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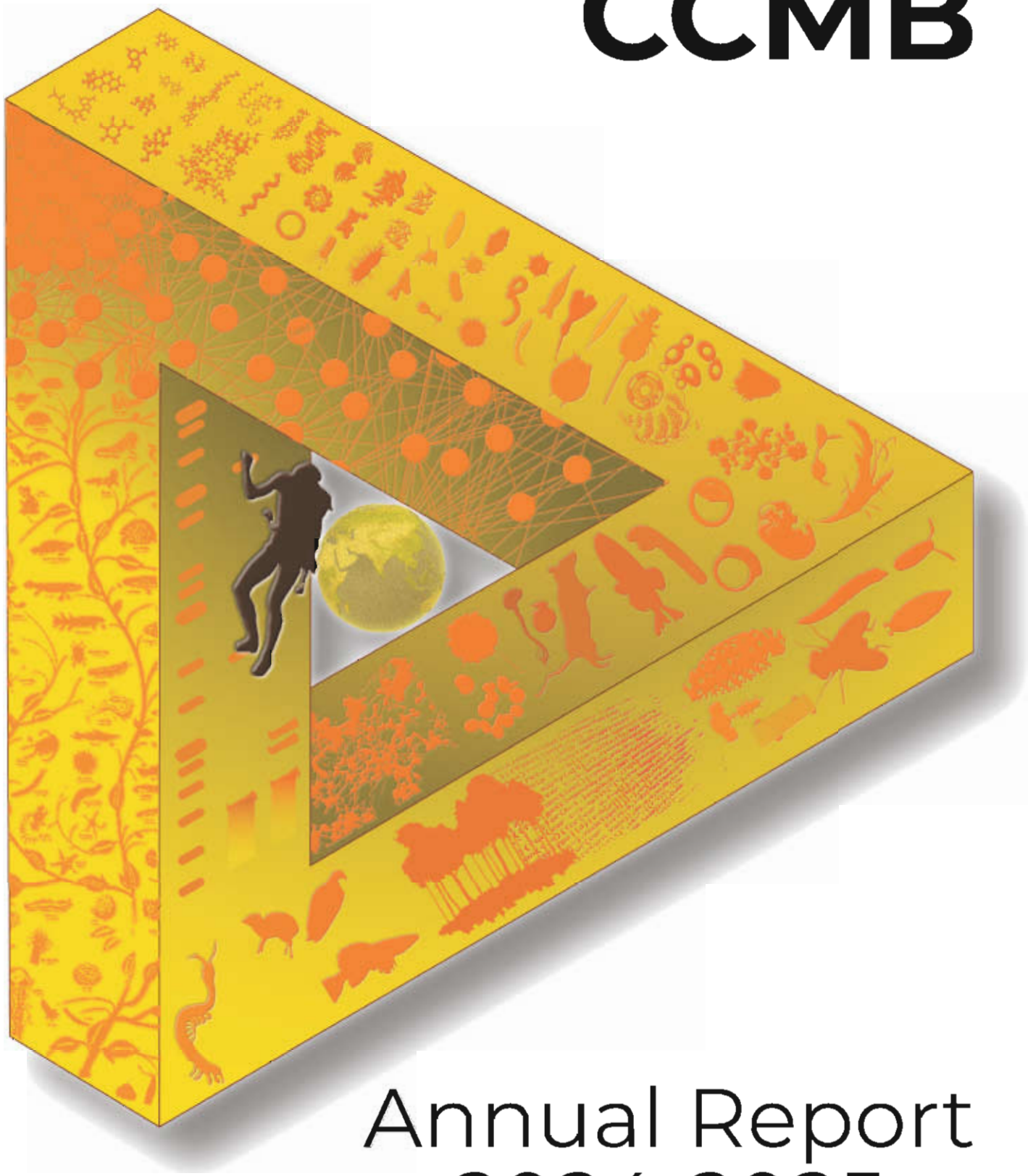

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2024-2025

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Front cover: The Penrose triangle is an impossibility in three dimensions. On it, the emergence of life from the interaction simple molecules into millions of species and their interplay in eco systems and larger scales is depicted. Us researchers are trying to glimpse the world having climbed the DNA ladder.

Back cover: From stardust emerges life generally with a shared structure. Some structures with similar function but vastly different forms and yet others that look the same but do entirely different things.

ANNUAL REPORT

2024-25

CCMB

CENTRE FOR CELLULAR AND MOLECULAR BIOLOGY,
HYDERABAD

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DIRECTOR'S FOREWORD



Vinay Kumar Nandicoori, Director, CSIR-CCMB



यह मेरा सौभाग्य है कि मैं सीसीएमबी के वार्षिक प्रतिवेदन 2024-25 की प्रस्तावना लिख रहा हूँ। आज, भारत जीव विज्ञान के क्षेत्र में उल्लेखनीय प्रगति कर रहा है, जिसमें जीनोम डिकोडिंग, आनुवंशिक इंजीनियरिंग विधियों का उपयोग करके संशोधित फसलें और वैश्विक उपयोग के लिए टीके विकसित करना शामिल है। आयुर्वेद से लेकर कृत्रिम बुद्धिमत्ता एआई-संचालित जीनोमिक्स तक की यात्रा हमारे समुदाय के लचीलेपन और अनुकूलनशीलता को दर्शाती है। सीएसआईआर-सीसीएमबी इन प्रगतियों में अग्रणी है। सीसीएमबी में, हम जैव सूचना विज्ञान, स्टेम सेल अनुसंधान और जलवायु जीव विज्ञान में अग्रणी हैं, साथ ही वनों, बाघों और तटरेखाओं के संरक्षण में भी सक्रिय हैं। पिछले 47 वर्षों में, सीसीएमबी ने डीएनए फ़िंगरप्रिंटिंग से लेकर वन्यजीव निदान तक, आधारभूत जीव विज्ञान के क्षेत्र में महत्वपूर्ण योगदान दिया है।

पिछले एक साल में, हमारे सीसीएमबी के सहयोगियों ने अपनी उपलब्धियों के लिए मान्यताएँ और पुरस्कार प्राप्त किए हैं, उच्च-स्तरीय शोध पत्र प्रकाशित किए हैं, चावल की एक नई किस्म का पता लगाया, और किफ़ायती पॉइंट-ऑफ़-केयर डायग्नोस्टिक्स विकसित किए हैं। डॉ. कुमारसामी थंगराज के जनसंख्या आनुवंशिकी और चिकित्सा जीनोमिक्स में दिए गए योगदान को मान्यता मिली है, और उन्हें सीएसआईआर भटनागर फेलो नामित किया गया है। डॉ. संतोष चौहान को आईएनएसए(INSA) का फेलो चुना गया है। बायोइन्फॉर्मेटिक्स एंड ड्रग डिस्कवरी सोसाइटी ने डॉ. राजन शंकरनारायणन को प्रोफेसर एन. श्रीनिवासन मेमोरियल लेक्चर अवार्ड से सम्मानित किया है। डॉ. रघुनंद तिरुमलाई को तेलंगाना विज्ञान अकादमी का फेलो चुना गया है। डॉ. गिरिराज चांडक ने सिकल सेल एनीमिया के लिए एक किफायती पॉइंट-ऑफ़-केयर ड्राई ब्लड स्पॉट टेस्ट विकसित और पेटेंट कराया और "लाइटनिंग लाइव्स" नाम से स्टार्टअप की स्थापना की। डॉ. हितेंद्र पटेल ने आईसीएआर के सहयोग से सांबा मसूरी चावल की धान श्रृंखला की किस्मों का पता लगाया, जो लवणता और दबाव सहनशीलता, जलवायु अनुकूलनशीलता, बेहतर उपज, बेहतर पोषण, रोग प्रतिरोधक क्षमता और सिंचाई की कम आवश्यकताओं के लिए जानी जाती हैं। डॉ. लेखा दिनेश कुमार ने एक संवेदनशील miRNA-आधारित परख (assay)विकसित किया है जो स्तन कैंसर के विभिन्न स्तरों, चरणों और प्रकारों का सटीक पूर्वानुमान लगाने में सक्षम है। इसके अतिरिक्त, सीसीएमबी के पूर्व छात्र डॉ. अरविंद पेनमत्सा को राष्ट्रीय विज्ञान पुरस्कार (विज्ञान युवा) से सम्मानित किया गया। स्नातक छात्रों और युवा शोधकर्ताओं को उनके वैज्ञानिक योगदान के लिए विभिन्न एजेंसियों द्वारा सम्मानित किया गया है, जिनमें अंतर्राष्ट्रीय सम्मेलनों के लिए यात्रा पुरस्कार, विदेशी प्रयोगशालाओं में शोध के लिए फेलोशिप, वैश्विक मंचों पर प्रस्तुति के लिए निमंत्रण और भारत एवं विदेश में वैज्ञानिक बैठकों में सर्वश्रेष्ठ पोस्टर पुरस्कार शामिल हैं। उन संकाय सदस्यों और छात्रों को बधाई जिनके कार्य को विभिन्न मंचों द्वारा मान्यता दी गई है।

प्रमुख जैविक पत्रिकाओं में हमारे प्रकाशन अग्रणी मौलिक अनुसंधान के प्रति हमारी निष्ठा को दर्शाते हैं। डॉ. इमरान सिद्दीकी की प्रयोगशाला द्वारा तैयार किया गया अध्ययन नेचर प्लांट्स में प्रकाशित हुआ है, तथा इससे हमें पौधों के विकास को समझने में मदद मिली है, क्योंकि वे द्विगुणित और अगुणित अवस्थाओं के बीच संक्रमण करते हैं। उनके अध्ययन से पता चला कि अरेबिडोप्सिस में, द्विगुणित स्पोरोफाइट नर युग्मकोद्भिद् (gametophyte) विकास को प्रभावित करता है। SHUKR जीन प्रोटीन अपघटन को बढ़ावा देकर कई अर्धसूत्रीविभाजन-पश्चात युग्मक जीनों को दबा देता है, जिससे पराग विकास के बारे में गहन जानकारी मिलती है। डॉ. कार्तिक भारद्वाज की टीम ने, यूरोपियन जर्नल ऑफ ह्यूमन जेनेटिक्स में प्रकाशित अपने अध्ययन में, CHM 13 संदर्भ का विश्लेषण करने के लिए "ऑप्टिकल जीनोम मैपिंग" का उपयोग किया, जिससे सेंट्रोमियर, टेलोमीयर और छोटे p-आर्म जैसे पहले से दूर के भूभाग के साथ-साथ बड़े डीएनए के पुनर्निर्माण का पता चला। यह प्रगति निदान को बेहतर बनाती है और सीसीएमबी को भारत में उन्नत आनुवंशिक परीक्षण में अग्रणी स्थान देती है। जर्नल ऑफ बायोजियोग्राफी में प्रकाशित डॉ. जाह्नवी जोशी की प्रयोगशाला के शोध से पता चलता है कि लंबे पैरों वाले इंडियन घरेलू सेंटीपीड (स्कूटीगेरोमॉर्फ) गोंडवाना के अवशेष हैं। जीनोमिक और जैवभौगोलिक आंकड़े बताते हैं कि वे लगभग 200 मिलियन वर्ष पहले अपने पूर्वजों से इंडियन प्लेट पर उत्पन्न हुए, वे बच गए, और ऑस्ट्रेलिया में आ गए, जिसके कारण संभवतः आज देखी जाने वाली विविधता का अधिकांश हिस्सा इन्हीं के कारण है। ईलाइफ में प्रकाशित हमारी प्रयोगशाला के शोध से पता चलता है कि टीबी के कारक माइकोबैक्टीरियम ट्यूबरकुलोसिस में एल-सिस्टीन का जैवसंश्लेषण अत्यंत महत्वपूर्ण है, और इसमें शामिल एंजाइम दवा के लिए भरोसेमंद लक्ष्य हैं। यूरोपियन जर्नल ऑफ ह्यूमन जेनेटिक्स में डॉ. के. थंगराज और डॉ. ज्ञानेश्वर चौबे द्वारा किए गए एक जीनोमिक अध्ययन में निकोबारी द्वीप समुदायों की उत्पत्ति पर दोबारा से विचार किया गया है, जिसमें दिखाया गया है कि वे दक्षिण और दक्षिण-पूर्व एशिया के ऑस्ट्रोएशियाटिक समूहों से निकटता से संबंध रखते हैं। लगभग~11,700 वर्षों के पूर्व अनुमानों के विपरीत, उनके पूर्वज संभवतः लगभग 5000 वर्ष पहले आए थे।

इस वर्ष, हमने 315 लोगों के बैठने की क्षमता के साथ नए पीएम भार्गव सभागार का उद्घाटन किया । ऑटोफैगी पर कार्यशालाएँ और टीबी में होस्ट और रोगजनक विषमता पर ईएमबीओ (EMBO) कार्यशाला आयोजित की गई, जिसमें रोग के अंतर्निहित जीव विज्ञान पर विशेष रूप से ध्यान केंद्रित किया गया। सीसीएमबी ने समूह प्रमुखों के लिए ईएमबीओ (EMBO) के लैबोरेटरी लीडरशिप कार्यक्रम का भी आयोजन किया। इसके अतिरिक्त, सीसीएमबी ने मांसपेशी जीवविज्ञानियों को एक साथ एक मंच पर लाने और इस क्षेत्र में अत्याधुनिक उपकरणों और ज़रूरी सवालों पर चर्चा करने के लिए " प्रजातियों के बीच मांसपेशियों का निर्माण और रोगों का इलाज" नाम से एक कार्यशाला का

आयोजन किया। सीसीएमबी युवाओं को लक्षित करते हुए अनेक आउटरीच गतिविधियाँ संचालित करता है। एक प्रमुख पहल के अंतर्गत "यंग इनोवेटर्स प्रोग्राम" है, जो हाई स्कूल के छात्रों को जीव विज्ञान में प्रयुक्त होने वाली प्रयोगशाला उपकरणों से परिचित कराता है। हमारा लक्ष्य है कि आजीविका संबंधी निर्णय लेने के इस शुरुआती चरण में, ये छात्र अपने भविष्य की राह तय करने के लिए जानकारी प्राप्त करें। पिछले एक साल में, सीसीएमबी ने सभी संवर्गों और विभागों में अधिकारियों एवं कार्मिकों की भर्ती की है। कई लोग पहले ही शामिल हो चुके हैं, और हमें उम्मीद है कि आने वाले वर्ष में हम सभी संवर्गों में और अधिक प्रतिभाशाली लोगों की भर्ती करेंगे। हमारे संस्थान में ऐसी वैज्ञानिक जीवंतता देखकर हमें बहुत खुशी होती है। नए सदस्यों के आगमन को देखते हुए, यह अत्यंत महत्वपूर्ण है कि वे हमारे अनुभवी सदस्यों के समान ही प्रतिबद्धता का स्तर प्रदर्शित करें, जिसमें समय प्रबंधन में अनुशासन, समर्पण और संगठन के प्रति निष्ठा शामिल हो। यह समर्पण हमें भविष्य में उत्कृष्ट और शानदार कार्य करने में सक्षम बनाएगा।

I am honored to write the foreword for the CCMB annual report 2024-25. Today, India is making significant progress in biology, including decoding genomes, engineering crops, and developing vaccines for global use. The journey from Ayurveda to AI-driven genomics reflects the resilience and adaptability of our community. CSIR-CCMB stands at the forefront of these advancements. At CCMB, we excel in bioinformatics, stem cell research, and climate biology, while also actively conserving forests, tigers, and coastlines. Over the past 47 years, CCMB has contributed crucially to foundational biology, from DNA fingerprinting to wildlife diagnostics.

Over the past year, our CCMB colleagues have received recognition and awards for their achievements, published top-tier research papers, introduced a new rice variety, and developed cost-effective point-of-care diagnostics. Dr. Kumarasamy Thangaraj's contributions to population genetics and medical genomics are recognized, and he has been named a CSIR Bhatnagar Fellow. Dr. Santosh Chauhan has been elected a fellow of INSA. The Bioinformatics and Drug Discovery Society awarded Dr. Rajan Sankaranarayanan the Prof. N. Srinivasan Memorial Lecture Award. Dr. Raghunand Tirumalai has been elected a Fellow of the Telangana Academy of Sciences. Dr. Giriraj Chandak developed and patented an affordable Point of Care dry blood spot test for Sickle Cell Anemia and founded the startup "Lightning Lives." Dr. Hitendra Patel, in collaboration with ICAR, introduced the Dhan series of Samba Masuri rice varieties known for salinity and stress tolerance, climate adaptability, high yield, improved nutrition, disease resistance, and lower irrigation needs. Dr. Lekha Dinesh Kumar developed a sensitive miRNA-based assay capable of accurately predicting different grades, stages, and types of breast cancer. Additionally, CCMB alumnus Dr. Aravinda Penmatsa received the Rashtriya Vigyan Puraskar (Vigyan Yuva). Graduate students and young researchers have been honored by various agencies for their scientific contributions, including travel awards for international conferences, fellowships for research in foreign labs, invitations to present at global forums, and best poster awards at scientific meetings in India and abroad. Congratulations to the faculty and students whose work has been recognized by various forums.

Our publications in leading biological journals underscore our dedication to pioneering fundamental research. Dr. Imran Siddiqi's lab, published in Nature Plants, and helped our understanding of plant development as they transition between diploid and haploid stages. Their study showed that in Arabidopsis, the diploid sporophyte influences male gametophyte development. The gene *SHUKR* suppresses many post-meiosis gamete genes by promoting protein degradation, offering deeper insights into pollen development. Dr. Karthik Bharadwaj's team, in their study published in European Journal of Human Genetics, used "Optical Genome Mapping" to analyze the CHM 13 reference, revealing previously inaccessible regions like centromeres, telomeres, and short p-arms, as well as large DNA rearrangements. This progress enhances diagnostics and establishes CCMB as a leader in advanced genetic testing in India. Research from Dr. Jahnavi Joshi's lab, published in the Journal of Biogeography, finds that Indian long-legged house centipedes (*scutigeromorphs*) are Gondwanan relics. Genomic and biogeographic data suggest they originated from ancestors on the Indian plate about 200 million years ago, survived India's drifting, and colonized Australia, likely driving much of the diversity seen today. Our lab's research published in eLife shows that L-cysteine biosynthesis in Mycobacterium tuberculosis, the TB causative agent, is crucial, with involved enzymes being promising drug targets. A genomic study led by Dr. K. Thangaraj and Dr. Gyaneshwar Chaubey, in the European Journal of Human Genetics,revises the origin of Nicobarese island communities, showing they are closely related to Austroasiatic groups in South and Southeast Asia. Contrary to earlier estimates of ~11,700 years, their ancestors probably

arrived around 5000 years ago.

This year, we inaugurated a new 315-seat PM Bhargava auditorium and hosted workshops on autophagy and an EMBO workshop on Host and Pathogen Heterogeneity in TB, focusing on the underlying biology of the disease. CCMB also organized EMBO's Laboratory Leadership Program for group leaders. Additionally, CCMB organized a workshop, "Muscling through Species and Treating Diseases," to bring together muscle biologists and discuss the cutting-edge tools and urgent questions being addressed in the field. CCMB engages in numerous outreach activities targeting young people. A flagship initiative is the "Young Innovators Program," which provides high school students with an introduction to laboratory tools used in biology. Our goal is that, at this early stage of career decision-making, these students gain insights to help shape their future paths. Over the past year, CCMB has recruited individuals across all cadres and departments. Many have already joined, and we hope to recruit more talented individuals across cadres in the coming year. It is gratifying to see such scientific vibrancy in our Institute. Given the influx of new members, it is crucial that they demonstrate a comparable level of commitment as our experienced members, including discipline in their time management, dedication, and loyalty to the organization. This dedication will enable us to accomplish great things in the future.

CHARTER

The Centre for Cellular and Molecular Biology (CCMB) is one of the constituent national laboratories of the Council of Scientific and Industrial Research (CSIR), New Delhi, India.

The objectives of the Centre are:

- To conduct research in frontier and multi-disciplinary areas of modern biology, and to seek potential applications of this work
- To carry out exploratory work in areas of biology with a view to aid the development of biochemical and biological technology in the country on a sound basis
- To train people in the advanced areas of biology to serve the needs of development in these areas, with special provision for short-term training of staff from other institutions in techniques for which adequate facilities may not exist elsewhere
- To provide centralized facilities in the country for new and modern techniques in the inter-disciplinary areas of biology, and to ensure that these facilities are so organized, maintained and administered that they can be put to maximal use by research workers from other laboratories and institutions in the country
- To interact adequately with other institutions doing basic or applied work in areas related to the activities of the Centre
- To collect, collate and disseminate information relevant to biological research

1.1 Research Programmes







The research programs at CCMB broadly fall under the following themes:

- Developmental biology
- Structural biology
- Genomics and epigenetic regulation
- Cell and stem cell biology
- Microbes and biology of infection
- Wildlife conservation and ecology
- Crop improvement





1.1A
Research Summaries



DEVELOPMENTAL BIOLOGY

Anant Patel
Dhananjay Chaturvedi
Imran Siddiqi
Megha Kumar
M Mohammed Idris
Sonal Nagarkar Jaiswal



ANANT B PATEL

Impact of anesthetics on neuronal and astroglial activity in the brain



From left to right: Hilal, Zubair, Bhargirdhar, Prajakta, Chaynita, Shalini, Anant, Sohini, Akila, Ajay, Vimala, Varadarajan

Research interests

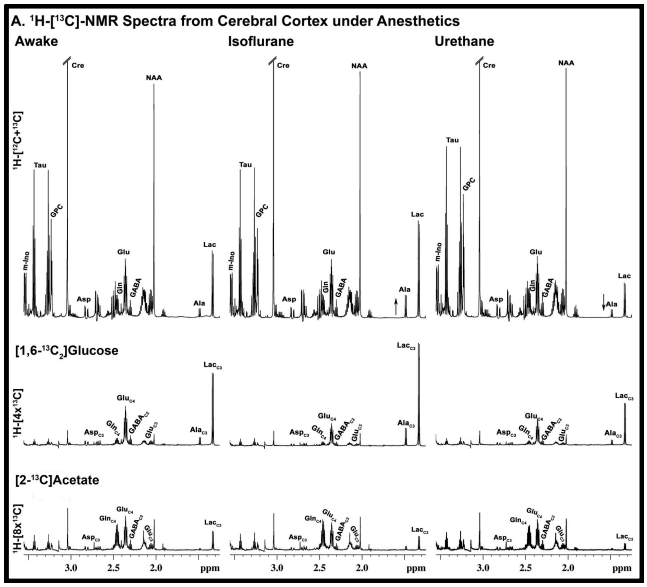
The major focus of our study is to investigate the energetics of glutamate and GABA neurotransmission in healthy brains, as well as in neurodegenerative disorders (Alzheimer's disease and amyotrophic lateral sclerosis) and psychiatric conditions (depression and addiction), using ^{1}H-[^{13}C]-NMR spectroscopy in conjunction with administration of ^{13}C-labeled glucose or acetate.

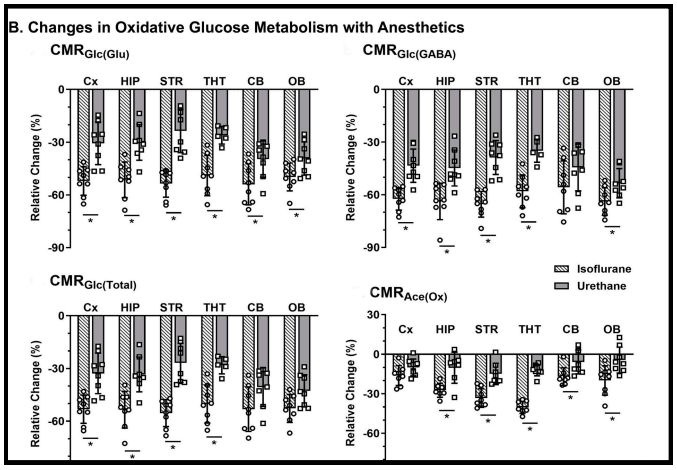
Anesthetics are routinely used during surgery and in animal experiments to immobilize subjects and reduce movement-related artifacts during anatomical and functional studies in rodents. However, the quantitative significance of their impacts on neuronal and astroglial activity remains unclear. We evaluated the impacts of isoflurane and urethane on the metabolic activity of glutamatergic neurons, GABAergic neurons, and astrocytes across different brain regions.

Male C57BL/6 mice were anesthetized with isoflurane (1.5 %) or urethane (1.5 g/kg, intraperitoneal), and administered with [1,6-$^{13}C_2$]glucose or [2-^{13}C]acetate intravenously for 10 or 15 minutes, respectively. Brain metabolism was arrested using focused beam microwave irradiation, and the ^{13}C labeling of neurometabolites was measured in brain tissue extracts ex vivo using ^{1}H-[^{13}C]-NMR spectroscopy for neurometabolic analysis. The cerebral metabolic rate of glucose and acetate oxidation

was estimated based on ^{13}C labeled trapped into amino acids from labeled glucose and acetate, respectively.

The levels of aspartate and succinate were decreased, while alanine increased across the brain in mice exposed to isoflurane compared to awake controls. The labeling of brain amino acids from [2-^{13}C]acetate was decreased in the isoflurane group, suggesting suppression of astroglial metabolic activity in the subcortical region. A pronounced reduction in ^{13}C labeling of brain amino acids from [1,6-$^{13}C_2$]glucose was observed in both isoflurane- and urethane-treated mice, indicating a strong inhibitory effect of these anesthetics on the metabolic activity of glutamatergic and GABAergic neurons. Isoflurane increased the ratio of anaerobic to oxidative metabolic ratio in glutamatergic and GABAergic neurons across the brain compared with awake mice. Furthermore, the metabolic activity of inhibitory neurons correlated positively with that of excitatory neurons. The findings indicate that isoflurane and urethane differentially reduce excitatory and inhibitory synaptic transmission in the brain. Notably, isoflurane shifts cerebral metabolism toward anaerobic respiration.





A) ^{1}H-[^{13}C]-NMR spectra from cortical extracts depicting labeling of brain metabolites from [2-^{13}C]acetate. B) Impacts of anesthetics on neurometabolic rates. Mice were anesthetized with isoflurane (1.5 %) or urethane (1.5 g/kg), and infused either [1,6-$^{13}C_2$]glucose or [2-^{13}C]acetate for 10 or 15 minutes, respectively. The brain metabolites were extracted using an ethanol extraction protocol and analyzed in ^{1}H-[^{13}C]-NMR spectroscopy. The cerebral metabolic rates of glucose and acetate oxidations were calculated using the tapping pool approach in different groups of mice. The percent reduction in the cerebral metabolic rate for a given anesthetic was calculated as: 100 x (Cerebral metabolic rate under anesthetic – Cerebral metabolic rate in awake mice) ⁄ Cerebral metabolic rate in awake mice. ∗p<0.05. Abbreviation used are: Ala_{C3}, alanine-C3; Asp_{C3}, aspartate-C3; Cre, creatine; $CMR_{Ace(Ox)}$, cerebral metabolic rate of acetate oxidation; $CMR_{Glc(Glu)}$, rate of glucose oxidation in glutamatergic neurons;CMR_{Glc}(GABA), rate of glucose oxidation in GABAergic neurons; $GABA_{C2}$, g-aminobutyric acid-C2; $GABA_{C3}$, g-aminobutyric acid-C3; $GABA_{C4}$, g-aminobutyric acid-C4; Glu_{C3}, glutamate-C3; Glu_{C4}, glutamate-C4; Gln_{C4}, glutamine-C4; GPC, glycerophosphocholine; Lac_{C3}, Lactate-C3; m-Ino, myo-inositol; NAA, N-acetyl aspartate; Tau, taurine.

DHANANJAY CHATURVEDI

in vivo Muscle Repair and Homeostasis



From left to right, back row: Ishita, George, Sarasij
Front row: Dhananjay, Swaraj, Haritha, Maheen

Research interests

We are uncovering principles of how skeletal muscles function *in vivo*. We do so by asking how the relatively large architecture of muscle syncytia coordinates activity along its length, and how a relatively tiny population of adult muscle stem cells contributes to repair.

Though skeletal muscle are common, their biology needs to be understood better for relevance to treatments of dystrophies. Studying molecular function *in vivo* has been a major technical challenge that we are overcoming through fruit flies. Much of what we know comes from *ex vivo* culture that decouples several cues, such as nutrition, physical cues and immune signals. In flies, we gain an integrated view of muscle functioning in a systemic environment.

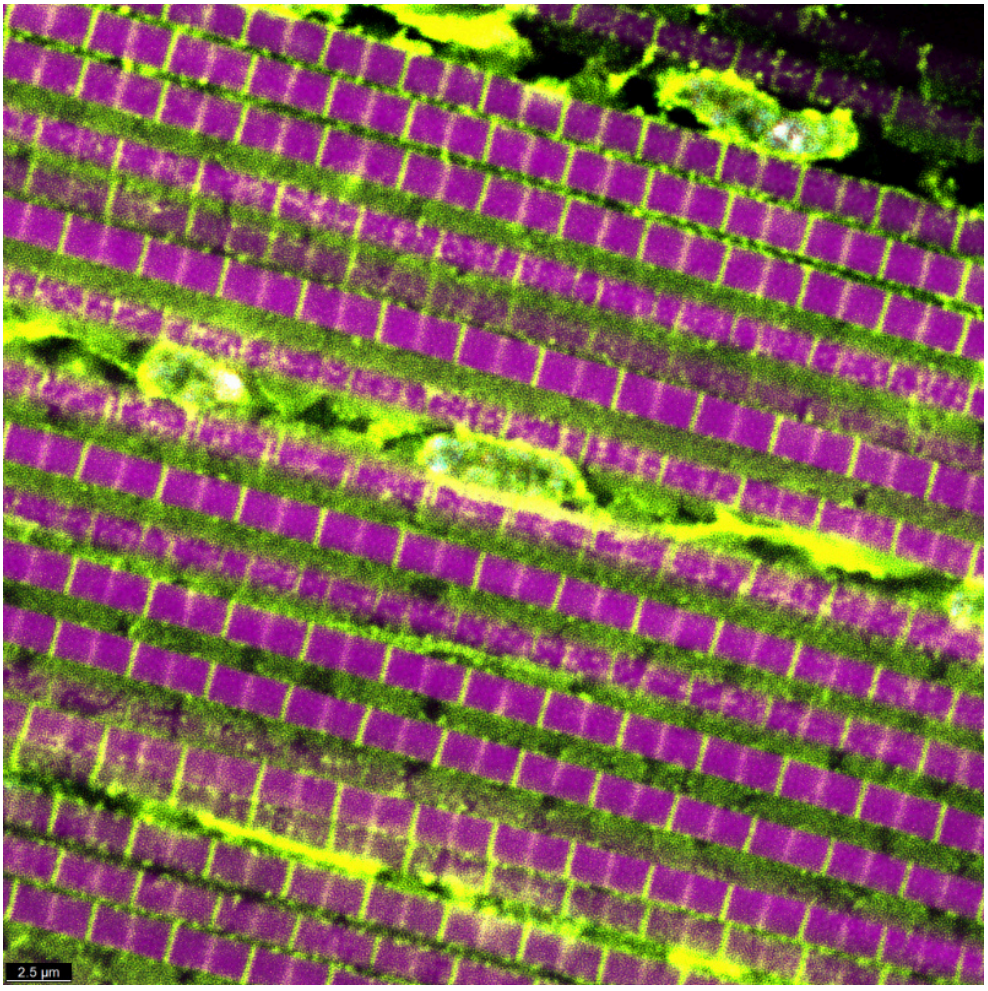
We're characterizing several genes whose transcripts appear heterogeneously distributed along the length of the muscles. These genes mostly have no functional annotation, reagents, and in some cases homology with vertebrate systems. So, we're glimpsing processes that are probably conserved, controlled by possibly new therapeutic targets or potential technological advances. In our investigations we can see protein distributions that do not match transcript enrichment, protein distributions that are distinct

in muscles that were formerly thought identical and proteins that may have localized requirements in syncytium.

Our investigations arising from these fundamental questions have led us to the process of fatty acid breakdown in muscles. Our findings that hint at its necessity are in contrast to the widely reported requirement only of sugars. Further, we find that an Acyl-CoA oxidase of our interest localizes not only to its canonical place of function, peroxisomes, but also on the physical infrastructure required for contraction and relaxation. Its enzymatic requirement at myofibrils will be quite revealing to the field.

Further, we have isolated a shorter variant, unreported in any database, which may regulate the function of the full length protein. Further, the short isoform out populates the full length protein with aging. We're looking to see if fatty acid breakdown through this enzyme may influence aging.

These findings, along with emerging observations on stem cell function are drawing interest from clinician partners.



An acyl-CoA oxidase of our interest (yellow) localizes not only to its canonical place of function, peroxisomes, but also on the physical infrastructure required for contraction and relaxation (myofibrils, magenta) and well as in and around nuclei (cyan).

IMRAN SIDDIQI

Plant Reproductive Biology



From left to right: Anand Singh, M Bhaskar Rao, V. Vaishnavi, G. Sai Kiran Gowd, M. Sai Kiran, Kaladhar Bethoju, Prakash Sivakumar, Imran Siddiqi, K. Gayathri (not in picture)

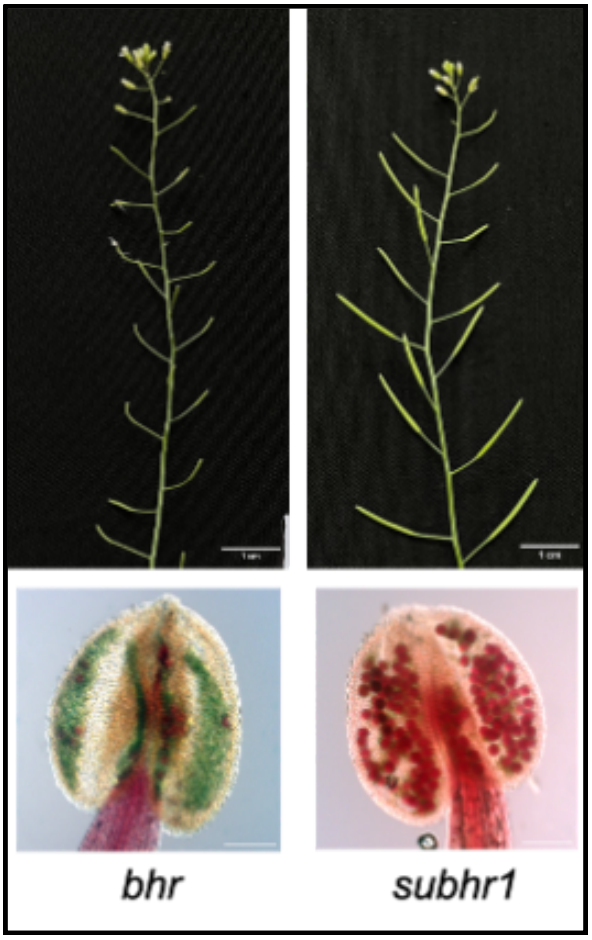
Research interests

Our laboratory works on understanding the control of meiosis and germ cell development in plants using *Arabidopsis* as a model. We study genetic and epigenetic mechanisms underlying the control of plant meiosis, meiotic chromosome organization, and gametogenesis. Information on the control of plant meiosis is useful for designing novel strategies for plant breeding.

The land plant life cycle alternates between two distinct generations, a diploid sporophyte and a haploid gametophyte. In bryophytes (mosses and liverworts) which retain features of ancestral land plants, the gametophyte is dominant and has an independent existence whereas in flowering plants the gametophyte is reduced to just a few cells and develops enclosed within the sporophyte. The transcriptional controls regulating early steps in gametophyte development show conservation between bryophytes and flowering plants leading to the view that the flowering plant gametophyte retains control of its development even after evolutionary reduction. Our recent work has shown that in fact the sporophyte exerts an important level of developmental control of the gametophyte by programming regulated turnover of proteins during gametophyte development via the ubiquitin proteasome system.

We identified a novel gene named SHUKR (SKR) which controls this process. SHUKR is expressed in meiosis and is required for expression of a large set of ubiquitin related genes that are normally expressed only after meiosis during male gametophyte development but express precociously during meiosis in an *skr* mutant. The *SHUKR* gene emerged recently in evolution, within eudicots and is under positive selection indicating an important role for variation in control of protein turnover during male gametogenesis.

Our current work involves delineation of the pathways and regulatory mechanisms controlling meiosis and postmeiotic gametogenesis using a range of approaches to identify genes and proteins that interact with SHUKR. We are also analyzing the function of a paralogue of SHUKR which we name BHRIGU (BHR). BHRIGU like SHUKR also acts in meiosis to control postmeiotic pollen development and is also involved in seed development.



The *bhr* mutant is male sterile. Restoration of male fertility in the *subhr1* suppressor line.

Recent publications

- Sivakumar P, Pandey S, Ramesha A, Davda JN, Singh A, Kumar C, Gala H, Subbiah V, Adicherla H, Dhawan J, Aravind L, Siddiqi I (2025) Sporophyte-directed gametogenesis in Arabidopsis. ***Nat. Plants*** 11(3): 398-409.

- Sivakumar P, Vaishnavi V, Gayatri K, Satheesh GR, Siddiqi I (2024) Improved validation of protein interactions using bicistronic BiFC (Bi2FC). ***Physiol. Mol. Biol. Plants*** 30(7): 1047-1054.

MEGHA KUMAR

Mitosis and Embryogenesis



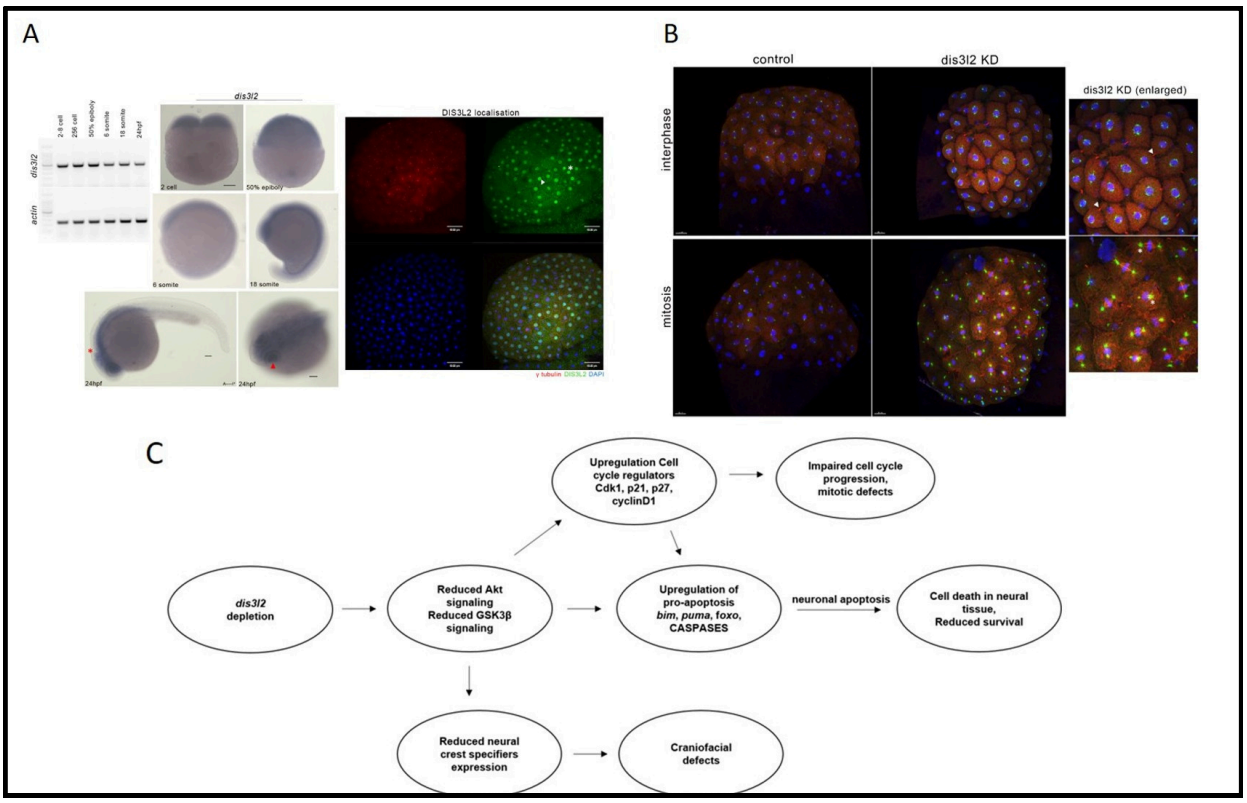
From left to right: Tuhina Prasad, Megha Kumar, Sharada Iyer

Research interests

Cell division is a fundamental cellular process involved in embryonic development and mitotic aberrations result in disorders such as microcephaly, aneuploidy syndromes and embryonic lethality. We study the molecular mechanisms regulating cell division to understand the basis of these developmental disorders.

My group is studying the mitotic machinery and the associated signaling pathways involved in various steps of cell division, resulting in faithful separation of DNA and cytoplasm during early divisions in the zebrafish embryo. As a molecular handle to the complex mitotic machinery, we are currently investigating the role of Centrosomal protein family (CEPs) during cell division. Our preliminary results indicate that CEP genes are required for proper spindle orientation, resulting in correct specification of cell fate and normal tissue architecture during early embryonic development.

In the past year we have also initiated ecotoxicological studies using zebrafish as a model system. In this project, we are exploring the developmental toxicity and the effects of common industry affluents such as byproducts of the perfume industry and washing powder industry which is routinely found in our water sources.



A: Spatiotemporal expression of dis3l2 across developmental stages.
B: dis3l2 is essential for early embryonic mitoses.
C: Summary of developmental functions of dis3l2 in during zebrafish embryogenesis.

M M IDRIS

Understanding the Biomechanism of Regeneration and Degeneration



From left to right: Anuhya T, Athira PV, Anusha PV, Mohammed Idris

Research interests

- Molecular and genetic mechanisms of tissue regeneration and degeneration
- Understanding the effect of ageing in development
- Molecular and genetic mechanism of complex diseases

Our group focuses on deciphering the molecular and genetic mechanisms that govern tissue regeneration, ageing, and complex diseases using alternative model organisms such as zebrafish, ascidians, and echinoderms. We aim to understand the remarkable regenerative capabilities of certain species to inform strategies for regenerative medicine and disease intervention.

A major area of research involves studying tissue and organ regeneration at the molecular level, where transcriptomics and proteomics approaches are applied to identify key genes, proteins, and signaling pathways involved in regenerative processes. By comparing regenerative responses across different species, our work highlights conserved and species-specific mechanisms that control cellular growth, differentiation, and repair.

