro-rata basis.

5. (a) Fixed assets have been created with core grants received from the Department of Biotechnology. No equipment procured out of project funds have yet been capitalized.

(b) Fixed Assets are stated at cost acquisition inclusive of custom duty (non-recoverable) and taxes, inward freight, incidental and direct expenses related to acquisition.

6. All purchases of chemicals, glassware, consumables and stationery have been charged to consumption at the time of purchase without working out closing stock at the end of the year.

7. Further all entries relating to purchase of consumables /equipment or other fixed assets in accounts are being passed only after submission of satisfactory Bill/Invoice, inspection/installation report irrespective of the date of actual receipt of the supplies /equipment.

8. Transactions denominated in foreign currency are accounted at the exchange rate prevailing at the date of transaction.

9. The institute has a policy of incurring expenditure on various projects in accordance with the sanctioned budget under various heads of accounts irrespective of the actual releases during a financial year. Since the actual release of money by the sponsoring agency is subject to various factors, the expenditure on approved heads of accounts is incurred within the overall sanction budget of the project.

सी. बी. यादव, प्रशासनिक अधिकारी (वित्त व लेखा)
C.B. YADAV, Administartive Officer (F&A)
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Regional Centre for Biotechnology

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10. The balances of the previous year have been rearranged/regrouped as per requirement and shown in Balance Sheet against the relevant heads.

11. Expenses and Overheads incidental to construction building of institute as well as other buildings in the NCR BSC, as reported by the Project Monitoring Unit are added to the capital work in progress to be capitalized along with the building only on submission of final accounts.

13. The Capital Work-in-progress booked in the accounts includes the construction of laboratory buildings of ATPC, Bio-incubator and hostels & faculty housing, common facilities, BSL-3 laboratory, Office of Connectivity Building, etc. under Phase-I Extension and Phase II. The expenditure under Phase-I was transferred to the respective stakeholders as per their contribution and area wise expenditure. Expenditure under Phase-I was capitalised during the FY 2019-20 Phase-II has been settled during FY 2022-23 & that of under Phase-I Extension has been settlement during 2023-24. The remaining WIP appearing in the Balance Sheet exclusively relates to under construction hostel building.

14. Interest earned on saving bank account and fixed deposits during the financial year 2024-25 amounting to **Rs.10.57 Lakhs** has been allocated to the respective projects on pro-rata basis.

15. No income tax or GST scrutiny is pending for any of the years.

Schedule 25: Contingent Liabilities

1. An Amount of **Rs.11.88 Lakhs** recovered from security deposit of M/s Disha Electronics due to non-completion of work by the contractor is presently classified as a contingent liability. Due to a dispute, the deposit has not been released, and arbitration proceedings are ongoing. Based on current information: (i) the possibility of an outflow, while not remote, is uncertain; (ii) the amount and timing of any outflow cannot be reliably determined; and (iii) therefore no provision has been made, but the matter is disclosed accordingly. The position will be reviewed at each reporting date.

(C.B. YADAV)
ADMINISTRATIVE OFFICER (F)

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फरीदाबाद - 121 001 (हरियाणा), भारत / Faridabad-121 001 (Haryana), India

सत्यमेव जयते

कार्यालय महानिदेशक लेखापरीक्षा,केन्द्रीय व्यय
पर्यावरण एवं वैज्ञानिक विभाग
नई दिल्ली-110 002
OFFICE OF THE DIRECTOR GENERAL OF AUDIT, CENTRAL EXPENDIT
ENVIRONMENT & SCIENTIFIC DEPARTMENTS,
A.G.C.R. BUILDING, I.P. ESTATE
NEW DELHI-110 002

स.म.नि.ले.प.के.व्य.(पर्या.एवं वै.वि)/नि/4(147)SAR/RCB/2024-25/337-338 दिनांकः 11.11.2025