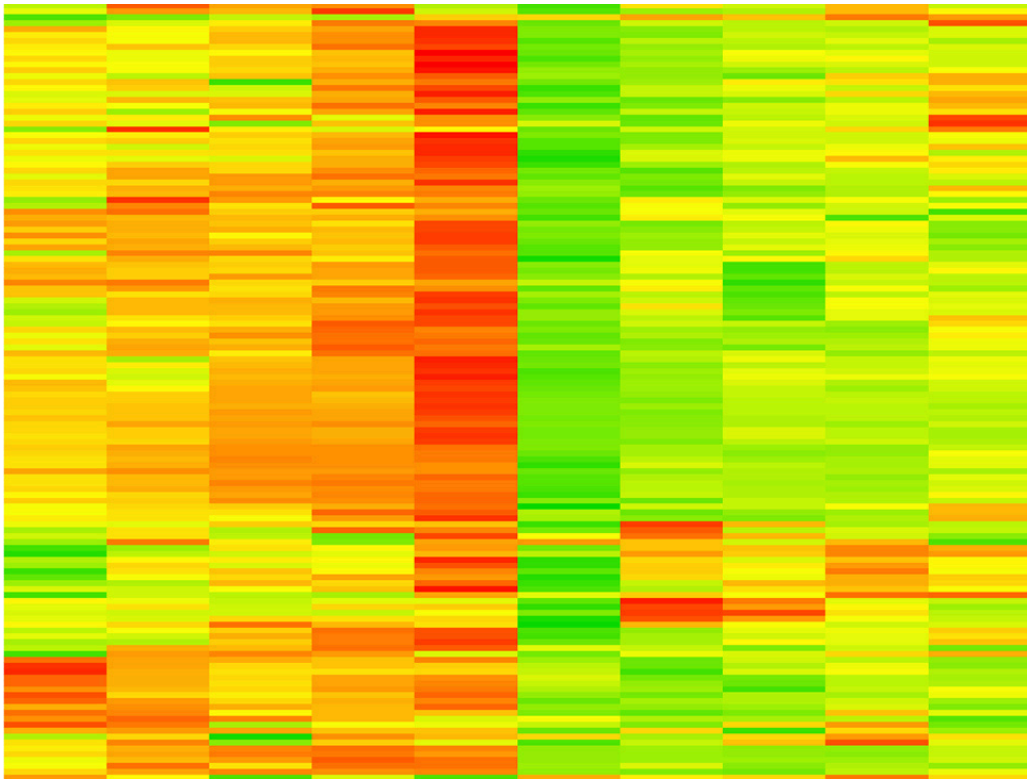
We also investigate the impact of ageing on development and regeneration, focusing on age-

associated molecular changes that diminish regenerative potential. These studies provide insights into biological factors contributing to reduced tissue repair capacity and age-related diseases, with the goal of improving regenerative therapies.

In collaboration, we addresses the molecular and genetic basis of complex diseases, particularly Non-Alcoholic Steatohepatitis. Utilizing advanced omics approaches, we identify biomarkers, molecular pathways, and therapeutic targets involved in disease progression and liver dysfunction, contributing to a deeper understanding of metabolic disorders.

Further, we engage in DNA barcode mapping of medicinal plants to establish reliable molecular identification methods. This ensures the authenticity and quality of herbal materials, supporting the standardization and scientific validation of traditional Unani medicine.

By integrating high-throughput data analysis with functional *in vivo* validation, our research advances a systems-level understanding of regeneration, ageing, disease mechanisms, and plant biodiversity, bridging basic and applied science.



Differential expression of genes across various ageing and regenerating time points

Recent publications

- Anusha PV, Tewari S, Philp C, Arvind A, Iyoob I, Idris MM (2025) Small molecule influence on caudal fin regeneration in zebrafish: A proteomic based study. ***BioRxiv*** doi.org/10.1101/2025.03.01.640803

- Banu S, Anusha PV, Mandal K, Idris MM (2025) Exploration of phosphoproteomic association during epimorphic regeneration. ***Sci. Rep.*** 15(1): 4854

SONAL NAGARKAR JAISWAL

Neural stem cell maintenance during development and disease



From left to right: Basker, Priyanka, Aishwarya, Andrea, Sachin, Sonal, Nandan, Ayesha, Rishabh, Prakriti and Deblina

Research interests

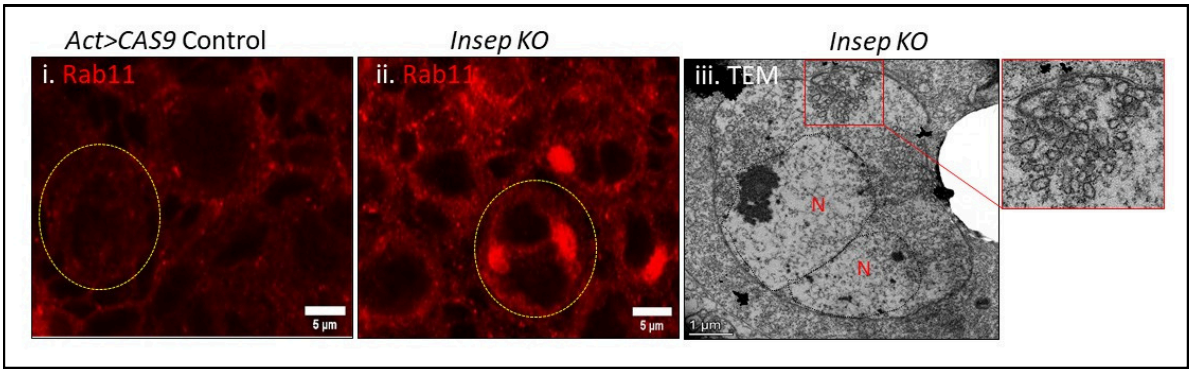
- Neural stem cell maintenance during development and disease
- Mitochondrial dynamics during development and disease
- Validation of human disease-causing genes using *Drosophila* as a model system

Theme 1: Neural stem cell maintenance during development and disease: Neuronal stem cells self-renewal and differentiation are highly regulated, any defects in these processes may lead to neurodevelopmental disorders such as microcephaly or brain tumor. Therefore, identifying the molecular players and understanding the mechanisms underlying these processes during brain development is crucial. Through genetic screens, we identified several evolutionarily conserved genes whose loss results in brain defects. These genes are predicted to be involved in various cellular processes, currently, we are focusing on genes that may play a role in vesicle trafficking. To study these genes, we use the *Drosophila* brain and human neuronal stem cells as model systems.

Theme 2: Mitochondrial dynamics during development and disease: Mitochondria are highly dynamic organelles, they undergo fission

and fusion to regulate to their size, distribution and function. These processes are necessary to main cellular homeostasis. Mitochondrial dynamics is altered in various physiological conditions and developmental stages and also during metabolic stress. We are interested in understanding how mitochondrial dynamics is regulated during development and metabolic stress. To study these processes, we use *Drosophila* and human cell lines as model systems.

Theme 3: *Drosophila* is an unparalleled genetically tractable *in vivo* model to study evolutionarily conserved regulatory processes in humans. About 65% of protein coding genes are conserved in human and approximately 75% of human disease causing genes have homologs in *Drosophila*. We work in collaboration with clinicians and use flies to assess human disease associated variants and determine how they impact the gene function and contribute to disease onset and progression.



Insep mutant NBs accumulate Rab11 vesicles: Confocal images of 68h AEL brain from i. Act-Cas9 controls (n=11) and ii. Insep KO (n=17) stained with Rab11, a yellow circle marks the cell boundary and depicts Rab11 punctate pattern in control and accumulation in KO, respectively. iii. Electron microscopy images of Insep KO NBs, the black inset indicates vesicles accumulated near the plasma membrane, the red inset shows a magnified view of the black inset in the respective image. N- Nucleus, Scale bar = 1µm

Recent publications

- Wang P, Sarkar S, Huan ZH, Zhang Z, Balasubramanian D, Jayaram N, Datta S, He R, Wu P, Chao P, Zhang Y, Washburn MP, Florens L, Nagarkar-Jaiswal S, Jaiswal M, Man Mohan (2024) DYRK1A interacts with Tuberous Sclerosis complex and promotes mTORC1 activity. ***eLife*** 12: RP88318

STRUCTURAL BIOLOGY

Amitabha Chattopadhyay
Janesh Kumar
Mandar V. Deshmukh
Rajan Sankaranarayanan
Saikat Chowdhury


LET'S
LIVES B

AMITABHA CHATTOPADHYAY

Role of Membrane Lipids and Actin in GPCR Function: Implications in Health and Disease



From left to right: Lipsa Dash, Shishu Pal Singh, Ashwani Sharma, Amitabha Chattopadhyay, Jayashree Pratha S, Subhashree S Sahu, K. Venkatalakshmi

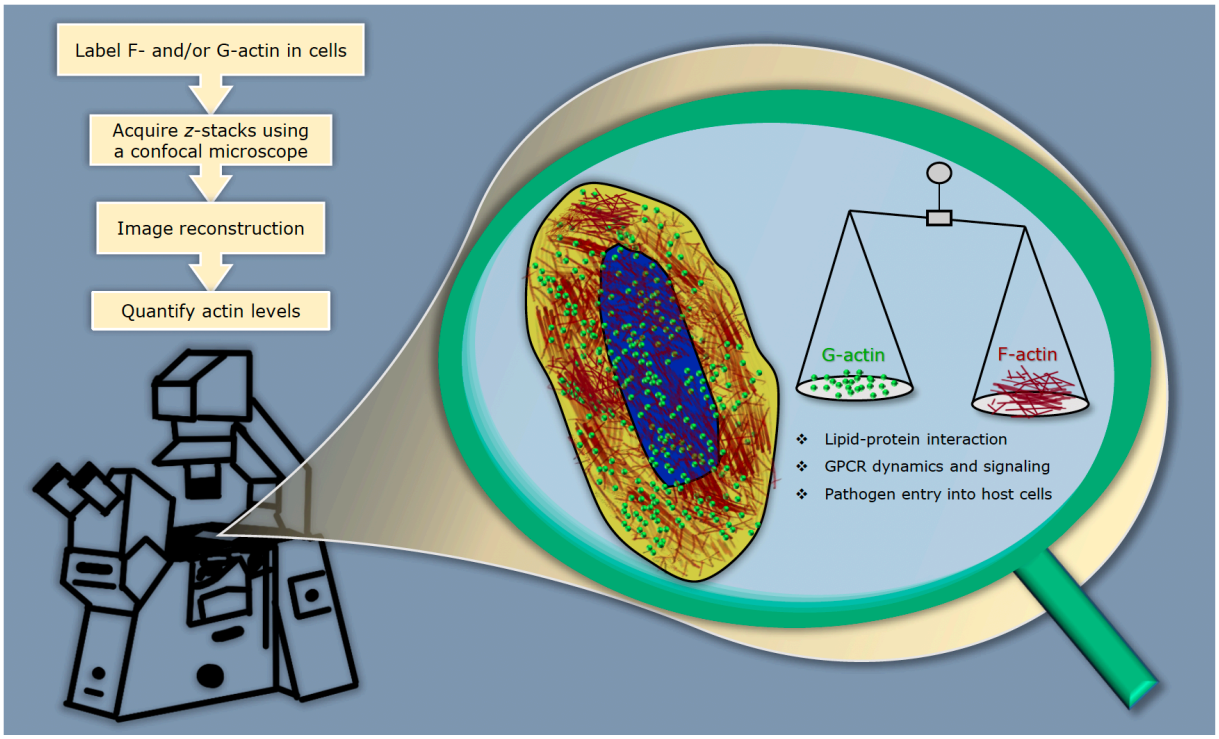
Research interests

The overall focus of our work is role of lipids and actin in function of G protein-coupled receptors (GPCRs) and its implications in health and disease. Recent work has centered on role of lipids and actin in endocytosis/intracellular trafficking of GPCRs and the entry of pathogens into host cells.

G protein-coupled receptors (GPCRs) constitute the largest class of membrane proteins that transduce signals across the plasma membrane, and have emerged as major drug targets in the development of therapeutics in all clinical areas. We study interactions of membrane lipids (such as cholesterol and sphingolipids) with GPCRs and its implications in health and disease. We are one of the first groups globally to work in this important area. We employ a judicious combination of biophysical, biochemical, cell biological and molecular dynamics simulation (coarse-grain and all atom) approaches in our work. We have shown that GPCR-cholesterol interaction is important for ligand binding, G-protein coupling, downstream signaling, oligomerization, and endocytosis of GPCRs. The choice of GPCR in our laboratory is the serotonin$_{1A}$ receptor, a neurotransmitter GPCR, which is implicated in anxiety and depression and serves as a popular drug target. We recently

showed that destabilizing the actin cytoskeleton leads to an increase in the constitutive internalization of the serotonin$_{1A}$ receptor. Notably, under these conditions, the receptor predominantly utilized the caveolin-mediated endocytic pathway for internalization. Interestingly, upon constitutive internalization, the serotonin$_{1A}$ receptor does not recycle back to the plasma membrane. These results would enhance our understanding of the interdependence of actin-GPCR endocytosis.

In another work using coarse-grain molecular dynamics simulations, we showed that palmitoylation of glucagon-like peptide receptor-1 (GLP-1R), a drug target in diabetes and obesity, modulates the binding of the receptor with lipids such as cholesterol and phospholipids. These results provide novel insight in understanding the molecular effects of lipid modifications in GPCRs.



Schematic representation of actin polymerization quantitation using confocal microscopy

Recent publications

- Sahu SS, Sarkar P, Chattopadhyay A (2024) Quantitation of F-actin in Cytoskeletal Reorganization: Context, Methodology and Implications. ***Methods*** 230: 44-58.

- Mohole M, Nagkekar A, Sengupta D, Chattopadhyay A (2024) Probing the Energy Landscape of the Lipid Interactions of the Serotonin$_{1A}$ Receptor. ***Biophys. Chem.*** 313: 107289.

JANESH KUMAR

Fine-Tuning Brain Signals: A Three-Way Control System for Kainate Receptors



From left to right, front row: Mukund, Shantanu, Bhavya, Ananya, Swathy, Suparna
Second row: Saurav, Janesh, Ithayaraja, Sanjay, Rahul, Jupitara, Rajesh
Last row: Aswini, Rajesh, Somnath

Research interests

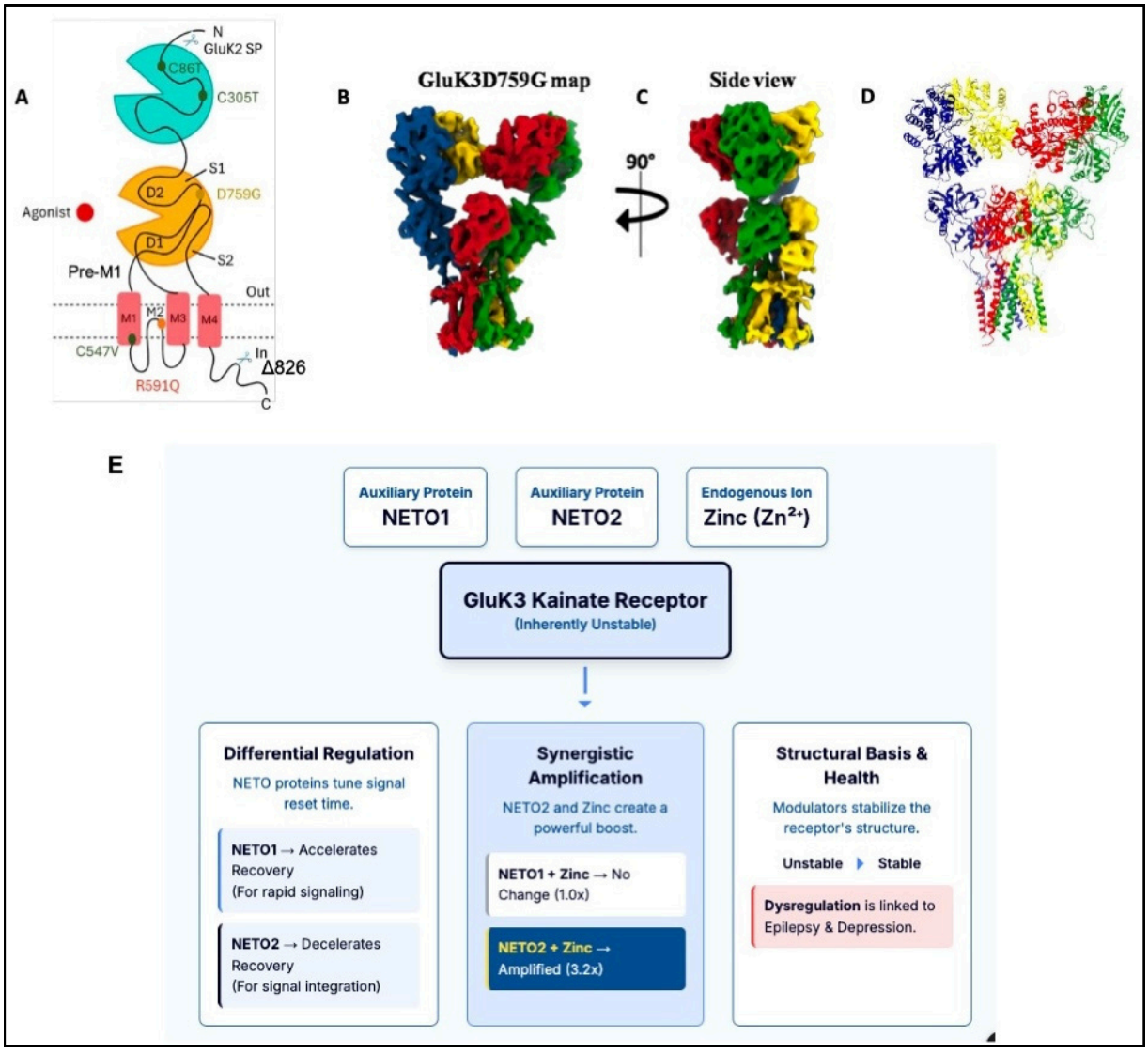
Investigations into the architecture and mechanisms of glutamate receptor signaling complexes in the Central Nervous System.

Communication between brain cells is fundamental to everything the brain does, from forming memories to controlling movement. This communication is regulated by specialized proteins called receptors. Our work focuses on a particular type, the GluK3 kainate receptor, which acts like a sophisticated dimmer switch for nerve signals, especially in brain regions critical for memory.

The function of GluK3 is controlled by two main factors: auxiliary proteins called NETO1 and NETO2, and the zinc ion, which is released alongside neurotransmitters at certain synapses. However, how these three components work together has remained a mystery. We investigated this tripartite system by measuring the electrical currents produced by the receptor in living cells and determining its three-dimensional structure using cryo-electron microscopy (Cryo-EM).

We discovered that NETO1 and NETO2 tune the GluK3 receptor in opposite ways, giving neurons a mechanism to either respond rapidly to incoming signals or to integrate them over longer periods. Most strikingly, we found that NETO2 and zinc work together synergistically, boosting the receptor's signal far beyond what either could achieve alone. Our structural data revealed that the GluK3 receptor is inherently unstable, explaining why it relies so heavily on these modulators to function correctly.

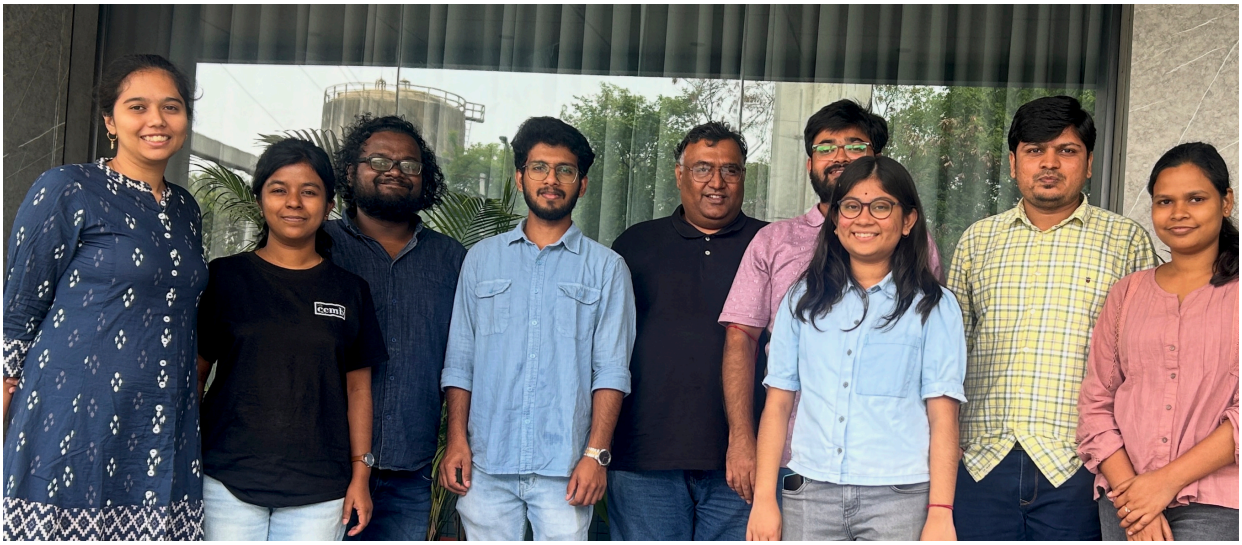
This research uncovers a multi-layered control system that allows for precise regulation of brain circuits. Understanding this system is crucial, as its dysregulation may contribute to neurological conditions like epilepsy and depression, opening new avenues for targeted therapies.



Tripartite Control of GluK3 Kainate Receptors. A. Schematic representation of GluK3 mutant (D759G) construct.
B & C. CryoEM density map segmented and colored as different chains (labelled as A, B, C, D) at 5.9 Å for GluK3 bound to Spermine and antagonist UBP310. Front and side views for the color segmented map.
D. Fitted atomic model colored to represent four receptor subunits.
E. This schematic shows how molecular modulators like NETO proteins and zinc (top) act on the unstable GluK3 receptor (center) to produce the study's major findings (bottom) on signal regulation, synergistic amplification, and links to neurological health. The arrows show the flow of influence from inputs to outcomes.

MANDAR V DESHMUKH

Mechanistic Insights into dsRBP-Mediated dsRNA Recognition in Plant RNAi



From left to right: Nilam Waghela, Aleena Treesa, Debadutta Patra, P. S. Aravind, Mandar V. Deshmukh, Jaydeep Paul, Supriti Das, Ramdas Aute, and Priti Chanda Behera

Research interests

We explore the role of RNA-binding gene regulatory proteins by studying the structure, inter-domain orientations, and dynamics to construe the initiation of the non-coding RNA-mediated gene regulation in eukaryotes. We find that the conformational dynamics in structurally homologous proteins incite specificity towards the dsRNA substrate that dictates RNAi pathway initiation.

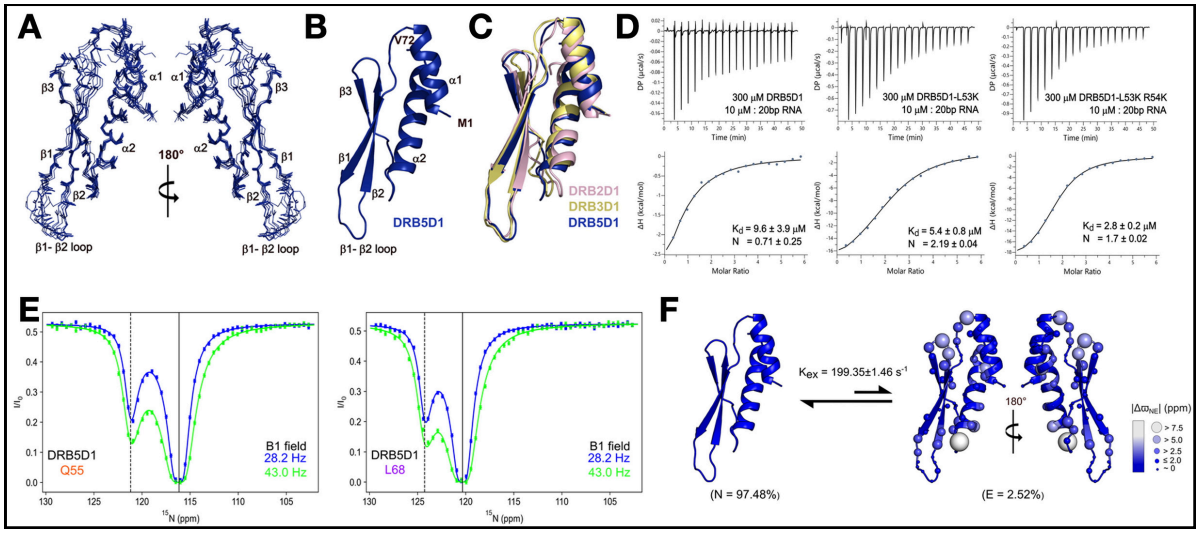
Double-stranded RNA-binding proteins play a crucial role in the antiviral defense and endogenous post-transcriptional gene regulation in higher eukaryotes. We have unravelled the structure and function of high molecular weight proteins, protein complexes, and nucleic acids such as RDE-4 (*C. elegans*), DRB2/DRB3/DRB4/DRB5/ DRB7.2:DRB4 (*A. thaliana*), R2D2 (*D. melanogaster*), and Crc (*P. syringae*), using ultra-modern and innovative NMR approaches. These findings highlight a delicate balance in highly homologous systems fine-tuned to direct the fate of small RNA-mediated gene silencing. Surprising heterogeneity in the structure and dynamics of dsRBPs suggests that the process of RNAi initiation is unique for each organism and is dependent on the step-wise assembly of the Dicer, dsRBP, and the trigger small RNA.

During this year, we have demonstrated that DRB2, DRB3, and DRB5 utilize their oligomerization-prone

dsRBD2 domains to form phase-separated condensates. We showed that these domains adopt a modified dsRBD fold, resulting in unique charge distributions and multivalent interaction surfaces that allow concentration-dependent self-association and the formation of liquid condensates driven by dsRNA, ATP, or molecular crowding, implying it to be a fundamental antiviral strategy.

In continuation of the earlier work on the dynamics of DRB2/3 dsRBD1, we showed that while DRB5 dsRBD1 exhibits a canonical dsRBD fold, it cannot recognize rigid dsRNA substrates. We showed that the weak affinity stems from the inherent ability of DRB5 dsRBD1 to sample a wide range of low-populated excited state conformations in the intermediate-slow timescale, indicating intrinsic plasticity enhances promiscuity in substrate recognition. We further show that the unique complex formation between the minimal interaction domains of DRB7.2:DRB4D3 is responsible for DCL3 suppression during the processing of endogenous inverted-repeat dsRNAs.

Collectively, these findings reveal distinct yet complementary strategies by which plant dsRBPs regulate RNA fate involving an array of mechanisms, such as phase separation, conformational exchange, and competitive sequestration.



Structure and Dynamics in DRB5D1. (A) Superposition of the ten lowest energy ensemble structures of DRB5D1 (average backbone RMSD = 0.78 Å). (B) Cartoon representation of the lowest energy structure of DRB5D1 (C) The structural alignment of DRB5D1 (blue) with DRB2D1 (PDB id 9JVC, pink) and DRB3D1 (PDB id 9JMT, yellow). (D) ITC plots with 20 bp RNA for DRB5D1, DRB5D1 (L53K), and DRB5D1 (L53K, R54K), respectively. The upper panels in the ITC plots represent the raw titration data, and the corresponding bottom panels depict the integrated enthalpy change (DH) per mole of protein injected into the cell containing 20 bp dsRNA. For DRB5D1, the data fitted with a Kd of 9.6 ± 3.9 μM. For single mutant DRB5D1 (L53K) and double mutant DRB5D1 (L53K, R54K), Kd equivalent to 4.2 ± 0.7 μM and 2.8 ± 0.2 μM were obtained, respectively. A single-site binding model was used for all analyses. (E) 15N-CEST profile for DRB5D1 residues Q55 and L68 (bottom panel), respectively. 15N-CEST profile for DRB5D1 shows a second dip for the low populated excited state at two different B1 fields (28.2 Hz and 43 Hz) fits in the two-state exchange model. The experimental data points are represented using blue and green circles for two B1 fields, 28.3 Hz and 48 Hz, respectively, and the uncertainties in the experimental measures are shown using error bars. The vertical dotted and solid lines in CEST profiles correspond to the chemical shift of the excited and native states, respectively. (F) Population for native (N) and excited state (E), Kex, and $\Delta\varpi_{NE}$ of the two states for DRB5D1 are plotted on the structure of DRB5D1. The diameter of the sphere plotted in the structure corresponds to the magnitude of $\Delta\varpi_{NE}$.

Recent publications

- Paturi S, Patra D, Behera PC, Aute R, Waghela N, Kinatukara P, Deshmukh MV (2025) The mechanism of DRB7.2:DRB4 mediated sequestering of endogenous inverted-repeat dsRNA precursors in plants. ***eLife*** 14: RP105762.

- Aute R, Waghela N, Deshmukh MV (2024) Key arginine residues in R2D2 dsRBD1 and dsRBD2 lead the siRNA recognition in the Drosophila melanogaster RNAi pathway. ***Biophys. Chem.*** 310: 107247

RAJAN SANKARANARAYANAN

Mechanistic understanding of Proofreading in Translation Machinery and Elucidating the structure- function relationship of lipid metabolite- producing Enzyme



From left to right: Priyam Chopra, Biswajit, Azeen Zehra, Shankhadeep Baksi, , Sakshi Shambhavi, Keerthana, Anurag, Mukul, Tamajit, Suhail, Daityari Nayak, Sankaranarayanan, Subashree, Santhosh , Nisha, Shobha Krupa Rani, Koushick, Lalitha, Sambhavi

Research interests

- Mechanistic and functional implications of proofreading mechanisms during translation quality control.
- Insights into lipid metabolite-producing enzymes: how cell fine-tunes lipid subspecies for cellular homeostasis and environmental adaptation.

I. Proofreading is a key process for translation quality control. However, the efficiency of proofreading has been shown to be modulated during stress.

Alanyl-tRNA synthetase and Threonyl-tRNA synthetase possess a common fold performing proofreading function. Both have an invariant Zn^{2+} binding motif across life forms. Our recent study revealed the role of Zn^{2+} ion in both the domains i.e., the metal ion is ubiquitous in one and inhibitor for the other. The universally conserved Zn^{2+} in AlaRS-Ed protects its proofreading activity from (ROS) whereas mistranslation of Thr-codons is well tolerated. Structural analysis has shown that a single residue rooted over ~3.5 billion years of evolution is primarily responsible for the functional divergence from the time of last universal common ancestor (LUCA). Thus, the distinct metal binding driven functional

dichotomy plays a key role that integrates redox signalling and translation quality control. Currently we are embarking on elucidating the mechanism of editing of AlaRS-Ed.

II. Disco-interacting protein 2 (Dip2), a eukaryotic protein found in fungi and animals, has been reported to influence several cellular processes such as neuronal morphology, cell migration, lung development, salivary gland development, virulence in pathogenic fungi, autism spectrum disorder, dyslexia, etc. Using Yeast as a model system, we have demonstrated that Dip2 is involved in homeostasis of specific diacyl-glycerols (DAG), which in turn, regulates several cellular properties including ER stress, osmoadaptation, vacuole membrane fusion, mitochondria-vacuole contacts, maintenance of proper mitochondrial form and functions, etc. On the other hand, Dip2 regulates Protein kinase C (Pkc) signalling in a specific DAG dependent manner and the absence of Dip2 leads to the translocation of Pkc to mitochondria. Further, our analysis suggests that multiple lipid divergence events happened across evolutionary timescale and interestingly, these events correlate with the phylogenetic branching points. Our present work is focussed on the structure function relationship.

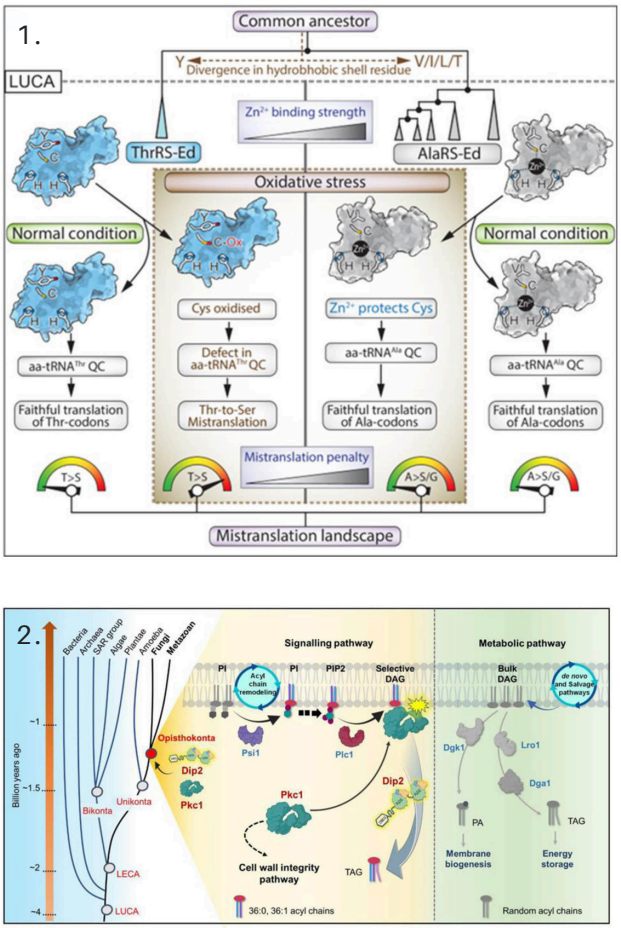


Fig 1: A schematic depicting the pre-LUCA evolutionary divergence of AlaRS-Ed and ThrRS-Ed in terms of Zn2+ binding potential and it is attributed to a residue surrounding the coordination sphere, leading to distinct sensitivities in their activities toward ROS.
Fig 2: A graphical representation depicting the emergence of Dip2-Pkc axis and the evolution of selective DAG-based Pkc signalling in Opisthokonta

Recent publications

- Kumar P, Sankaranarayanan R (2024) When Paul Berg meets Donald Crothers: an achiral connection through protein biosynthesis. ***Nucleic Acids Res.*** 52(5): 2130-2141.

SAIKAT CHOWDHURY

Structural biology of cytoskeletal assembly and macromolecular machines



From left to right: Saikat Chowdhury, Justus Francis, Kiran Vyshnav Eliyan, Sridhar S, Oushnik Goswamy, Manisha Pani, Amarttya Bagchi, Rajesh Palle, Pragati Pandey, Pathri Achyutha Krishna, Kulvinder Kaur, Palash Kumar Seal, Kankipati Teja Shyam

Research interests

- Elucidating the molecular mechanisms of actin cytoskeletal nucleation by diverse nucleators in response to cellular cues and signaling pathways
- Deciphering the molecular basis of crosstalk and coordination between distinct cytoskeletal systems
- Advancing cryogenic electron microscopy methods to capture and determine structures of dynamic macromolecular assemblies

Decoding how cells build and remodel their actin architecture one molecule at a time.

Every living cell relies on a dynamic internal scaffold called the actin cytoskeleton. This network of protein filaments gives cells their shape, enables movement, and drives processes such as division and intracellular transport. At the heart of this system is Arp2/3 complex, a molecular machine that initiates and organizes actin filaments into diverse architectures. However, Arp2/3 does not function alone; it is tightly regulated by a host of activators and stabilizers that together determine how cells build and sustain actin networks.

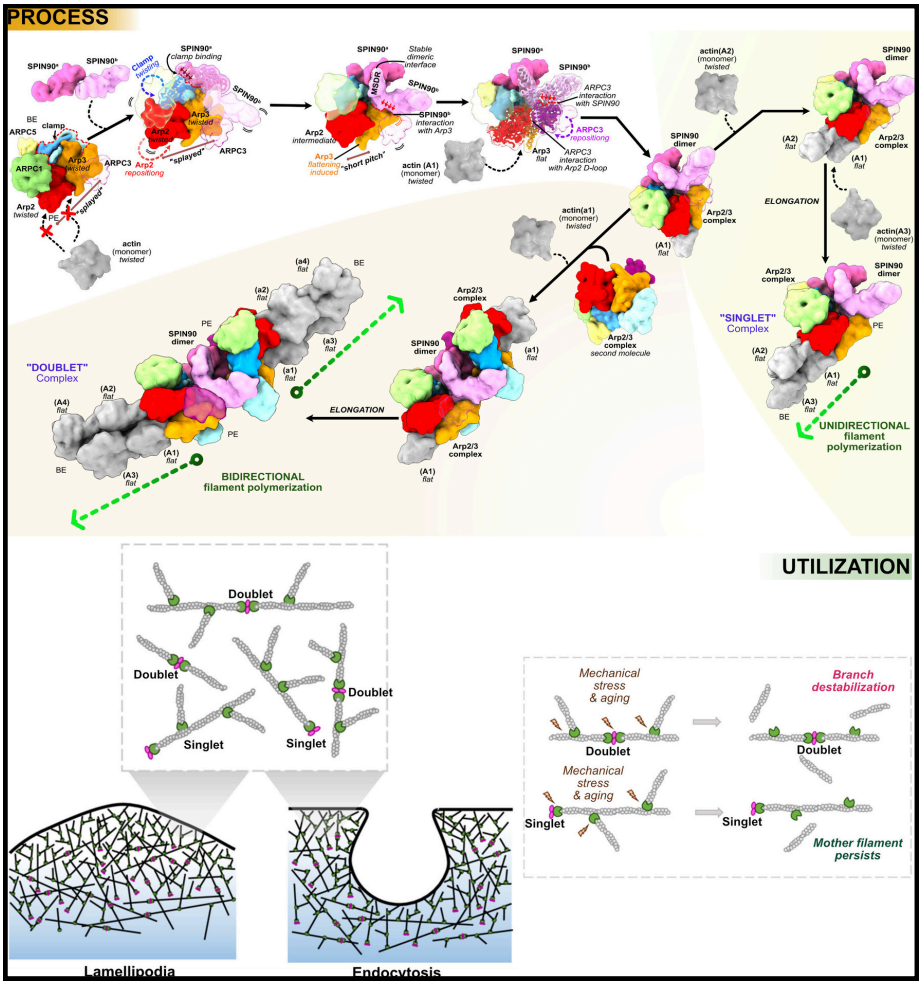
Our laboratory investigates how Arp2/3 complex and its regulatory partners coordinate the formation, architecture, and stability of actin filament networks. We use state-of-the-art cryo-electron microscopy (cryo-EM), complemented

by biochemical reconstitution and biophysical analyses, to visualize these protein assemblies at near-atomic resolution and capture how they change shape and interact during actin nucleation.

In the past year, we uncovered a previously unknown activation mechanism of Arp2/3 complex by a vertebrate nucleation-promoting factor, SPIN90. Our cryo-EM structures revealed that SPIN90 forms a dimeric assembly that binds and reshapes Arp2/3 complex to nucleate linear actin filaments, distinct from the canonical branched actin formation. Remarkably, two SPIN90–Arp2/3 complex assemblies can associate in a head-to-head configuration, generating filaments of opposite polarity, adiscovery that suggests a potential mechanism for linking linear and branched actin networks in cells.

These findings redefine our understanding of how cells initiate and sustain actin networks and provide insights into how dysregulation of this machinery contributes to diseases such as cancer and neurodegeneration.

Moving forward, our research aims to explore how interplay of stimulators and regulators orchestrate cytoskeletal remodeling during processes such as cell migration, endocytosis, and mechanotransduction. By bridging structural and cellular biology, we strive to build a comprehensive molecular framework of cytoskeletal regulation.



Actin assembly by SPIN90 protein and Arp2/3 complex

Recent publications

- Fu Z, Crooks EJ, Irizarry BA, Zhu X, Chowdhury S, Van Nostrand WE, Smith SO (2024). An electrostatic cluster guides Aβ40 fibril formation in sporadic and Dutch-type cerebral amyloid angiopathy. ***J. Struct. Biol.*** 216(2):108092.

GENOMICS AND EPIGENETIC REGULATION

Divya Tej Sowpati
G.R. Chandak
Ishwariya Venkatesh
K. Thangaraj
Mukesh Lodha
Rakesh K. Mishra
Shrish Tiwari
T. Karthik Bharadwaj


STOP

DIVYA TEJ SOWPATI

Computational Genomics



From Left to Right, Top: Ramakanth, Abishek, Venkat, Siddharth, Sriram, Reuben, Nitesh, Pruthvi
Bottom: Anukrati, Pooja, Ankit, Shreya, Sofia, Tej, Pratheusa, Isha, Sreelekshmi

Research interests

- Genetic variation in Indian populations, and their consequences
- Structural variations and tandem repeats
- Single cell genomics
- Algorithms in big data analysis and visualization

DNA present within cells, collectively known as the genome, is the instruction manual read by the cellular machinery to live and function. Hence, all the complexity and variation seen in life on earth is encoded in the genome. My lab is interested in understanding how the variation in genomes of Indians predisposes them to disparities in health and disease. We study this at two levels. First, we identify genetic variation of individuals using cutting-edge high throughput sequencing technologies. As part of large nation-wide population genomics programs, we map the natural variation in healthy genomes. Using this as the baseline, we study individuals with specific disorders to understand their genetic basis.

In particular, our interests lie in two classes of variations known as structural variations and tandem repeats. Structural variations are large changes in the genome that affect more bases than SNPs and small InDels. Tandem DNA

repeats are loci where a small DNA motif is repeated several times. The number of times a motif is repeated is highly dynamic, and correlates with phenotypes including several disorders. We also study how the same DNA sequence can give rise to different phenotypes, as observed in various cell types of a single organism. Despite having an identical genome, cells can be regulated differently via epigenetic mechanisms that result in cell specific gene expression patterns. Using single cell genomic technologies, we analyze the gene expression and epigenetic profiles of various cells to understand cell heterogeneity. Finally, we develop new computational methods that enable faster and better analysis of complex biological data, as well as more interactive and intuitive data visualization.

Recent publications

- Sharma A, Sowpati DT (2025) Analysis of tandem repeats in seven telomere-to-telomere primate genomes. ***J. Genet.*** doi: 10.1007/s12041-025-01503-2.

- Banu S, Mk K, George JK, Siby E, Bhagat R, Ms S, Patil SJ, Phadke SR, Sowpati DT, Tallapaka KB (2024) Enhanced resolution of optical genome mapping utilizing telomere-to-telomere reference in genetic disorders. ***Eur. J. Hum. Genet.*** 33(7): 956-959.

GIRIRAJ RATAN CHANDAK

Epigenomics of Childhood Cognitive Function and Inflammation



From left to right, first row: Sohail Mansuri, Alagu Sankareswaran, Jayasuriya, Md Sufail, Sumit Paliwal, Archana Dharavath
Second row: Giriraj Ratan Chandak, Aditya Soni, PSKDB Punyasri, R Dhanyashree, Pranavi Garimella, Anusha Dharavath, Jhansi Rani, Sumati Swain, Swetha Ghanate
Third row: Shagufta Tasneem, Seema Bhaskar, Akshita Jukanti, Dimple Lavanuru, Bithika Pramanik, Netravati Chavan, Swati Bayyana
Fourth row: Arumalla Manisha, Priyanka Baberwaal

Research interests

Genetic and epigenetic basis of complex diseases like Diabetes mellitus and related intermediate traits, with reference to gene-gene and gene-nutrient interaction and pre- and peri-conceptional nutritional intervention to understand casuality.