सेवा में,

डॉ. अरविंद के. साहू,
कार्यपालक निदेशक,
क्षेत्रीय जैव प्रौद्योगिकी केन्द्र,
तृतीय मील पत्थर, फरीदाबाद-गुडगांव एक्सप्रेसवे,
फरीदाबाद-121001

विषयः क्षेत्रीय जैव प्रौद्योगिकी केन्द्र, के वर्ष 2024-25 के लेखों पर पृथक ऑडिट रिपोर्ट।

महोदय,

मुझे क्षेत्रीय जैव प्रौद्योगिकी केन्द्र के वर्ष 2024-25 के लेखों पर ऑडिट रिपोर्ट अग्रेषित करने का निर्देश हुआ है।

संसद के दोनों सदनों में प्रस्तुत करने से पहले वर्ष 2024-25 के वार्षिक लेखों को क्षेत्रीय जैव प्रौद्योगिकी केन्द्र द्वारा अपनाया जाए। प्रत्येक दस्तावेज जो संसद में प्रस्तुत किया जाए उसकी तीन प्रतियां इस कार्यालय तथा दो प्रतियां भारत के नियंत्रक एवं महालेखापरीक्षक को अग्रेषित की जाए। संसद के दोनों सदनों में प्रस्तुत करने की तिथि (या) भी इस कार्यालय को सूचित की जाए।

आपसे अनुरोध है कि पृथक ऑडिट रिपोर्ट का हिन्दी अनुवाद अपने कार्यालय में कराने के पश्चात सॉफ्ट कॉपी तथा हार्ड कॉपी दोनों में हमें भेज दें ताकि हिन्दी प्रति को शीघ्र अग्रेषित किया जा सके।

यह महानिदेशक महोदया द्वारा अनुमोदित है।

भवदीय,

संलग्नकः यथोपरि।

10/11

उप-निदेशक (निरीक्षण)

OPINION OF THE COMPTROLLER & AUDITOR GENERAL OF INDIA ON THE ACCOUNTS OF REGIONAL CENTRE FOR BIOTECHNOLOGY, FARIDABAD FOR THE YEAR ENDED 31 MARCH, 2025

Opinion

We have audited the Financial Statements of Regional Centre for Biotechnology, Faridabad, which comprise the Statement of Financial Position as at 31st March, 2025 and the Income & Expenditure Account/Receipts & Payment Account for the year then ended and notes to the Financial Statements, including a summary of Significant Accounting Policies under Section 19(2) of the Comptroller & Auditor General's (Duties, Powers & Conditions of Service) Act, 1971 read with Section 32 (1) of RCB Act, 2016.

This Audit Report contains the comments of the Comptroller & Auditor General of India (CAG) on the accounting treatment only with regard to classification, conformity with the best accounting practices, accounting standards, disclosure norms etc. Audit observations on Financial Transactions regarding compliance with the Law, Rules and Regulations (Propriety & Regularity) and efficiency cum performance aspects, etc., if any, are reported through Inspection reports/ CAG's audit reports separately.

In our opinion the accompanying Financial Statements of RCB read together with the accounting policies and Notes thereon and matters mentioned in the Separate Audit Report, which follows, **give a true and fair view** of the Financial Position of the autonomous body as at March 31, 2025, and of its Financial Performance and its cash flows for the year then ended in accordance with uniform format of accounts applicable to the RCB.

Basis for Opinion

We conducted our audit in accordance with the CAG's auditing regulations/standards/manuals/guidelines/guidance-notes/orders/circulars, etc. Our responsibilities are further described in the *Auditor's Responsibilities for the Audit of the Financial Statements* section of our report. We are independent of the autonomous body in accordance with ethical requirements that are relevant to our audit of the Financial Statements, and we have fulfilled our other ethical responsibilities in accordance with these requirements. We believe that the audit evidence we have obtained is sufficient and appropriate to provide a basis for our opinion.