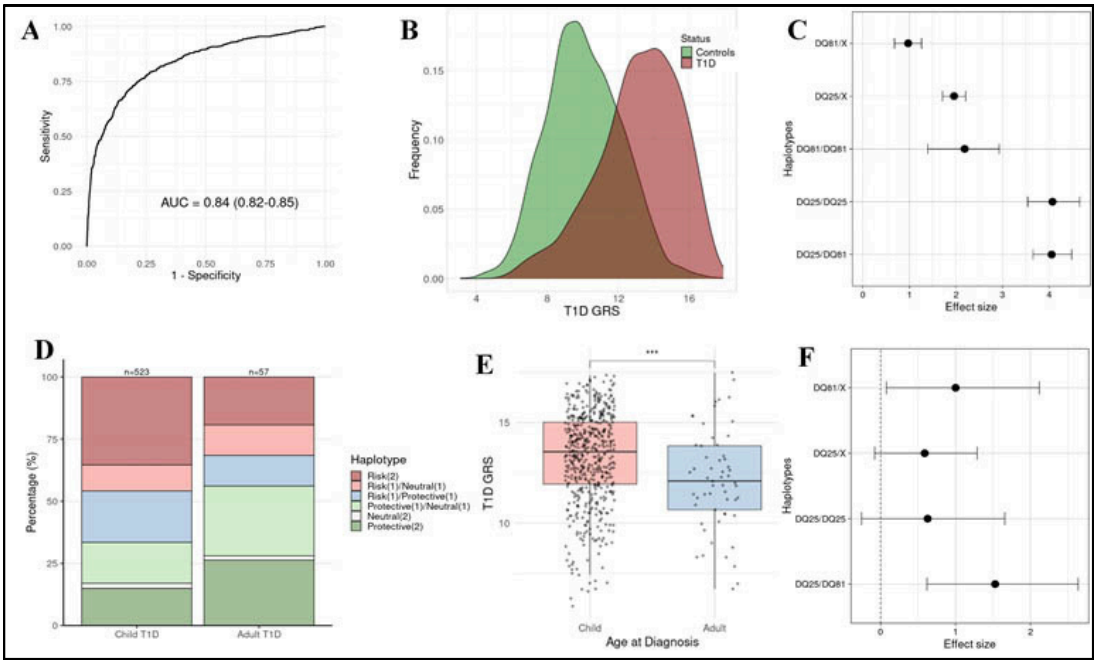
Type 1 diabetes (T1D) is a chronic autoimmune disorder characterized by the destruction of insulin-producing pancreatic β-cells. Children are more frequently affected than adults, often presenting with severe symptoms such as diabetic ketoacidosis and poor glycemic control. While the precise triggers of autoimmunity remain unclear, T1D has strong genetic heritability, largely attributable to the *Human Leukocyte Antigen* (*HLA*) region. Our earlier work demonstrated the utility of a genetic risk score (GRS) in differentiating T1D from type 2 diabetes (T2D) in an Indian cohort from western India. Given India's diverse genetic background, evaluating the performance of a unified T1D GRS across populations was essential.

In this multi-centric study spanning Indo-European and Dravidian populations, we assessed the discriminative ability of a unified T1D GRS. We found no significant frequency

differences in T1D-associated SNPs among controls, indicating shared genetic architecture across Indian populations. Using receiver operating characteristic (ROC) curve analysis, the GRS achieved an area under the curve (AUC) of 0.84, consistently across cohorts. This highlights the potential of a single unified GRS for screening and diagnosis in Indians, irrespective of population structure.

However, recent data indicate that nearly half of new T1D diagnoses now occur in adults, underscoring the heterogeneity of its clinical presentation. This presents a major diagnostic challenge in India, where early-onset T2D is highly prevalent. Our data showed that while the GRS discriminated T1D well in both groups, performance was higher in children (AUC: 0.84) compared to adults (AUC: 0.72; $P < 0.0001$). On comparing the frequencies of the T1D associated *HLA-DQ* haplotypes, we found that adults carried a higher proportion of protective haplotypes and a lower proportion of susceptible ones, which may help explain the delayed onset of disease in this group. Globally, two haplotypes, DQ25 and DQ81, are recognized as the major contributors to T1D risk. In our earlier work, we observed that DQ25 conferred greater risk in Indians, in contrast to Europeans where DQ81 exerts a stronger effect. This difference was consistently replicated in the present study as well. Follow-up analysis stratified by age at onset groups revealed a distinct pattern. Haplotypes with DQ81 combinations were associated with childhood onset T1D whereas the DQ25 combinations were not associated. However, their heterozygous combination is also associated with the early-onset.

Together, these findings underscore the value of a unified GRS for T1D in India while highlighting age-specific differences in genetic risk. Larger studies are needed to explore gene–gene interactions and the genetic basis of adult-onset T1D in diverse Indian populations.



A) Receiver operating characteristic curve of the T1D GRS between T1D and controls. B) Density plot of the T1D GRS between T1D and controls. C) Forest plot showing the association of high risk HLA-DQ haplotypes between T1D and controls. D) Stacked bar plot showing the distribution T1D risk and protective haplotypes between child and adult-onset T1D. E) Boxplot of the T1D GRS between child and adult-onset T1D. F) Forest plot showing the association of high risk HLA-DQ haplotypes between Child and Adult onset T1D.

Recent publications

- Liu T, Sankareswaran A, Paterson G; Genes & Health Research Team; Fraser DP, Hodgson S, Huang QQ, Heng TH, Ladwa M, Thomas N, van Heel DA, Weedon MN, Yajnik CS, Oram RA, Chandak GR, Martin HC, Finer S (2025) Investigating misclassification of type 1 diabetes in a population-based cohort of British Pakistanis and Bangladeshis using polygenic risk scores. ***Sci. Rep.*** 15(1):1168
- Ghosh S, Laxmaiah A, Chandak GR, Meshram II, Raman R, Sengupta S, Yajnik CS, Kurpad AV, Sachdev HS; Vitamin B12 India Study (2025) Anaemia and iron deficiency in India: a venous blood-based survey of adolescents, adults, and the elderly in eight states. ***Eur. J. Clin. Nutr.*** 79(5):443-451.

ISHWARIYA VENKATESH

Molecular Control of Axon Growth



From left to right, Standing: Faheem Farooq, Prakash C, Venkatesh, Dhruva Kumar, Netra Krishna, Athul Narayan, Shringika Soni, Meghana Konda, Praveena K, Dhanuush Balakannan
Sitting: Manojkumar Kumaran, Yogesh Sahu, Anisha S Menon, Ishwariya Venkatesh, Aarthi Sukumar, Rutuja Pendharkar, Katha Sanyal

Research interests

Our research investigates the molecular pathways that limit axon regeneration in adult mammals and explores whether developmental mechanisms can be recapitulated for repair, using bioinformatics, genomics and *in vivo* models.

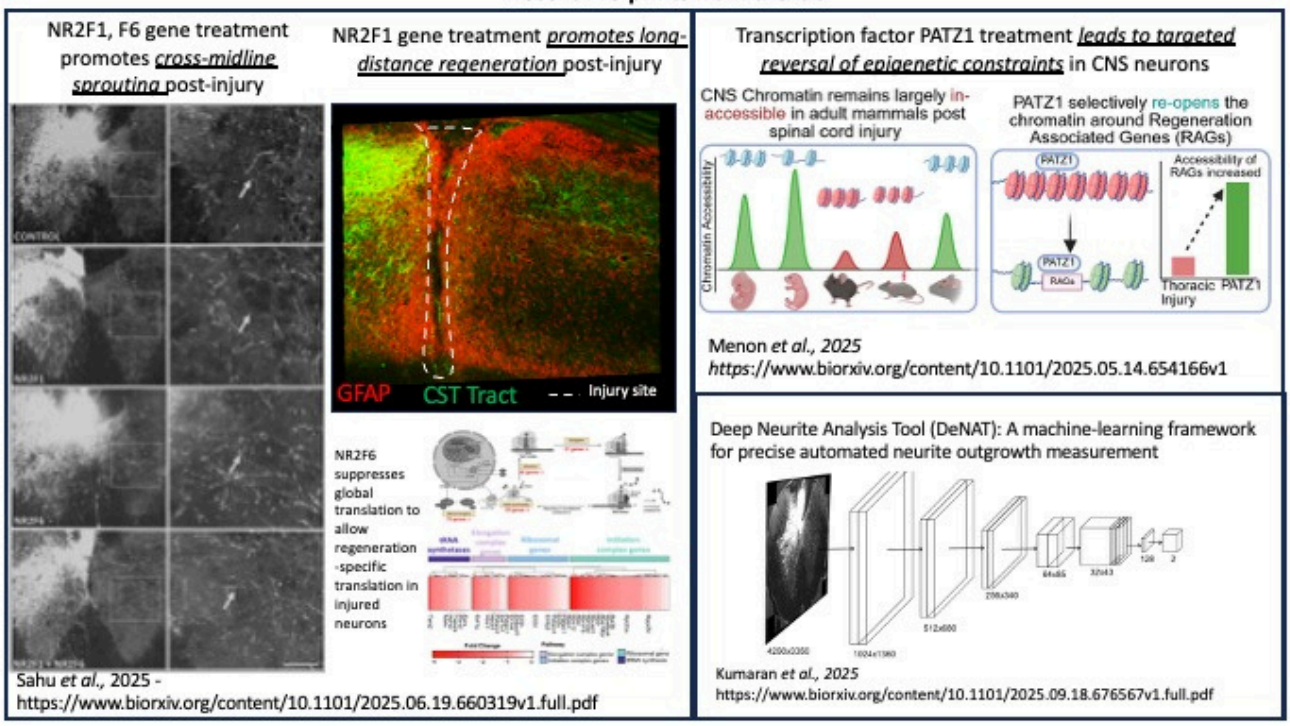
How is axon growth regulated during development and regeneration in mammals?

Communication in the nervous system is achieved via long cables called axons which connect neurons in the brain with the rest of the body. Intact axons are critical for proper nervous system function. When injured, young neurons are remarkably good at regeneration and repair. In contrast, adult neurons fail to regenerate resulting in permanent irreversible nervous system damage.

What molecular pathways drive the observed loss of regenerative capacity across development? What regulatory mechanisms modulate developmental axon growth? Does successful Central Nervous System regeneration in adult neurons require a faithful recapitulation of developmental mechanisms? Are there development independent pathways that co-ordinate repair? These are some of the questions

we are currently tackling. To get at these questions, we use a combinatorial approach which includes Bioinformatics, Functional Genomics (Single-cell RNA-Seq, ATAC-Seq, Hi-C, ChIP-Seq), in vitro assays of growth, in vivo mouse models of injury and behavioral assessments.

Recent Pre-prints from the lab



Scale bars, experimental conditions, and statistics as indicated in the respective preprints. Links: Sahu et al. (NR2F1/NR2F6), Menon et al. (PATZ1), Kumaran et al. (DeNAT)

Recent publications

- Wang, Z.; Kumaran, M.; Batsel, E.; Testor-Cabrera, S.; Beine, Z.; Alvarez Ribelles, A.; Tsoulfas, P.; Venkatesh, I∗.; Blackmore, M. G∗. Single-Nuclei Sequencing Reveals a Robust Corticospinal Response to Nearby Axotomy but Overall Insensitivity to Spinal Injury. J. Neurosci. 2025, e1508242024. https://doi.org/10.1523/JNEUROSCI.1508-24.2024.

K THANGARAJ

Evolutionary and Medical Genetics



From left to right: G. Mala, Sushmitha Raj Nitta, S. Deepa Selvi Rani, K. Thangaraj, Deepak Kumar Kashyap, Pratheusa Machha, Mahfuj Hasan

Research interests

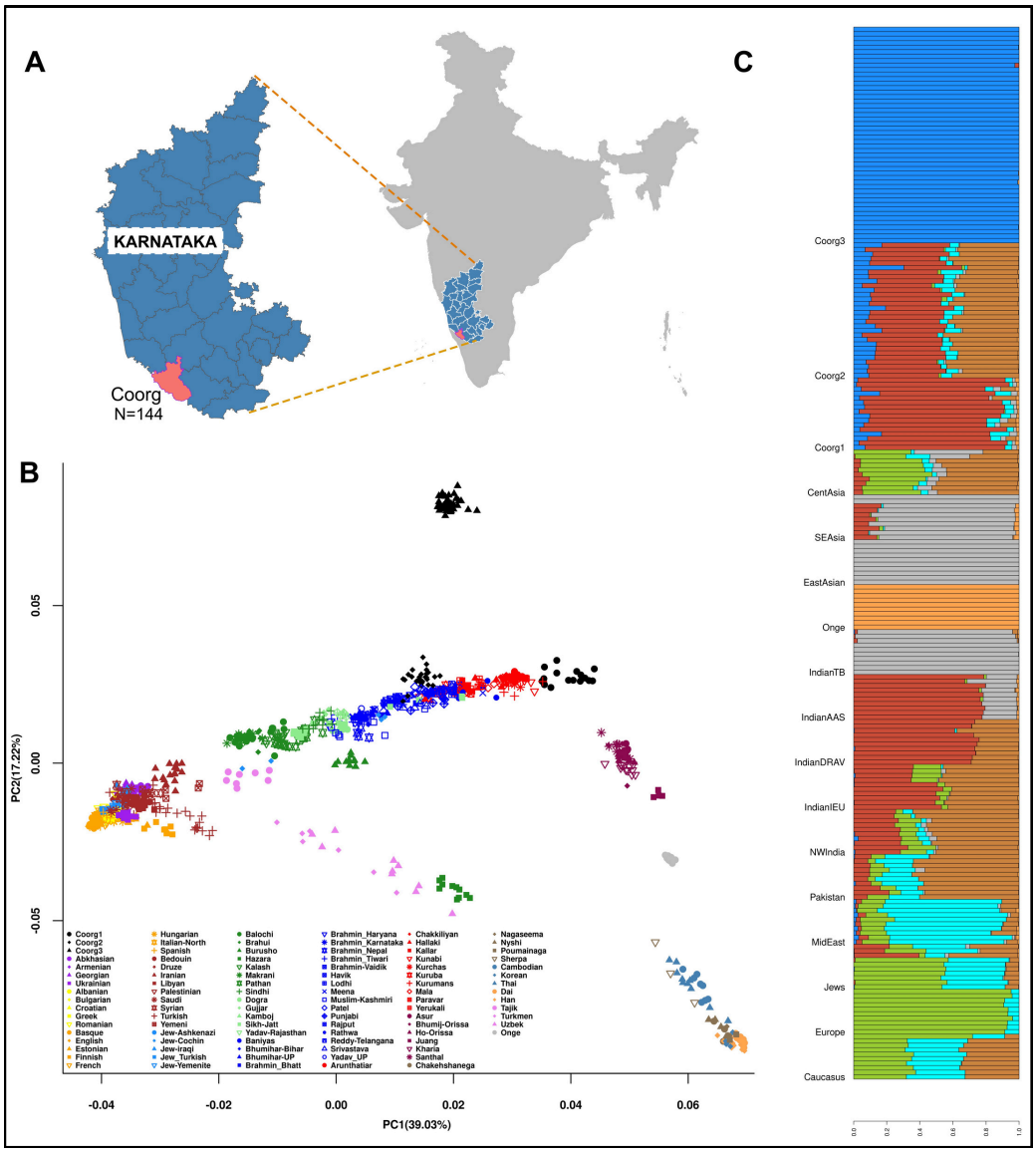
Main research interest of my group has been in the field of evolutionary and medical genetics, which includes origin and affinities of modern human, genetic basis of rare diseases, cardiovascular diseases, mitochondrial disorders, male infertility and sex determination.

The extraordinary genetic diversity of contemporary Indian population is the result of thousands of years of population mixing and eventual isolation. During the year, we have established the origin and affinities of a few populations, some of which are as follows:

The Coorgs are a small community in Karnataka, India. Our analyses suggest population substructure among Coorgs and showed significant population drift (Figure 1). The mtDNA analysis revealed that the Coorgs possess about 40% South Asia-specific mitochondrial lineages; while Y chromosome analysis revealed a predominance of Eurasian, Middle Eastern, and Indian-specific haplogroups (*Commun. Biol.* 2025). In another study, we have analysed three Ladakh populations (Changpa, Brokpa and Monpa) and found that Changpa and Monpa have shared close maternal ancestry compared to Brokpa, which is very distinct and probably experienced historical Bottleneck (*Mitochondrion*, 2024).

We also analysed the Nicobarese and found that they showed close affinities with Htin Mal language speakers and might have arrived on the Nicobar Islands in the last 5000 YBP (*Eur. J. Hum Genet.*, 2024).

Founder events influence recessive diseases in highly endogamous populations. Therefore, we performed whole-exome sequencing of 281 individuals, characterized by high IBD scores. We identified 1284 unreported exonic variants, of these, 23 are deleterious, all of which are heterozygous; they may be pathogenic when exist in homozygous (*J. Genet. Genome* 2025). In addition to population studies, we have also analysed patients with cardiomyopathy. We screened for a common 5bp deletion polymorphism in Troponin T (*TNNT2*) gene and found a high frequency of del/del genotype in patients with hypertrophic cardiomyopathy (*J. Clin. Cardiol. Cardiovasc. Interven.,* 2024).



Sample collection location and population structure within Coorg. A The geographical and sampling locations of contemporary Coorg samples. B Biplot of principal component analysis of Coorgs with modern Eurasian populations with first two components; C Stacked barplot of the ADMIXTURE analysis with K = 7 with global populations ordered geographically. (IndianIEU -Indian Indo-Eur- opean, IndianDRAV—Indian Dravidian, IndianAAS—Indian Austroasiatic, IndianTB—Indian Tibeto-Burman)

Recent publications

- Kumar L, Rajpal R, Ahlawat B, Singh Sehrawat J, Spalzin S, Singh Fonia R, Thangaraj K, Rai N (2024) The Maternal Genetic Origin and Diversity of the Extant Populations of the Ladakh Region in India. *Mitochondrion* 75:101828.

MUKESH LODHA

Epigenetic inheritance and plant development



From left to right: Kamala Radhakrishnan, Vyshnavi K, Mukesh Lodha, Prashanth Namdigalla, Fuzail Malik

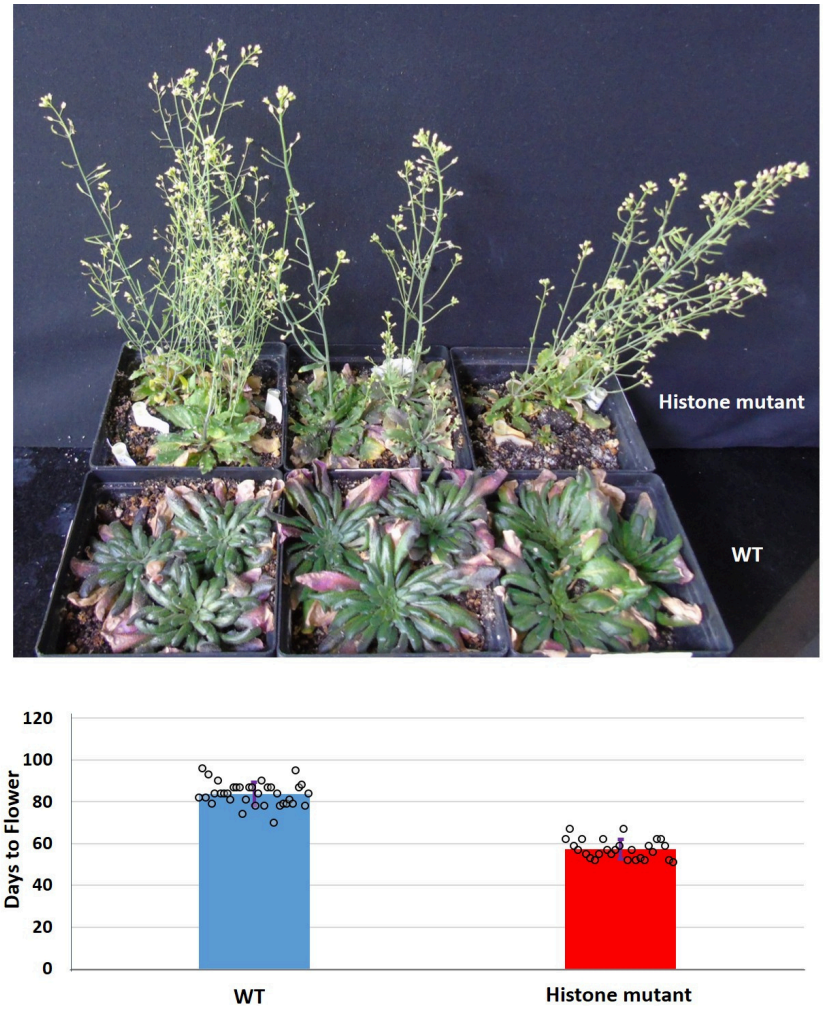
Research interests

We are interested in role of epigenetic regulations in plant development. Particularly, we are studying role of histone post translational modifications in leaf development and flowering time.

Epigenetic information is heritable during cell divisions but it is not encoded in the genetic material. An important question that remains underexplored is the mechanism of inheritance of epigenetic cellular memory. We are particularly interested in role histones in transmitting epigenetic memory during cell division. Using developmental context of leaf complexity and flowering time in model plant *Arabidopsis thaliana*, we are trying to understand mechanisms of epigenetic inheritance. SHOOT MERISTEMLESS (STM), a homeobox transcription factor is an important regulator of leaf complexity. We found binding sites for Polycomb and Trithorax complexes in the promoters of STM. Polycomb is a repressor and Trithorax is a depressor of transcription. Our experiments show that distance and interaction between binding sites of these complexes are important in determining leaf complexity. A repressive loop is formed between the binding sites in simple leaf species which does not allow

STM expression in the developing leaves. In compound leaf species, repressive loop is diminished, allowing expression in the developing leaves and cause the leaf lamina to divide and give rise to compound leaf.

Prolonged cold (vernalization) accelerates flowering in winter-annual accessions of *Arabidopsis*. On one hand, we are taking genetic approach to map the genes responsible for vernalization sensitivity, as there is difference in vernalization response in different accessions. We have generated F2 population of cross between differentially sensitive accessions for vernalization. map based cloning approach is being taken to identify the causal genetic difference in the vernalization response. On the other hand, we are trying to identify histone residues which are important for vernalization response. In this approach, we are complementing Histone mutant plant with either wild type or mutant histone and studying their vernalization response. After identifying the amino acid residues on histone, we will characterize the posttranslational modification which is important in vernalization response.



Mutation in histone genes cause early flowering in *Arabidopsis thaliana*

RAKESH K MISHRA

Genome Organization and Epigenetic Regulation



From left to right, top row: Rakesh K. Mishra, K. Phanindhar, Sheikh Suhail, Ravina Saini
Bottom row: Sonu Yadav, Saketh Murthy, Sanskruti Wadi, Anil Komanduru

Research interests

- Comparative and functional genomics of non-coding DNA
- Organization and regulation of Hox genes: evolutionary logic of animal body plan
- Epigenetic regulation of development and ageing

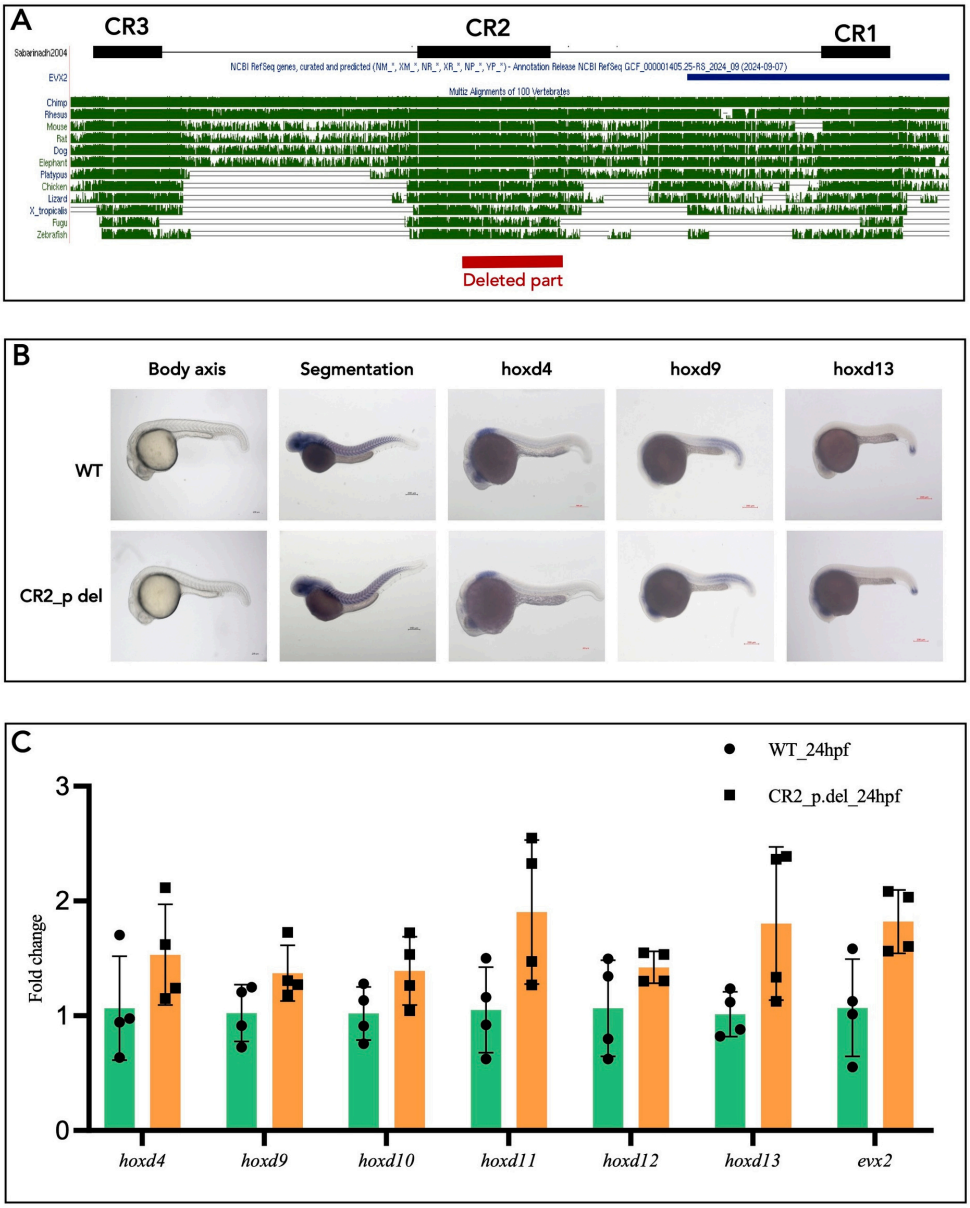
Our laboratory previously identified three ultra-conserved non-coding DNA regions (CRs) located adjacent to the vertebrate HoxD complex, which is well known for its role in regulating segmentation and body-axis patterning. Using reporter assays in mammalian cell lines and early zebrafish embryos, we demonstrated the regulatory potential of these CRs. However, their precise target genes and mechanisms remain unresolved.

To investigate their function, we employed genome-editing technology to delete two CRs (CR2 and CR3). Only a partial deletion line of CR2 (designated CR2_p.del) could be maintained. Repeated attempts to generate large deletions were unsuccessful, suggesting that such extensive loss is not compatible with viability.

Detailed phenotypic and molecular analyses were conducted on the CR2_p.del line. We did not observe any obvious morphological abnormalities or major phenotypic changes.

Expression patterns of HoxD genes along both the primary and secondary anterior–posterior axes remained unaltered at 24 and 48 hpf (hours post-fertilization) following CR2 deletion (Figure). Interestingly, RT-PCR analysis revealed a modest increase in the expression levels of most HoxD genes at both 24 and 48 hpf, supporting the repressor activity we previously observed in mammalian cell culture experiments.

These findings suggest that the majority of CRs are indispensable, and only the comparatively less conserved portions in lower vertebrates can be deleted. Population-level studies indicate that such ultra-conserved regions are typically depleted among copy-number variants and segmental duplications, implying that their disruption may not be tolerated. Notably, partial deletion of CR2 does not impair zebrafish development, highlighting potential differences in the requirement for these elements between lower and higher vertebrates. Further work is needed to elucidate the function of CRs, which appear to have originated early in vertebrate evolution and expanded in size with increasing organismal complexity.



Deletion of ultra conserved regions of HoxD complex.
A. Deleted part of CR2
exhibits a few variations across vertebrates compared to the rest of the region.
B. Body axis, segmentation and expression pattern of hoxd genes in wt and CR2_p.del embryos.
C. Relative expression level of all the hoxd genes wt and mutant embryos.

SHRISH TIWARI

Discovering genotype to phenotype correlations



From left to right: Shrish Tiwari, Prachi Singh and Deepti Rao

Research interests

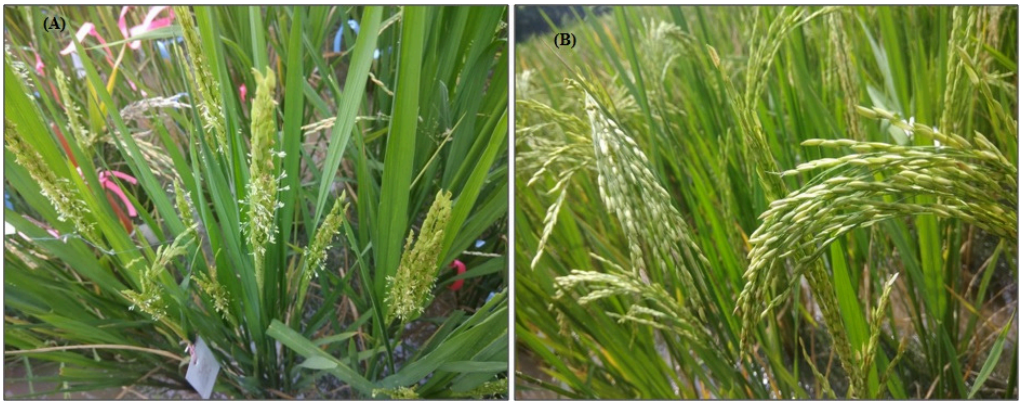
The research interests of the group are in elucidating genotype to phenotype correlations using variation analysis of genomes. This involves NGS analyses, comparative genomics as well as expression analysis. We use rice as our model system. We have also done some work involving analysis of noncoding RNA.

We have built a chromosomal level assembly for Samba Mahsuri (SM), using short read- and long read-sequences, as well as optical mapping of the genome. We are now using this assembly as the reference genome against which we can align reads from mutant genomes to identify variations.

Earlier we used the Nipponbare genome as proxy, by aligning reads from wild type SM and mutant SM to Nipponbare genome and the filtering out SNPs that were unique to the mutant. We re-analysed the mutant genome SM93, which has the desired characteristics of high yield and early maturation, with the SM reference genome and found the all the loci associated with early flowering that had come up in the previous analysis. In addition, we found a new locus associated with the phenotype of interest. Aligning our reference SM genome to Nipponbare genome revealed a 6MB inversion near the centromere of chromosome 6. This

inversion was missing when we aligned SM to the Indica genome. Since there are several rice genomes available, we confirmed this inversion by aligning SM to all available rice genomes. We are now looking at the evolutionary implications of this discovery.

We are also sequencing *Aeluropus lagopoides,* which is a mangrove grass that secretes salt in its stems and leaves. The short read sequencing is done and we are waiting for the long read sequencing and optical mapping data to complete the assembly of its genome.



Left: Wild type samba mahsuri (SM). Right: SM93 an early maturation variant. As can be seen while SM is in the flowering stage, SM93 has entered the grain-filling stage.

T KARTHIK BHARADWAJ

Genomics for human health and disease



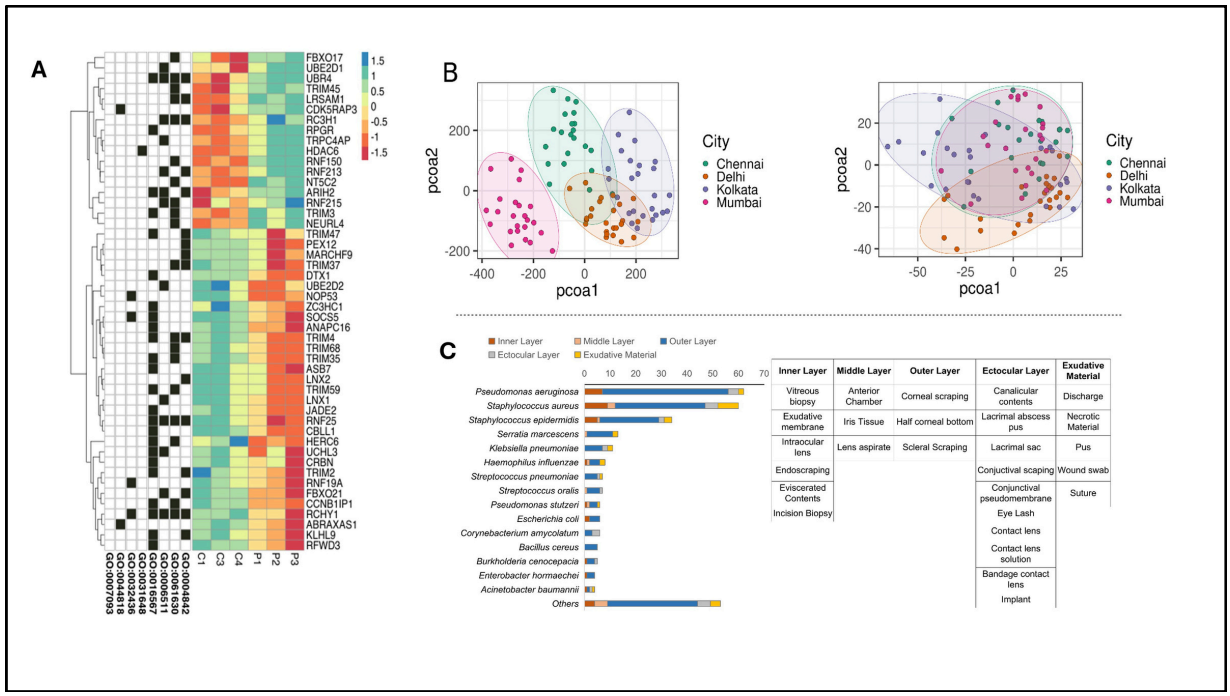
From left to right, top row: Pranjal, Bishwadeep, Srinivas, Vinay, Osed, Jafri, Balakrishna, Rakesh
Middle row: Hari Charan, Joel, Dibya Rana, Karthik, Aruna, Sushmita, Valli, Elizabeth , Aneek
Bottom row: Parvathi, Mounika, Pratima, Nandini, Kanakavalli, Shreya, Jyothi, Tulasi, Deepshika, Swetha, Niharika

Research interests

My lab is interested in application of the knowledge of genetics in human health and disease with special focus on rare genetic disorders.

With rapid advancement of sequencing technologies, it is becoming more and more possible to discern the impact of genetics on human health and disease. Our lab intends to capitalize on this progress in understanding the etiopathogenesis of ultra rare genetic disorders/syndromes. In this context, we are currently working on a novel intellectual disability syndrome caused by mutations in DPH2 gene and CHFR related hereditary cancer predisposition syndrome. We use cutting-edge technologies like long read sequencing and optical genome mapping in addition to short read sequencing to facilitate the diagnosis of genetic diseases and identify genetic modifying factors contributing to disease predisposition and prognostication. In collaboration with our clinical partners, we are currently investigating various disease cohorts like FSHD and other neuromuscular disorders, Intellectual disability & autism spectrum disorders, complement mediated kidney disease, etc.

In addition, our lab is currently handling diverse projects like Genome India, Indian Breast Cancer Genome Atlas and various genomics-based pathogen surveillance activities. In addition to understanding pathogen abundance and AMR signature from environmental samples, we also look at specific clinical cohorts like ocular infections, diarrheal diseases and acute febrile illnesses.



A. The genes and gene products that are annotated to CHFR-associated GO-BP terms and are differentially expressed ($p < 0.05$) between control (n = 3) and patient samples (n = 3) are presented in the heatmap. B. PCoA plot (Aitchison distance) based on bacterial species abundances showing distinct city specific clustering of samples but not when based on ARG abundances. C. Distribution of bacterial isolates sequenced from different layers of the eye

Recent publications

- Pal P, Devireddy S, Bhat S, George JK, Kakkar S, Das Bhowmik A, Tallapaka KB (2025) Case report of a 21-year-old woman with Gabriele-de Vries syndrome and autoimmune hypothyroidism. ***Clin. Dysmorphol.*** 34(3): 79-82.

- Banu S, Mk K, George JK, Siby E, Bhagat R, Ms S, Patil SJ, Phadke SR, Sowpati DT, Tallapaka KB (2025) Enhanced resolution of optical genome mapping utilizing telomere-to-telomere reference in genetic disorders. ***Eur. J. Hum. Genet.*** 33(7): 956-959.

- Aggarwal S, Vineeth VS, Padwal SS, Bhat SA, Singh A, Kulkarni A, Patil M, Tallapaka K, Pasumarthi D, Venkatapuram V, Thotakura PL, Dalal A, Bhandari R (2024) SERPINA11 related novel serpinopathy - A perinatal lethal disorder. ***Clin. Genet.*** 106(3): 367-373.

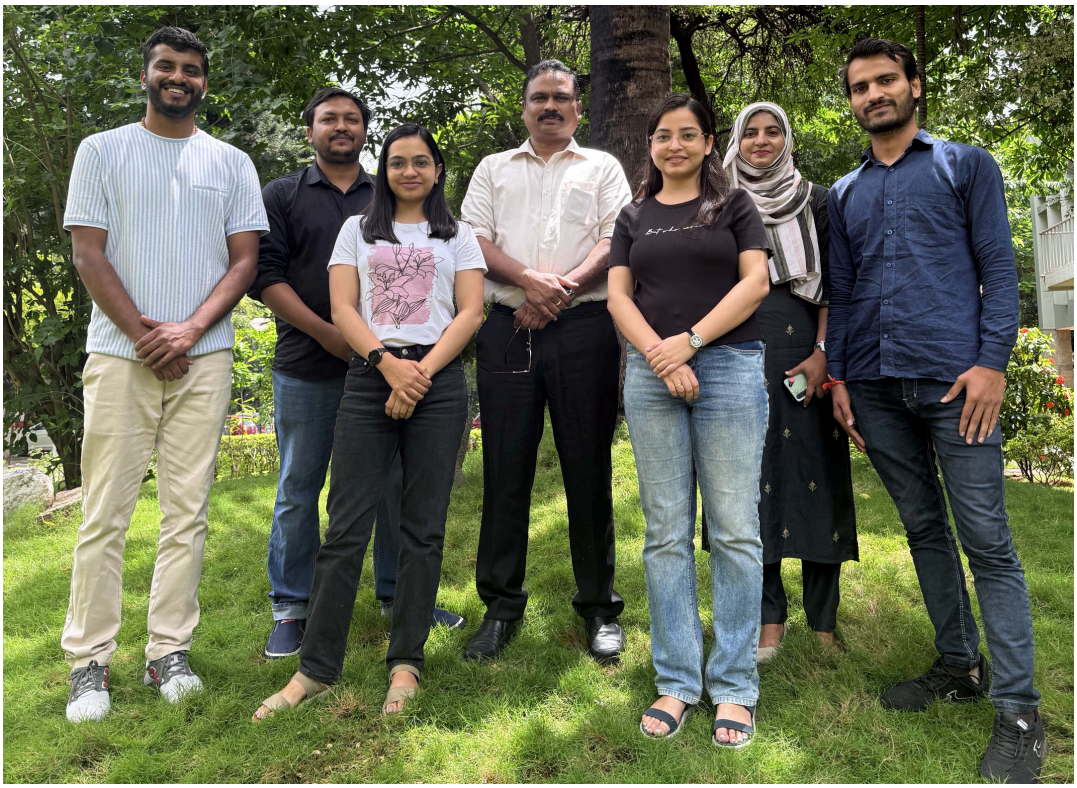
CELL AND STEM CELL BIOLOGY

A.S. Sreedhar
B. Kiran Kumar
P. Chandra Shekar
Regalla Kumaraswamy
Santosh Chauhan
Santosh Kumar
Suman Siddharth Thakur
Swasti Raychaudhuri
Tripura Sundari C.B.
Venkat R. Chalamcharla



A S SREEDHAR

Heat Shock Proteins in Biology and Medicine



From left to right: Anit Antony, Vivek Chaudhary, Priyadarshini Singh, Amere Subbarao Sreedhar, Prateekshya Das, Kainat Fatima, Nitesh Kumar Gupta

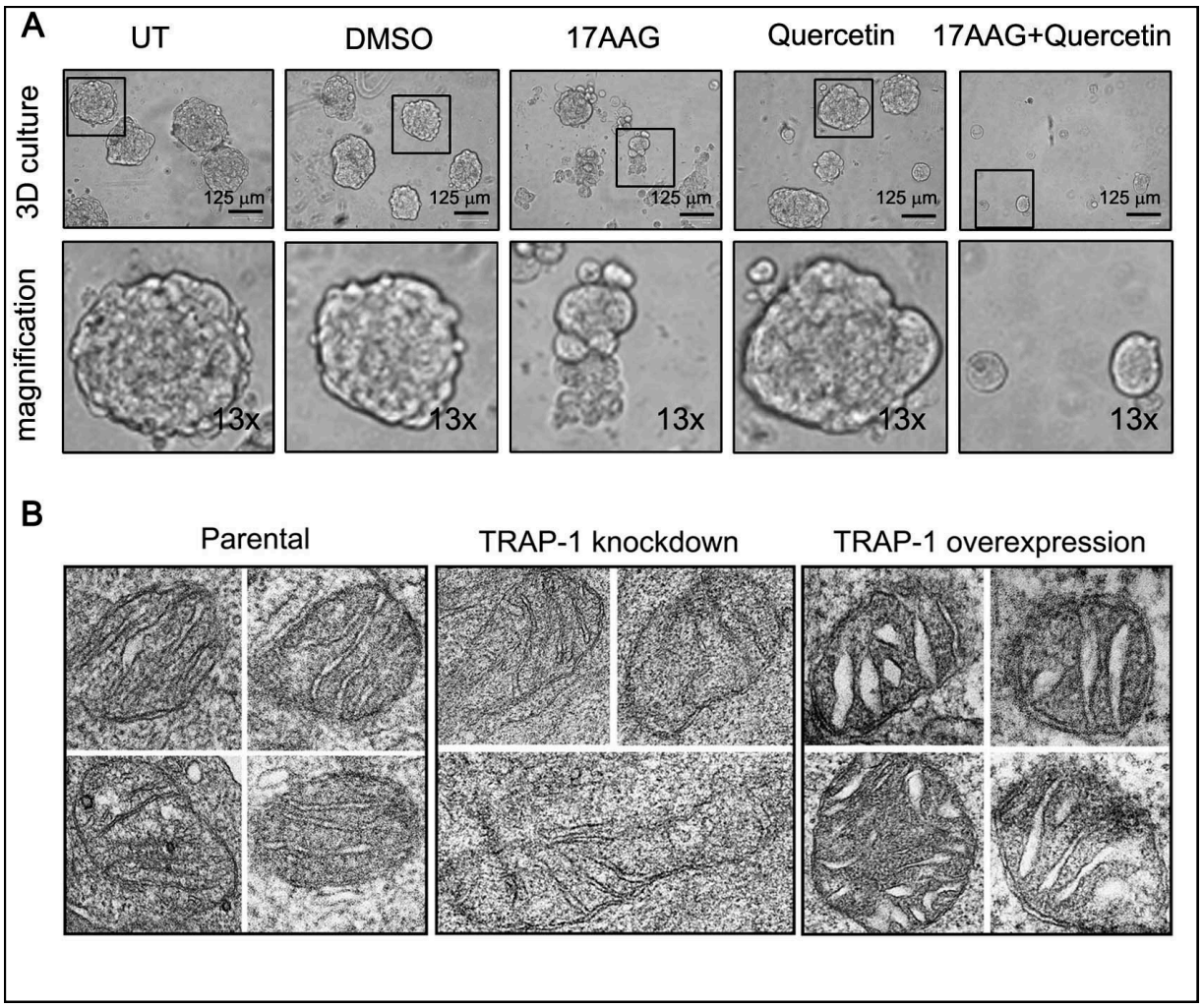
Research interests

Understanding the molecular basis of stress adaptations across species, tumor heterogeneity, multidrug resistance, iron addiction and metabolic adaptations leading to disease progression.