Emphasis of Matter –Nil

Responsibilities of Management for the Financial Statements

The Body of Governors of Regional Centre for Biotechnology, Faridabad is responsible for the preparation and fair presentation of the Financial Statements in accordance with uniform format of accounts, and for internal control as management determines it necessary to enable the preparation of Financial Statements that are free from material misstatement, whether due to fraud or error.

Auditor's Responsibilities for the Audit of the Financial Statements

Our objectives are to obtain reasonable assurance about whether the Financial Statements as a whole are free from material misstatement, whether due to fraud or error, and to issue an auditor's report that includes our opinion in accordance with CAG's auditing regulations /standards/ manuals/ guidelines/ guidance-notes/ orders/ circulars etc.

Separate Audit Report on the Accounts of Regional Centre for Biotechnology, Faridabad for the year 2024-25

A. Balance Sheet

A.1 Liability

A.1.1 Current Liabilities and provisions ₹29.11 crore

As per Uniform Format of Accounts, amounts received as grant or assistance or retained by the entity to be utilised for specific or earmarked purposes and remaining to be expended/utilised for the specific purpose for which these are intended, are required to be disclosed under the Schedule 3: 'Earmarked/Endowment Funds'.

RCB booked balances of project grants and fellowships amounting to ₹947.76 lakh under 'Schedule-7: Current Liabilities' instead of 'Schedule-3: Earmarked/ Endowment Funds'. This led to understatement of Earmarked/Endowment Funds by ₹947.76 lakh and overstatement of Current Liabilities by the same amount. It also led to insufficient disclosures of capital and revenue expenditure incurred under these projects which were required to be depicted in Schedule 3.

B. Income and Expenditure Account

B.1 Income ₹1.60 crore

PHD fees receivable amounting to ₹10.40 lakh from Centre for DNA Fingerprinting and Diagnostics (CDFD) is not booked for FY 2018-19 to 2024-25. Hence, Income and Fees Receivable and are understated by ₹10.40 lakh. The prior period income by ₹10.40 lakh for 2018-19 to 2023-24 and current year income is understated by ₹.40 lakh and Surplus are understated by ₹10.40 lakh.

B.2 Expenditure

B.2.1 Understatement of Expenditure

An amount of ₹93.99 lakh pertaining to the expenditure for the FY 2024-25 is booked in FY 2025-26 and for which no provision was made in the annual accounts of RCB in the FY 2024-25. This resulted in understatement of expenditure besides understatement of Current Liabilities both by ₹93.99 lakh (Annexure).

C. Accounting Policies

Accounting policy adopted by RCB for chemicals, glassware, consumables and stationary was not in conformity with generally accepted accounting principles, as all purchases of chemicals, glassware, consumables and stationery were charged to consumption at the time of purchase.

Chemical consumptions booked by RCB amounting to ₹928.51 lakh and stationery of ₹21.23 lakh is fully charged as consumption, which is in contravention of Uniform Format of Accounts prescribed by Government of India for Autonomous Bodies.

This issue was also reported in previous years' Audit Reports (for the years 2023-24 and 2022-23).

D. General

D.1 TDS & TCS Recoverable

The amount of ₹62,98,975.50 pertaining to TDS refund have remained outstanding since 2011-12. Without realisation of TDS from Income Tax Department despite repeated follow ups, these amounts have not been refunded or adjusted in the books of account**.**

E. Management Letter

Deficiencies which have not been included in this Separate Audit Report have been brought to the notice of the Management through a Management Letter issued separately for remedial/corrective action.

F. Assessment of Internal Controls

(i) **Adequacy of Internal Control System**: No deficiencies were noticed.
(ii) **Adequacy of Internal Audit System**: Internal Audit has been conducted by Regional Centre for Biotechnology, Faridabad till FY 2022-23.
(iii) **System of Physical verification of fixed assets**: Physical verification of Fixed Assets has been done up to November 2024.
(iv) **System of Physical verification of inventory**: Physical verification of Inventory has been done up to November 2024.
(v) **Regularity in payment of statutory dues**: No discrepancies noticed.
(vi) **Other matters relating to functioning of the entity:** Nil

G. Grants in Aid

Out of the Grants in Aid of ₹66.92 crore received during the year, the organisation could utilise a sum of ₹64.76 crore leaving a balance of ₹2.16 crore as unutilised grant as on 31 March 2025.