Cellular stress response is accompanied by heat shock proteins (Hsps), which function as molecular chaperones. Adaptive stress responses are linked to civilisation-associated disorders such as cancer. Among Hsps, Hsp90 functions as a cancer chaperone, making it a molecule of interest to biologists and clinicians. Apart from this, Hsp90 contributes to cellular adaptations, including responses to oncogenes, drugs, and metabolic changes, which can lead to disease conditions. We study unconventional roles of Hsp90 in cancer adaptations. Since Hsp90 buffers mutations and increases canalisation, resulting in intra-tumour heterogeneity, we study the molecular basis of tumour heterogeneity mediated by Hsp90.

We demonstrated that Hsp90 regulate tumour heterogeneity in an isoform-specific manner, where Hsp90α functions as a cancer chaperone and Hsp90β contributes to tumour dormancy and stem cell mimicry via NOTCH2. Earlier, we had demonstrated that its mitochondrial

homologue TRAP-1 contributes to metabolic rewiring via increased glycolysis in the presence of glucose and glutaminolysis in the absence of glucose. We could establish a hypothesis that TRAP-1 modulates iron uptake, heme and iron-sulfur cluster biosynthesis to rewire metabolism. We are now elucidating the role of TRAP-1 in modulating cristae organisation and OXPHOS efficiency. Since the acquisition of multidrug resistance poses a challenge to current anti-cancer treatments, we study the molecular basis of the epigenetic mechanism underlying drug adaptation. We observed Hsp90-dependent cross-talk between chromatin regulatory complexes and histones, which exhibits differential regulation of the multidrug resistance gene 1 (MDR1) promoter in induced and acquired multidrug resistance in cancers. Studies are underway to unfold this regulation.



A. Chemotherapy-induced intra-tumour heterogeneity is intervened by quercetin treatment in human breast cancer cells. Note decreased mammosphere formation on 3D cells in the combination treatments.
B. TRAP-1 influences on cristae organisation leading to decreased OXPHOS efficiency. Note TRAP-1 overexpression decreases cristae junctions and increases cristae volume, while parental and TRAP-1 knockdown cells show normal cristae organisation.

B KIRAN KUMAR

Understanding molecular pathways governing the initiation of regeneration, with a focus on understanding the role of stem cells in tissue repair and the signaling factors that regulate their differentiation



From left to right: Renuga Devi, Vuddhav Reddy, Nandha Kumar, Sreekanth, B Kiran Kumar, Sreenivas, Khyathi Ratna, Deepika, Shruthi Sri, Anmol Kamath

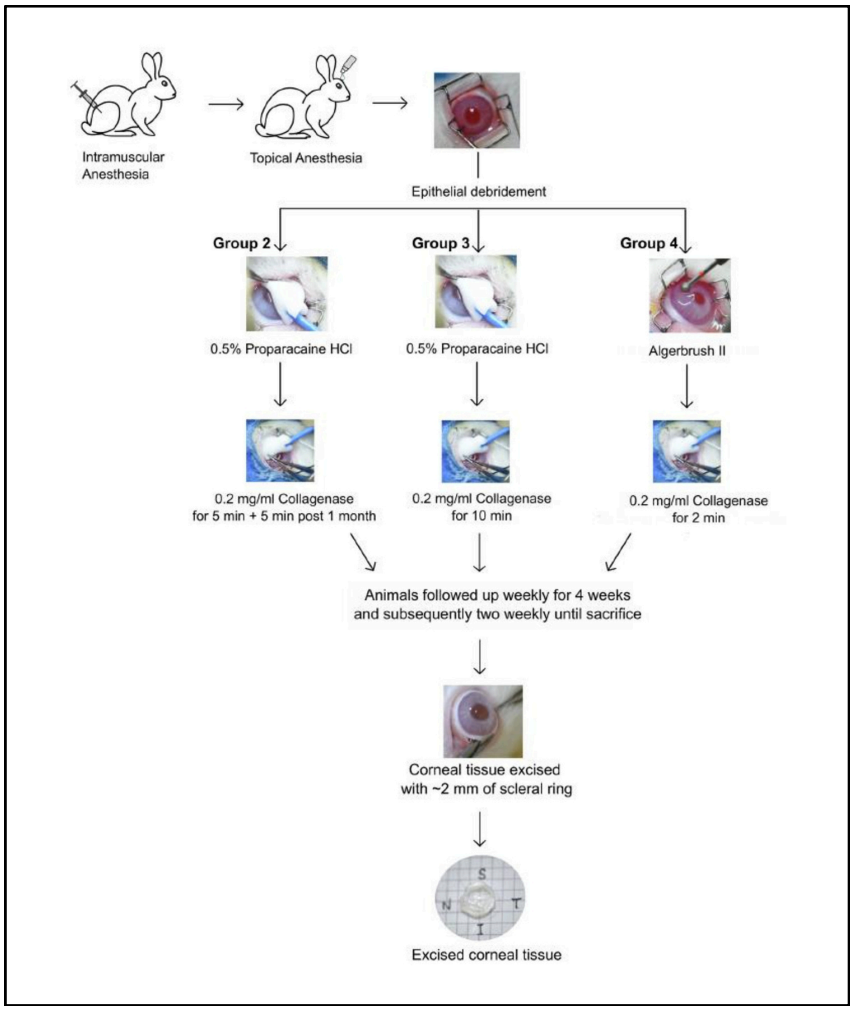
Research interests

Develop human-relevant animal and organoid models to advance disease modeling and therapeutic applications.

Keratoconus (KC) is a degenerative disorder resulting from the degradation of the stromal collagen fibril network in the cornea, leading to its thinning and conical deformation. Various studies have established animal models of KC by using the collagenase type II enzyme to gain a better understanding of the pathogenesis. However, long-term monitoring or follow-up of the models have not been reported so far.

Our study evaluates the long-term stability of collagenase type II-induced KC in a rabbit model. Six New Zealand rabbits were divided into 4 study groups with 3 eyes per group. The groups were control (group 1), 0.5% proparacaine + 5 min collagenase treatment on day 0 and day 30 (group 2), 0.5% proparacaine + 10 min collagenase treatment on day 0 (group 3) and, mechanical debridement + 2 min collagenase treatment on day 0 (group 4). Inflammation was observed in group 4 till week 10. Significant decrease in the central corneal thickness was observed in group 3 by week 4 ($p < 0.001$).

However, the thickness was regained in the subsequent follow-ups in all the groups. Keratography results showed no changes in K_m values but an increased astigmatic power in all groups. Scanning electron microscopy images revealed thinner collagen fibrils arranged in a mesh-like pattern above the uniform layer of the collagen lamellae in the central part of the treated corneas. Similarly, histological staining revealed loosely packed stromal fibrils in the anterior portion of the cornea. This corroborates with the immunofluorescent staining results. This study revealed the remodeling of the corneal structure by eight weeks of collagenase treatment. Consequently, the possibility of creating a rabbit keratoconus model induced by collagenase may warrant further consideration.



Schematic representation of the workflow of creating KC model. The protocol involved epithelial debridement followed by topical application of Collagenase enzyme using spear sponge in New Zealand White Rabbits. Based on the model of epithelial removal and duration of enzymatic treatment, rabbits were categorized into three groups. Post-surgery follow ups and corneal tissue extraction was performed for further analysis to assess the extent of KC development. N: Nasal, T: Temporal, I: Inferior and S: Superior regions of the cornea.

Recent publications

- Ealla KKR, Durga CS, Sahu V, Kumari N, Venkatesan J, Veeraraghavan VP, Ramani P, Bokara KK, Ramalingam K (2025) Doxycycline-integrated silk fibroin hydrogel: preparation, characterizations and antimicrobial assessment for biomedical applications. ***BMC Oral Health*** 25(1): 177.

- Shankar S, Thacker M, Sahoo A, Aindla AR, Padala KR, Jaffet J, Bokara KK, Basu S, Singh V (2024) Revisiting rabbit models for keratoconus: A Long-term Study on Collagenase-Induced Disease Progression. ***Exp. Eye Res.*** 241: 109811

P CHANDRA SHEKAR

Mechanistic insights into stem cell state transition in pluripotent stem cells



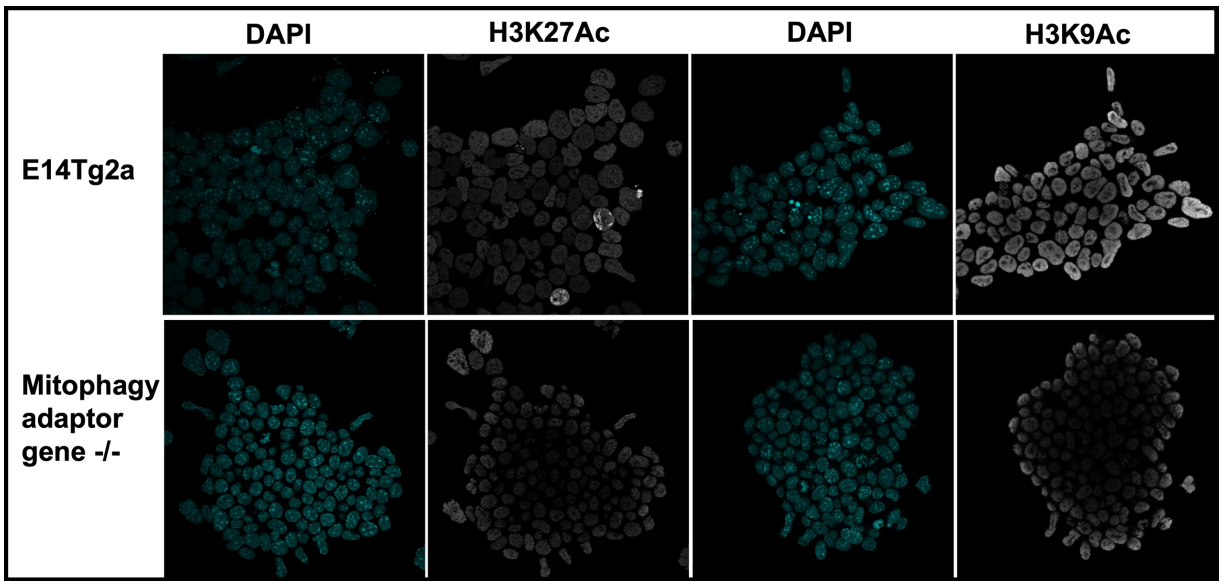
From left to right: Pratham Tanotra, Elarani Majhee, Niharika Tiwary, Priyanshi M Patel, Dhthri Bollepalli, P Chandra Shekar, Karthik M, Sudheer, Divya Kumari, Syeda Afraa Fatimah

Research interests

Understanding the molecular mechanisms of pluripotency state transition and self-organisation of stem cells into embryo like structures. Development of stem cell models of embryos to understand human embryonic development and developmental disorders

Multiple types of stem cells have been derived from the pre implantation embryos, with varying developmental potentials with unique transcriptome and chromatin state. These stem cells represent 2-cell stage or morula (2CLCs), naive epiblast or inner cell mass (ESCs) and post implantation epiblast (EpiSCs) etc. When cultured in appropriate media conditions, the pluripotent stem cells can transit from one stem cell state to another implying an inherent plasticity. The mouse pluripotent stem cells are known to exist in a unique state called a metastable state where the stem cells in one state can give rise to the stem cells of another state seamlessly. In metastable state, all stem cell states exist in a dynamic equilibrium in the same culture. The mechanisms regulating these stem cell state transitions are not understood. In our pursuit to understand these mechanisms, we have identified a mitophagy adaptor gene that is essential for the stem cell state transition. The loss of this gene leads to loss of state transition in mouse stem cells. Also the loss of the gene leads

to loss of metastable state. We further show that the protein of the gene interacts with the enzymes like Isocitrate dehydrogenase and regulates their abundance and activity. Loss of the gene leads to increase in the metabolites like alpha ketoglutarate (Alpha-KG) and alteration in other metabolites. The altered abundance of the metabolites resulted in global decrease of H3K4me3, H3K27me3, H3K27Ac and H3K9Ac marks. The cells in this global altered chromatin state exhibit resistance to stem cell state transitions. Our finding suggest that the stem cell state transition are regulated by the mitophagy regulator, which in turn regulates the abundance of enzymes required for generating metabolites for demethylation and acetylation of chromatin.



The global reduction in histone acetylation of the ESCs lacking mitophagy adopter gene. The analysis of H3K27Ac and H3K9Ac expression levels by immuno fluorescence. The ESCs lacking the mitophagy adapter gene show lower levels of H3K27Ac and H3K9Ac compared to the WT cells (E14Tg2a)

Recent publications

- Kumar U, Sudhakar DVS, Kumar N, Moitra A, Kale HT, Jha RK, Rawat S, Verma G, Gupta NJ, Deenadayal M, Tolani AD, Raychaudhuri S, Chandra Shekar P, Thangaraj K (2024) TEX13B is essential for metabolic reprogramming during germ cell differentiation. ***Hum Reprod.*** 10.1093/humrep/deae094.

KUMARASWAMY REGALLA

Cardiovascular Biology



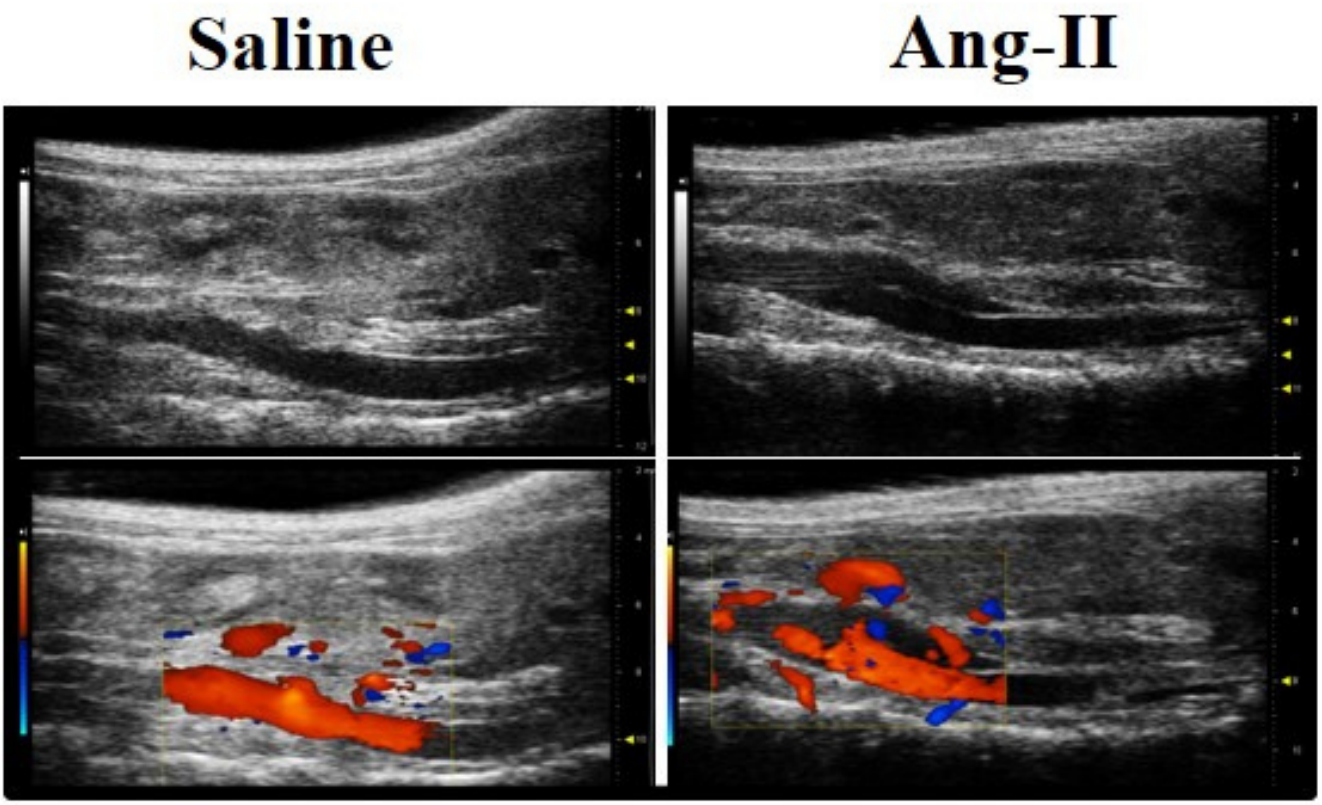
From left to right: Abhishek, Kumarswamy, Mallesh, Disha, Jyothi, Shreyas and Priyanka

Research interests

- RNA Biology
- Cardiovascular diseases
- Non-coding RNAs
- Animal models
- Translational research

Heart diseases are the leading cause of death worldwide. In India about 40% of all deaths in urban areas and 30% in rural areas are attributed to cardiovascular diseases. Incidence of heart diseases in India has steadily increased from about 2% (1960) to 10.5% (2000). Although available therapies improve symptoms, they are not able to reverse fibrosis or activate hibernating myocardium. Recently, interest in non-coding RNAs as therapeutic-targets for chronic diseases is increasing. It is known and that less than 2% of our genome codes for proteins. Recent advancements in transcriptomics have unveiled thousands of transcripts which are relatively abundant yet they have very little protein coding potential. These non-coding RNA based on their size can be classified as small non-coding RNA (miRNA, piRNA, 21-22nts long) or long non-coding RNA (lncRNA). LncRNA are defined as transcripts that are longer than 200 nucleotides in length, having very little coding potential. Generally,

these lncRNAs are poorly conserved and have a tight spatiotemporal expression. While the role of microRNAs is well studied, information about the role of long non-coding RNAs (lncRNAs) in cardiovascular diseases is scarce. In our lab we investigate the role of lncRNAs in patho-physiology of the heart. We identified several lncRNAs that participate in cardiac hypertrophy, fibrosis or aortic aneurysm.



Abdominal Aortic Aneurysm (AAA) induced in mice by treating with angiotensin-II (Ang II). Imaged using Vevo-2100 ultra sound imager in live mice

SANTOSH CHAUHAN

Cell death and tissue regeneration



From left to right: G. Bhanu, Ramya, Devender, Santosh K, Rinku, Prince, Sahidur, Megha, Jagamohan, Souradeepa, Kollori, Soumya, Santosh. C, Shivram, Vennela, Kanitha, Sameekshya, Anikta, Nivedita, Ruchika, Ashwani, Sarika, Rina, Sunita

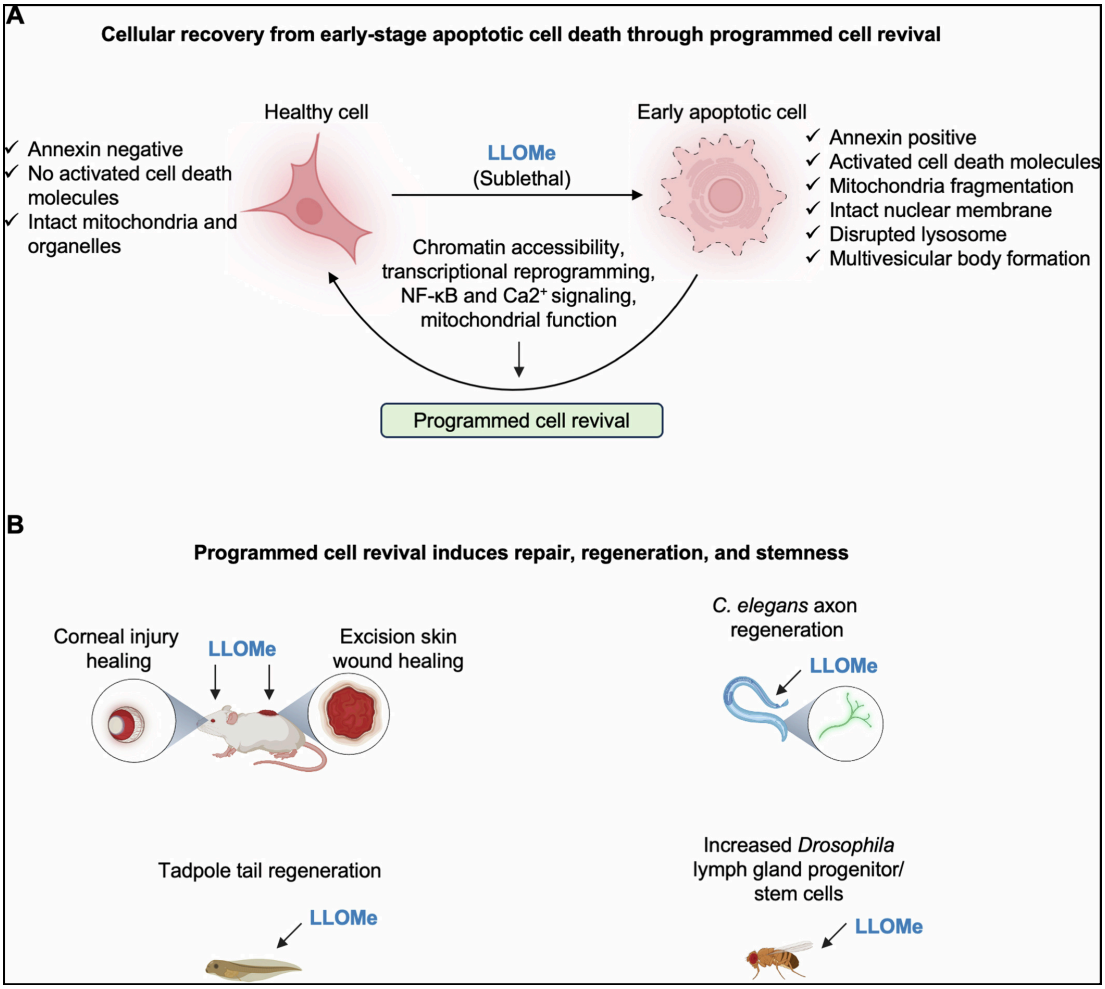
Research interests

- Understanding host cell autonomous defense systems- autophagy and innate immunity.
- Identifying new targets and therapeutic small molecules against viruses and cancer

Programmed cell revival from imminent cell death enhances tissue repair and regeneration

Cell recovery from near-death states is a critical yet poorly understood aspect of cell biology. Here, we describe a tightly-regulated programmed cell revival process after exposure of cells to cell death-inducing lysosomotropic agents, such as L-leucyl-L-leucine methyl ester (LLOMe). In the initial stage of cell recovery, we observe increased chromatin accessibility and upregulation of genes and pathways associated with embryonic development, regeneration, stemness, and inflammation. Subsequently, vital pathways governing metabolism, organelle biogenesis, membrane trafficking, transport, and cytoskeleton remodeling are activated, resulting in the complete renewal of cells. Consistent with the links of this transcriptional profile to tissue repair and regeneration, we found LLOMe to enhance the healing of skin wounds and corneal alkali burns in mice, promote hematopoietic

progenitor/stem cell production in *Drosophila melanogaster,* induce tadpole tail regeneration in frogs, and mediate axon regeneration in *Caenorhabditis elegans*. Using both genetic and pharmacological approaches, we show NF-κB signaling to be critical for both cell revival and regeneration. This study characterizes cell revival from near-death conditions as a programmed cell-intrinsic mechanism, which could be harnessed for therapeutic applications in regenerative medicine.



Inducing programmed cell revival promotes repair, regeneration, and stemness.
(A) In response to a sublethal dose of LLOMe, cells initiate apoptosis, but then undergo a revival mechanism mediated by NF-κB signaling, calcium (Ca^{2+}) signaling, and mitochondrial function. (B) This "programmed cell revival" promotes repair, regeneration, and stemness in multiple species Figure is adopted from Balamurugan Sundaram and Thirumala-Devi Kanneganti. EMBO J 2025 doi.org/10.1038/s44318-025-00538-6.

SANTOSH KUMAR

Understanding human NK cells and harnessing their therapeutic potential



From left to right: Apoorva, Rashmi, Sushree, Sankar, Aashutosh, Santosh

Research interests

Signaling pathways in human NK cells and exploring them for cancer immunotherapy

Natural killer (NK) cells constitute an important effector cell population of our immune system, which are critical in providing protection against infection and cell transformation. We are working to understand the biology of NK cells and harness their therapeutic potential.

Regulation of NK cell cytotoxicity by Zn^{2+} ions

NK cells from Zn^{2+}-deficient individuals are seen to exhibit diminished cytotoxicity. In this study, we have investigated the role of Zn^{2+} in the cytotoxicity of human NK cells. Upon conjugation with sensitive target cells, NK they display a cell-wide increase in intracellular free Zn^{2+} level. This increase is observed, although to a lesser extent, despite the presence of EDTA, a cell-impermeable Zn^{2+} chelator. These results suggest an intracellular redistribution of Zn^{2+} that elevates free Zn^{2+} levels in NK cells at NK-target cell cytotoxic synapses. Further, NK cell cytotoxicity remained normal despite the presence of

extracellular EDTA, indicating that NK cell cytotoxicity is independent of extracellular Zn^{2+}. However, depletion of intracellular Zn^{2+} with the cell-permeable chelator TPEN reduced NK cell cytotoxicity. Supplementation with exogenous Zn^{2+} restored intracellular Zn^{2+} levels and rescued NK cell cytotoxicity in the presence of TPEN. Taken together, these findings indicate that an intracellular Zn^{2+} redistribution enhances free Zn^{2+} levels in NK cells at cytotoxic synapses and that intracellular Zn^{2+} promotes NK cell cytotoxicity.

NK cell responses in Helicobacter pylori infection

H. pylori plays causative roles in gastric tumours. *H. pylori* is seen to be present in established gastric tumours. How *H. pylori* controls the anti-tumour activities of NK cells is unclear. Our in-culture experiments indicate that H. pylori upregulates the surface expression of the MHC-I molecule HLA-C on cancer cells, and thereby protects them from the cytotoxic attack of NK cells. We are heading towards extending this work in gastric tumours from patients.

Recent publications

- Apoorva E, Jacob R, Rao DN, Kumar S (2024) Helicobacter pylori enhances HLA-C expression in the human gastric adenocarcinoma cells AGS and can protect them from the cytotoxicity of natural killer cells. ***Helicobacter*** 29: e13069.

SUMAN SIDDHARTH THAKUR

Mass Spectrometry based Proteomics and Cancer Biology

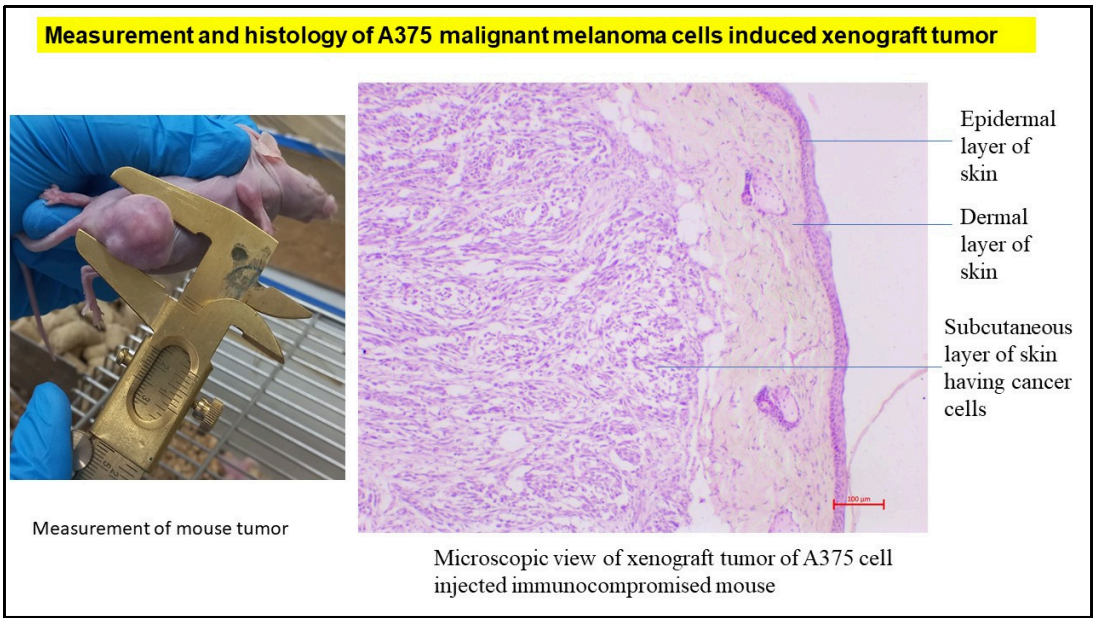


From left to right: Niharika, Keerthana, Suman Thakur, Anena, Saveri

Research interests

Our research interests involve understanding the initiation of cancers and their progression in cancer development, including metastasis for the childhood and aggressive cancers. Furthermore, the biomarkers involved in the cancer initiation and progression will serve as targets for developing cancer therapeutics.

Cancer is one of the most intricate and life-threatening diseases. Our research interests involve understanding the initiation of cancers and their progression in cancer development, including metastasis for the childhood and aggressive cancers. We are especially interested in investigating the role of the loss of cancer suppression genes and the involvement of post-translational modifications in the initiation of cancers using cell biology, mouse models, and modern biology approaches including mass spectrometry based quantitative and targeted proteomics, metabolomics and transcriptomics. Furthermore, the biomarkers involved in the cancer initiation and progression for childhood and aggressive cancers will serve as targets for developing cancer therapeutics. Further, we are also interested to understand and study the progression and impact of pandemic diseases including COVID-19 on human health and disease.



The xenograft tumors derived from A375 malignant melanoma cells in immunocompromised mice, along with histological analysis (microscopic view)

Recent publications

- Chatterjee B, Thakur SS (2024) Valuable Contributions and Lessons Learned from Proteomics and Metabolomics Studies of COVID-19. ***J. Proteome Res.*** 23(10): 4171-4187.

SWASTI RAYCHAUDHURI

Fundamentals of protein homeostasis insufficiency in age-related disease models



From left to right, sitting: Suhail, Anubhab, Swasti, Gururaj, Cheshta, Aanchal
Standing: Bhavika, Pallavi, Shreya, Suparna, Navyatha, Pooja Gupta, Alivelu, Pooja Joshi, Gayathri

Research interests

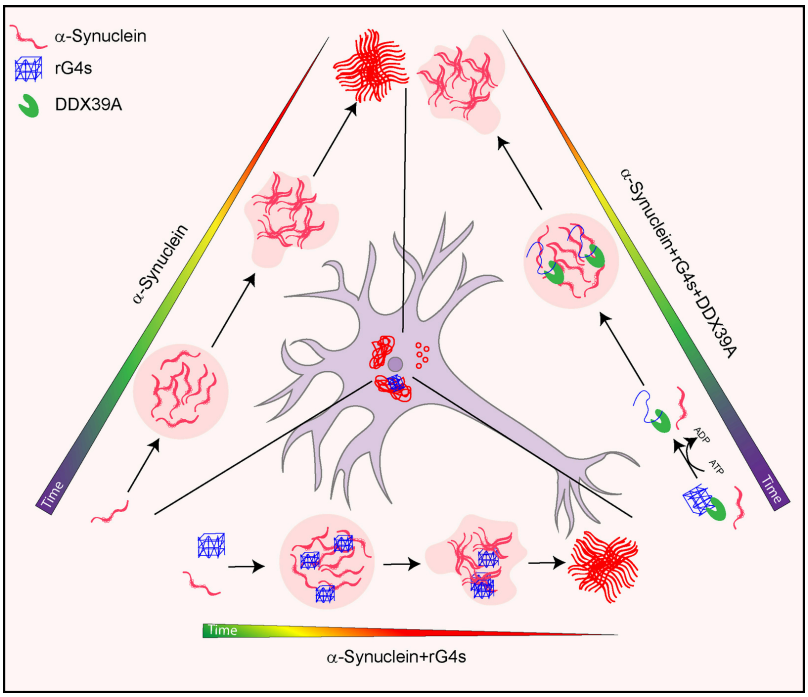
- Quality control of respiratory complex biogenesis
- Cause and consequences of intracellular spatiotemporal organization of protein inclusion bodies
- Large scale plasma proteomics and metabolomics studies to identify prognostic and diagnostic biomarkers in Indian population with a focus on Cardiovascular diseases and Sickle Cell Anaemia

Respiratory complexes are multi-subunit protein complexes with central function in aerobic respiration. Earlier, we found that the protein subunits of respiratory complexes are aggregation-prone. We also observed that individual complexes associate and engage in higher-order supercomplexes to protect cellular respiration during stress. We recently figured out that subunits embedded into the mitochondrial inner membrane are sequence-conserved within eukaryotic kingdoms but diverged beyond. Our results suggest that lipid-interactions of inner membrane subunits calibrate the kingdom-specific sequence evolution of eukaryotic respiratory complexes. We are currently studying how the heterogeneity of mitochondrial import mechanisms regulate the structural and functional assembly of respiratory complexes.

We also work with α-Synuclein which is an amyloidogenic protein associated with Parkinson's Disease (PD). Soluble α-Synuclein shuttles between cell membrane, cytoplasm, nucleus, and other cell organelles while its

aggregates are predominantly cytosolic. We find that α-Synuclein restricted outside nucleus interacts with a specific set of RBPs that bind to mRNA-secondary structures. These interactions coincide with the appearance of enlarged processing bodies in the cytoplasm. Biogenesis of large α-Synuclein aggregates is simultaneously decelerated. Elevating cellular load of RNA G-quadruplexes (rG4s), including rG4s from the genomes of RNA viruses, perturbs this interaction equilibrium and expedites α-Synuclein amyloidogenesis. This offers a mechanistic explanation of the well-established link between viral infections and an enhanced long-term risk of PD. We have identified ATP-dependent DEAD-Box Helicase 39A (DDX39A) as an exclusive interactor of α-Synuclein in the cytoplasm. We demonstrated that a tripartite cytosolic interaction network between α-Synuclein, viral rG4s, and DDX39A calibrates the phase-transition landscape of α-Synuclein towards amyloidogenesis.

In addition, we performed plasma proteome analysis of Sickle Cell Anaemia patients to identify diagnostic and prognostic biomarkers in Indian population. We are also involved in the "Phenome India-CSIR Health Cohort Knowledgebase" project and aim to generate plasma proteomic and metabolomic variables linked with chronic lifestyle diseases in Indian population.



RNA-mediate α-Synuclein amyloidogenesis. rG4 - RNA-G quadruplex

Recent publications

- Gupta P, Chakroborty S, Rathod AK, Kumar KR, Bhat S, Ghosh S, Rao T P, Yele K, Bakthisaran R, Nagaraj R, Manna M, Raychaudhuri S (2025) Kingdom-specific lipid unsaturation calibrates sequence evolution in membrane arm subunits of eukaryotic respiratory complexes. ***Nat. Commun.*** 16(1): 2044.

- Borar P, Biswas T, Chaudhuri A, Rao TP, Raychaudhuri S, Huxford T, Chakrabarti S, Ghosh G, Polley S (2025) Dual-specific autophosphorylation of kinase IKK2 enables phosphorylation of substrate IκBα through a phosphoenzyme intermediate. ***Elife*** 13: RP98009.

- Mansuri S, Jain A, Singh R, Rawat S, Mondal D, Raychaudhuri S (2024) Widespread Nuclear Lamina injuries defeat proteostatic purposes of α-Synuclein amyloid Inclusions. ***J. Cell Sci.*** 137(7): jcs261935.

TRIPURA SUNDARI C B

Chronic Liver Disease- Mechanism, Diagnosis and Regeneration



From left to right: Joanna, Rajashree, Vyshnavi, Tripura, Khushboo, Anusha

Research interests

- Understanding the progression of non-alcoholic fatty liver disease (NAFLD). The role of inflammatory mediators in progression and deciphering mechanism to identify non-invasive molecular biomarkers for early diagnosis
- Targeting hepatic stellate cells (HSCs) to develop anti-fibrotic therapies, while also exploring HSC role in liver regeneration

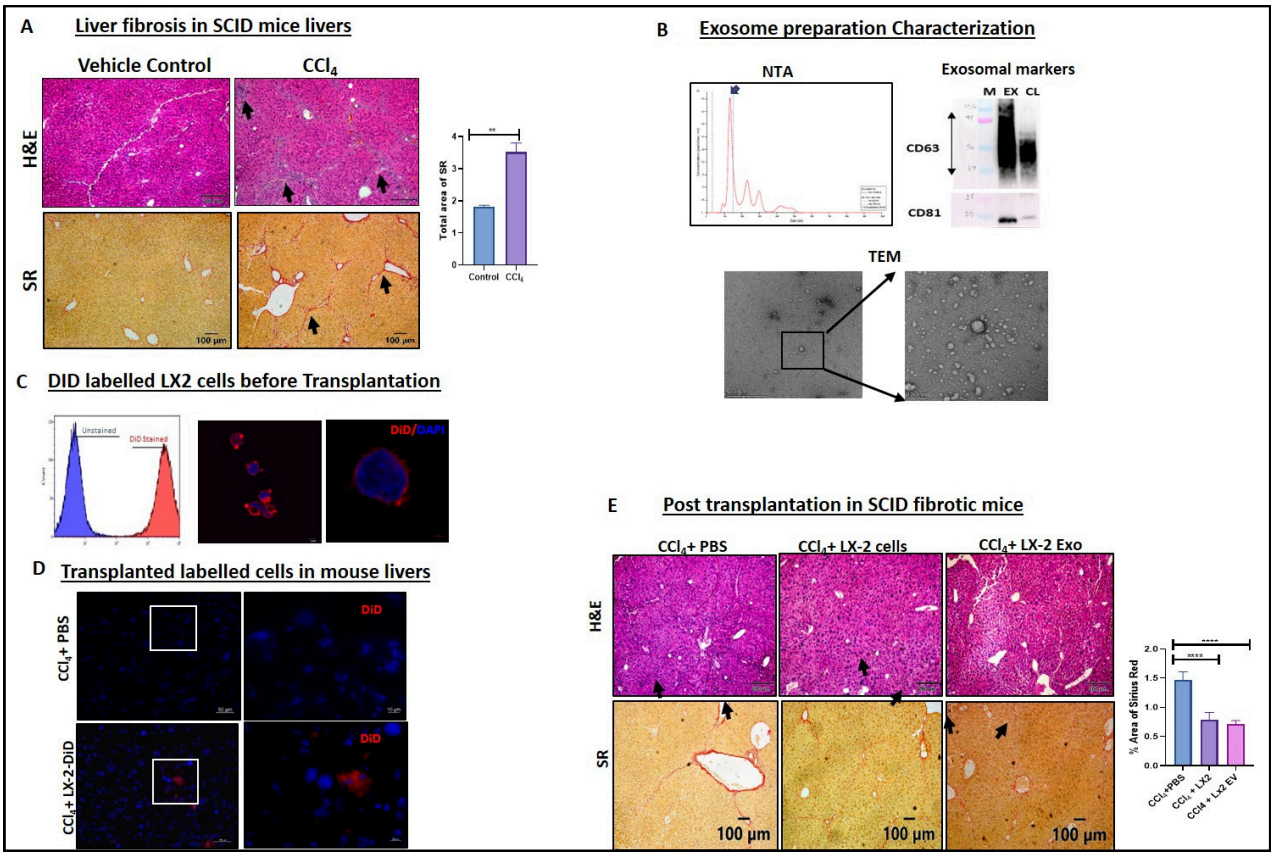
Chronic liver disease (CLD) is a significant global health challenge, with ongoing liver inflammation, loss of liver tissue, and impaired repair mechanisms leading to fibrosis, cirrhosis, and ultimately liver failure. Our lab investigates the key drivers of NAFLD progression from simple steatosis to steatohepatitis focusing on inflammatory pathways of non-infectious origin. We are keen on the novel inflammasomes that are involved in the process. With a global increase in NAFLD where early diagnosis is limited due to lack of specific biomarkers, we employ a multi-omics approach using clinical samples to identify novel, non-invasive molecular markers that can facilitate early detection and improve patient outcomes.

We also, explore strategies to alleviate liver fibrosis by targeting hepatic stellate cells (HSCs), the primary fibrogenic cells of the liver. Additionally, we are focusing on the regenerative role of HSCs, in repair and regeneration while preventing pathological scarring. Through these

interconnected research themes, we seek to advance both diagnostic and therapeutic approaches for CLDs.

To further our understanding of the role of HSCs in liver repair and regeneration, exosomes were isolated from the cultured human hepatic stellate cells adapted to low serum conditions and both the cells and exosomes transplanted individually into SCID mice with established liver fibrosis.

Interestingly, a reduction in fibrosis as compared to the untreated mice is observed with both the cells and the exosomes. Proteomic profiling revealed the presence of protein signatures involved in wound healing pathways in different levels in both the cell lysate and the exosomal preparation. The regulatory molecules that are further involved in regeneration are being explored.



LX-2 cell derived exosomes alleviate liver fibrosis.

(A) SCID mice were injected with CCl4 to induce liver fibrosis (SCID-Fibrosis mice) which was confirmed by histological analysis of H&E staining and Sirius red for collagen deposition. A significant increase in collagen in the CCl4 mice is shown (graph). (B) Exosomes were purified from cultured human hepatic stellate cells (LX-2 cells) and characterized by nanoparticle tracking analysis (NTA) and TEM. Western blot was done to confirm the exosomal membrane markers CD63 and CD81. (C) Before transplantation, cells were labelled with DiD and confirmed by flow cytometry. Confocal microscopy imaging shows the dye to be distributed uniformly on the membrane. (D) Cells and exosomes were transplanted via tail vein injection into the SCID-Fibrosis mice and after 2 weeks the mice were sacrificed and livers were checked for presence of DiD signal which was shown only in the transplanted mice confirming the homing of the cells/exosomes to the liver. (E) Histological analysis of the liver tissue showed decrease in inflammatory cells (H&E) and reduced fibrosis (Sirius red) in the mice livers transplanted with the cells and the exosomes as compared to the mice that received PBS alone.