H. Lack of response – Nil

For and on behalf of the CAG of India

Director General of Audit, Central Expenditure
(Environment and Scientific Departments)

Place: New Delhi
Date: 11.11.2025

Annexure

Sl. No.	Voucher No.	Voucher Date	Amount (In ₹)	Bill Date	Purpose
1.	PV/39/RCB/25-26	15-Apr-25	13,246.00	21-Mar-25	Material
2.	PV/38/RCB/25-26	15-Apr-25	99,897.00	27-Feb-25	Material
3.	PV/37/RCB/25-26	15-Apr-25	83,393.00/	28-Mar-25	Material
4.	PV/36/RCB/25-26	15-Apr-25	31,101.00	24-Mar-25	Material
5.	PV/35/RCB/25-26	15-Apr-25	4,57,600.00	28-Mar-25	Material
6.	PV/34/RCB/25-26	15-Apr-25	23,452.00	24-Mar-25	Material
7.	PV/33/RCB/25-26	15-Apr-25	55,480.00	24-Mar-25	Material
8.	PV/32/RCB/24-25	15-Apr-25	2,29,388.00	28-Mar-25	Material
9.	PV/31/RCB/24-25	15-Apr-25	99,180.00	20-Mar-25	Material
10.	PV/29/RCB/25-26	11-Apr-25	3,00,489.79	13-Mar-25	Article Processing Charge
11.	PV/24/RCB/25-26	08-Apr-25	19,824.00	19-Feb-25	Material
12.	PV/23/RCB/25-26	08-Apr-25	34,593.00	07-Mar-25	Material
13.	PV/22/RCB/25-26	08-Apr-25	44,100.00	06-Mar-25	Material
14.	PV/21/RCB/25-26	08-Apr-25	2,03,472.00	07-Mar-25	Material
15.	PV/20/RCB/25-26	08-Apr-25	1,02,814.00	04-Mar-25	Material
16.	PV/19/RCB/25-26	08-Apr-25	4,98,429.00	10-Mar-25	Material
17.	PV/18/RCB/25-26	08-Apr-25	3,62,440.00	04-Mar-25	Material
18.	PV/17/RCB/25-26	08-Apr-25	5,00,464.00	05-Mar-25	Material
19.	PV/16/RCB/25-26	08-Apr-25	4,43,680.00	11-Mar-25	Material
20.	PV/15/RCB/25-26	08-Apr-25	28,334.00	05-Mar-25	Material
21.	PV/12/RCB/25-26	08-Apr-25	1,89,216.00	10-Feb-25	Conference
22.	PV/06/RCB/25-26	08-Apr-25	14,98,637.00	21-Feb-25 to 5-Mar-25	Conference
23.	PV/87/RCB/25-26	21-Apr-25	24,501.00	22-Mar-25	Material
24.	PV/86/RCB/25-26	21-Apr-25	26,068.00	24-Mar-25	Material
25.	PV/84/RCB/25-26	21-Apr-25	2,29,962.00	22-Mar-25	Material
26.	PV/83/RCB/25-26	21-Apr-25	1,13,969.00	21-Mar-25	Material
27.	PV/82/RCB/25-26	21-Apr-25	13,446.00	10-Mar-25	Material
28.	PV/81/RCB/25-26	21-Apr-25	63,720.00	25-Mar-25	Material
29.	PV/80/RCB/25-26	21-Apr-25	4,31,631.00	11-Mar-25	Material
30.	PV/79/RCB/25-26	21-Apr-25	73,691.00	21-Mar-25	Material
31.	PV/78/RCB/25-26	21-Apr-25	17,802.00	03-Mar-25	Material
32.	PV/77/RCB/25-26	21-Apr-25	19,686.00	24-Feb-25	Material
33.	PV/76/RCB/25-26	21-Apr-25	14,383.00	27-Feb-25	Material
34.	PV/75/RCB/25-26	21-Apr-25	30,943.00	22-Feb-25	Material

35.	PV/74/RCB/25-26	21-Apr-25	29,028.00	28-Feb-25	Material
36.	PV/73/RCB/25-26	21-Apr-25	10,152.00	05-Mar-25	Material
37.	PV/72/RCB/25-26	21-Apr-25	49,997.00	21-Mar-25	Material
38.	PV/71/RCB/25-26	21-Apr-25	17,157.00	24-Mar-25	Material
39.	PV/70/RCB/25-26	21-Apr-25	1,27,321.00	04-Mar-25	Material
40.	PV/69/RCB/25-26	21-Apr-25	60,202.00	27-Feb-25	Material
41.	PV/68/RCB/25-26	21-Apr-25	1,99,267.00	26-Feb-25	Material
42.	PV/67/RCB/25-26	21-Apr-25	1,31,688.00	26-Feb-25	Material
43.	PV/66/RCB/25-26	21-Apr-25	26,662.00	28-Feb-25	Material
44.	PV/65/RCB/25-26	21-Apr-25	39,079.00	15-Jan-25	Material
45.	PV/64/RCB/25-26	21-Apr-25	34,810.00	21-Feb-25	Material
46.	PV/63/RCB/25-26	21-Apr-25	12,377.00	17-Feb-25	Material
47.	PV/62/RCB/25-26	21-Apr-25	1,39,588.00	14-Feb-25	Material
48.	PV/61/RCB/25-26	17-Apr-25	1,41,600.00	18-Feb-25	Material
49.	PV/60/RCB/25-26	17-Apr-25	33,040.00	22-Mar-25	Material
50.	PV/59/RCB/25-26	17-Apr-25	2,06,463.00	24-Feb-25	Material
51.	PV/58/RCB/25-26	17-Apr-25	29,258.00	04-Mar-25	Material
52.	PV/57/RCB/25-26	17-Apr-25	12,823.00	04-Mar-25	Material
53.	PV/56/RCB/25-26	17-Apr-25	32,568.00	20-Feb-25	Material
54.	PV/55/RCB/25-26	17-Apr-25	1,21,083.00	22-Feb-25	Material
55.	PV/54/RCB/25-26	17-Apr-25	9,98,327.00	18-Mar-25	Material
56.	PV/53/RCB/25-26	17-Apr-25	1,01,965.00	24-Mar-25	Material
57.	PV/51/RCB/25-26	17-Apr-25	3,54,850.00	21-Feb-25 to 25-Feb-25	Conference
58.	PV/41/RCB/25-26	15-Apr-25	1,10,802.00	05-Mar-25	Material
Total			**93,99,138.79**		