VENKAT CHALAMCHARLA

Transcription and Chromatin Regulation



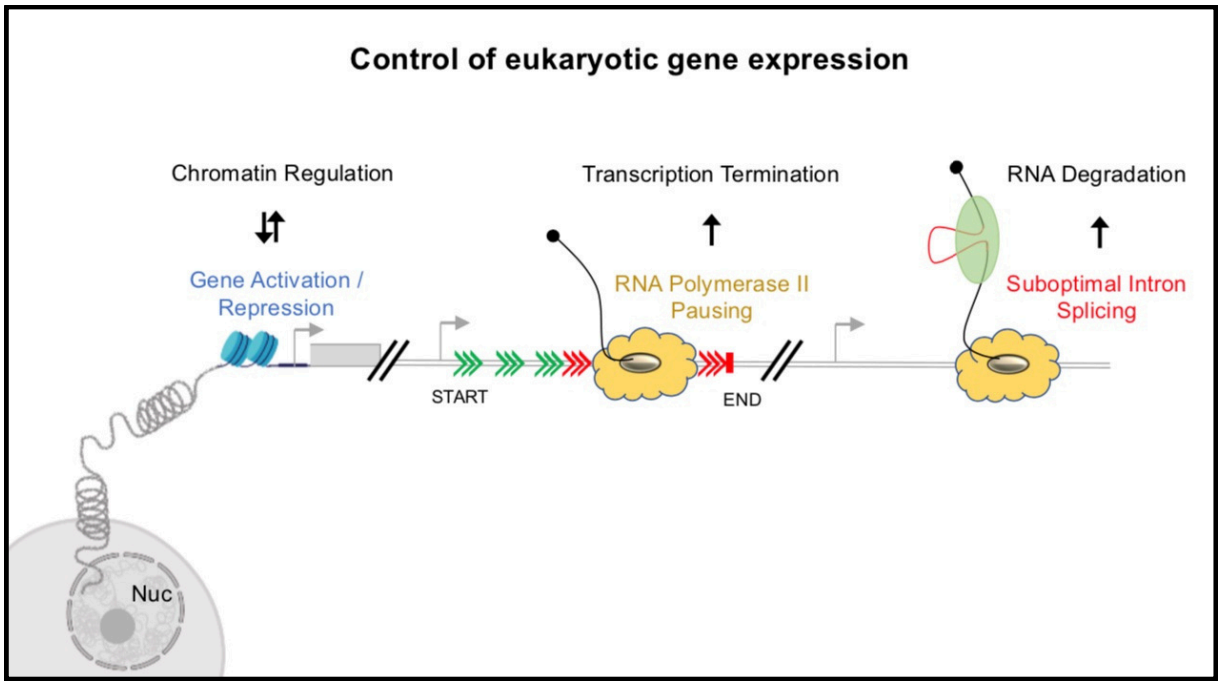
From left to right: Anubhav, Vaishnav, Sauvik, Harsh, Venkat, Annapoorna, Monika, Aarthi, Sahithi

Research interests

- Pre-mRNA processing
- Chromatin dynamics
- Gene regulation
- Genome instability
- Cellular quiescence
- Yeast genetics

Our lab pursues work in three areas: chromatin dynamics, transcription elongation and nuclear mRNA quality control, which are highly complex and coupled steps in eukaryotic gene expression. Currently, using the fission yeast Schizosaccharomyces pombe as a modelorganism, we are focused on understanding: (A) the gene regulatory mechanisms that promote the cellular transition from a non-diving quiescent state to proliferation, (B) the molecular events that trigger the end of transcription elongation by RNA Polymerase II (Pol II), and (C) the specificity determinants for co-transcriptional degradation of splice-defective pre-mRNAs. To this end, we have identified several transcriptional and chromatin regulators required for the long-term maintenance of the cellular quiescence (non-dividing, G0 phase) in *S. pombe*. Importantly, we discovered a transcription control mechanism that preserves the genome 3D structure of ageing quiescent cells and governs their remarkable longevity; G0 chromatin

perturbation could lead to aneuploidy, which has been linked to ageing and age-associated diseases in humans. Besides, we have identified a key determinant of the Cdk9-PP1 kinase-phosphatase switch that triggers Pol II termination and advanced our understanding of how the conserved exoribonuclease Xrn2 targets suboptimal spliceosomes to ensure splicing fidelity. The latter studies could provide valuable insights into mRNA quality control mechanisms that preserve the integrity of the proteome in eukaryotes.



Schematic representation of our current research focus. We are working to define the basic mechanisms by which quiescent non-dividing (G0) cells maintain their condensed chromatin structure and control gene expression as they re-enter the cell division cycle. Besides, we are investigating the mechanisms of fidelity in pre-mRNA splicing and transcription termination by RNA Polymerase II in eukaryotic cells.

MICROBES AND BIOLOGY OF INFECTION

Krishnan H. Harshan
Manjula Reddy
Nitin C. Tupperwar
Puran Singh Sijwali
Raghunand R. Tirumalai
Sriram Varahan
Vinay K. Nandicoori



KRISHNAN H HARSHAN

Metabolic interphase of innate antiviral response regulated through mitochondria



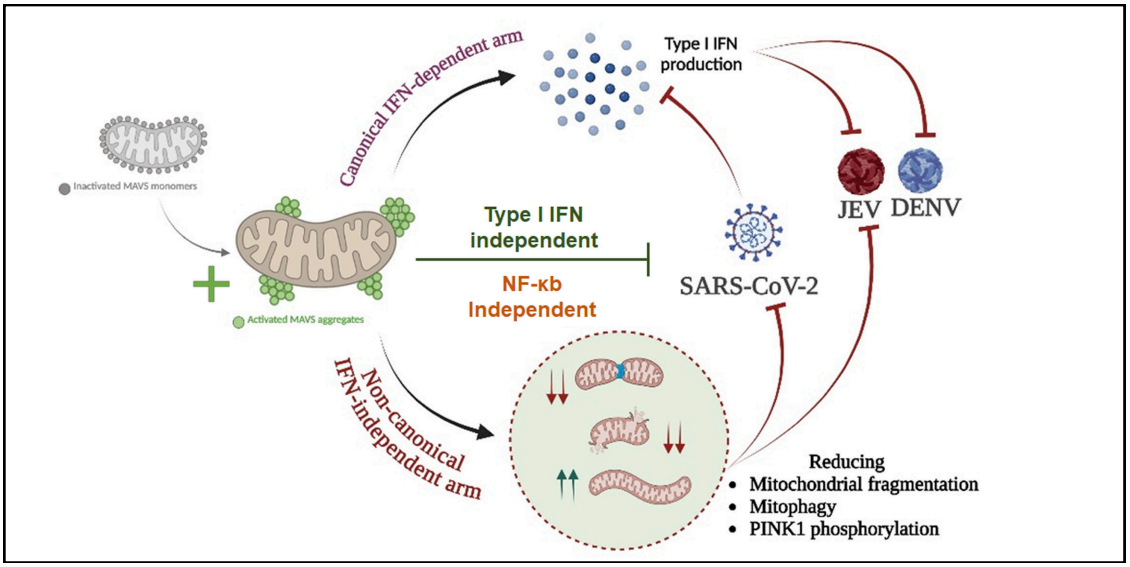
From left to right: Dixit Tandel, Prangya Parmita Sahoo, Vishal Sah, Krishnan H Harshan, Poojitha Sai Potharaju, Mohan Singh Moodu, Jaya Surya

Research interests

- Host-Virus interaction
- RNA Viruses
- Innate Immune Response
- RLR pathway
- SARS-CoV-2
- Dengue
- Antiviral therapeutics

For the past several years, we have been investigating the interphase of innate antiviral response to RNA viruses and mitochondria-mediated regulations. Previously, we had demonstrated that SARS-CoV-2 variants had evolved over the course of the pandemic to better deal with the innate antiviral response. Delta variant acquired capabilities to enforce long-term suppression of IFN activation in comparison with the earlier isolates that were effective in silencing the RLR pathway for upto the initial 24 hrs of infection. Our subsequent investigation revealed that SARS-CoV-2 achieves the shutdown of the RLR pathway by preventing the aggregation of mitochondrial antiviral signaling molecule (MAVS), a key adaptor molecule in the pathway. MAVS, that resides on the outer mitochondrial membrane (OMM) aggregates upon their activation by the RLRs. This aggregation facilitated by its CARD domain is critical in the formation of MAVS signalosome that is responsible for the IFN production. Our studies show that MAVS, apart from its critical role

in the IFN production, is also a key molecule in orchestrating a potent, IFN-independent antiviral response. We have now demonstrated that MAVS is critical for safeguarding mitochondria from virus-induced mitophagy and this is sufficient to generate an strong, IFN-independent antiviral response. We have shown that MAVS is crucial for the proper association of TOM complex on mitochondrial membrane, which is key for mitochondrial protein import. Upon MAVS loss, a disturbed TOM complex leads to mitochondrial protein import block, thus resulting in higher mitophagy. This function of MAVS in protecting mitochondria from mitophagy is not just virus-specific, but is effective against the common mitotoxins such as CCCP. This study positions MAVS as a key regulator of mitochondrial health, and by protecting mitochondria, MAVS imparts a broad antiviral response, encompassing both IFN-dependent and independent mechanisms.



Proposed model for non-canonical antiviral arm of MAVS: Upon activation, MAVS aggregates on the outer mitochondrial membrane, initiating two distinct signalling branches. The canonical IFN-dependent arm activates IRF pathways, leading to type-I IFN production and antiviral defence. This pathway is targeted and suppressed by several RNA viruses, including SARS-CoV-2, JEV, and DENV, to evade host immunity. The non-canonical IFN-independent arm regulates mitochondrial homeostasis by controlling mitochondrial fragmentation, mitophagy, and PINK1 phosphorylation. SARS-CoV-2 disrupts this arm by dampening MAVS-mediated mitochondrial surveillance mechanisms, contributing to increased mitochondrial dysfunction and enhanced viral replication. Thus, MAVS acts as a central hub balancing antiviral immunity and mitochondrial integrity, both of which are compromised during infection.

MANJULA REDDY

Understanding bacterial cell wall synthesis and its regulation



From left to right: Krishna Chaitanya, Shambhavi Garde, Meher Fathima, Vishnu Vachana, Manjula Reddy, Vaidehi Rajguru, Debnita Mongal, Harikrishnan Selvaraj, Suraj Meher, Bhargavi Gundavarapu, Stuti Chatterjee

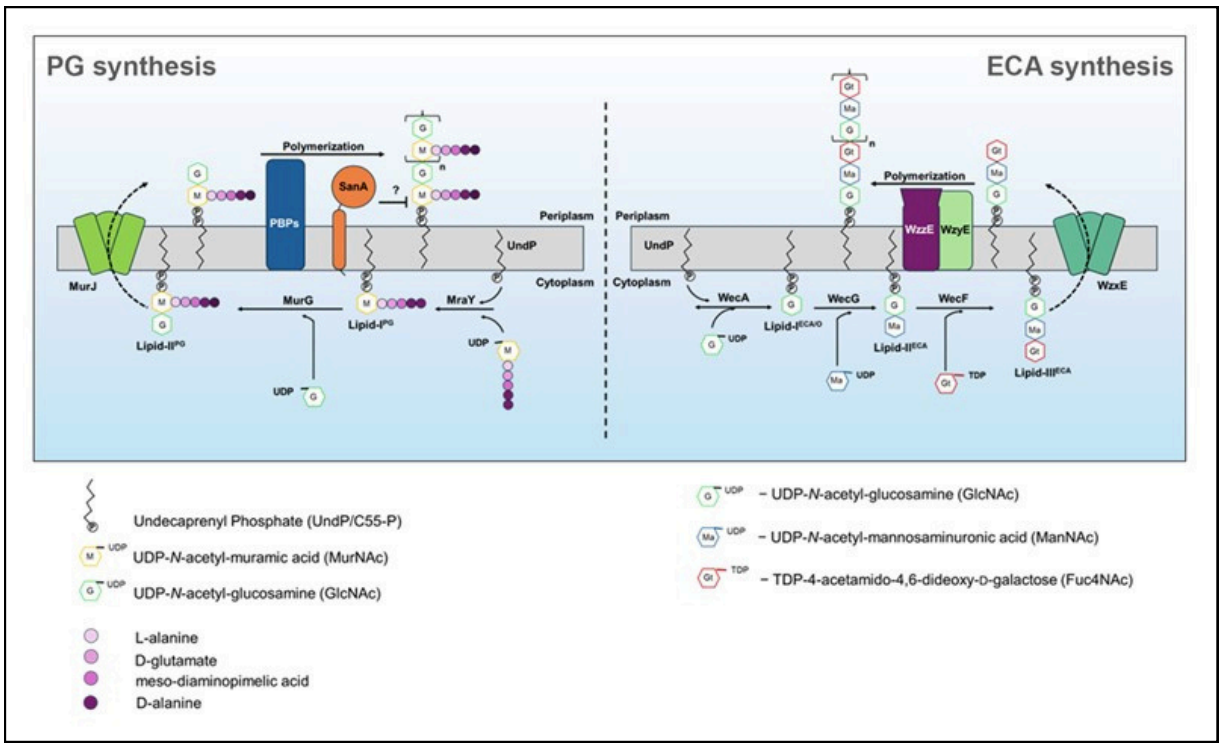
Research interests

Research in my lab is focused towards understanding the bacterial cell envelope structure, synthesis and its regulation using a Gram-negative model organism, *E. coli*

Gram-negative bacterial cell envelope consists of a surface-exposed lipid bilayer (outer membrane or OM) that serves as a permeability barrier to maintain the cellular integrity. Beneath the OM is the periplasmic space that harbours peptidoglycan (PG), a highly cross-linked mesh-like glycan polymer closely encasing the inner membrane (IM). During growth of a bacterium balanced synthesis of the envelope components is required to maintain the cellular integrity, of which little is known.

During the year, we identified that sanA, an ORF of unknown function encoding a predicted IM-anchored protein as a factor contributing to balanced synthesis of PG in *E. coli*. Absence of SanA increased the rate of nascent PG strand incorporation, and restored growth and viability to several mutants defective in either cell division or cell elongation. Detailed mutant analysis of sanA showed that it is defective in the envelope barrier properties. Interestingly, overexpression of

the periplasmic endopeptidases that cleave the cross-links of the PG mesh was able to alleviate the phenotypes of sanA mutant implying the envelope defects are due to alterations in the PG sacculus. Additionally, a SanA variant (SSDsbA-SanA) targeted to the periplasm, complemented the SanA- phenotypes suggesting it functions in the periplasmic phase of the PG synthesis. Further, we find that SanA functions independently of its paralog, ElyC, known to regulate the synthesis of enterobacterial common antigen (ECA), a surfacepolysaccharide found in the cell envelopes of most enteric bacteria. Overall, our results suggest a role for SanA in the maintenance of optimal PG synthesis, providing evidence for the existence of an additional layer of regulation in Gram-negative cell envelope biogenesis.



Schematic representation of the peptidoglycan (PG) and Enterobacterial common antigen (ECA) biosynthetic pathways. PG synthesis occurs in two distinct cellular compartments. In the cytoplasm, UndPP-MurNAc (pentapeptide)-GlcNAc (Lipid-IIPG) moieties are synthesized, flipped across the IM into the periplasmic space by MurJ flippase, and subsequently polymerized into the growing sacculus by the activity of PG synthases (PBPs). Herein, our study provides evidence for SanA, a protein of unknown function to be a novel regulator of PG biosynthesis, likely controlling the step of nascent PG formation in the periplasm. In parallel, the biosynthesis of ECA begins in the cytoplasm wherein a series of enzymatic reactions leads to the formation of Lipid-IIIECA (UndPP-GlcNAc-ManNAc-Fuc4NAc) which is then translocated across the IM into the periplasm by the flippase WzxE. In the periplasm, the three-sugar unit is polymerized through WzzE-WzyE complex to generate the mature ECA polymer.

Recent publications

- Rajguru V, Chatterjee S, Garde S, and Reddy M. (2024). Crosslink cleaving enzymes: the smart autolysins that remodel the bacterial cell wall. ***Trends in Microbiology*** doi: 10.1016/j.tim.2023.11.004

PURAN SINGH SIJWALI

Investigation of the regulatory mechanisms of cell division, genome fidelity and organelle biogenesis in apicomplexan parasites



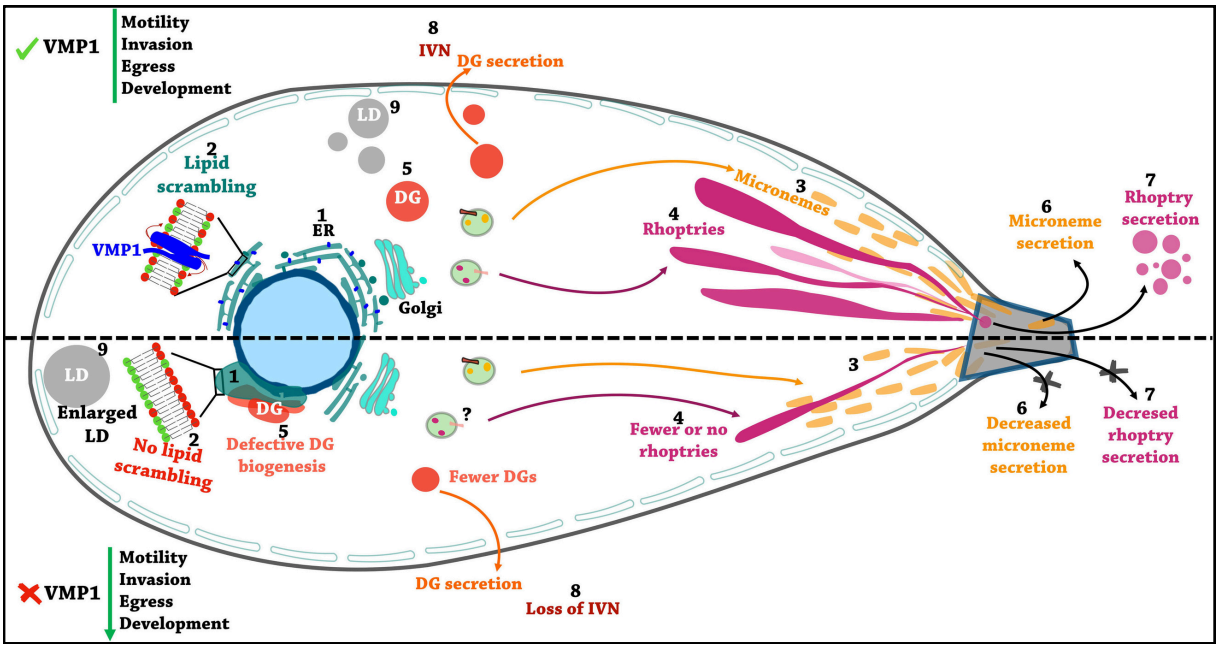
From left to right, First row: Deeksha, Anjana, Parvathi, Rashmi, Pragati, Kanika
Back row: Somesh, Pritam, Nandkumar (alumnus), Viswagithe, Srinivas, Shivam, Manash, Puran, Amarttya

Research interests

- Ubiquitin proteasome system
- Autophagy
- Cullin-RING ubiquitin E3 ligases
- DNA-protein crosslink repair
- *Plasmodium* & Malaria
- *Toxoplasma* & Toxoplasmosis
- Cell division
- Organelle biogenesis
- Proteases

Apicomplexan parasites, including *Plasmodium falciparum* and *Toxoplasma gondii,* contain specialized secretory organelles such as micronemes, rhoptries, and dense granules, which are essential for parasite motility, invasion of the host cells, development, and egress. DedA superfamily proteins are implicated in lipid mobilization, which is a key requirement for organelle biogenesis. We identified and investigated the vacuole membrane protein 1 (VMP1), a DedA superfamily member, of *P. falciparum* (PfVMP1) and *T. gondii* (TgVMP1). PfVMP1 and TgVMP1 are ER-localized lipid scramblases. TgVMP1 depletion adversely affected parasite development, motility, host cell invasion, and egress. These phenotypes were consistent with impaired rhoptry and dense granule biogenesis, and decreased secretion of micronemes and rhoptries in TgVMP1-depleted parasites, indicating a crucial role for TgVMP1 in the biogenesis and function of these organelles. TgVMP1 depletion impaired lipid droplet

homeostasis and ER organization, and caused loss of intravacuolar network in the parasitophorous vacuole, which are key for parasite development. Restoration of the ER-localized lipid scramblase by complementing TgVMP1-depleted parasites with PfVMP1 or a homolog as distant as human VMP1 rescued the depleted parasites, indicating their functional conservation and a crucial role for ER- resident lipid scramblase activity in the biogenesis and function of secretory organelles. The essentiality of TgVMP1 for parasite development and likely functional conservation of apicomplexan VMP1 proteins highlight their drug-target potential.



A model for the functions of VMP1. The figure shows indicated cellular structures and processes in wild type (upper half) and TgVMP1-depleted tachyzoite (lower half). TgVMP1 is an ER-localized lipid scramblase, and is most likely required for translocation of lipids in ER and/or the vesicles containing proteins destined to the secretory organelles (micronemes, rhoptries, and dense granules). The loss of TgVMP1 impairs biogenesis of rhoptries and dense granules (DG), function of secretory organelles, lipid droplet (LD) homeostasis, IVN formation, and ER organization, resulting in the decreased parasite motility, host cell invasion, egress, and overall parasite development.

RAGHUNAND R TIRUMALAI

Identification of Carbapenem resistance genes in *Mycobacterium tuberculosis*



From left to right, back row : Dasari Vatsalya, Simran Sharma, Rohit Macharekar, Ananya Pai, Korak Chakraborty, Md Saquib Ali
Front row: Raghunand Tirumalai, Shristy Kothiwal, Veigyabati Devi, Mihina Pradhan, Sayani Dasgupta

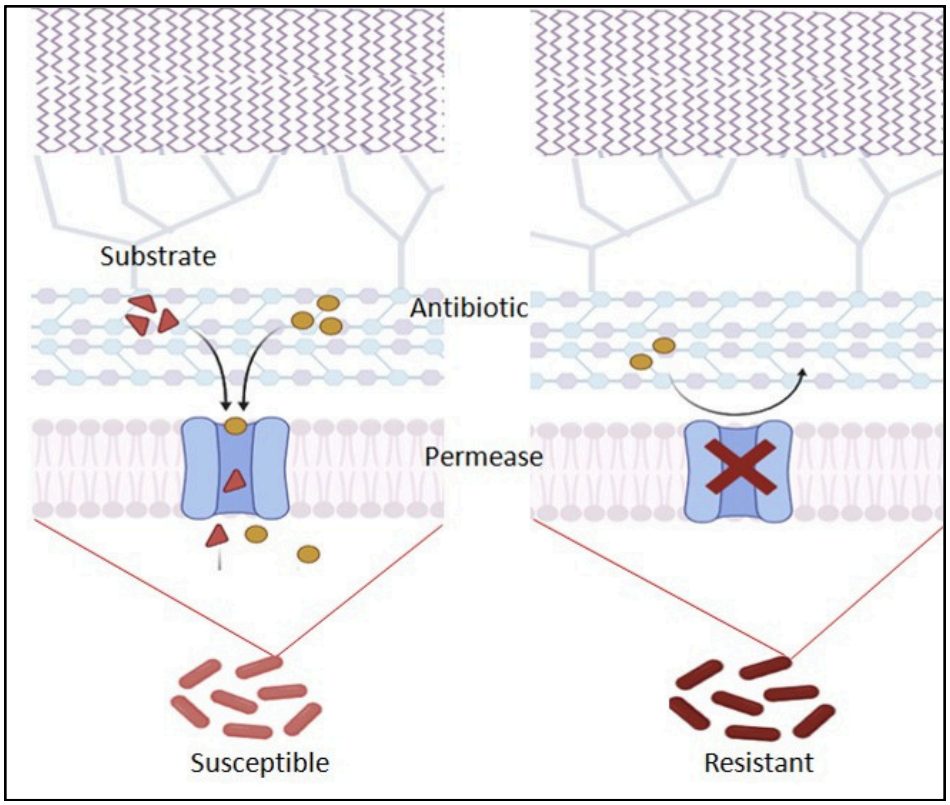
Research interests

- Ubiquitin proteasome system
- Autophagy
- Cullin-RING ubiquitin E3 ligases
- DNA-protein crosslink repair
- *Plasmodium* & Malaria
- *Toxoplasma* & Toxoplasmosis
- Cell division
- Organelle biogenesis
- Proteases

The global effort to eradicate Tuberculosis has been hampered due to the emergence of multidrug resistant strains of *M.tb*, the spread of which poses a growing health threat to all nations. The presence of β-lactam hydrolysing enzymes in *M.tb*, has raised the question whether this group of antibiotics can be used as a treatment option for TB. Among the β-lactams, Carbapenems possess the broadest spectrum of activity and greatest potency against Gram-positive and Gram-negative bacteria and are relatively resistant to β-lactamases. Since clinical studies on the anti-TB efficacy of Carbapenems have led to WHO recommending its use to treat drug-resistant infection, it is of utmost importance to identify mechanisms that could lead to β-lactam resistance in *M.tb*. To identify genes involved in Carbapenem resistance we constructed a library of 30,000 transposon mutants of *Mycobacterium smegmatis* mc26 using the mycobacteriophage MycomarT7, carrying the Himar1 transposon. These mutants

were then screened for resistance at concentrations of 2x and 5x MIC of Meropenem over the wild-type strain respectively. Resistant mutants were cultured, and their transposon insertion sites were identified. This approach led to the identification of a candidate Meropenem resistance gene MSMEG_2772, annotated as an amino acid permease - a homolog of which is also present in *M.tb*.

Complementation of the mutant HV13 with the WT gene and its M.tb homolog, led to the restoration of Meropenem sensitivity. We are using a combination of genetic and biochemical approaches to determine the mechanistic role of the identified gene in mycobacterial resistance to Meropenem.



Working model depicting the role of the permease encoded by MSMEG_2772 in mycobacterial resistance to Meropenem

Recent publications

- Sharma SS, Macharekar RM, Raghunand TR (2024) Transport mediated Antibiotic Resistance in *Mycobacterium tuberculosis*. ***Indian J. Biochem. Biophys.*** 62: 267-280.

- Savanagouder M, Mukku RP, Yeruva CV, Nagarajan N, Peddapuvala UK, Sharma Y, Raghunand TR (2024) Dissecting the Ca^{2+} dependence of *Mycobacterium tuberculosis* DesA1 function. ***FEBS Lett.*** 598(13): 1620-1632.

- Ramachandran G, Yeruva CV, Swarup G, Raghunand TR (2024) A cytoprotective role for optineurin during mycobacterial infection of macrophages. ***Biochem. Biophys. Rep.*** 38: 101672.

SRIRAM VARAHAN

A Unified Metabolic Framework to Understand Fungal Morphogenesis



From left to right: SJoel Philip, Sudharsan M, Pallavi Phatak, Ojasvi Chopra, Siddhi Gupta, Dhrumi Shah, Sriram Varahan, Mary Shejo, Uma Mahto, Adishree M, Nikita Rewatkar, Ishvarya Suresh, Shathya Sekar

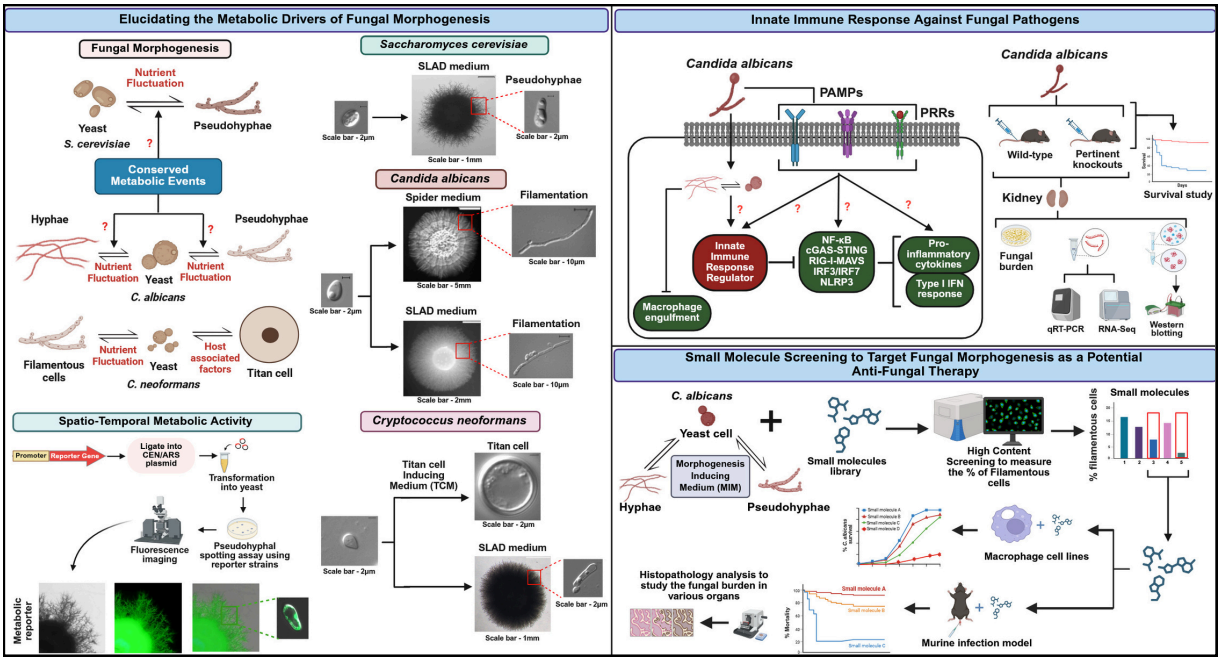
Research interests

- Elucidating the metabolic drivers of fungal morphogenesis
- Identification of novel host innate immune responses against fungal pathogens
- Development of anti-fungals targeting human-fungal pathogens

Fluctuations in nutrient availability is one of the most common challenges encountered by microorganisms. A common strategy employed by microorganisms to adapt to continual changes in nutrient availability is to reversibly transition to alternate cell states better suited for growth and survival in that particular environment. Fungi respond to nutrient fluctuations by undergoing reversible morphological transitions termed as 'Fungal Morphogenesis'. This allows them to efficiently forage for nutrients, form complex biofilm communities and establish persistent infections in a variety of hosts. Current studies have largely focused on identifying gene regulatory networks that control this phenomenon. However, we lack a complete understanding of the driving metabolic processes behind such cellular decision-making events, and how they are regulated.

Our laboratory uses multiple fungal model systems including *Saccharomyces cerevisiae* and

human fungal pathogens including *Candida albicans* and *Cryptococcus neoformans* to elucidate the metabolic regulation of fungal morphogenesis and its implications in fungal pathogenesis using murine infection models. Our laboratory is also interested in understanding the interplay between the host innate immune response and fungal pathogens and how this ultimately affects infection outcome. Specifically, we are interested in deciphering the role of the master innate immune response regulator, IRGM1, in fungal pathogenesis.



1) Elucidating the Metabolic Drivers of Fungal Morphogenesis
2) Identification of Novel Host Innate Immune Responses Against Fungal Pathogens
3) Development of Anti-Fungals Targeting Human-Fungal Pathogens

Recent publications

- Phatak PS, Suresh I, Shah D, Shejo M, Mathivathanan S, Varahan S (2025) A Conserved Metabolic Network Regulates Titan Cell Formation in *Cryptococcus neoformans*. ***bioRxiv*** 2025.09.02.673682; doi: https://doi.org/10.1101/2025.09.02.673682.

- Shah D, Adishree M, Rewatkar N, Gupta S, Mathivathanan S, Varahan S (2025) Glycolysis-dependent Sulfur Metabolism Orchestrates Morphological Plasticity and Virulence in Fungi. ***bioRxiv*** 2025.05.14.654021; doi: https://doi.org/10.1101/2025.05.14.654021.

- Kundu S, Chauhan S, Dhar K, Varahan S, Chauhan S (2025) Chats and Spats of Autophagy and Innate Immune Systems. ***J. Mol. Biol.*** Aug 11: 169387. doi: 10.1016/j.jmb.2025.169387.

VINAY K NANDICOORI

Elucidating the molecular mechanisms that regulate the survival of the pathogen *Mycobacterium tuberculosis* (*Mtb*)



From left to right, Front: Abhishek, Bitan, Debatri, Vinay, Sutashree, Priyadarshini, Jagadeeshwari, Amit
Back line: Baburam, Praveen, Asis, Purushotham, Rakesh, Madhu, Sathya

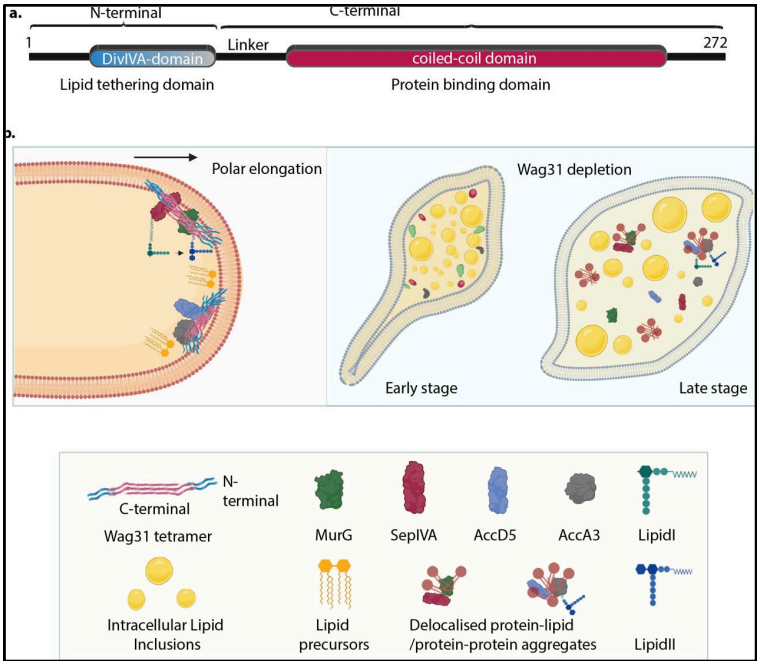
Research interests

- Delineate the underlying serine/threonine protein kinase-mediated signaling mechanisms that regulate multiple cellular processes such as cell division, cell wall synthesis, secretion, transcription, and survival in the host.
- Determine the function of transcription initiation factors such as sigma factors and characterize novel transcription factors that are non-essential for bacillary growth but play an essential role in the host.
- Determine the role of RNA polymerase subunits and transcription elongation factors and translation initiation factors in modulating the Mtb stress response.
- As part of the InTGS consortium, sequence 13000 clinical tuberculosis genomes to identify novel mutations associated with drug resistance and develop a POC next-generation sequencing method to detect drug resistance.

Wag31, a membrane tether, is crucial for lipid homeostasis in mycobacteria

Cell division is a critical event in the life of a bacterium, as it is the prime mode of bacterial growth and reproduction. The DivIVA protein of *Mtb* called Wag31 is known to regulate both cellular growth and morphology, which makes it an exciting candidate to investigate. Wag31 has a characteristic N-terminal DivIVA-domain and a C-terminal coiled-coil domain. While the role of Wag31 in polar elongation is known, there is limited mechanistic insight on how it orchestrates growth and elongation. We endeavoured to address the lacunae in the functionality of Wag31 by asking the following questions- i) what are the ultrastructural changes that occur in mycobacteria due to the absence of Wag31, ii) do Wag31 deficient cells undergo transcriptional rewiring to adjust to cell division defects, iii) is the change in cellular morphology from 'rod-to-round' accompanied by altered lipid levels, iv) what is the interactome of Wag31, v) what are the functions of its N and C-terminal domains and finally vi) what is its relationship with the mycobacterial membrane.

We show that Wag31 predominantly interacts with several membrane-associated proteins involved in lipid metabolism, cell wall synthesis and division. Native levels of Wag31 are critical for the maintenance and distribution of membrane lipids. Both depletion and overexpression of Wag31 perturbs lipid homeostasis, leading to the formation of intracellular lipid inclusions (ILIs). Protein-lipid crosslinking and imaging studies reveal that purified Wag31 can bind and effectively tether Cardiolipin (CL)-containing liposomes. We further show that the tethering activity lies in the DivIVA-domain containing N-terminal of Wag31 while the C-terminal mediates protein-protein interactions of Wag31. Despite retaining its ability to interact with partner proteins, the DivIVA domain-deleted Wag31 mutant shows defects in liposome tethering in vitro and non-polar localization of CL in vivo, which eventually causes lethality. This study suggests that membrane tethering 'licenses' Wag31 to form scaffolds that help orchestrate protein-lipid and protein-protein interactions necessary for mycobacterial growth and survival.



a) Model of Wag31 showing the N- and C-terminals. N-terminalhouses the DivIVA-domain that is involved in membrane-tethering and the C-terminal is the protein-binding domain that facilitatesinteractions of Wag31 with other proteins. (b) Left: Illustration showing Wag31 scaffolds bound to cardiolipin in the membranevia N-terminal, tetheringit and creating CL-microdomains at the poles. The C-terminal of Wag31 bound to protein-partners, localizethem to the membrane, facilitating several membrane-centric processes such as PG and lipid synthesis, that ensure mycobacterial survival. The right panel shows thetime-dependent consequences of Wag31depletion i.e. early and late stage. The cells are bulged at one pole and start accumulating ILIs in the early stage and as the time progresses, the effect of Wag31 depletion becomes severe, rendering the cells round and full of ILIs. In the absence of Wag31, CL-microdomains become delocalised due to the lossof tethering, pulling awayseveral membrane-associated proteins causing non-polar growth and loss of curvature.

Recent publications

- Khan MZ, Hunt DM, Singha B, Kapoor Y, Singh NK, Prasad DVS, Dharmarajan S, Sowpati DT, de Carvalho LPS, Nandicoori VK (2024) Divergent downstream biosynthetic pathways are supported by L-cysteine synthases of Mycobacterium tuberculosis. ***Elife*** 12: RP91970.
- Agarwal M, Bhaskar A, Singha B, Mukhopadhyay S, Pahuja I, Singh A, Chaturvedi S, Agarwal N, Dwivedi VP, Nandicoori VK (2024) Depletion of essential mycobacterial gene glmM reduces pathogen survival and induces host-protective immune responses against tuberculosis. ***Commun. Biol***. 949.
- Sanyal P, Nandicoori VK (2025) Preparation of Mycobacterium tuberculosis Culture Filtrate to Understand TB Pathogenesis. ***J. Vis. Exp.*** 217.

WILDLIFE CONSERVATION AND ECOLOGY

Ajay Gaur
G. Umapathy
Jahnavi Joshi
Karthikeyan Vasudevan
P. Anuradha Reddy
Siddharth Shrikant Kulkarni


Sriram Varahan Photography

AJAY GAUR

Conservation Genetics of Endangered Indian Species



From left to right: Akshar, Yukta, Ajay Gaur

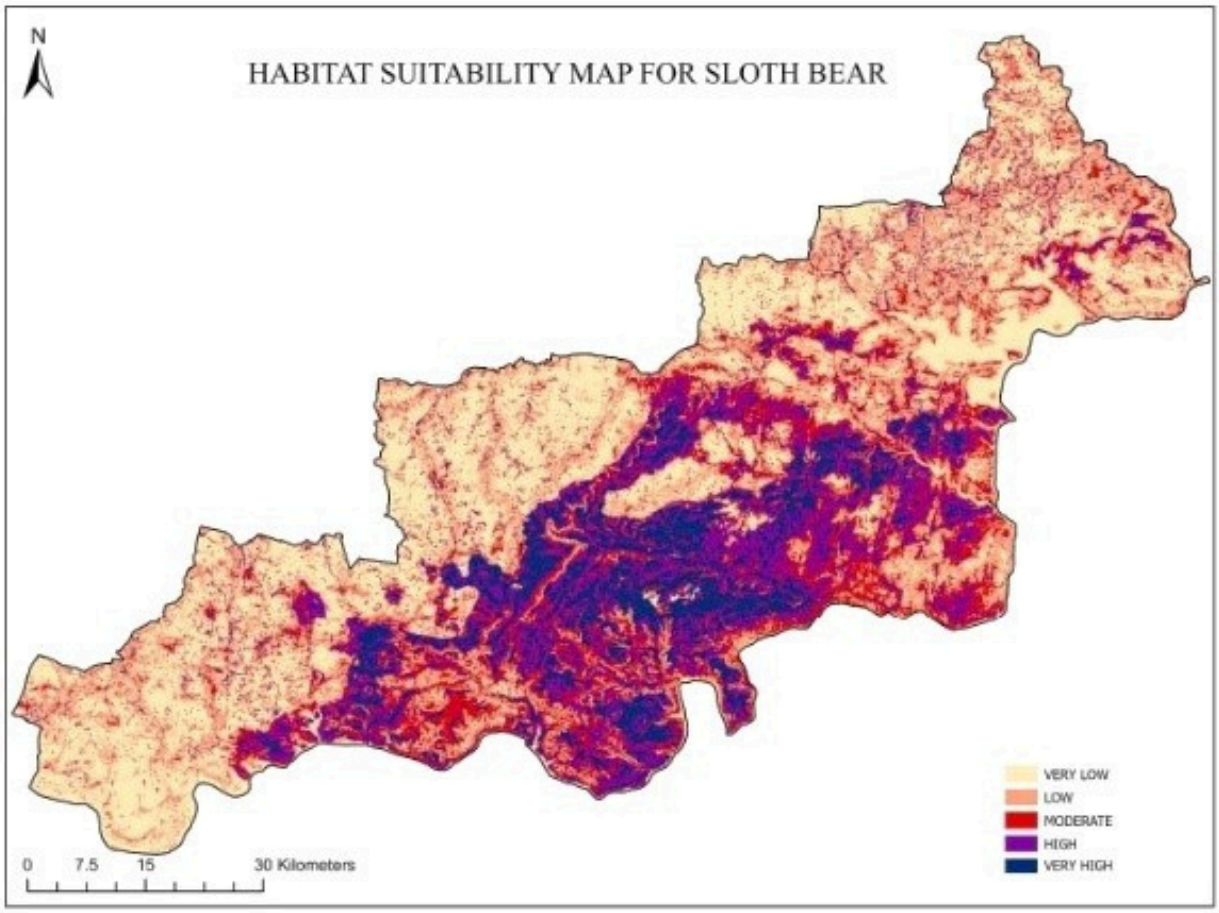
Research interests

- Population genetics
- Evolutionary genetics
- Wildlife forensics
- Conservation breeding

Our research focuses on conservation genetics of Indian endangered species. Our major efforts are towards the use of non-invasive sampling protocols and development of species – specific DNA markers to investigate the genetic structure of existing populations. The sloth bear (*Melursus ursinus*) is a large wide-ranging carnivore species endemic to the Indian subcontinent. However, their distribution has gradually decreased and become patchy due to habitat loss and fragmentation. Multiple studies have been conducted to understand population genetics of other bear species, but no information is available on population and landscape genetics of sloth bears. Owing to their generalist diet, inconsistent occupancy, and limited information about their dispersal range and pattern, it is an important question how the sloth bear allelic diversity is distributed within the Eastern Ghats landscape.

We initiated our genetic study of sloth bears by employing non-invasive sampling methods

across various forest patches in the Eastern Ghats. This year sampling expanded to cover additional protected areas such as the Lankamalla Reserve Forest, Kuldiha Wildlife Sanctuary, and Satkosia Tiger Reserve. Parallel to this, we advanced our species distribution modeling (SDM) work to better understand habitat suitability and landscape use by sloth bears within Amarabad Tiger Reserve. Using an ensemble Random Forest framework, we integrated updated environmental and anthropogenic variables such as land surface temperature, terrain ruggedness, vegetation indices (NDVI), and proxies for human disturbance. Species occurrence data, derived from field-collected scat samples, systematic camera trap deployments, and records from the M-Stripes monitoring platform, formed a comprehensive dataset for model training and rigorous validation. The resulting models demonstrated strong predictive accuracy (AUC > 0.9; TSS > 0.8) across all species, confirming their robustness in this heterogeneous tropical dry forest landscape. Habitat suitability maps revealed species-specific preferences emphasising that rugged terrain and heterogeneous forest cover were critical for sloth bears.



Habitat suitability map for Sloth Bear (*Melursus ursinus*) in Amrabad Tiger Reserve, Telangana

G UMAPATHY

Historical Demography, Species Distribution and Speciation in Primates of Northeast India



From left to right: VInay Teja, Himanshu Kothorai, Anuja Pandey, Manisha Ray, Sri Lakshmi, MS Ram, Gopi Krishnan, G. Umapathy, Vinod Kumar, Neeldeep Ganguly, Samuel Singh, Abhilash Nair, Gayatri Divakar, Caroline Rose

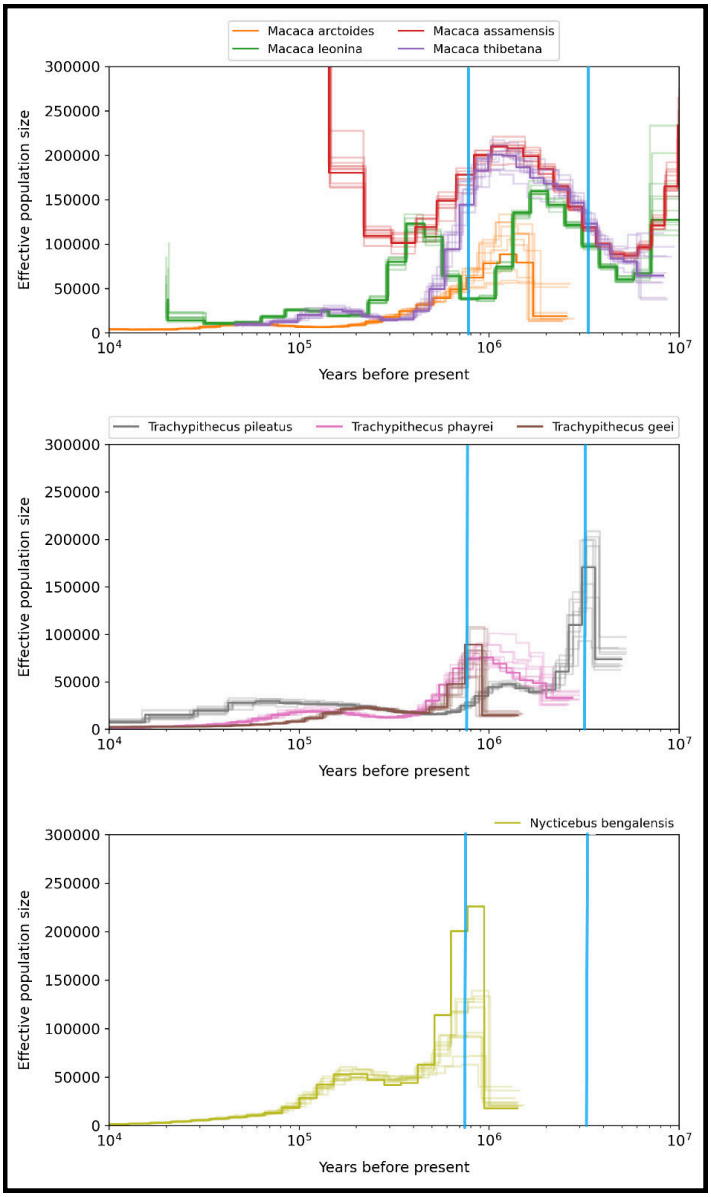
Research interests

- Understanding species' extinction in human-dominated landscapes
- Conservation physiology
- Environmental DNA
- Genomics in biodiversity conservation

How species accumulate in a particular geographic region:

Past climate change is one of the important factors influencing primate speciation. Populations of various species could have risen or declined in response to these climatic fluctuations. Northeast India harbors a rich diversity of primates, where such fluctuations can be implicated. Recent advances in climate modeling as well as genomic data analysis have paved the way for understanding. We utilized these methods to explore the primate diversity in this unique region in relation to past climate change. To ascertain the population level changes, we inferred the demographic history of nine species of primates found in Northeast India and compared it with species distribution models of the Pliocene and Pleistocene periods. Through this study, we are able to provide a detailed picture of how past climatic changes have resulted in the present species diversity and this mixture of species have either originated in the

region or have dispersed from mainland Southeast Asia. We observe that effective population size has decreased for all the species, but distributions are different for all the four genera: Macaca, Trachypithecus, Hoolock and Nycticebus. It also gives an idea about how each species is affected differently by climate change, and why it should be given emphasis in framing species-wise conservation models for the future climate.



Demographic history of the genus Macaca (top), Trachypithecus (middle) and Nycticebus bengalensis (down), with perpendicular blue lines showing two SDM time points of, 3.3 million years ago (right) and 787,000 years ago (left). (A) All Macaca species show an increase between the time points of Pliocene and Pleistocene, and then there is a stark decline towards the present. Also, a clear divergence can be seen between *M. assamensis* and *M. thibetana* after the Pleistocene, suggesting their evolutionary split. (B) The ancestor of *Trachypithecus pileatus* and *T. geei* has the largest population size at about 3.3 million years. *T. geei* and *T. phayrei* have their respective peaks at 787 kya. (C) Sudden decline of *N. benghalensis* after 3.3 my marks reflects its vulnerability to the climatic fluctuations of the Pleistocene.

Recent publications

- Hameed S, Ali MN, Manu S, Arekar K, Khaleel M, Bashir T, Umapathy G (2024) Genetic Diversity, Geographical Structure, and Demographic History of the Kashmir Gray Langur (*Semnopithecus ajax*). ***Int. J. Primat.*** 46(1): 122-144.

- Ray M, Manu S, Rastogi G, Umapathy G (2024) Cyanobacterial genomes from a brackish coastal lagoon reveal potential for novel biogeochemical functions and their evolution. ***J. Mol. Evol.*** 92: 121–137.

- Pandey A, Iyer P, Kumar V, Umapathy G (2025) Assessing the impact of Livestock Grazing on Fecal Glucocorticoid Metabolites Levels and Gastrointestinal Parasites in Himalayan Ibex in Spiti Valley, Western Himalayas. ***J. Wild. Sci.*** 2(1): 20-25.

JAHNAVI JOSHI

Examining the pace, patterns and predictors of biotic diversification in peninsular India



From left to right, Row 1st: Sudhanshu, Karunakar, Abhishek, Marwa
Row 2nd: Pragyadeep, Swathi, Shalini, Jahnavi, Madhumitraa
Row 3rd: Pooja, Nivedita, Shriya, Sharvani

Research interests

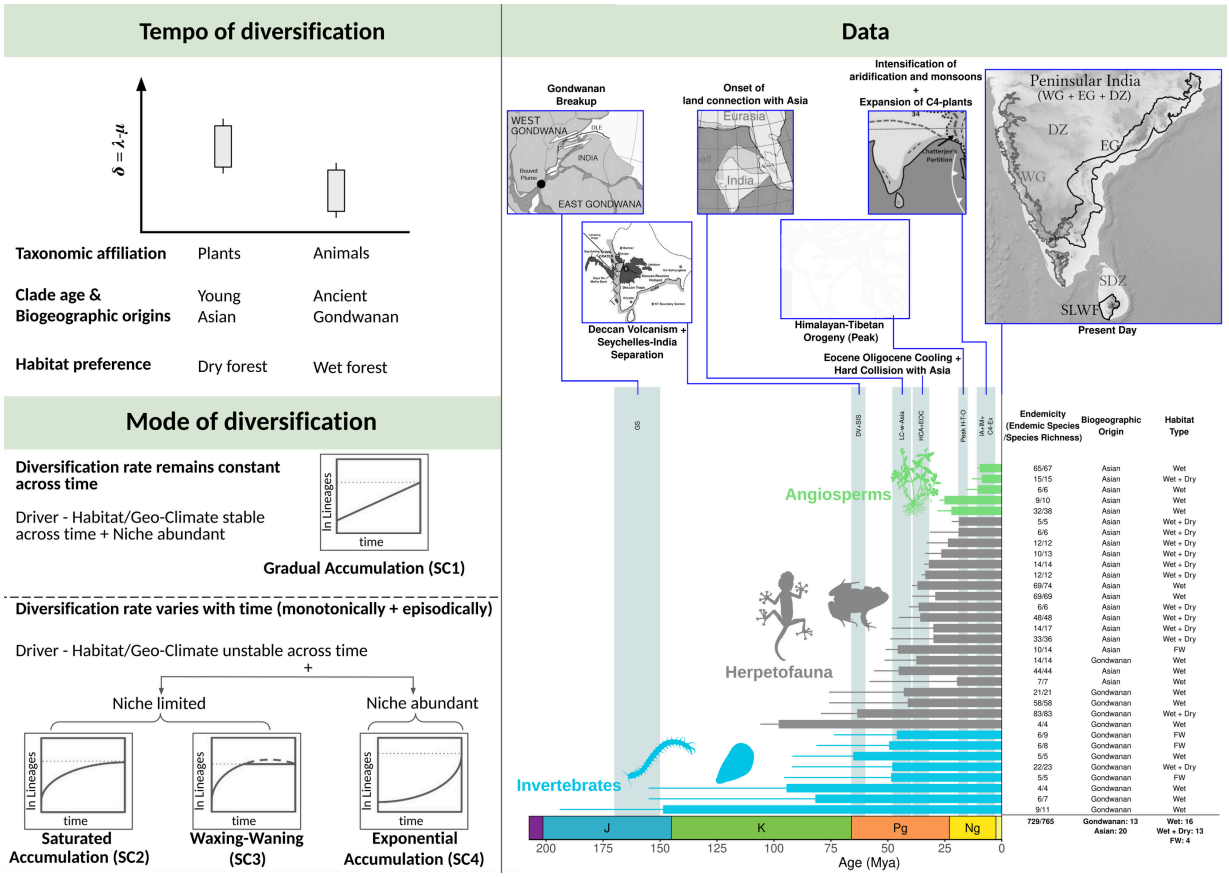
Our research aims to understand the ecological and evolutionary factors driving tropical biodiversity, with a focus on peninsular India—an ancient Gondwanan landmass in tropical Asia that supports a rich and highly endemic biota, much of which faces increasing threats from global change.

We address the overarching question: What generates and maintains high biodiversity in tropical forests? To achieve this, we employ a multidisciplinary framework that integrates extensive field ecology with molecular and analytical approaches, including integrative taxonomy, phylogenetics, population genomics, biogeography, community ecology, and comparative methods. We conduct extensive fieldwork to build natural history collections from the largely unexplored taxa and landscapes of the Western and Eastern Ghats, with a particular focus on documenting invertebrates, plants, and threatened bird species. These collections form the foundation for investigating how geo-climatic history, continental break-up events, and ecological processes together shape diversification, genetic diversity, and community assembly in tropical Asia.

Idiosyncrasies unveiled: examining the pace, patterns and predictors of biotic diversification in peninsular India:

Understanding the tempo and mode of diversification and its consequences for tropical biodiversity remains a key challenge as different clades and regions exemplify distinct patterns and processes. The evolution of the Peninsular Indian biota, one of the oldest regions of differentiation in tropical Asia with a complex geological history and high species diversity with endemism, remains poorly explored. Using birth-death models and their variations, we examined diversification rates and drivers across 33 well-studied endemic lineages in peninsular India. We show that 19 lineages supported gradual species accumulation, suggesting that the historical stability of the landscape was an important driver.

Additionally, paleotemperature, Miocene aridification, monsoon intensification and existing species diversity explained time-varying diversification patterns among the other 15 lineages. The species richness across clades was driven by net-diversification rates rather than clade ages, where speciation mainly drove diversification, as extinction rates remained low across taxa. Our results highlight the importance of regional biogeographic, phylogenetic, and geoclimatic history on diversification dynamics. This is critical to understanding the evolution of high tropical diversity and predicting how it may respond to global change.



Predictions for the tempo and mode of diversification and the data used in the study. (Left panel) The mean diversification rate can be influenced by taxonomic affiliations, clade age, biogeographic origins and habitat preference as illustrated in the box plot. The mode of diversification can follow multiple scenarios due to speciation and extinction rate dynamics as depicted. (Right panel) Our dataset of 33 endemic clades from the PIP. They vary in clade age, number of species, endemicity, biogeography, and habitat affinities. Key geological events are highlighted by grey vertical bars. Maps used in the figure have been extracted and edited from multiple studies, and the map for the present day has been generated using QGIS (Ali and Aitchison 2008; Chatterjee et al. 2013; Morley 2018).
WG: Western Ghats; EG: Eastern Ghats; DZ: Dry Zone; SLDZ: Sri Lanka Dry Zone; SLWF: Sri Lanka Wet Forests.

Recent publications

- Manivannan M, Gurung N, Edgecombe G, Joshi J (2024) A Passage through India: The Biotic Ferry Model Supports the Build-up of Indo-Australian Biodiversity of an Ancient Soil Arthropod Clade. ***J. Biogeogr.*** 51(12): 2395-2411.

- De-Kayne R, Schley R, Barth JM, Campillo LC, Chaparro-Pedraza C, Joshi J, ... Cerca J (2024) Why Do Some Lineages Radiate While Others Do Not? Perspectives for Future Research on Adaptive Radiations. ***Cold Spring Harbor Perspectives in Biology***, a041448.

KARTHIKEYAN VASUDEVAN

Wildlife disease ecology and snake venom biology



From left to right, top row: Yashwant Singh, Harika Segu, Karthikeyan Vasudevan, Shibi Muralidhar, Vishal Raut Bottom row: Shreya Upadhaya, Jeevan Nayak, Jyoti Kumari, Krinaveni C, Suchetana Gupta, Athira Regu, Shubalakshmi Swain, Avni Blotra, Swapnil Kiran

Research interests

- Wildlife disease ecology: understanding the long-term consequences of disease burden in amphibians and reptiles
- Wildlife conservation ecology: identifying drivers of human-wildlife conflict and develop models of area based conservation approaches
- Snakebite ecology: understanding the complex interactions between snakes, humans, and the environment that lead to snakebite envenomings

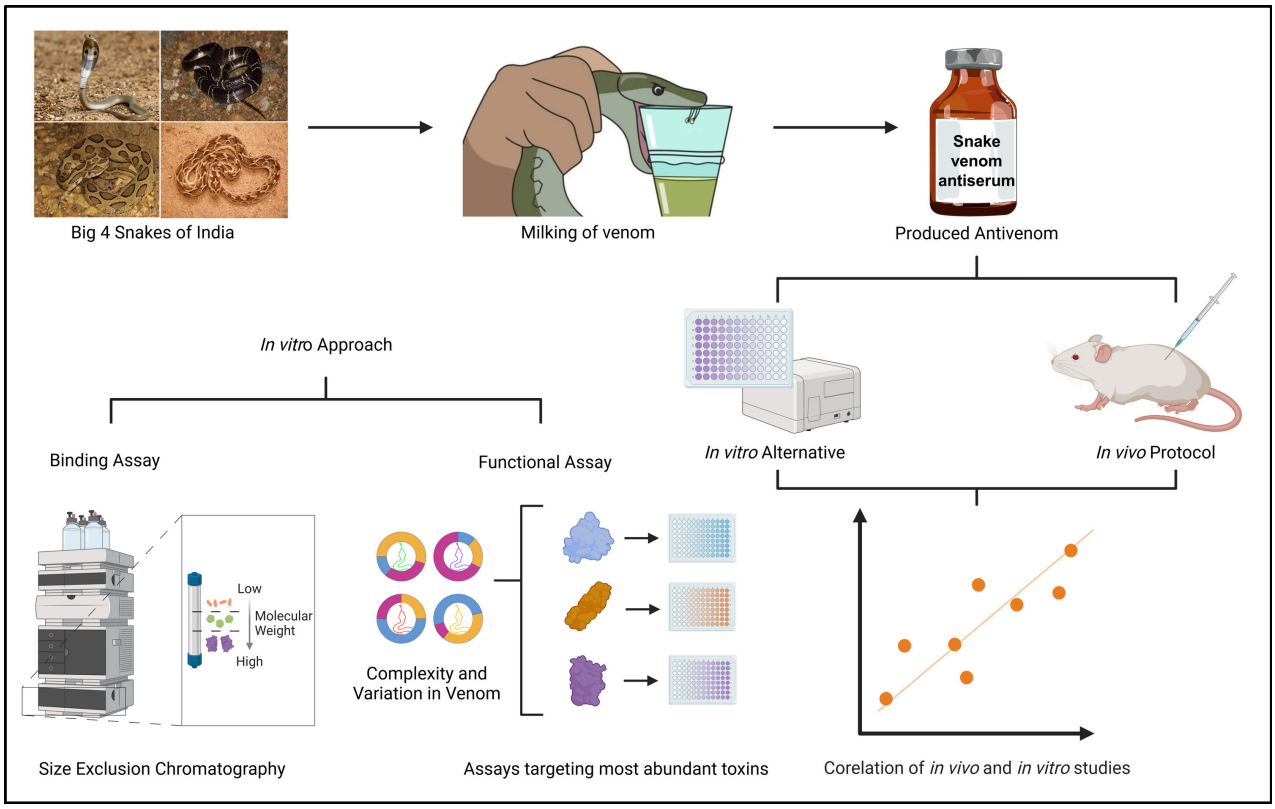
A century of chytridiomycosis in Indian amphibians:

Chytridiomycosis, caused by the Chytrid fungus *Batrachochytrium dendrobatidis* (*Bd*) contributes to the global decline of amphibians. *Bd* poses a significant threat to 600 threatened species globally. We sampled 5802 amphibians, that included 802 historical (from 1911 to 2020) and 1900 contemporary (from 2021 to 2023) from different locations in India. *Bd* was present in 15% of historical (museum) samples. *Bd* has been infecting amphibians in India for over a century, with the earliest detection in 1912 from Shimla, Himachal Pradesh. Bd prevalence was higher in in 1960s, but after the 1970s, there was no increase in prevalence. We hypothesize that *Bd* originated in South Asia, since both phylogenetic studies and data on frog leg trade from India prior to its ban in 1985 substantiate this. We are identifying the *Bd* lineage and its variation over time in India. We postulate that the host immunity

might have coevolved with pathogen virulence. This research is crucial for understanding of the global spread of the pathogen.

Implementing 3Rs in Polyvalent Antivenom production:

Snakebite is a neglected tropical disease, and India carries the heaviest burden, with more than 64,000 deaths each year. Polyvalent antivenoms (PAVs) raised against the spectacled cobra, common krait, Russell's viper, and saw-scaled viper. The production PAVs relies heavily on *in vivo* quality control, with animal-based efficacy tests performed at multiple stages of production. Annually, a manufacturing unit uses 3,700 mice. Along with the ethical implications, they are expensive. To address this problem, we are developing a panel of *in vitro* alternatives, aligned with the 3R principles. Given the biochemical complexity of snake venoms we are employing a combinatorial approach, involving binding assays and functional assays. Venom–antivenom binding is assessed using size-exclusion chromatography and functional assays target the dominant toxin families of each species.



Schematic representation of workflow for development in vitro assays to implement 3 Rs in Polyvalent Antivenom production

Recent publications

- Bletz MC, Gratwicke B, Belasen A, Catenazzi A, Duffus ALJ, Lampo M, Olson D, Vasudevan K (2024) Chapter 6. Infectious diseases: Advances and challenges in addressing emerging pathogens. Pages 148-176, In. IUCN SSC Amphibian Specialist Group (2024). The Amphibian Conservation Action Plan: A status review and roadmap for global amphibian conservation. Wern, S., Borzée A., Marcec-Greaves, R., Angulo, A. (Eds.). IUCN SSC Occasional Paper, No 57. Gland, Switzerland: IUCN. ISBN: 978-2-8317-2279-5. DOI: https://doi.org/10.2305/QWVH2717.
- Tapley B, Johnson, K, Michaels, CJ, Bradfuekdm K, Barber, D, Randall, L, Vasudevan, K, Paszkowski, C, Griffiths, RA, Calatayud, N, Griffit, E, Kacoliris, F (2024) Chapter 11. Conservation breeding. Pages 267-283, In. IUCN SSC Amphibian Specialist Group (2024). The Amphibian Conservation Action Plan: A status review and roadmap for global amphibian conservation. Wern, S., Borzée A., Marcec-Greaves, R., Angulo, A. (Eds.). IUCN SSC Occasional Paper, No 57. Gland, Switzerland: IUCN. ISBN: 978-2-8317-2279-5. DOI: https://doi.org/10.2305/QWVH2717.
- Srivastava T, Hameed J, Kumar V, Segu H, Narayan S, John M, --- Umapathy G (2025) Establishing reproductive seasons for the conservation of the critically endangered Kashmir red deer Cervus Hanglu. ***Sci. Rep.*** 15: 4955.

P ANURADHA REDDY

Conservation Biology and Genetics of Endangered Species



From left to right: Gausiya Kelawala, Anuradha Reddy, Vedam Pruthvi Pavankumar, Kavita Bisht, Moitrayee Sarkar and Anuradha Joshi

Research interests

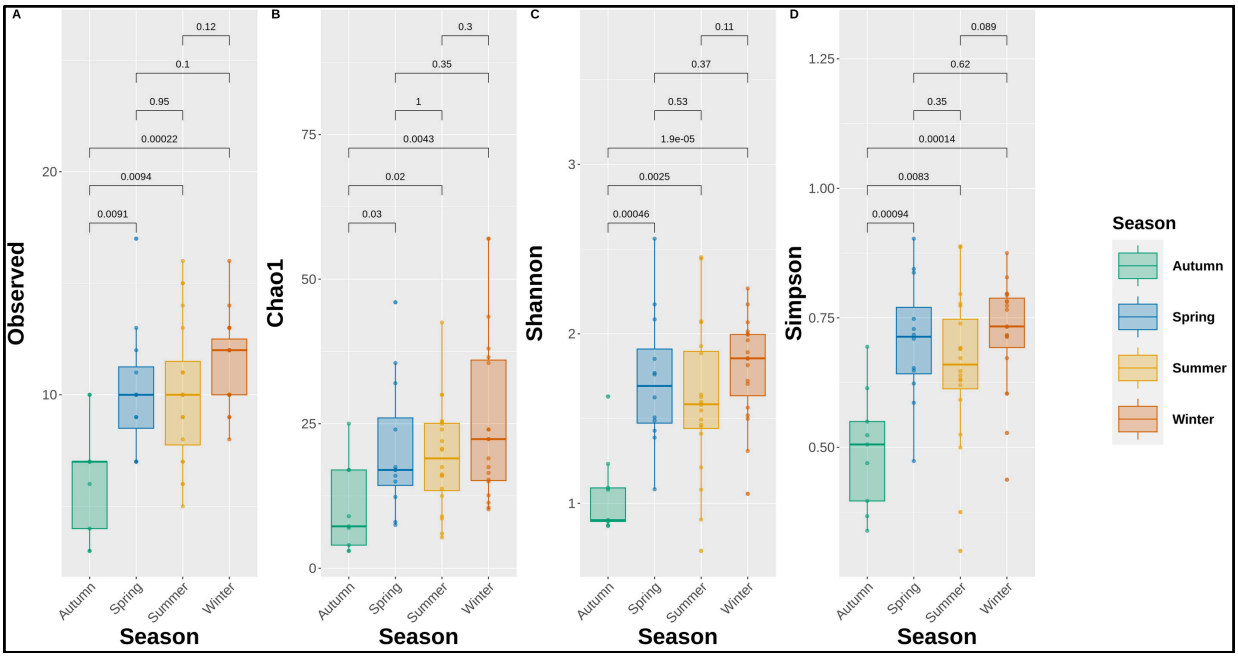
- Population and landscape genetics
- Gut microbiome and health of animals, both in the wild and in captivity

Integrated landscape management of key population areas and the corridors linking them is important for the conservation of several endangered and wide-ranging species. Robust and large-scale data on animal movement within and between protected areas can be obtained through genetic analyses. Identifying landscape factors influencing population connectivity is essential to delineate core areas, corridors and barriers to population connectivity. We are now exploring how meta-populations of wide-ranging and elusive species like tiger is linked to presence of its prey species and population dynamics of co-predators like leopard and dhole in the Eastern Ghats, and the North-eastern Hills and Brahmaputra plains, both landscapes reeling under several conservation threats.

All future conservation breeding plans of endangered species should be integrated within a hybrid management framework, wherein the captive-bred population is part of the larger metapopulation. We had earlier assessed the

largest existing population of the critically endangered hangul (*Cervus hanglu hanglu*) in Dachigam NP in the Kashmir Himalaya. Non-invasive genetic analysis yielded identities of 293 individuals with moderate genetic diversity (He=0.62), no evidence of recent bottlenecks, and a population estimate of 394 ± SE 26 individuals, providing a baseline for captive breeding and habitat connectivity initiatives to mitigate inbreeding risks. We then analysed seasonal variations in the gut microbiota of wild hangul, and found *Firmicutes* and *Bacteroidota* as the dominant phyla, with significant seasonal shifts in microbial diversity and composition.

We observed marked reduction in microbial richness in autumn (indicating reduced forage quality/ diversity), increased lactose and galactose degradation pathways in spring, and enhanced methanogenesis in winter. These findings provide mechanistic insights into how hangul copes with environmental stressors, reinforcing the need to preserve habitat heterogeneity and forage diversity. Understanding gut microbiota dynamics is crucial for captive populations, where dietary modifications and probiotic interventions could enhance health and adaptation to controlled environments.



Comparison of alpha diversity indices for hangul samples collected in different seasons from Dachigam National Park, wherein the microbial diversity in autumn samples is significantly lower ($p<0.05$) than that in other seasons.

Recent publications

- Adhya T, Singh S, Gottumukkala HV, Banerjee A, Chongder I, Maity S, Reddy PA (2024) Making Noah's Ark work for fishing cat conservation: A blueprint for connecting populations across an interactive wild *ex situ* spectrum. *Animals* 14: 2770.

SIDDHARTH KULKARNI

Genomic determinants of asymmetric evolution under global climate change



From left to right: Shreya Salunkhe, Siddharth Kulkarni, Pratik Khopkar, Arjun CK

Research interests

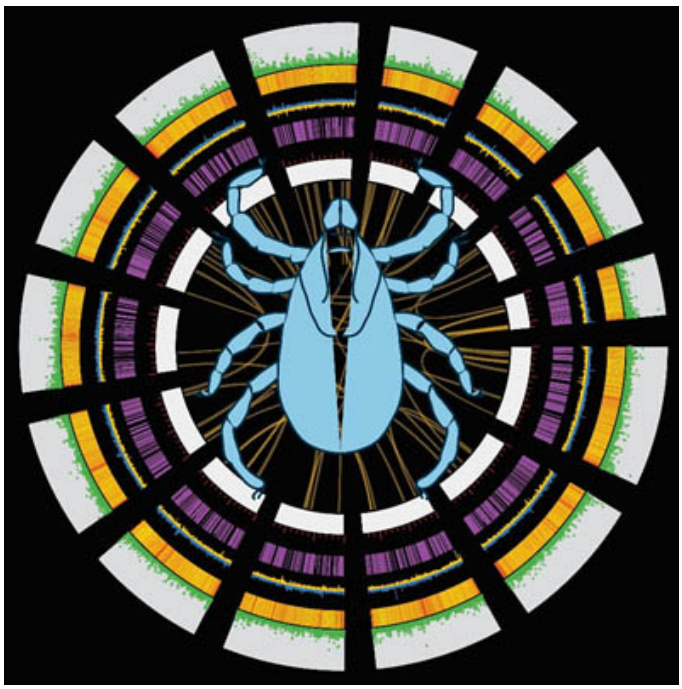
- Asymmetric diversification
- Conservation genomics
- OneHealth
- Evolutionary history
- Comparative genomics
- Bioinformatics

Biodiversity is strikingly uneven across space and time. A staggering diversity of some lineages over other disparately microdiverse groups pose a fundamental question– what makes a lineage asymmetrically diverse than its close relatives on a changing planet? We explore the *modus operandi* of maintaining high diversity of lineages using chelicerata (parasitic ticks, mites, spiders, etc.) as a study system with advanced genomic, computational and experimental approaches.

After joining CSIR-CCMB in March 2025, we have explored the conserved synteny, rare genomic changes in the ticks and mites using *de novo* and existing genomes. We discovered primitive group of mites and generated its *de novo* chromosomal level genome to explore the ancestral configuration of genomic structure and function. We have sampled acarine parasites from cattle to study the tempo and mode of parasitism and explore the genomic signatures of the parasite.

We are resently working on testing the role of whole genome duplications in increased rates of speciation, trait diversification, neo-/subfuntionalization, etc within spiders.

In the light of past mass extinction events and climate change, we are testing if whole genome duplication aided in surviving the bottleneck events.



A self-synteny circos plot show degree of inter-chromosomal duplications in arachnids with gene density and GC-skew on periphery and a tick silhouette representing an asymmetrically diverse group within Arachnida

Recent publications

- Siddharth Kulkarni, Benjamin C Klementz, Prashant P Sharma (2025) A chromosome-level genome of the giant vinegaroon Mastigoproctus giganteus exhibits the signature of pre-Silurian whole genome duplication. ***Journal of Heredity*** esae074.

CROP IMPROVEMENT

Hitendra K. Patel



HITENDRA K PATEL

Plant - Pathogen Interactions and Crop Improvement



From left to right, first row: first row: Hitendra K. Patel, Raju Madanala, Vinoth Kumar K, Md. Jamaloddin, Gokulan CG, Deepti Rao, Rennya PR; Second row: Anjana Sharma, Praveen Kumar Nayak, Amita Rani Supriyo, Sarath Dev GP, Apoorva Masade,Sumedha C Prabhu, Preethi KP
Third row: K Shashi Kiran, Deepika M, Kirtana R, Tata Sreenivasa Rama Satya Sandeep, Raihana Najla N, Erum Khan, Molieswar J; Fourth row: D Swetha, Hemsagar Patel, Rupdhar Yadav, Kumar Sumit, Lokesh Choudhury, Dheeraj Patel, Sandhya

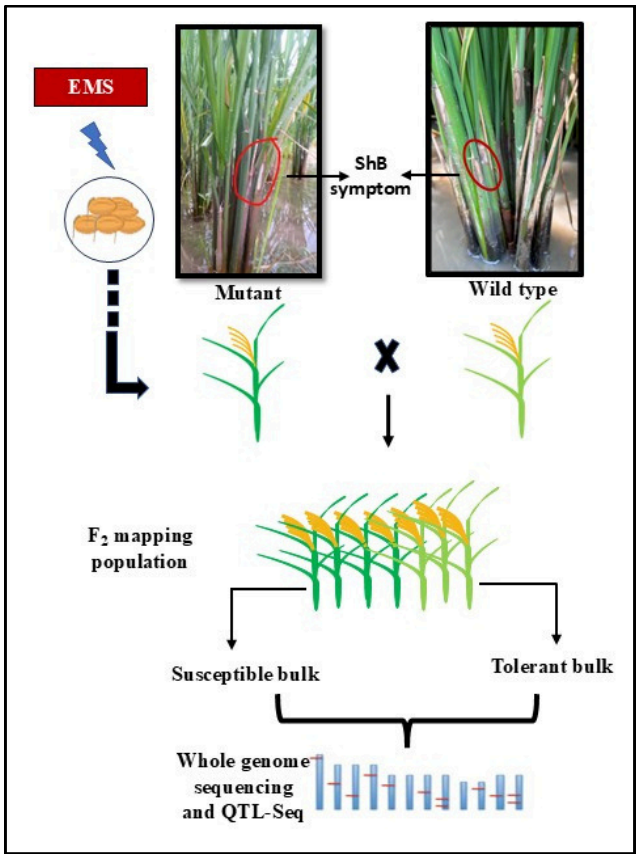
Research interests

- Rice functional genomics
- Molecular plant-microbe interactions
- Crop improvement through marker-assisted selection and genome editing

Rice, a staple for over half the global population, is crucial for food security and economic stability. However, the vast rice agro-ecosystem is threatened by pests and pathogens, jeopardizing yield and quality, highlighting the urgent need for resilient rice varieties. Mutagenesis stands as one of the most powerful tools for generating plant varieties with novel alleles conferring biotic and abiotic stress resistance traits. Over 10,000 EMS (Ethyl methanesulfonate) induced mutant lines were generated in the background of Samba Mahsuri (SM; BPT-5204), a rice variety prized for its fine grain, excellent cooking quality, wide adaptability, and high yield. Through rigorous screening, the stable mutant lines exhibited valuable traits, including enhanced resistance to major biotic stresses such as Bacterial Blight (BB), Sheath Blight (ShB), Yellow Stem Borer (YSB) and important agronomic traits like high yielding, early flowering, strong culm. The rice mutant lines identified as having important agronomic traits include SB23, BB42, SM48, SM74, Ti-3, Ti-17, Ti-26, Ti-35, Ti-87, Ti-112, Ti-128, Ti-166,

HKP-2, HKP-52, HKP-9, HKP-15, HKP-62.

Sheath Blight (ShB), caused by the soil-borne necrotrophic fungal pathogen *Rhizoctonia solani* (*R. solani*), is one of the most devastating rice diseases, with yield losses of up to 50% in favourable conditions. Sustainable management of ShB is challenging as no source of complete resistance is identified within the rice germplasm, forcing reliance on harmful agrochemicals to manage the disease; hence, the EMS-generated mutant resource serves as an excellent source for understanding disease-resistant mechanisms and for breeding advancements. To map the genetic loci linked to ShB resistance in the rice mutants SB23 and Ti87, QTL-Seq mapping approach was deployed (Fig. 1). Markers developed from this study can aid in marker-assisted selection and the development of highly resilient, disease-resistant rice varieties, ensuring more robust and sustainable crop production.



Schematic representation of Quantitative Trait Loci Mapping

Recent publications

- Gokulan CG, Bangale U, Balija V, Ballichatla S, et al. (2024) Multiomics-assisted characterization of rice-Yellow Stem Borer interaction provides genomic and mechanistic insights into stem borer resistance in rice. ***Theor. Appl. Genet.*** 137(6): 122.

- Ballichatla S, Gokulan C G, Barbadikar KM, Hake AA, et al. (2024) Impairment in a member of AP2/ERF and F-box family protein enhances complete panicle exsertion in rice. ***J. Exp. Bot.*** 75(18): 5611-5626.

- Rana R, Sharma A, Madhavan VN, Korpole S, Sonti RV, Patel HK, Patil PB. (2024) *Xanthomonas protegens* sp. nov., a novel rice seed-associated bacterium, provides *in vivo* protection against *X. oryzae* pv. *oryzae*, the bacterial leaf blight pathogen. ***FEMS Microbiol. Lett.*** 371: fnae093



1.1B
Institutional Projects



Establishment of Advanced Bioinformatics Centre for Disease/Epigenomics/Futuristic Genomics (ABCDEFG)

PIs: Divya Tej Sowpati, Shrish Tiwari, Vinay K Nandicoori

This project, funded by the Department of Biotechnology (DBT), seeks to establish a Bioinformatics Centre at CCMB. The main objective of our Centre is to provide a state-of-the-art bioinformatics facility and trained personnel that can analyze large scale whole-genome data and extract biologically meaningful results and conclusions. In particular, ABCDEFG has achieved the following since the project inception in 2022:

- An improved computational pipeline for reliable discovery of structural variants from short-read and long-read data
- An accurate tool to identify imperfect tandem repeats from whole genome sequences based on comparison of 2-bit representations of DNA sequences
- Single cell transcriptomics data analysis from Mouse Embryonic Stem cells as part of a collaborative project
- Lectures on transcriptomics data analysis to empower many students to handle their own RNA-seq analysis

As an extension to the establishment of ABCDEFG, the National Network Project (NNP) of CSIR-CCMB, funded by DBT, encourages development of novel computational methods in collaboration with scientists outside CCMB. In this project, we are collaborating with IIT Hyderabad, and our work revolves around:

- Benchmarking various tools and models currently available for identification of DNA modifications from Oxford Nanopore data using both public and in-house generated datasets. DNA modifications are crucial in epigenetic control of gene expression.
- Development of a neural network model for accurate identification of specialized DNA base called 6-methyladenine from Oxford Nanopore sequencing data.
- A tandem repeat genotyper for long-read data. The tool is technology agnostic and works with both PacBio and Oxford Nanopore data. It runs much faster than other existing tools while performing on par in terms of accuracy.

Indian Breast Cancer Genome Atlas (IBCGA)

PI: Karthik T Bharadwaj

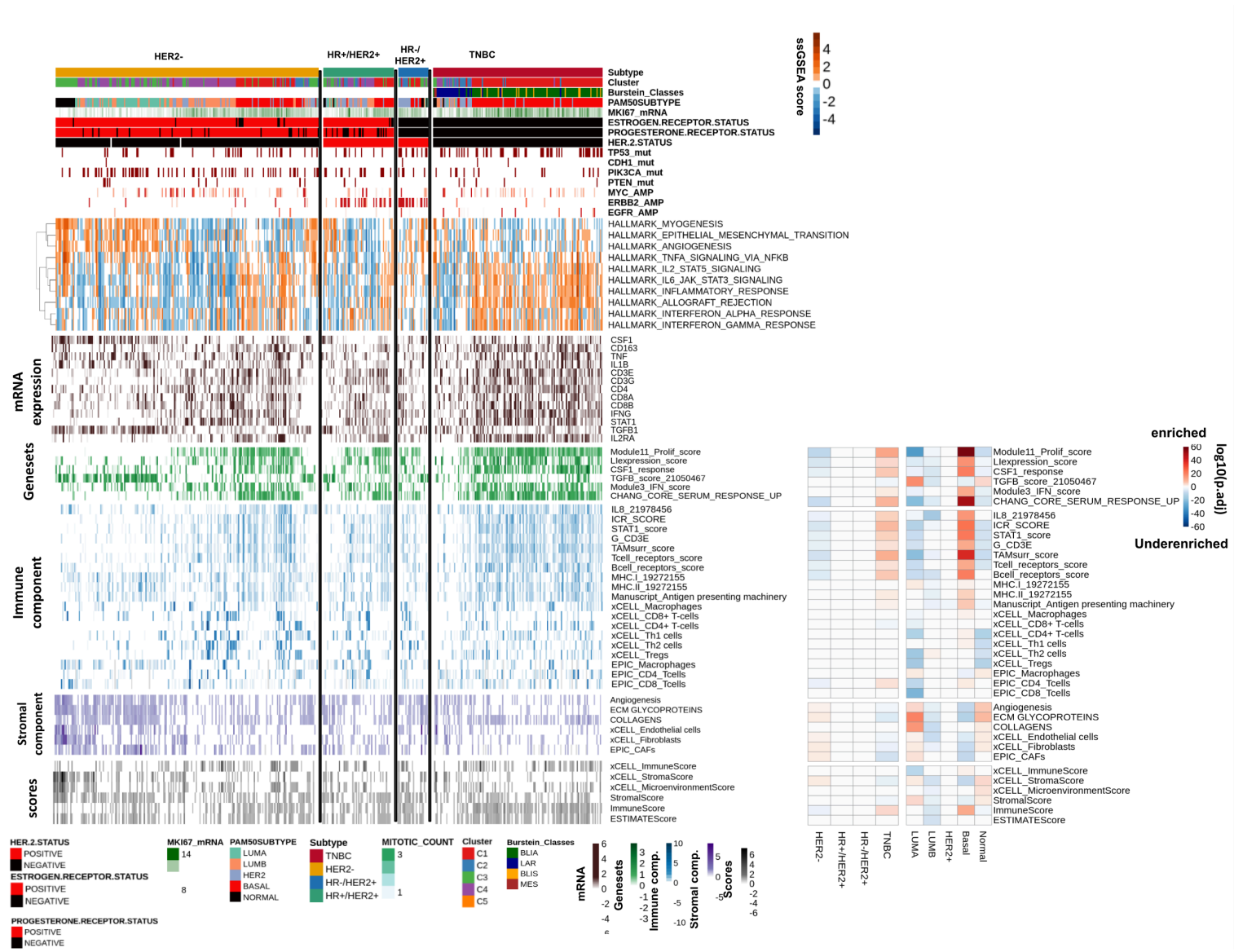
Despite harboring around a quarter of the world's population, South Asia remains significantly underrepresented in the global cancer genomics datasets. To address this gap, in the IBCGA project, we performed systematic genomic and transcriptomic profiling of breast tumors from Indian patients affected with breast cancer. Using genomic and transcriptomic (mRNA) data from 438 Breast Cancer samples, we performed structural variant and immunophenotype analyses, respectively.

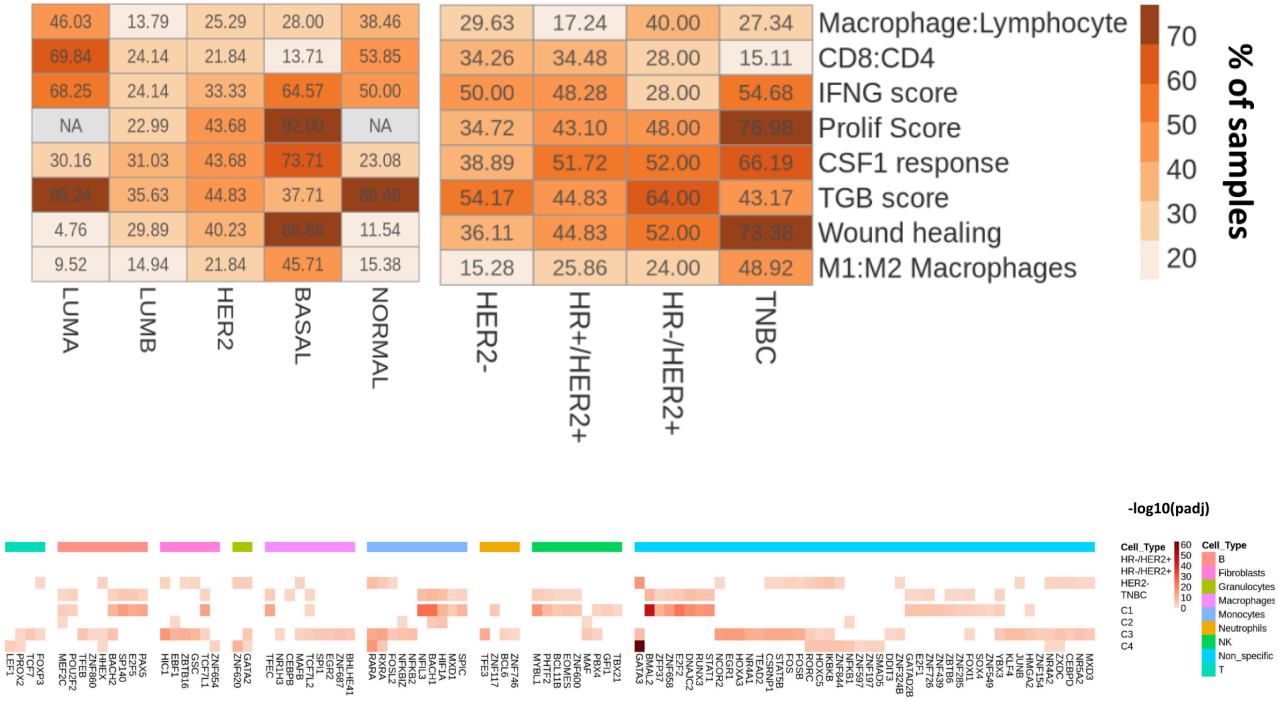
In particular, the structural variant analysis revealed specific types of genomic changes that align with the biology of these tumors. For example, the genomes of HR-/HER2- (Triple Negative Breast Cancer) samples revealed morefrequent tandem duplications with high similarity to the Structural Variation signature 3 (SV3), indicative of failure in the repair of DNA double-stranded breaks (Homologous Recombination Deficiency). Whereas, the HR+/HER2+ genomes showed a higher frequency of inversions alongside

recurrent rearrangements in the chromosomal region 17q12–q21.

The transcriptome analysis has identified i) immune-cell-associated pathways and, ii) transcriptional factors specific to each of the tumor subtypes. The HR+/HER2- samples showed overexpression of transcriptional factors related to estrogen signaling (GATA3) and retinoic acid-related nuclear receptors superfamily (RXRA, RORC, RARA). A subset of these HR+/HER2- tumors that are of Luminal-A molecular subtype exhibited high TGF-beta activity with increased stromal cell infiltration, and enrichment of collagen/ECM glycoproteins as compared to HR+/HER2- luminal-B tumors (Figure 1a).

On the other hand, the HR-/HER2- (TNBC) samples showed significantly higher enrichment of leukocyte, CSF1 response, and IF-gamma gene signatures, indicating high levels of immune cell infiltration (Figure 1b). We also observed significantly higher putative fractions of macrophages and CD4+ T-cells in HR-/HER2- samples. We also found overexpression of transcriptional factors (STAT1, RUNX3, STAT4) involved in the differentiation of T-helper cells in the HR-/HER2- samples (Figure 1c).