DGA(ESD)/Inspection/4(147)/SAR/RCB/2024-25/337-338 **Date: 11.11.2025**

Management Letter

1. As per Uniform format of Accounts, debtors exceeding six months are to be shown as prescribed in Schedule 11 - Current Assets, Loans & Advances. During audit on test check basis, cases of debtors exceeding six months were observed. However, bifurcation of debtors exceeding six months was not made as per the prescribed format.
2. NCBS Receivable A/c has opening balance of ₹0.26 lakh since April, 2016 which has not been adjusted so far. Hence, it is suggested that this issue shall be followed vigorously.
3. RCB conducted road show during the financial year and generated revenue by charging stall charges, during audit it is noticed that Road Show amounting to ₹0.40 lakh are booked in Misc. Receipt instead of Income from Road Show resulted understatement of income under the head Income from Road Show and subsequently overstatement of income in Income from Misc. Receipt by ₹0.40 lakh. In Addition to above para, road show is taxable supply under GST Act, amounting to ₹40,000 against GST liability ₹7,200 (₹40,000 at the rate of 18 per cent) which was not booked resulting in understatement of Duties and Taxes Liability under Current Liabilities & Provisions by ₹7,200. Subsequently, this was also to be shown in GST return and paid tax accordingly.
4. A.1.2 As per Uniform Format of Accounts prescribed by Government of India for Autonomous Bodies the head Current Liabilities and Provisions does not consist of Contingent Liabilities. However, RCB withheld an amount of ₹11.88 lakh for the work executed by M/s Disha Electronics which was reflected as Contingent Liability in Schedule 7 of Current Liabilities & Provisions. It should have been disclosed only in notes to accounts under head Contingent Liabilities.
5. A.1.3 RCB had shown an amount of ₹20.38 lakh in suspense head under Schedule 7 - current Liabilities & Provisions. Annual accounts should not contain a Suspense Head as it indicates unclassified or unmatched transactions. All transactions should be properly categorised and allocated to their appropriate accounts before finalisation of accounts to ensure accuracy and transparency.

6. In Schedule 8, additions of assets during the year under the following heads was not shown correctly:

Head	Half year period	Amount shown in Schedule 8	Actual purchase as per Assets Register	Difference	Rate of Depreciation (In *per cent*)	Difference in Depreciation
Lab Equipment	1st	3,18,74,090	1,94,85,886.99	1,23,88,203.01	15	18,58,230.45
Lab Equipment	2nd	3,61,76,403	4,52,68,727.50	-90,92,324.50	7.5	-6,81,924.34
Furniture and Fixture	1st	42,44,718	36,51,135	5,93,583	10	59,358.30
Furniture and Fixture	2nd	27,20,471	16,26,766.08	10,93,704.92	5	54,685.25
Office Equipment	1st	4,52,933	3,62,994.37	89,938.63	15	13,490.79
Office Equipment	2nd	27,09,044	10,93,390.24	16,15,653.76	7.5	1,21,174.03
Computer and Peripherals	1st	1,11,20,935	50,59,573	60,61,362	40	24,24,544.80
Computer and Peripherals	2nd	63,19,309	51,37,732.31	11,81,576.69	20	2,36,315.34
Total		**9,56,17,903**	**8,16,86,205.49**	**1,39,31,697.51**		**40,85,874.62**

This incorrect depiction of assets resulted in overstatement of assets by ₹98.46 lakh (₹139.32 lakh less ₹40.86 lakh depreciation thereon), overstatement of liabilities by ₹139.32 lakh and overstatement of expenditure by ₹40.86 lakh.

7. Expenditure amounting to ₹23.08 lakh pertaining to the year 2023-24 and ₹61.66 lakh pertaining to 2022-23 is booked in FY 2024-25 and for which no provision was made in the annual accounts of RCB in the respective years. This resulted in overstatement of expenditure besides understatement of prior period expenses by ₹84.74 lakh. (Annexure)
8. Receipts and Payments Account was not as per Uniform Format of Accounts prescribed by the Government of India for Autonomous Bodies as it contained various heads like 'Current Liabilities', 'Current Assets', 'Fixed Assets', which are not part of Receipt and Payment Account as per Uniform Format of Accounts.
9. The accounting policy 2 of the Schedule of Significant Accounting Policies does not fulfil the disclosure requirements as prescribed in AS 15.

भवदीय

उपनिदेशक (निरीक्षण)

Dr. Arvind K. Sahu
Executive Director,
Regional Centre for Biotechnology,
NCR Biotech Science Cluster,
3rd Milestone, Faridabad- Gurugram Expressway,
Faridabad, Haryana- 121 001.