(a) Heatmap of IBCGA samples (n = 438) grouped into either of the four clinical subtypes (HR+/HER2-, HR+/HER2+, HR-/HER2+ and TNBC) using the ssGSEA scores of Hallmark pathways, mRNA expression of select markers, ssGSEA scores of immunooncologic genesets, immune cell abundances, stromal cell abundances and estimates of overall stromal and immune abundances derived from deconvolution algorithms. The annotation columns (top) of the heatmap are color-coded to display the following: i) sample attributes: Subtype, cluster, Burstein class, MKI67 mRNA expression, ER status, PR status, HER2 status; ii) Mutation status: TP53, CDH1, PIK3CA, PTEN and iii) CNV status: MYC, CDKN2A, ERBB2 and CCND1. The heatmap on the right depicts the level of significance (-log10(padj)) for the above immune cell estimates for each of sample groups classified based on PAM50 subtype and receptor status. for the above immune signatures (b) The heatmap exhibits percentage of samples having higher scores than median value for the immune estimates with respect to PAM50 classification (left) and subtypes based on receptor status. (c) Plot depicts the level of significance (-log10pval) of upregulation of immune TFs across each of the four subtypes (HR+/HER2-, HR+/HER2+, HR-/HER2+ and TNBC) and unsupervised sample clusters obtained by Iterative Consensus Clustering.

Phenome India - CSIR Health Cohort Knowledgebase

PIs: Swasti Raychaudhuri, Karthik T Bharadwaj, GR Chandak

CSIR-CCMB finished the first and second phase of sample collection from all CSIR institutes in South India. It has performed targeted metabolomic analysis of >1500 samples, with ~450 metabolites per sample. Targeted proteomic analyses are underway. ~2800 samples have been subjected to high throughput genotyping using GSA v3.0 Illumina Chip (800K genetic variants) and a



pilot association analysis with medically important traits is ongoing after proper quality control and data imputation.

Setting up pathogen surveillance systems beyond SARS-CoV-2

PIs: Rakesh K Mishra, Vinay K Nandicoori, Karthik T Bharadwaj

The Alliance for Pathogen Surveillance Innovations (APSI)-India, established in 2021 at CSIR-CCMB, Hyderabad, with support from the Rockefeller Foundation, is a pan-India consortium with a collaborative network of academic, research and medical institutions. Its partners include TIFR-NCBS, TIGS, Ashoka University, CSIR-IGIB, CSIR-NCL, IISER, Pune Knowledge Cluster and Pasteur Institute, Shillong. APSI focuses on advancing pathogen surveillance through genome sequencing, bioinformatics and standardized protocols to monitor pathogens of public health concern utilizing wastewater based epidemiology. The Phase 1 of the consortium's efforts during 2021-2022, focused on developing robust surveillance systems to monitor and detect SARS-CoV-2 variants circulating across India.

The Phase 2, during 2023-2025, focused on expanding activities to establish monitoring procedures and detection systems for other viral and bacterial pathogens including those contributing to antimicrobial resistance. APSI's cost-effectiveness models demonstrated wastewater surveillance's potential to reduce outbreak-related healthcare costs. APSI integrated surveillance technologies into public health systems, developed low-cost, indigenous pathogen detection tools and advocated for national surveillance networks. APSI has significantly advanced India's surveillance capabilities, establishing sustainable systems and protocols to enhance public health preparedness under the One Health approach.

CSIR-Sickle Cell Anemia Mission

PI: GR Chandak

CSIR-CCMB started contributing in the Sickle Cell Anemia (SCA) 2018 onward. From 2018-24 (barring 2020-22 due to COVID-19 pandemic), they have done population-level screenings in Chattisgarh, Maharashtra, Madhya Pradesh and Rajasthan.

In this project, they have screened 3.5 lakh people. Of them, they treated 4500 patients with hydroxyurea and followed up with them to check for improvement. They offered 387 couples with prenatal screening for Sickle Cell Anemia.

They developed the CSIR Scan Test, which is validated by ICMR and now a part of SCA testing under National Health Mission of Maharashtra, Madhya Pradesh, Rajasthan and Jharkhand. The test has helped understand the true prevalence of the disease in the country.

CCMB has facilitated and obtained the CDCSO approval for hydroxyurea use for Sickle Cell Anemia treatment. Formulations of 200 mg in tablet and syrup formats for the same are now available.

Creation of a national network of existing and upcoming high risk pathogens laboratories (BSL-3/4) labs across departments and keeping their "interlinkages" functional for use during outbreak response across sectors" under NOHM component of PM_ABHIM

PIs: Santosh Chauhan, Vinay K Nandicoori

Under the National One Health Scheme, ICMR is establishing a robust network of high-risk pathogen laboratories (BSL-3/4) across various departments to ensure a rapid and coordinated response during disease outbreaks. This network, which includes institutions like the CCMB, aims to maintain functional interlinkages nationwide, facilitating swift detection and diagnostics of emerging infectious diseases.

ICMR has provided essential funding and specialized training, with nearly five training sessions for CSIR-CCMB staff and students. These trainings covered handling advanced equipment, standard operating procedures (SOPs) for decontamination, and safe handling of high-risk pathogen samples. By strengthening laboratories and fostering collaboration, this network plays a pivotal role in India's public health response, ensuring timely outbreak containment and improved health security.

Establishment of Centre for Advanced Research for Rapid Development of Host-directed Broad Antivirals

PIs: Santosh Chauhan, Krishnan H Harshan

CSIR-CCMB has been awarded a CAR grant for developing host-directed broad-spectrum antiviral strategies. The rapid evolution of viruses often renders conventional antivirals ineffective due to drug resistance. This project takes a host-centric approach, targeting cellular pathways hijacked by viruses and enhancing the body's innate antiviral defense.

The team which also includes scientists from THSTI, IISER Mohali, and IIT Ropar will work to:

- Establish high-throughput pipelines to identify small molecules targeting host lipid metabolism and endocytic/autophagic pathways essential for viral entry and replication;
- Develop a structure-based drug discovery platform to modulate interferon-stimulated genes and strengthen host antiviral programs; and
- Design therapeutic strategies to minimize inflammation-induced tissue damage. With proof-of-concepts already established, this project positions CCMB at the forefront of pandemic preparedness through multipronged, host-directed antiviral pipelines.

Whole Genome Sequencing of *Mtb* Clinical Strains for Determining Drug Resistance and Strain Lineage in India: A Structured Nationwide Approach

PIs: Vinay K Nandicoori, Divya Tej Sowpati

Tuberculosis, caused by the bacterium *Mycobacterium tuberculosis,* is one of the deadliest infectious diseases in India. However, TB is curable with rapid diagnosis and timely initiation of the correct therapy. Worryingly, drug-resistant TB has become common in many countries significantly complicating treatment strategies and increasing risk associated with TB.

To tackle the global health challenge of TB and contribute to the national mission of TB elimination, the Indian TB genome sequencing consortium (InTGS) has been formed. In a nutshell, InTGS aims to make mapping drug resistance possible through genomics and artificial intelligence to allow rapid identification of drug-resistant TB strains in patients and facilitate strategies for better control of TB. Under the InTGS project, the goal is to develop a well-characterized repository of 32,000 *Mycobacterium tuberculosis* (Mtb) clinical isolates consisting of their whole genome sequence data.

Since the inception of this project in October 2023, the consortium has performed high-coverage (>500x median) of more than 15,000 Mtb isolates. Out of these, half were sequenced at CCMB. Our results indicate that most isolates belong to the Indo-Oceanic (lineage 1.1) and East-African Indian (lineage 3.1) lineages.

In addition to the sequence data, a strain repository of these isolates is being made, and the antibiotic sensitivity profiles are also being developed. By correlating the genomic signatures with the phenotype data, we envisage a data-driven approach to mitigate the burden of TB.

Translational Neuroscience: Pharmacological Validation of Key Biological Pathways Involved in Neurodegeneration

PI: Ishwariya Venkatesh

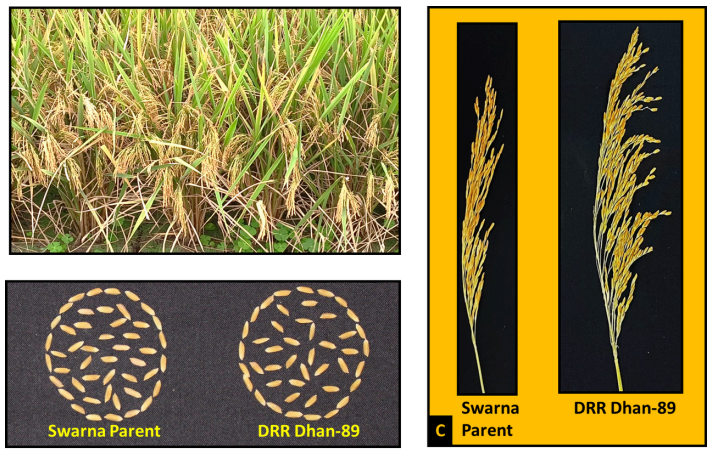
We are developing small-molecule agonists of RARβ to reinstate intrinsic growth capacity in adult neurons after injury. In collaboration with CSIR-IICT, structure-guided design has yielded aryl-amide analogs with improved stability over retinoic acid. Screening in Neuro2a cells identified a compound as a potent regulator of neurite growth, increasing neurite length and branching while inducing RARβ target genes. In adult mouse spinal-injury models, the compound has shown improved functional performance on machine-learning–based gait analyses and enhanced axonal growth, consistent with repair. In human iPSC assays, it promoted neural induction and elevated early neurogenesis markers, supporting relevance for neuronal replacement strategies.

Current efforts include comparative testing of additional analogs, pharmacokinetics, target engagement, and SAR-guided optimization to refine potency, selectivity, and delivery.

Development of climate resilient and high-yielding trait improved varieties of Swarna; a mega rice variety of India

PI: Hitendra K Patel

Swarna rice variety, possessing high yield, short bold grain type was released by Rice Research Station, Maruteru, APAU, Andhra Pradesh, India in 1982. Despite being a very old rice variety, Swarna is still being enthusiastically grown on more than 6 million hectares across India. However, Swarna is highly susceptible to BB, blast disease and also to submergence and lodging stresses. Depending on the severity, these stresses account for a yield loss of 20-80% (a minimum of 1000 crores/annum) to rice farmers. Under this project, CSIR-CCMB and ICAR-IIRR are jointly addressing the above-mentioned lacunae in Swarna through the marker-assisted breeding strategy to develop superior versions of the Swarna variety. The yield improvement and low input cost of agrochemicals will be additional benefits to the rice farmers of our country.



DRR Dhan 89: Climate resilient- high yielding, medium slender grain type rice variety released for cultivation in Odisha, Bihar, West Bengal and Chhattisgarh. A: Field view of DRR Dhan 89 showing high-yielding phenotype. B: DRR Dhan 89 shows a similar seed phenotype to that of the Swarna parent. C: DRR Dhan 89 panicle with high-yielding phenotype compared to the Swarna parent.

Genome Editing for Crop Improvement (GE-CROP)

PI: Hitendra K Patel

Contemporary rice breeding strategies for disease resistance rely on marker-based introgression/pyramiding of multiple race-specific resistance gene loci into rice. For example, Improved Samba Mahsuri (ISM) was jointly developed by CSIR-CCMB and ICAR-IIRR, Hyderabad by pyramiding three resistance loci using marker-assisted selection (MAS). It is becoming widely popular due its bacterial blight resistance and low glycemic index. However, it is possible that bacteria will eventually evolve and infect the ISM variety.

Hence, it is necessary to keep improving existing varieties so that the tolerance of these cultivars do not break down in the field. MAS may also have issues of negative linkage drag, that is bring in undesirable traits into crops. CRISPR-mediated genome editing, when optimally standardized and integrated with conventional breeding programs, has the potential to overcome these and other problems.

It can accelerate breeding cycles and leading to faster, cheaper, and more predictable outcomes. In this project, we are developing genome-edited lines of the indica rice cultivar Samba Mahsuri (BPT5204) to enhance tolerance to diseases and improve agronomic traits that contribute to yield and productivity.

Dissecting plant responses to growth promoting microbes

PI: Hitendra K Patel

Soil microorganisms offer a promising approach for promoting plant growth and enhancing crop yields. We aim to understand the growth promotion attributes of a beneficial soil bacterium and understand the plant role in the recruitment and response of/to selected microbiomes, by investigating the underlying molecular mechanisms in plant-microbial interactions.

We will focus on the effect of the microorganisms on promoting productivity using rice as the model species. The proposed study is being carried out as a collaborative DBT Network Project between four pioneering institutes, ICGEB New Delhi, NIPGR, New Delhi, ICAR-IIRR, Hyderabad and CSIR-CCMB, Hyderabad.

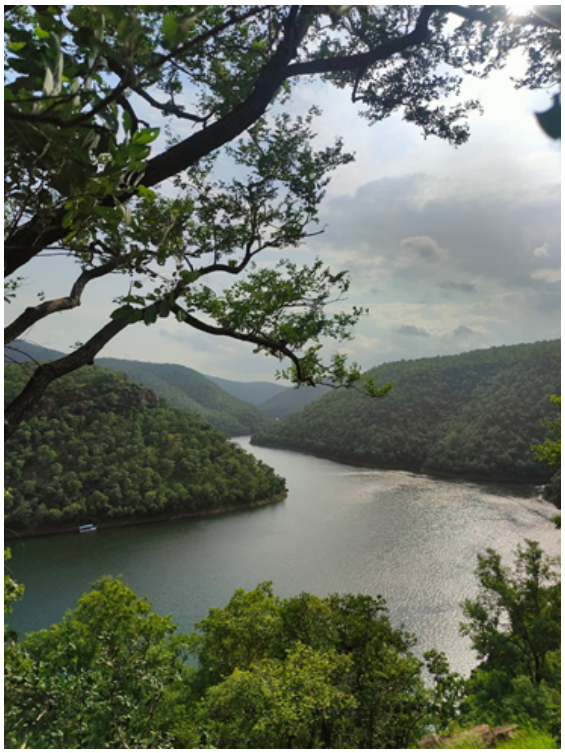
Discerning The Eastern Ghats For Improving Conservation Outcomes

PIs involved from LaCONES-CCMB;
Nodal PI: G Umapathy

The project aims to enhance biodiversity knowledge and management through integrative research and conservation planning. Key achievements include extensive soil arthropod surveys conducted across Tamil Nadu, Andhra Pradesh, Telangana, and Odisha, along with DNA metabarcoding to explore diversification and biogeographic histories.

Aquatic biodiversity was assessed using environmental DNA collected from 204 samples across 68 water bodies, which resulted in the identification of metazoan diversity and the creation of a custom genetic reference database for fish. Large carnivore studies mapped populations of tigers, leopards, wild dogs, and sloth bears using non-invasive genetics, scat surveys, and habitat suitability models.

Restoration efforts focused on understanding the genetic identity of wild buffalo and implementing assisted reproductive technologies. Additionally, research on plant communities examined the impacts of the invasive species Lantana and drought on forest resilience.



A picturesque landscape along the Nagarjuna Sagar backwaters in the Eastern Ghats

Training workshops, collaborations, and student mentoring were conducted to build scientific capacity. Overall, the project explores essential data and tools for conserving the fragmented yet biodiverse landscape of the Eastern Ghats.

Genomic Characterization of the Deep-Ocean Virome in the Indian EEZ

PI: G Umapathy

The objective of the project is to explore viral diversity and ecological roles in deep-sea ecosystems, a largely unstudied area in India's waters. Significant progress has been made in field sampling and laboratory standardisation over the last year. A total of 15 sediment samples and 85 water samples were collected at depths of up to 2,000 meters from the Andaman and Lakshadweep islands. Protocols for viral enrichment, nucleic acid isolation, and sequencing were optimized.

Using Oxford Nanopore sequencing, we generated approximately 6.4 million high-quality reads from 13 water and four sediment samples, including ultra-long reads of up to 78.7 kb. In total, 58,715 assemblies were produced, of which 21,180 were identified as viral genomes.

Taxonomic assignments revealed 11 viral subfamilies and 15 families distributed across two major classes (Caudoviricetes and Megaviricetes). However, most assemblies remain unclassified, indicating a vast reservoir of novel viruses.

We also established a functional annotation pipeline to analyze the metabolic potential of these viruses. In addition to data generation, the project contributed to building capacity in viral genomics, bioinformatics, and advanced imaging, with young researchers trained in sequencing and analysis. These outcomes lay a strong foundation for mapping deep-ocean viral diversity, understanding host-virus interactions, and developing resources for future ecological and biotechnological applications.



CCMB-LaCONES scientists as a part of a cruise for sampling in the Andaman and Nicobar Islands

1.1C
Research Facilities



riram Varahan Photography





Advanced Microscopy and Imaging Facility (AMIF)

The Advanced Microscopy and Imaging Facility offers a variety of advanced microscopes for imaging to assist all research groups with capturing and analyzing images. We also provide training for students and researchers, supervise their image capturing and analysis, and help them publish high-quality images.

List of equipment

- Leica TCS SP8 3X STED Super-Resolution Microscope
- Leica TCS SP8 Confocal Microscope.
- 3i Marianas diSPIM Light Sheet Microscope.
- Nanonics Multiview 1000 Atomic Force Microscope (AFM)
- Zeiss LSM 880 Confocal Microscope with Airyscan
- Olympus FV3000 Confocal Microscope (Live-Cell Imaging)
- Renishaw inVia Raman Microscope (Raman and Rapid Raman Imaging System)
- Zeiss AxioZoom V16 Stereo Microscope with Apotome
- Zeiss AxioImager Z2 with Apotome
- Zeiss AxioImager Z2 Upright Fluorescence Microscope
- Zeiss Axioplan 2 Upright Fluorescence Microscope

Achievements of the year

- The automated booking portal ensures fair and transparent access to the microscopy facility for all users. It streamlines scheduling, reduces conflicts, and helps researchers manage instrument time efficiently. Additionally, it provides a clear record of bookings, enhancing overall transparency and convenience.
- Mr. Suman Bandari, Senior Technical Officer, received the Best Employee Award for his valuable contributions to the facility.
- Achieved ₹2.79 lakhs in facility revenue, the highest in the past five years.
- Conducted live demonstrations of advanced imaging systems, including Leica Mica, Andor BC43, and ZEISS Axiovert 5 Digital Widefield Microscope and Leica Thunder

Facility staff

Nandini Rangaraj
Venkata Mahesh Nitla
Suman Bandari
N.R. Chakravarthi
Sajid Ahmed Shareef



Sajid Ahmed Shareef, Suman Bandari, Venkata Mahesh Nitla, N.R. Chakravarthi, Nandini Rangaraj



Animal House

The CCMB Animal House has been registered under CPCSEA [Committee for the purpose of control and supervision of Experimental Animals] ,Ministry of Animal Husbandry & Dairying, Government of India since the year of 1999. The registration number is 20/GO/RBi/S/99/CPCSEA, and it is for the purpose of research and breeding of mice, rats, rabbits and hamsters for In-house purpose and commercial for trading purpose.

The main objective of the Animal House is to supply genetically defined various strains of mice, rats and rabbits to CCMB's scientific community under strict regulation from CPCSEA, Government of India. All animal house activities are regulated by ONTEXA [Online indenting system for experimental animals] software In which all PIs can raise an online animal request as per IAEC approved project for supply of animals. This inventory platform software helps to regulate animal census, mortality, animal production and supply details. It's a monitoring platform software to generate data of microbial, genetic monitoring with micro environmental parameters of animal rooms such as temperature and relative humidity.

The Animal House provides orientation and training programme to authorized animal house users [students & project staff] to maintain standards of humane, ethical and responsible use of animals in their research. The animal facility maintains 89 strains of various inbred, out bred mice including different transgenic & knock-out mouse models, immuno-compromised (nude &scid) mice, two strains of rats, one strain of hamster and one strain of rabbit. All the mice and rat colonies are housed in individually ventilated caging system (IVCs) where supply air is filtered through a HEPA filter system and these machines were imported from Techniplast, Italy and double-sided racks from Orchid Scientifics.

Key features of the facility

The facility is under electronic surveillance system CCTV and Biometric system so that only those who are authorized can enter the facility to minimize the risk of infection to animal colonies. All animal rooms are environmentally controlled and monitored for temperature, humidity and automatic lighting system to control 12hrs/12hrs light and dark cycle.

The experiments conducted on animals at this facility are through the approval of IAEC (Institutional Animal Ethics Committee). A total of 124 projects were approved for animal experimentation under IAEC in 2024-2025.

The Animal House has various disease models of Transgenic and Knock-out mice. Around 89 strains are available in Animal house facility, sourced from Jackson laboratory USA, Riken Institute Japan, Charles River USA, Cardiff University UK, National Cancer Institute USA, MMRRC USA, St Jude Children's Research hospital USA,NII Delhi, ILS Bhubaneshwar.



Conducted Skill Development training programme on "Genetic and Microbial Monitoring of laboratory animals" from 26th August 2024 to 31st August 2024

The training Program focused on developing practical applications for maintaining Animal health with cutting-edge, Skills related to the genetic and Microbial monitoring of animals. This program benefited approx.10 participants.

Animals supplied during this year for various experiments in-house:

Species	Number of animals supplied
Mice	7562
Rats	153
Rabbits	46

The Animal House team comprises of one veterinarian, one Sr. Technical Officer(3), one Sr. Technical Officer(1) and 2 trained technicians who are involved in breeding and maintenance of various lab animals and also providing technical support to a various ongoing research projects. Also, regular genotyping and microbial screening by a Project Associate,and 12 HLS staff provide technical support in various animal house day to day activities.



DNA Microarray Facility

Microarray is a high-throughput technique for analyzing expression levels of thousands of genes or genotyping large numbers of SNPs in a single experiment. The microarray facility is equipped to do genome wide analysis with applications in basic research as well as in biomedicine and agro-biotechnology. Microarrays (also known as DNA/gene chips) are generated by a technology that integrates molecular biology and information technology.

The facility combines dedicated cubicles for wet lab experiments, data generation and data analysis using high-end computing systems. It houses the Illumina HiScan System for sensitive and accurate imaging of Illumina Bead Arrays for Gene Expression, high throughput Genotyping & DNA Methylation and the Affymetrix Gene Chip System for analyzing Affymetrix Chips related to generating similar kind of data. The entire microarray facility is housed in a dust-free room at CCMB main building. The applications that have been used are largely in the areas of gene expression analysis, microRNA profiling, and genotyping. Gene expression studies have been done with mammalian (mouse, rat and human), plants (rice and *Arabidopsis*), and insects (*Drosophila*) systems. Similarly, the genotyping studies have been carried out in the area of human population genetics and disease association studies.

Biophysics Central Facility

The facility offers a large panel of state-of-the-art equipment to address queries regarding the structures, folding/stability, and interactions of protein-protein/DNA biomolecules. Our state-of-the-art instruments and techniques are customized to support cutting-edge research in nanomaterials, enabling precise characterization of nanoparticles and their properties.

List of equipment

The facility is equipped with various spectroscopic and calorimetric instruments for studying biomolecular structures, folding, binding thermodynamics, kinetics, and quantification. Our facility offers a wide range of calorimetric instruments for precise biomolecular interaction analysis, including PEAQ-ITC, ITC200, VP-ITC, and VP-DSC, along with recent technology Microscale thermophoresis (NanoTemper Monolith N115.) Furthermore, we have advanced spectroscopic and characterization tools such as Jasco J-815 Circular Dichroism (CD) Spectrometer (Peltier-based temperature control) for precise structural analysis, Horiba Dynamic Light Scattering (DLS) for quick and reliable molecular size characterization and zeta potential measurements, Bruker Alpha FT-IR Spectrometer for detailed infrared spectroscopy Advanced Fluorimeters for sensitive fluorescence measurements. Our comprehensive suite of instruments ensures that scientists can perform high-quality experiments and gather valuable insights into their biomolecular research. Recently, we have bought DeNovix spectrofluorimeter, a dual instrument that combines UV-Vis spectrophotometry and fluorescence measurements in a single device, typically designed for biomolecule quantification.

Achievements of the year

Our work has been well-received in research council (RC) presentations and posters by various research groups at CCMB and other academic research institutes and universities across India. Some of the research studies conducted at our facility have already been published in reputed journals suchas JACS, eLife, Small methods etc with more results and outcomes expected in the near future. Additionally, we have signed Memorandums of Understanding (MOUs) with prominent companies to collaborate on biomaterial characterization and interaction studies. Through our AnalytiCSIR initiative, we also offer instrument access in partnership with the business development group, creating a source for revenue generation.

Facility staff

Shiv Pratap Singh Yadav, Scientist
R. Phanindranath, Sr. Technical Officer (2)



Instruments in the facility and Various training programs and activities through out the year



From left to right: R Phanindranath, Janesh Kumar, Shiv Pratap Singh Yadav

BSL2 / BSL3

The BSL-2/3 facility at CSIR-CCMB provides a secure and well-equipped environment for handling high-risk pathogens and supporting advanced infectious disease research. The facility enables work with a range of bacterial, viral, and parasitic organisms and adheres to all national biosafety and biosecurity standards.

Organisms Handled:

Mycobacterium tuberculosis H37Ra
Mycobacterium bovis BCG
Mycobacterium smegmatis
Helicobacter pylori
Hepatitis C Virus (HCV)
Japanese Encephalitis Virus (JEV)
Dengue Virus
Lentivirus
Plasmodium falciparum
Plasmodium berghei
Plasmodium yoelii
Plasmodium chabaudi
Toxoplasma gondii
Mycobacterium tuberculosis H37Rv
SARS-CoV-2
Kyasanur Forest Disease Virus (KFDV)

List of equipment

- Biosafety Class-II B2 and A2 Type Cabinets
- BECKMAN COULTER Avanti J-30I Bio-safe Centrifuge
- Biosafety Ultracentrifuge
- CO_2 Incubators (Thermo Scientific Reach-in, Sanyo)
- Deep Freezers and Biomedical Freezers (-30°C)
- Inverted Microscope and LightCycler 480 II/98 PCR System
- Eppendorf Vapo.protect Mastercycler
- Bio-Rad Gene Pulser Xcell
- Julabo TW 20 Water Bath
- Innova 40 Incubator Shaker Series, Roller Mode TE8
- Mini Bead Beater, Vortex-2 Genie
- Double- and Single-Door Autoclaves
- Invitrogen Countess Automated Cell Counter
- Weighing Machines and Electronic Balances
- Millipore Milli Vac Maxi
- Eppendorf Thermomixer Comfort
- Ultraspec 10 Cell Density Meter
- Refrigerators, Water Baths, and Shaker Incubators

Achievements of the year

- Supported multiple research projects from within CSIR-CCMB and external academic and research institutions.
- Facilitated high-impact studies on bacterial, viral, and parasitic pathogens.
- Contributed to national capacity building through training programs in biosafety and infectious disease research. A new extension of facility is established.

Facility staff

Amit Kumar , Techincal Officer

Animal Tissue Culture Facility

The Animal Cell Tissue Culture Facility is one of the institute's major facilities and serves more than 25 research groups interested in cell and developmental biology. The facility maintains many cancerous and non-cancerous mammalian cells and cellular models for cardiovascular, musculoskeletal and neurological disorders, as well as a repertoire of human and mouse stem cells from different origins. It also provides organoid models from iPSCs, particularly intestine and brain organoids, with conserved parental gene expression and retains the functional and biological characteristics of the parental cells.

In addition to providing routine training to facility users, we also conduct skill development programs periodically for researchers, students, and faculty members from different research institutes in India and abroad. These participants are trained in basic cell culture methods, such as maintaining cell lines, primary cell cultures, and hybridoma cell lines to produce monoclonal antibodies, transgene expressions in the host cells, establishing stable cell lines with transgene expression and cryopreservation of cells for long-term storage. Cell lines in the repository are authenticated by STR profiling and using Gene Mapper Software.

List of equipment

- Laminar flow hoods
- CO_2 water jacketed incubators
- FLoid imaging system
- Olympus fluorescence microscope
- Nucleofecter
- Liquid nitrogen tanks
- Deep freezers

Histology Facility

The various techniques and services provided are processing and sectioning of paraffin and frozen blocks of tissues. The faciliity has expert staff who helps in staining with special stains like Grocott Methenamine Silver (GMS) stain (a common technique used to identify fungi on tissue sections), Masson Trichrome stain (used to differentiate between collagen and smooth muscle in tumors and the increase of collagen in diseases such as cirrhosis), Van Gieson stain (to visualize elastin in tissues), Sirius Red stain (to visualize collagen and to study collagen networks in different tissues) and also routine staining like Hematoxylin & Eosin (for viewing cellular and tissue structure detail).

The facility also provides training to students and researchers for general tissue processing and histology study methodologies.

List of equipment

- Cryomicrotome - Leica ; Model no: CM 1950 with Ag Protect TM and U.V. protection
- Rotatory Microtomes: (a) Leica ; Model no: RM21 ; (b)Jinhua Yidi ; Model no: YD-355AT
- Tissue Embedding Station - Leica; Model no: EG1140 H/ C

Facility Staff:

Avinash Raj, Sr. Technical Officer (2)

Electron Microscopy Facility

The Electron Microscopy Facility (EM Facility) at the CSIR-CCMB is a cutting-edge, state-of-the-art facility established to uncover the hidden complexities of the living world, spanning from the organism level to the atomic structures of life's fundamental components. We provide a range of advanced services, including Single Particle Reconstruction, morphology analysis of cellular organelles, cell-cell interactions, host-pathogen interactions, exosome characterization, nanoparticle analysis, and Micro-ED. Since its establishment, the EM Facility has served numerous internal and external users, including pharmaceutical and biotechnology companies nationwide, thereby enhancing their research capabilities.

List of equipment

- Ultra-microtome Leica EM UC7 with FC7
- Thermo Scientific Vitrobot Mark IV
- Quorumtech New Gloqube plus
- Talos L120C Transmission Electron Microscope
- Talos Arctica Cryo-TEM
- S-3400N Scanning Electron Microscope
- Quorum Q150T Sputter Coater

Facility staff

Ravikumar Reddi, Scientist
A Harikrishna, Senior Technical Officer
Sandeep Shrivastava, Sr. Technical Officer
Amol Mandlik, Technical Officer



1) Talos Arctica Cryo-TEM, 2) Talos L120C TEM, 3) S-3400N SEM, 4) Vitrobot Mark IV, 5) Ultra-microtome Leica EM UC7 with FC7, 6) Quorumtech New Gloqube plus, 7) Quorum Q150T Sputter Coater, 8) Turbo-Pumped Thermal Evaporator



From left to right: K. Sanjeev Kumar, Ravikumar Reddi, A. Harikrishna, Sandeep Srivastava, Amol Mandlik

Flow Cytometry

The FACS facility is used to measure the multi-parameters which are expressed by a single, multiple cells or particles on the basis of differences in their light scattering and fluorescence properties. The facility has been used in CSIR-CCMB to analyse and high speed sterile sorted cells for further cultures or isolate nucleic acids /proteins. The facility provides training to their students/project staff as well as support in designing and analysis of experiments to all investigators in the institute and to the local scientific community. FACS is being used more and more frequently by various research groups such as working in Cell biology, Stem cell biology and Infection biology, and offers completely new possibilities for the analysis and purification of cells and cell organelles by sterile sorting. These groups are supported and guided in the planning and carrying out of experiments as well as the subsequent analysis.

List of equipment

- Gallios (Flow cytometry analyzer with 405nm,488nm,640nm Lasers) Beckman Coulter 2016 Cell cycle, ROS, Cell Viability, Apoptosis, Immuno fluorescence of different markers, Stem cell marker analysis and all Cell biology assays including Fluorescence proteins analysis up to 10 colours and 12 parameters
- LSR Fortessa with HTS (96 plate reader) (Flow cytometry analyzer with 488nm,561nm,640nm Lasers) Becton & Dickinson 2017
- Cell cycle, ROS, Cell Viability, Apoptosis, Immuno fluorescence of different markers, Stem cell marker analysis and all Cell biology assays including Fluorescence protein analysis up to 10 colours and 12 parameters
- MoFlo XDP (High speed Cell sorter with 351nm, 488nm, 640nm Lasers) Beckman Coulter 2015
- Flow cytometer for Single cell sorting into 96,384,1536 well plates, Cell cycle, Side population sorting, four-way sorting, Multi-colour analysis, and Fluorescence proteins based sorting up to 10 colours / 12 parameters (with Sterile sorting and Temperature control)
- Aria Fussion (High speed Cell sorter with 405nm,488nm,561nm,640nm Lasers) Becton & Dickinson 2019
- Flow cytometer for Single cell index sorting into 96, 384, 1500 well plates, Cell cycle, Side population sorting, four-way sorting, Multi-colour analysis, and Fluorescence proteins based sorting up to 10 colours / 12 parameters (with sterile sorting and temperature control)

Facility staff

G. Srinivas, Sr. Technical Officer (2)

Fly Lab

The fly facility offers a great collection of *Drosophila* strains either with mutations or tools for their perturbation. This facilitates detailed molecular analysis of tissue functions like the brain and muscles, including the context of inherited disease-like conditions. These are supported with a large and efficient setup in which to grow and manipulate flies.

List of equipment

We are equipped with over a dozen fly stations (stereoscopes and CO_2 supply), six incubators to hold animals at different temperatures, the climate controlled stock room; a fluorescent stereomicroscope with attached 20MP camera with staking capabilities, an embryo injection setup, a fully equipped behavior room with illumination control geared towards mobility, learning and memory studies at all stages of fly development. The support facility called Nectar is devoted to satisfying user requirement of food formulations in different formats exclusively with RO water.

This is possible because of automated fly food preparation and dispensing, ovens for drying food and cold cabinets for storage and autoclaves for sterilization and disposal. In short, the facility can cater to the detailed requirement of experimental design of any throughput.

Achievements of the year

Apart from catering to the substantial needs at CSIR-CCMB, we provide service to other universities/institutes. Students and teaching staff from different national and international universities visit the Fly Lab to get a hands-on experience of *Drosophila melanogaster* culture and maintenance. The Fly Lab also provides flies to different colleges in the city for teaching purposes and various strains to other research institutes in India for research purposes.

Facility staff

V. Bharathi, Principal Technical Officer





High Performance Computing Facility

The high-performance computing (HPC) facility of CCMB has been a vital resource for advancing genomic and structural biology research at CSIR-CCMB. It provides infrastructure support for large-scale genomic data analysis, processing CryoEM data, docking, molecular simulations, modeling, and curation of biological databases.

List of equipment

- Ramanujan Cluster: ~1500 CPU cores, >56000 GPU cores, 15 TB RAM, 1 PB PFS, computing power of >100 TFLOPS
- EpiHeD cluster: 280 CPU cores, 4.5TB RAM, 300TB storage, peak power of 5 TFLOPS
- Illumina DRAGEN server: Hardware acceleration for genomic data processing
- BioNano cluster: Dedicated computational resource to process Optical Genome Mapping data
- Total network attached storage: 3PB+

Achievements of the year

- Procurement of two GPU nodes, increasing total GPU cores to >56000
- Upgradation of Ramanujan cluster storage to 1 petabyte
- Basecalling of population scale Oxford Nanopore data
- Processing of CryoEM data

Facility staff

Geetha Thanu
Aparna Kumari
Biswajit Roy
Computational Resources Committee: Dr Janesh Kumar, Dr Saikat Chowdhury, Dr Jahnavi Joshi, Dr Divya Tej Sowpati







Clockwise from top left: New Smart Data Centre, Ramanujan Cluster, EpiHeD Cluster

National Wildlife Genetic Resource Bank

Systematic collection and preservation of tissues, gonads, gametes, and development of cell lines of wild animals. These samples serve as a biological repository for conservation research and species management in the future.

List of equipment

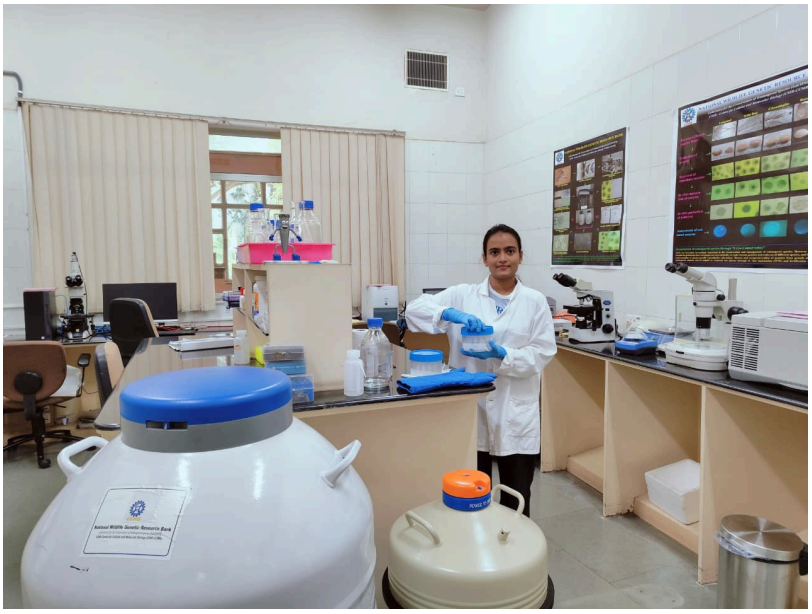
Biosafety cabinets, CO_2 incubators, -70°C freezers, liquid nitrogen containers for storage of biological samples, compound microscopes, inverted fluorescent microscopes, fluorescent upright microscope, stereo zoom microscopes, refrigerated centrifuge, veterinary blood biochemistry analyzer, and computer-assisted sperm analyzer.

Achievements of the year

To set up the regional biobanks in Indian zoos, CCMB signed MOUs with Padmaja Naidu Himalayan Zoological Park (PNHZP), Darjeeling, West Bengal, and Nandankanan Zoological Park, Bhubaneswar, Odisha. Mentoring the zoos in the establishment and operation of biobanks. PNHZP is the first zoo in India to have a biobanking facility. To raise awareness about biobanking, we trained the field staff of Maharashtra and Chhattisgarh forest departments on sample collection in a one-day workshop organized by Indravathi Tiger Reserve, Bijapur, Chhattisgarh. We delivered a talk on biobanking in a workshop conducted for Indian zoo biologists at Indira Gandhi Zoological Park, Andhra Pradesh. Testicular tissue of wild-caught sloth bear (*Melurus ursinus*) collected post-mortem was cryopreserved. Cell lines of tiger (*Panthera tigris*), lion (*Panthera leo*), and leopard (*Panthera pardus*) were shared with the National Centre for Biological Sciences, Bengaluru, for conservation research on big cats; these cell lines were developed previously from the tissues collected post-mortem at Nehru Zoological Park, Hyderabad.

Facility staff

B Sambasiva Rao
Shubhalakshmi Swain



Next Generation Sequencing Facility

The Next Generation Sequencing (NGS) facility at CSIR-CCMB is a state-of-the-art genomics facility that caters to all internal research groups at the institute, and also plays a key role in successful implementation of large scale genomics projects of national importance. Sequencing is also offered as a service to other researchers outside the institute and private companies.

List of equipment

- Illumina NovaSeq 6000: An ultra high throughput short read sequencer, generating as much as 3 Terabases (3 trillion bases) of data per flowcell, and 20 billion paired end reads of up to 150nt. This translates to approximately 30 full human genomes. This sequencer has been instrumental in powering our population-scale genomics projects such as the Genome India project and the Indian Breast Cancer Genome Atlas.

- MGISEQ 2000: A medium throughput short read sequencer which generates up to 480 Gigabases of data per flowcell. It is typically used for whole transcriptome and whole exome sequencing, and has been a key resource for our clinical genomics facility.

- Oxford Nanopore PromethION: A high throughput long read sequencer capable of generating 100 gigabases of data per flowcell, and can run 24 flowcells in parallel. Reads are typically in the range of 15-100 kilobases in length. PromethION comes with its own data analysis tower, which is powered by dual Nvidia A100 GPUs. We are utilizing this to sequence human genomes for better analysis of large variations known as Structural Variants.

- Oxford Nanopore GridION: A lower throughput long read sequencer from Oxford Nanopore, capable of running 5 flowcells at once, and each flowcell generating up to 30 gigabases of data. This sequencer is used for metagenomic studies, base modification detection, and direct RNA sequencing.

- BioNano Saphyr: An optical genome mapper, which generates data for detection or large chromosomal changes and structural variants, particularly in heterogeneous samples such as leukemias. The data is also useful for accurate assembly of large vertebrate genomes. The machine can generate data for up to 3 samples in parallel.

- In addition to the above machines, the facility harbors liquid handlers (Tecan, MGI, Mosquito, and Dragonfly) that enable fast, automated sample processing that minimize hands-on time as well as improve reproducibility.

Achievements of the year

The facility was instrumental in successfully implementing wastewater surveillance to detect pathogens of public health concern. Wastewater surveillance can guide public health interventions to slow down or stop the spread of infectious diseases, especially when associated with seasonal changes. The facility is powering the WGS and transcriptome data generation in the Indian Breast Cancer Genome Atlas project, which is using a multi-omic approach to delineate the molecular signatures of breast cancers in Indians. It has contributed significantly to the Indian tuberculosis sequencing consortium (InTGS), a nationwide initiative to map the clinical strains, diversity, and antimicrobial resistance patterns of

Mycobacterium tuberculosis in India.

In addition, the NGS facility has contributed to various omics related projects of researchers within CSIR-CCMB and other research institutes and universities.

Facility staff

Md Jafurulla
Sreenivas Ara
Tulasi Nagabandi
Kanakavalli Prakash
Valli Undamatla
Sangepu Jyothi
Balakrishna T



From left to right: Sreenivas, Valli, Jyothi, Tej, Karthik, Jafri, Tulasi, Balakrishna



List of equipment (from top left to bottom right): Illumina NovaSeq 6000, Oxford Nanopore GridION, MGISEQ 2000, Oxford Nanopore PromethION, BioNano Saphyr, Tecan Liquid Handler

Nuclear Magnetic Resonance Facility

The facility is useful to perform structural studies of dynamic biomolecules that are difficult to crystallize (e.g., multi-domain proteins, and majorly disordered proteins). The spectrometer is routinely used to derive biologically relevant conformational flexibility of proteins and nucleic acids *in situ*.

List of equipment

600 MHz NMR Spectrometer equipped with cryogenically cooled CP-TCI probe and a four-channel transreceivers and dedicated amplifiers for 1H, 13C, 15N, and 2H NMR of biomolecular samples such as nucleic acids and proteins.



The 600 MHz NMR Spectrometer

Achievements of the year

Published over seven articles in journals like: Biomolecular NMR Assignments, Biophysical Chemistry, ACS Pharmacology & Translational Science (in collaboration with CSIR - IICB), eLife and the Journal of the American Chemical Society.

Facility staff

Mandar V. Deshmukh



(from left to right) NMR Magnet, Mandar, and the electronic console.

Proteomics Facility

Mass spectrometry (MS) based proteomics is fast becoming an essential analytical tool for biological scientists. Modern instrumentation and data analysis software can identify and quantify hundreds or thousands of proteins from complex biological mixtures such as cell lysates or body fluids. At CSIR-CCMB, we are equipped with state-of-the-art chromatography systems and mass spectrometers for LC-MS and LC-MS/MS, with a wide range of bioinformatic tools for data interpretation and evaluation. The facility provides a range of services, including:

- Intact molecular weight measurement of proteins
- Protein identification from gel bands
- Protein identification from complex mixtures
- Identification of post-translational modifications
- SILAC, iTRAQ, and label-free quantification of peptides and proteins

List of equipment

Our instrument platforms include cutting-edge Orbitrap Exploris 240, Q-Exactive-HF, Q-Exactive, QTRAP 6500+, and MALDI TOF/TOF mass spectrometers, coupled to ultra-high performance EASY-nLC 1200 Systems.