Annexure

Sl. No.	Voucher No.	Voucher Date	Amount (In ₹)	Bill Date	Purpose
Expenditure pertaining to the FY 2023-24					
1.	PV/67/RCB/24-25	19-Apr-24	6,33,186	14-Feb-24	Services
2.	PV/60/RCB/24-25	18-Apr-24	26,788	22-Mar-24	TA
3.	PV/56A/RCB/24-25	16-Apr-24	4,86,833	13-Mar-24	Material
4.	PV/55/RCB/24-25	16-Apr-24	43,413	14-Mar-24	Material
5.	PV/53/RCB/24-25	16-Apr-24	4,20,791	Fellowship for March 2024	Fellowship for March 2024
6.	PV/48/RCB/24-25	15-Apr-24	3,08,295	10-Mar-24	Services
7.	PV/47/RCB/24-25	15-Apr-24	2,58,132	11-Mar-24	Services
8.	PV/43/RCB/24-25	12-Apr-24	1,31,020	17-Feb-24	Material
			23,08,458		
Expenditure pertaining to the FY 2022-23					
9.	PV/42/RCB/24-25	12-Apr-24	61,65,760	Contribution for the month of Jan 2023	Services
			61,65,760		
TOTAL			**84,74,218**		

Institutional Governance

रजिस्ट्री सं० डी० एल०—(एन)04/0007/2003—16 REGISTERED NO. DL—(N)04/0007/2003—16

भारत का राजपत्र
The Gazette of India

असाधारण
EXTRAORDINARY
भाग II — खण्ड 1
PART II — Section 1
प्राधिकार से प्रकाशित
PUBLISHED BY AUTHORITY

सं० 43] नई दिल्ली, शनिवार, जुलाई 30, 2016/श्रावण 8, 1938 (शक)
No. 43] NEW DELHI, SATURDAY, JULY 30, 2016/SHRAVANA 8, 1938 (SAKA)

इस भाग में भिन्न पृष्ठ संख्या दी जाती है जिससे कि यह अलग संकलन के रूप में रखा जा सके।
Separate paging is given to this Part in order that it may be filed as a separate compilation.

MINISTRY OF LAW AND JUSTICE
(Legislative Department)

New Delhi, the 30th July, 2016/Shravana 8, 1938 (Saka)

The following Act of Parliament received the assent of the President on the 29th July, 2016, and is hereby published for general information:—

THE REGIONAL CENTRE FOR BIOTECHNOLOGY ACT, 2016

No. 36 OF 2016

[29*th July*, 2016.]

An Act to provide for the establishment of an institution of national importance to be known as Regional Centre for Biotechnology and to provide for matters connected therewith or incidental thereto.

WHEREAS an agreement for the establishment and operation of the Regional Centre for Biotechnology Training and Education in India was entered into between the Government of India and the United Nations Educational, Scientific and Cultural Organisation on the 14th day of July, 2006;

AND WHEREAS in pursuance of the said agreement, the Central Government through an executive order dated the 20th April, 2009, established the Regional Centre for Biotechnology Training and Education at Faridabad, Haryana;

AND WHEREAS it is expedient to make provisions for strengthening and to make the Regional Centre for Biotechnology an institution of national importance for imparting education, training and conducting research in the areas of Biotechnology and related multi disciplinary areas.

BE it enacted by Parliament in the Sixty-seventh Year of the Republic of India as

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• **Director (Ex-officio Member)** National Institute of Immunology, Delhi 110 067	• **Dr. Niloo Srivastava (Ex-officio Member)** RCB Nodal Officer and Scientist-F, Department of Biotechnology Govt. of India, New Delhi
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Controller of Administration
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Executive (Finance & Services)
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Mr. Avdesh Khankriyal

United Nations
Educational, Scientific and
Cultural Organization

क्षेत्रीय जैव प्रौद्योगिकी केन्द्र
Regional Centre
for Biotechnology

REGIONAL CENTRE FOR BIOTECHNOLOGY

An Institution of National Importance for Education, Training and Research

Established by the Dept. of Biotechnology, Govt. of India

Under the Auspices of UNESCO

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