We also have multiple High Performance Liquid Chromatography (HPLC) instruments. These analytical instruments are routinely used for separation and quantification of mixture of proteins/chemical compounds derived either from natural products or synthetic processes. HPLC-facility offers viable solutions due to vast choice of stationary phases and mobile phase options. The different modes and choice of detectors allows analysis of wide range of samples.

Achievements of the year

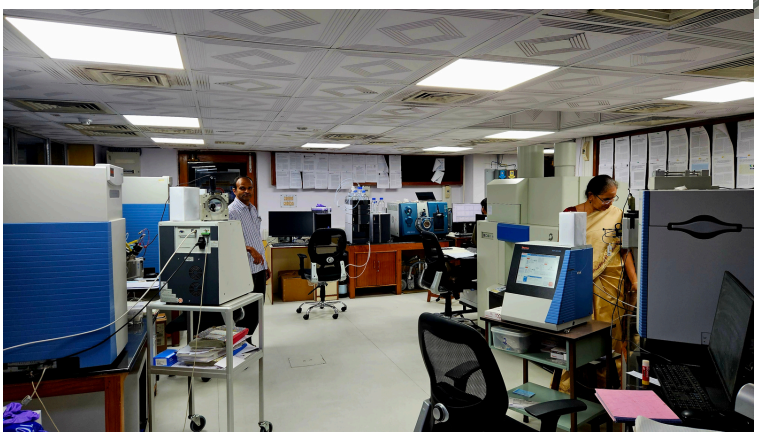
In addition to catering internal users in CSIR-CCMB, we provide mass spectrometry-based proteomics services to external users including many government-funded or private research labs as well as to biotechnology industry.

Facility staff

Y. Kameshwari, Principal Technical Officer
B. Raman, Principal Technical Officer
K. Ranjith Kumar, Technical Assistant



From left to right: Raman, Swasti, Ranjith, Kameswari



Mass spectrometers in the facility

Radioisotope Facility

The facility offers procurement, usage, storage, disbursement of radioisotopes from BRIT and BARC to the institute.

Safety precautions are followed during usage and disposal.

List of equipment

- Geiger-Müller counter
- Radiation survey meter
- A phosphor Imager (a digital instrument used to detect and quantify radioactivity in a sample by scanning a phosphor screen).

Achievements of the year

We use unsealed source for our research purpose. Phosphorus-32 is a commonly used radio nuclide with a half-life of 14.3 days, emitting beta particles with a maximum energy of 1.71 MeV (Million Electron Volts). The beta particles travel a maximum of 20 feet in air at maximum energy. We have separate Storage, Usage room and Hood allocated by AERB at CSIR-CCMB. We use very low concentrations of activities of 0.25 and 0.5 millicuries for our studies.

Short-lived waste is normally held for radioactive decay by Radiation Safety procedures. Following decay for a time period of 10 radioactive half-lives, the waste is monitored for the presence of residual radioactivity. If no residual radioactivity is detected the waste was disposed of as non-radioactive. Containers used to store short-lived waste was returned to the authorized user after disposal of the contents.

Disposal of liquid waste is typically performed using the following methods as appropriate for the isotopes, concentration, and form:
Consolidate compatible materials,
Sample and analyse for isotope/quantity,
Hold materials for radioactive decay, and discard after three or six months. Release liquids with radioactivity levels below the ALARA action levels.

Training is provided to the personnel whosoever are handling radioactive sources for their experiments, TLD badges are worn by the users to detect their exposure. These TLD badges are exchanged for every three months from AVANTTEC Laboratories. Procurement of source is done after approval of NOC from AERB. Safety precautions and disposal are followed as per the rules of AERB.

Facility staff

Dr. P. Shobha Krupa Rani, Sr. Prl. Scientist



X-Ray Crystallography - SAXS & Crystallization

X-ray facility is part of Integrative Structural Biology at CSIR-CCMB that provides state-of-the-art resources for structure-function characterization of macromolecules and their complexes.

List of equipment

It is equipped with powerful microfocus rotating anode generators: 1) MicroMax™ 007 HF (Rigaku) Cu anode generator with Mar345-dtb image plate detector and Oxford cryosystem 2) FR-E+ SuperBright (Rigaku) dual wavelength Cu/Cr anode generators with R-axis IV++ image plate detector and X-stream cryosystem. FR-E+ system is the most intense home lab source available for macromolecular crystallography, with focusing optics that can deliver a flux comparable to second generation synchrotron beamlines. Data collected from single crystal diffraction is processed using crystallographic computational software to elucidate three dimensional structures of macromolecules and their complexes at atomic level. Molecular-modeling studies are performed using linux-based workstations.

High Throughput (HT) Crystallization

A state-of-the-art HT-Crystallization facility provides complete solution for crystallization of macromolecules. Mosquito and Oryx 4 are automated liquid handling robots used for crystallization drop setting by accurately dispensing protein and precipitant solutions into crystallization plates. Users program the robots via software to define the drop volumes, concentrations, plate layouts, and any additives, such as seed stocks or other reagents, for screening and optimization. Incubators set to 4°C and 20°C are used for crystallization screening and storage to optimize crystal formation by allowing for experimentation at different temperatures. Microscopes with a polariser for the inspection of crystal growth. The facility is supported by dynamic light scattering (DLS, NaBiTech) equipment, a useful tool to diagnose size distribution, stability, and aggregation state of macromolecules in solution prior to crystallization.

Small Angle X-ray Scattering SAXS

The X-ray facility is also equipped with Small Angle X-ray Scattering (SAXS) System, BioSAXS-2000 (Rigaku) with 2-D Kratky collimation, mounted on the existing left port of MicroMax™ 007 HF Cu anode X-ray generator, for deciphering physical and structural features of macromolecules in solution. It is equipped with OptiSAXS Confocal Max-Flux (CMF) for higher brilliance at the sample position and data collection times in the range of minutes. The configuration incorporates an Automatic Sample Changer for unattended overnight operation and an Automatic Analysis Pipeline based on ATSAS package from EMBL Hamburg.

SAXS allows to probe size, shape, quarternary structure and complex formation of molecules without crystallization. It helps in understanding (i) structural parameters [radius of gyration (Rg), maximum Dimension (Dmax), partial-specific volume (Vp) etc], (ii) dynamics of molecules and (iii) generation of low-resolution shapes of macromolecules.

Several structural biology projects from CCMB and other research institutes / universities outside CCMB are handled at these facilities.

Facility staff

Integrative Structural Biology Facility Chairman: Janesh Kumar, Sr Principal Scientist

X-ray facility staff:

R. Rukmini, Principal Technical Officer (facility incharge)
K. Mallesham, Sr Technical Officer (1)

Instrumentation staff:
Amol Mandlik, Technical Assistant



From left to right: Amol Mandlik, K. Mallesham and R. Rukmini

Transgenic and Gene Knock Out Facility

The Transgenic and Gene Knock-Out Facility was established to create, procure, and maintain transgenic and gene knock-out mice models. Gene targeting in embryonic stem cells, micromanipulation, and survival surgeries are performed in this facility. The facility generates transgenic animals by pronuclear injections into F1 embryos. The facility generates targeted ES cell lines, which are used in blastocyst injection experiments to generate gene knock mice models. This includes designing the vectors, CRISPR-based gene editing, microinjection, genotyping, and breeding of the gene-edited mice. The facility supports many research groups in CSIR-CCMB in generating transgenic and knock mice for their research. It also provides technical help for phenotype analysis of transgenic and gene knock-out mice. The facility provides extensive hands on training in transgenic and gene knockout technology for users from other institutions.

List of equipment

Micromanipulators, Nepa-gene electro-porator, surgery hoods, Tri-gas incubator

Achievements of the year

- The facility generated chimeric embryos by morula injection.
- The facility has established ES cell-morula injection SOPs to generate chimeric embryos capable of contributing to trophoblast lineage.

Facility staff

S Purnima Sailasree, Sr. Technical Officer
Asha Kumari, Sr. Technical Officer



Zebrafish Facility

State-of-the-art Zebrafish facility is equipped with large-scale breeding & embryo collection capacities, live feed (artemia) hatching facility, and centralized air facility. Advanced automated standalone systems maintain transgenic lines for developmental biology, toxicology, cell biology, and behavioral studies. The facility is also equipped with a micromanipulation system and trained staff to help researchers generate transgenic fish and perform genetic manipulations.

List of equipment

The stock room has been reorganized to house all the stock transgenic lines and wild type strains of the facility. The molecular biology room has been remodelled into light dark and temperature controlled room to house adult zebrafish. Each of these housing rooms are equipped with aeration and pump systems.

Achievements of the year

The facility has completed civil, electrical renovations and caters to the needs of different research groups of CCMB and Collaborative projects of various institutes (CDFD, LVPEI). Apart from providing staged embryos and adult fishes for research, we also help users with micromanipulation to generate and maintain desired transgenic fish lines. Recently, an industry collaboration has been initiated with SSS, Sweden and its Indian counterpart to determine the ecotoxicological impact of industrial byproducts which are disposed of in the industrial waste water.

Facility staff

Megha Kumar, Sr Scientist
M.L. Arvinda Swamy, Sr Technical Officer



(from left to right): Arvind M. L. Swamy, G. Raju, G. Nagesh



Snapshots of the zebrafish facility





1.1D
Research Resources



Instrumentation

The Instrumentation Group at CSIR-CCMB plays a vital role in ensuring the seamless functioning of Rs 250 crores worth of scientific instruments through its strong technical expertise and dedicated support. The team provides comprehensive technical support for the installation, maintenance, and repair of scientific instruments across three campuses of CCMB. The group ensures the smooth functioning of core research facilities by undertaking in-house servicing of instruments, thereby minimising dependence on external annual maintenance contracts (AMCs). With proven expertise in troubleshooting, repairing instruments and electronic circuit boards down to the component level—often by sourcing parts from the local market—the group has been instrumental in reducing equipment downtime and achieving significant cost savings. In addition to maintaining scientific instruments, the group is responsible for the upkeep of UPS systems and audio-visual projection facilities.

The group supports scientists in the procurement of new equipment by drafting technical specifications and preparing detailed technical evaluation reports of bids.

The group further contributes by undertaking in-house design, development, modification, and fabrication of instruments as required, and by extending technical advice to other institutes regarding the procurement and usage of scientific equipment.

Capacity-building is an important mandate of the group. Orientation and training programs on the basic principles, safe and effective use of instruments are conducted annually for new research scholars, with additional sessions organised for research staff throughout the year.

The group support extends to major institutional events such as symposia, seminars, workshops, CCMB Open Day, and other academic programs, particularly by providing audio-visual and UPS support.

Through these multifaceted activities, the Instrumentation Group ensures that CCMB's state-of-the-art facilities and scientific instruments in individual labs are managed efficiently, with minimal downtime, thereby enabling uninterrupted research operations.



From left to Right: Manoj Hanumant Pandhram, Sajid Ahmad Shareef, Sudatt T Tambe, Dattatrya N. Gurukhel , Angothu Ramesh, A. Syam Kumar, K. Sanjeev Kumar, Amol Mandlik, N. Ravindra Chakravarthi, Chetan Khapekar, A. Bala Murugan, Devender Sundi, Vinod Kumar Yadav



Instrumentation facility / services for repair, maintenance, design of scientific equipment



Fine Biochemicals

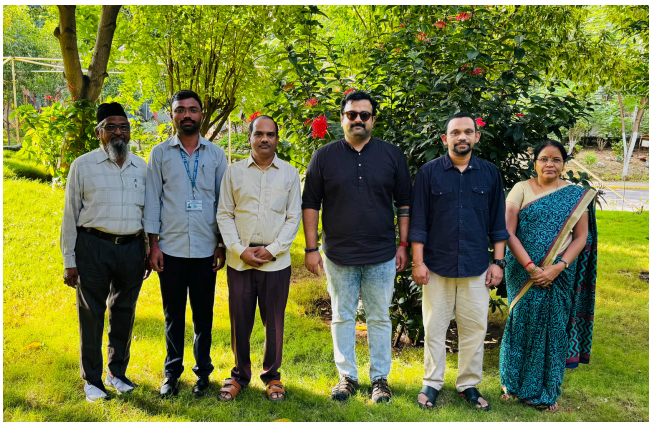
Our facility maintains critical chemicals, consumables and issues them all the research groups and facilities of CSIR-CCMB via an online software developed and maintained by the institute's IT department. We also receive, make entries and distribute consumables and chemicals ordered by various research groups in CSIR-CCMB. We are also involved in the storage and distribution of rectified spirit to the entire institute.

List of equipment

- Walk-in -20 Deep Freezer
- Walk-in Cold Room
- -20 Deep Freezer (Sanyo)
- Horizontal -80 Deep Freezer

Facility staff:

Sriram Varahan, Sr.Scientist, Facility In-Charge
T Avinash Raj, Senior Technical Officer
V Purushotham, Senior Technical Officer
Syed Sayeed Abdul, Technician
Santhosh Kumar, Technician



FBC Team (Left to Right): Syed Abdul, Santhosh Kumar, Avinash T, Sriram Varahan, Purushotham V, Radha



Fine Biochemicals Facility at CSIR-CCMB

Information Technology Group

The IT group looks after the IT infrastructure services and maintenance, and in-house software development.

Achievements of the year

The Information Technology Department plays a vital role in supporting research activities. The group actively maintained the complete IT infrastructure across the main campus and two annex campuses — entirely without any AMC support.

The laboratory's website, along with other portals including recruitment, e-portals, and online databases accessible over the Internet, were secured against hacking attempts and cyberattacks. All systems across campuses were continuously monitored and protected against data breaches to safeguard sensitive information from corruption, theft or unauthorized access.

The Data Centre, hosting the High-Performance Computing (HPC) systems and NAS & SAN storage servers, was efficiently maintained by the IT team. During the year, GPU servers were added, and storage capacity was significantly expanded, enhancing computing and storage capabilities.

At the LaCONES campus, the Wi-Fi network was expanded to cover all buildings, including hostels, and upgraded to centralized management by installing dedicated controllers.

New features were incorporated into existing in-house applications developed for CSIR-CCMB and CSIR, including CSIR-HRDG-EMR-II, CSIR-HRDG-ASPIRE, and CSIR-FIRST. In addition, several new applications were developed for managing various facilities during the year.

The IT team also maintained surveillance cameras, CCTV systems, fire alarms, biometric systems, BMS, and telephone networks across all three campuses. A few in-house applications were shared with CSIR-IIIM, CSIR-IGIB, CSIR-IICT and CSIR-IMTECH.

Facility staff

Geetha Thanu, Sublari Balaraju, Aparna Kumari, Biswajit Roy, Nagalinga Chary, Radhakrishna Murthy, Sambasiva Rao, Siva Rama Prasad, Padmavathi, Rama Chary, Sreekanth, Vishal Rasakatla



Server Room



Information Technology (IT) group

Laboratory Technical Services

The Lab Technical Services (LTS) in CCMB acts as a bridge between the scientific staff and the engineering Services. Thus it is the single contact point for them for all their needs that require involvement of engineers. Major services for which LTS sections attends to (i) House keeping, (ii) Manpower supply, (iii) Painting, (iv) Lifts, (v) Pest control services (vi) Horticulture, (vii) Arrangements include planning & coordination of various institutional events, conferences, workshops, meetings, etc.

The services of this group span across the CCMB main campus at Habsiguda, LaCONES, CCMB Annex1 at Attapur and Medical Biotechnology Complex, CCMB Annex-2 at Uppal.



Rajbhasha Unit

This unit helps the Institution mainly in complying with various provisions of Official Language envisage by the GOI. It provides training to the officials in Hindi, Hindi typing & stenography and also conducts Hindi workshops to its employees at regular intervals. This unit helps scientists in bringing out the papers, articles, reports in Hindi. The unit also ensures issue of official documents in Hindi as per the OL Act Provisions and also facilitates issuing of press releases and advertisements in Hindi.

This year marks the Golden Jubilee of the Rajbhasha Vibhag, MHA, GOI. To commemorate this significant milestone, a grand celebratory event was organized in Hyderabad, bringing together various Central Government departments, academic institutions, and research organizations. As part of the celebrations, the Centre for Cellular and Molecular Biology (CCMB) had the honor of participating in the event. The occasion served as a platform to recognize the contributions made by various institutions towards promoting the use of Hindi as the official language in government functioning, in alignment with the objectives of the Rajbhasha Vibhag. CCMB's active involvement reflected its commitment to Rajbhasha policies and to fostering inclusive communication in the scientific community.

Under Hindi Teaching Scheme, 09 staff members from various sections of CCMB were nominated for the 'Parangath' course during the year. The 'Parangath' level is an advanced course designed to enhance proficiency in Hindi, with a focus on vocabulary, grammar, translation, and official noting and drafting in Hindi. After successfully completing the course and passing the examinations, the trained staff members have been able to significantly contribute towards the implementation of the Official Language Policy at CCMB. Their enhanced proficiency in Hindi enables them to carry out official correspondence, documentation, and day-to-day administrative tasks in Hindi more effectively.

In alignment with the GOI's continuous efforts to monitor and enhance the implementation of the Official Language Policy, an inspection of official work related to Rajbhasha (Hindi) was conducted at the CCMB by Regional Implementation Office (Southern Region), Bangalore, functioning under the Department of Official Language, Ministry of Home Affairs.

Rajbhasha Unit conducts HINDI PAKHWADA in the month of September every year and various Hindi competitions and programs are organized during the occasion. This year Hindi Fortnight has been conducted from 23 Sep to 03 Oct. Various competitions were organized during that. This year, Hindi Book exhibition was also laid. The winners of the competitions were given away the prizes and cash awards were given to the officials who are doing their Official work in Hindi and contributing their part for the implementation of Hindi in the organization under Hindi Incentive scheme.

The unit regularly conducts Hindi workshops for the staff and Officers for training and upliftment of progressive usage of Hindi in the organization. Currently, we are conducting Hindi workshop in every quarter with the joint aegis of CSIR – CCMB, CSIR – IICT and CSIR - NGRI. Staff from all the three labs participate in the workshop. This brings staff of all the three labs under one roof and helps in building mutual relationship and communication among each other for the betterment and upliftment of the usage of Hindi in Official work towards effective implementation of Rajbhasha rules and policies. This year, we have conducted 04 one - day Hindi workshops.

The Unit provides opportunity to students and staff to show-case their cultural and literary talents by organising a programme named PRATIBHA. The main aim of PRATIBHA programme is to provide a platform to the inherent talents of research students and staff of CCMB. The programme is held annually, usually in the month of June-Jul. The programme mainly includes literary and cultural activities.

Apart from this Hindi section helps in translating all the necessary documents, Reports, Oms etc.. especially the documents falling under Rajbhasha Rule 1963, section 3(3). It also works towards the translation of Press notes and Press communiques.

The Rajbhasha Unit has a very rich library consisting 3337 Hindi Books on various subjects viz., classic works of Hindi literature, science, translations and books of general interest, personality development, etc. This year 77 books have been added to this collection. Thus, the Rajbhasha unit takes care of CCMB in respect of implementation of Official Language asprescribed by GOI time to time.







1.2 Academics



1.2A Academic Cell & PhD Program

The CCMB PhD Program is managed by the Academic Cell, which comprises an Academic Coordinator, In-Charge (Academic Cell), and an AcSIR Executive Assistant. The cell oversees all academic activities related to PhD students, including selection and recruitment, coursework coordination, laboratory allotment, Doctoral Advisory Committee (DAC) meetings, Comprehensive Examinations, and PhD thesis submission. It also maintains records of students' academic performance, progress reports, and all AcSIR-related documentation.

For the JNU-CCMB PhD Program, administrative matters are handled separately by the JNU-CCMB Committee.

PhD admissions at CSIR-CCMB are conducted twice a year, in January and August. Eligible candidates are shortlisted through a written test, followed by two rounds of interviews held at CCMB. Applications are invited through CCMB-AcSIR.

Since its inception, CSIR-CCMB has produced 499 PhD graduates. The program aims to train students for research careers in interdisciplinary areas within and beyond academia, providing a strong technical foundation, fostering analytical thinking, and preparing them to address emerging scientific challenges for the benefit of science and society.

During 2024-25, 10 students joined the PhD program in August 2024 and 8 students in January 2025. As of March 2025, there are 146 PhD students on roll. During this period, 13 students presented their PhD colloquia, 19 students submitted their theses, and 24 students were awarded the PhD degree under JNU/AcSIR.



1.2B PhDs Awarded

List of students awarded with PhD degrees during April 2024 to March 2025

P. Sai Uday Kiran
Understanding $Ca2^{+}$ Induced Functional Diversity of Calcium-binding Proteins (19.04.2024)
Guide: Yogendra Sharma / R. Sankaranarayanan

Deepti Rao
Functional Analysis of Rice Genome Sequences: Samba Mahsuri and its Related Line (30.04.2024)
Guide: Imran Siddiqi / Ramesh V. Sonti

S. Purnima Sailasree
Regulation of cell fate choice by FGFBP1 in early mouse development and pluripotent cells (15.05.2024)
Guide: P. Chandra Shekhar

Sachin Singh
Elucidating Neurometabolic and Molecular Mechanisms in Metabolic Disorder Induced Neuropsychiatric Disorders (24.05.2024)
Guide: Arvind Kumar

S. Soujanya
Investigating the role of vertebrate GAGA factor in genome organization during myogenesis (30.05.2024)
Guide: Rakesh Mishra

Aute Ramdas Annasaheb
Structural and functional insights of dsRNA binding proteins and Dicer interaction domains in Drosophila RNAi pathway (23.07.2024)
Guide: Mandar V. Deshmukh

Sitanshu Kumar Sarangi
Understanding killer cell immunoglobulin-like receptor signaling in human natural killer cells (26.07.2024)
Guide: Santosh Kumar

Ravi Kumar Singh
Study of Gharial (Gavialis gangeticus) population in Chambal River, India, using biotechnological approaches (02.09.2024)
Guide: Karthikeyan Vasudevan

Priyanka Pant
Exploration of the regulatory functions of long non-coding RNAs in cardiac hypertrophy and failure (30.09.2024)
Guide: Regalla Kumaraswamy

Manu S
Exploration and Assessment of Biodiversity across the Tree of Life using Extracellular eDNA (14.10.2024)
Guide: G. Umapathy

R. Abishek Bharadhwaj
Long non-coding RNA TUG1 regulates smooth muscle cell differentiation in aortic aneurysm (28.11.2024)
Guide: Regalla Kumaraswamy

Annapoorna P. Karthyayani
Deciphering the role KDM7 and KDM4 families of histone lysine demethylases in depression (02.12.2024)
Guide: Arvind Kumar

G. Srinivas Reddy
Investigation of the roles of vacuole membrane protein 1 in apicomplexan parasites Plasmodium falciparum and Toxoplasma gondii (12.12.2024)
Guide: Puran Singh Sijwali

Harshit Vaish
Role of membranes in stress signaling and protein homeostasis (13.12.2024)
Guide: Swasti Raychaudhuri

P. Sivakumar
Sporophyte Directed Gametogenesis via the Ubiquitin Proteasome System in Arabidopsis (17.12.2024)
Guide: *Imran Siddiqi*

Pratheusa Machha
Endogamy and high prevalence of deleterious mutations in India: evidence from strong founder events (18.12.2024)
Guide: K. Thangaraj/ Divya Tej Sowpati

Aditya Undru
Investigating the molecular pathways in neuroprotection following hypoxic preconditioning in adult male Zebrafish (30.12.2024)
Guide: Arvind Kumar

Disha Nanda
To study the role of long intergenic noncoding RNA linc-p21 in fibroblast activation during cardiac fibrosis (07.01.2025)
Guide: Regalla Kumaraswamy

Yogita Kapoor
Investigating the role of DivIVA-domain containing proteins in mycobacterial growth and division (15.01.2025)
Guide: Vinay Nandicoori

Ananga Ghosh
Exosomes as modulators of muscle stem cell function during regeneration (27.01.2025)
Guide: *Jyotsna Dhawan*

Sara Sajjadi
Genetic and Epigenetic Basis of Vitamin D Mediated Fetal Programming of Cardiometabolic Phenotypes (07.02.2025)
Guide: *G.R. Chandak*

Jaydeep Paul
Structural and Functional Study of DRB3 in Plant RNAi (18.02.2025)
Guide: *Mandar V. Deshmukh*

Ravina Saini
Mechanism of Transgenerational Epigenetic Inheritance in *Drosophila melanogaster* (28.02.2025)
Guide: *Rakesh Mishra*

A S Priti
Understanding centrosome-ciliary dynamics in regulation of cell cycle arrest (10.03.2025)
Guide: *Jyotsna Dhawan*

1.2C Training Programs

Dissertation Research Training Program (DRTP)

CCMB offers an interdisciplinary program for M.Sc/ M.Pharm/ M.Tech/ MD/ B.Pharm/ BDS/ B.Tech students to do six or twelve-month research projects. Applications are invited online only (www.ccmb.res.in > Academics > Training Programs > Dissertation Research Training Program) throughout the year. The students must work under the supervision of a scientist at CSIR-CCMB to complete a small research project as part of their partial fulfilment of the academic degree. The program offers one-week lectures on good laboratory practices, biosafety, research methodology, scientific writing, research ethics, recent research developments, and career opportunities in the life sciences. Student visits are organised to other annexes of CSIR-CCMB as part of training. After completing their research, students must present a poster to the CSIR-CCMB scientific community. After submitting the dissertation report, they will receive a certificate. Since we receive many applications, a stringent selection criterion will be applied to select the students. In 2024-2025, 60 students completed dissertation research training in CSIR-CCMB.

Project-based Student Training Program (PBST)

This program encourages students who have completed their studies in M.Sc/ M.Pharm/ M.Tech/ MD/ B.Pharm/ BDS/ B.Tech/ MBBS and would like to spend time learning and improving their laboratory skills. Unlike the dissertation research training program, students can choose their supervisor based on their research interest and take their consent to work in their laboratory for six months, with the training extendable to one year. The extension will be based on their research progress, and they will submit their application online (www.ccmb.res.in > academics > training programs > project-based student training program). The program also offers one-week lectures on good laboratory practices, biosafety, research methodology, scientific writing, research ethics, recent research developments and career opportunities in life sciences. In the 2024-25 academic year, 38 students benefited from the program.

Summer Training Program

The program is open to students from all branches of life sciences studying at any Indian university, college, or research institute. However, the program is offered to students who are still pursuing their studies. M.Sc/ M.Tech students who completed at least two semesters, B.Tech/ B.Pharm students who completed six semesters, and integrated B.Tech-M.Tech/ B.Sc-M.Sc students who completed eight semesters, MBBS/ BDS students in any year of their study and B.Sc. Biosciences (4-year program) students who have completed six semesters are eligible to apply. The training tenure is 60 days, from May to July, every year. Online applications (www.ccmb.res.in > Academics > Training Programs > Summer Training Program) are invited through a notification in March of every year. Selected students will be assigned to a CCMB staff scientist who will mentor them in executing small project work. A lecture series on scientific ethics, good laboratory practices and opportunities in life sciences will be organised for the students. At the end of the program, students must submit a 'Project Report' of the work done and are also required to make a poster presentation to the CCMB scientific community. The program primarily aims to provide students with real-time exposure/ hands-on experience in research. In 2024, we accommodated 43 students, including four students sponsored by the Indian Academy of Sciences and IISc.

Team: A.S. Sreedhar, C. B. Tripura, V. Anitha

Skill / Training Development Program

CSIR-CCMB has been conducting its Skilling/Training Programs under the CSIR-Integrated Skill Initiative since 2017 with a view to cater to both academia and industry needs. These programs target students and employees from government labs/ institutes, industries, hospitals, pathology laboratories, universities. In general, for each training program, as per the course curriculum, 20% theory and 80% practical sessions are conducted. Provision of hand-out information on teaching modules, tutorials (personal attention), multimedia-assisted lectures, central facility visits within the laboratory and evaluation by assignments are held. A certificate is issued to the successful candidates.

Skill Development Program 2024-25

	Course code	Training Date	Fee/sponsored	Name of the Course	No. Of Participants
1	FACS-1	10th -14th Jun 2024	Fee-based	Basics of Flow Cytometry	6
2	RECOMB-4	1ST TO 16TH JULY 2024	Fee-based	Molecular Cloning and Protein Expression	11
3	eDNA-1	23rd -27th Jul 2024	Fee-based	Environmental DNA (eDNA) and its applications	9
4	WBE-1	29th Jul - 3rd Aug 2024	Sponsored	Molecular approaches towards Pathogen & AMR Detection in Wastewater	16
5	NANO-2	5th -9th Aug 2024	Fee-based	Nanotechnology and Biodiagnostics	13
6	GMMA1	26st - 31st Aug 2024	Fee-based	Genetic and Microbial Monitoring of Animals	9
7	BTACC- 5	2nd to 6th September 2024	Fee-based	"Basic Techniques in Animal Cell Culture"	6
8	DNAMB	15th to 18th October 2024	Fee-based	DNA Metabarcoding Workshop	22
9	MTSTD	4th to 7th November 2024	Semi-Sponsored	Muscling Through Species to Treating Diseases	15
10	BIOPHY-1	18th to 22nd November 2024	Fee-based	Advanced Biophysical tools for Protein-DNA/Bimolecular Interactions	5
11	MedSRT-4	16th to 28th Dec 2024	non-Fee-based	Medical Students Research Training (MedSRT-4)	30
12	IPRPAT-2	08th to 10th Jan 2025	Fee-based	Introduction to IPR and Patents	12
13	NMRbM	27th to 31st Jan 2025	Fee-based	NMR - based Metabolomics	12
14	FDP	17th to 28th Feb 2025	Non-Fee-based	FDP on "Basic Techniques in Genetics & Molecular Biology"	14
15	WF-14	17th to 21st March 2025	Fee-based	"Wildlife DNA Forensics" (WF-14)	11
16	PROTEO-4	24th to 29th March 2025	Fee-based	LC-MS Based Proteomics	12
					203





1.3
Innovation Hub (iHUB)



1.3 A Services

Molecular and Chromosomal Diagnostics

CSIR-CCMB has offered dedicated diagnostic solutions for the last two decades, to address the significant burden of rare genetic disorders. The centre offers a full range of molecular and cytogenetic testing, including advanced Next-Generation Sequencing based tests to address conditions which, while individually uncommon, collectively represent a significant public health challenge.

Achievements of the year

CCMB provides diagnostic testing for a wide range of single-gene (monogenic) disorders. Using specialized techniques like TP-PCR, fragment analysis, and targeted gene sequencing (e.g., for the HBB gene), we identify or confirm the genetic cause of numerous conditions. The diseases covered include neuromuscular disorders, neurodegenerative diseases, cystic fibrosis, hereditary pancreatitis, and various haematological (blood-related) and metabolic disorders.

When symptoms present a medical puzzle, the answer is often hidden in our genes. Instead of searching for one specific genetic "typo" at a time, exome and genome sequencing tests act like a spell-check for your body's entire instruction manual. By examining 20,000 genes at once through exome test (1-2% of the whole genome) or the entire genome through whole genome sequencing, we offer a thorough way to understand the link between a person's DNA (genotype) and their symptoms (phenotype).

The facility also provides Optical Genome Mapping (OGM) test, an advanced cytogenetic technique for the high-resolution, genome-wide detection of structural variations (SVs). As a powerful alternative or complement to conventional methods, OGM is being adopted in clinical settings to more effectively identify a broad range of genomic abnormalities in both oncology and constitutional disorders, offering higher-resolution results that can uncover critical genetic anomalies other techniques might miss.

Altogether, 2902 patients from 2659 families have benefited from our testing services in the last financial year. In addition, we've improved our genetic services further by adding several new tests listed below.

FISH (Fluorescence *In Situ* Hybridization)

- Bcr-Abl Translocations
- DiGeorge, Kallmann, Miller-Dieckers, Prader-Willi, and William-Beuren Syndromes

MLPA (Multiplex Ligation-dependent Probe Amplification)

- Angelman Syndrome / Prader-Willi
- Beckwith-Wiedemann / Silver-Russell Syndrome
- Haemolytic Uremic Syndrome (HUS)
- Congenital Adrenal Hyperplasia

Other Specialized Tests

- Haemophilia A (Analysis for inversions in introns 1 and 22 of the Factor VIII gene)
- Biotinidase Deficiency

Facility staff:

T. Karthik Bharadwaj, Aneek Das Bhowmik, MK KanakaValli, Elizabeth Siby, Joel Kiran George, Vinay Mandaloji, Pratima Pal, Mounika Meher, Shreya R, Parvati A



From left to right, top row: Elizabeth Siby, Dr Aneek Das Bhowmik, Vinay Mandaloji, Joel Kiran George
Bottom row: T Karthik Bharadwaj, Pratima Pal, Mounika Meher, M K KanakaValli, Parvati A, Shreya R

Wildlife Diagnostics

The Universal Primer technology developed and patented by CSIR-CCMB allows identification of a biological specimen of unknown origin and delineates its utility to the level of family, genus and species. Wildlife DNA Forensics Laboratory at CRF campus of CSIR-CCMB, Hyderabad provides DNA-based species & individual identification, sexing, relatedness and rehabilitation services to the nation for the purpose of wildlife crime investigation. Biological specimens confiscated in wildlife related crime cases are forwarded by state forest, judiciary and police departments to Wildlife Forensics lab. Thus, CSIR-CCMB plays an important role in unambiguously identifying species involved in wildlife crime and illegal trade by providing reports to law enforcement agencies. Wildlife DNA forensics bring awareness and speed up reporting of crime involving poaching, illegal hunting and trade, thereby, speeding up justice process directly contributing to conservation of the endangered Indian species.

Achievements of the year

During the period (April 2024 – March 2025), we received a total of 279 wildlife crime cases for different analyses. More than 670 forwarded biological samples comprised of cooked/raw meat, skin, tusks, bones, claws, hair, feces, blood stains, saliva swabs and Hatha Jodi samples. During this period, a revenue of more than Rs. 45 lakhs was generated towards the DNA analysis fee charges.

We have been conducting regular training and hands-on-workshops on Wildlife DNA Forensics, as part of CSIR-Skill Development Initiative for skilling officers of forest, police, judiciary and other enforcement agencies on the use of DNA technology, its applications in detection of wildlife crime and proper collection, preservation and transportation of biological samples. We actively participate in capacity building programmes regularly conducted by Maharashtra Forest Department and Wildlife Crime Control Bureau.

- Conducted 5 days SDP/Hands on Trainings for skilling for 11 participants including graduate students, veterinarians, government officers from livestock department and private airports on DNA technology and its use in combating wildlife crime from 17th to 21st March 2025.

- Pallab Maiti, MSc. Biotechnology student of Department of Life Sciences and Biotechnology, South Asian University, New Delhi completed his Summer Internship on "Species Identification from Biological Samples Collected and Preserved on FTA Papers", from June-July 2024.

- Vaishnavi BK, MSc. Forensic Science student at National Forensic Science University, Goa completed her dissertation on "DNA-based species identification from biological samples of unknown origin", from February-July 2024.

Facility staff:
Ajay Gaur
Swati Chauhan
Deepanwita Purohit
OV Padmalatha
B. Kranthi
Raghvendra Babu
Stanley JB



From left to right: Deepanwita, Padmalatha, Ajay Gaur, Swati, Kranthi, Raghavendra, Stanley



A glimpse of hands-on session during the Skill Development Program on Wildlife Forensics conducted during March 2025

1.3B Atal Incubation Centre-CCMB

This year, the Atal Incubation Centre (AIC) at CCMB was not just a centre for innovation; it was a launchpad for the future of Indian biotechnology. From fostering early-stage student ideas to forging global partnerships, we transformed ambitious concepts into tangible, real-world solutions. This report captures a year defined by relentless entrepreneurship, strategic collaboration, and a strengthened commitment to building a world-class life sciences ecosystem.

Nurturing the Next Wave of Innovators

AIC-CCMB's core mission remains to identify and support high-impact ideas. Our tailored programs provided a robust pipeline for innovators at every stage, from initial concept to market-ready startups.

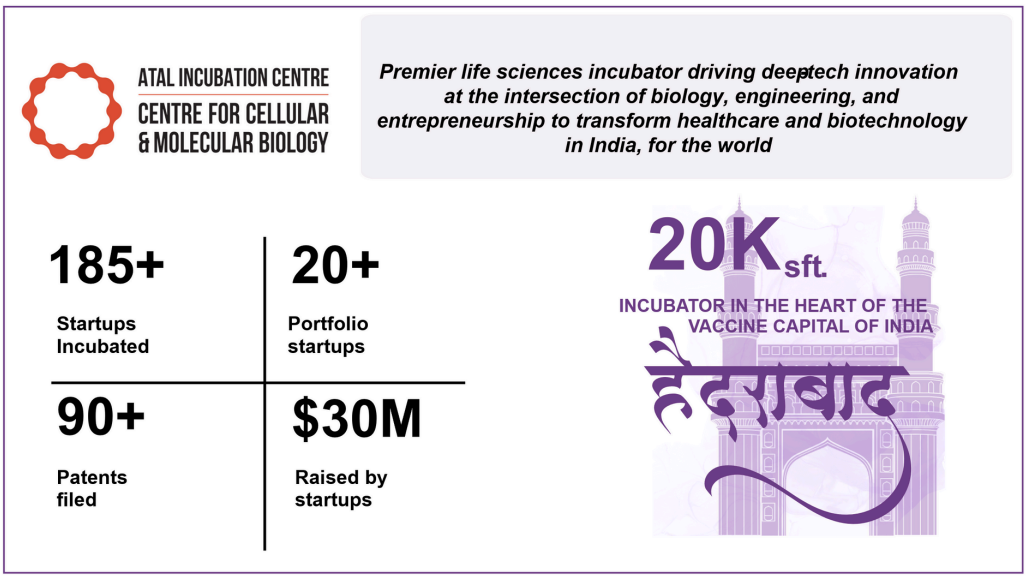
- **Café Mandala Propel:** AIC-CCMB's flagship knowledge sharing and networking event, Café Mandala took on a new avatar as the pitch event for our biotech startups. This showcase event provided a launchpad for passionate life science startups to pitch their ideas directly to investors, gaining invaluable feedback, mentorship, and exposure. We are happy to report that out 11 startups who pitched, one got funded.

Program Highlights and Capacity Building

- **NIDHI-PRAYAS (Cohort 2):** We continued to empower innovators to turn their ideas into working prototypes. This cohort received essential funding, infrastructure, and mentorship to develop practical solutions for real-world challenges in the life sciences sectors.

- **MeitY TIDE (Cohort 5):** Through the TIDE 2.0 scheme, we provided targeted support to technology startups, enabling them to refine their products and business models. This program underscored our efforts to integrate digital innovation into the biosciences ecosystem.

- **SIP Bootcamp:** In December 2024, we hosted a Student Innovator Program (SIP) Bootcamp for students from DPS Nacharam, DPS Miyapur, and CMR International School. The sessions focused on design thinking, business models, and pitching, concluding with a student prototype showcase.



Strategic Partnerships and Global Outreach

A cornerstone of our partnership strategy this year was the inauguration of the **Thermofisher Centre of Innovation**. This centre serves as a vital resource hub, providing our startups with critical access to advanced instrumentation and specialized training.



- **CSIR - Norway Delegation:** Dr. Nalam Rao, CEO of AIC-CCMB, joined a CSIR delegation to Norway to explore new opportunities for scientific collaboration and innovation partnerships with leading research institutions.

- **CSIR Innovation Centre- Mumbai Collaboration:** We joined hands with the newly inaugurated CSIR Innovation Centre in Mumbai. This partnership will strengthen the national innovation ecosystem through shared resources and joint programs focused on deep science ventures.

Building Bridges and Forging the Future

This year was marked by a significant expansion of our ecosystem, strengthening ties both locally and globally.

Ecosystem Engagements

- **ISBACON 2024:** The 16th annual conference of the Indian STEPs and Business Incubators Association (ISBA), hosted by AIC-CCMB along with CSIR – CCMB and IICTCCMB) in Hyderabad from October 17 to 19, 2024. It brought together over 250 delegates including startup incubators, investors, government representatives, industry experts, and thought leaders from across India.



Key discussions focused on the latest trends in startup incubation, investment opportunities, policy frameworks, and fostering collaboration between public and private sectors to drive Industry 5.0 in India.

- **TANDEM Connect (India-Germany Exchange):** In partnership with DWIH New Delhi and DAAD, we hosted an international immersion program to strengthen innovation exchange between Indian and German entrepreneurs through knowledge-sharing and networking.

- **Café Mandala CSR Conclave:** On January 20, 2025, we united CSR leaders from firms like **Apollo MedSkills, Cipla Foundation**, and **Cognizant** to explore corporate-driven social impact.

- **Enduring Excellence in Biological Research:** We were recognised for our contribution to the Telangana startup ecosystem by MATH AI @T-hub.

- **BFI-BIOME (Cohort 1):** This program accelerated biotech and health-tech innovation. The Fellowship Program at AIC-CCMB is focused on supporting researchers translating their leads to Proof of Concept. The first cohort included Dr. Ramdas Aute, Dr. Ashwathy Menon as well as Renovo Cell Biologics under the Kickstarter Program. The program provides for 9 months of fellowship stipend of Rs 50000/ month and ₹10 lakh in funding, incubation, and investor access to help them scale.

- **जंगli-IDEATHON** – This national-level competition by AIC-CCMB gained a lot of attention as it encouraged innovative solutions for wildlife conservation challenges. The competition aimed on themes such as Human-Animal Conflict, Anti-Poaching Technologies, Interactive Wildlife Tourism, and Deforestation Prevention. Participants, either individuals or teams of two (aged 18+), are invited to submit their innovative tech-enabled ideas that can address these pressing issues. It drew 33 entries, with top honours going to Noark Tech (₹75,000), and runners-up Debugging Earth (₹35,000) and Greenverz (₹35,000).



Centre for Predictive Human Model Systems (**CPHMS**) is India's first science and policy think-tank dedicated to advancing human-relevant models in biomedical research. Established in 2019 with support from Humana World for Animals, we focus on innovative technologies such as Microphysiological systems and computational biology.



In Bootcampswe trained researchers in emerging Microphysiological systems (MPS) technologies in Bangalore and Gujarat. An awareness session was also held for regulators at CDSCO, New Delhi, to advance non-animal testing methods, with the representatives of CDSCO,ICMR, DBT, CROs and Academia.



Follow us on LinkedIn, Facebook, Instagram and X for new calls and our activities.



2.1 Administration & Management



Research Council

Research Council of a laboratory under CSIR provides direction and vision and helps it to formulate R&D programmes keeping in view the national priorities and opportunity niches and facilitates to design a road map to achieve it. The following are the constituent members of the Research Council of CCMB:

Dr M Srinivas **Chairman**
Director
All India Institute of Medical Sciences
Ansari Nagar, New Delhi - 110029

Ms Deepanwita Chattopadhyay **Member**
Chairperson and CEO
IKP Knowledge Park
Genome Valley Hyderabad- 500101 &
Koramangala, Bengaluru

Prof Vidita A Vaidya **Member**
Professor and Chairperson
Department of Biological Sciences
Tata Institute of Fundamental Research
Homi Bhabha Road
Colaba, Mumbai - 400005

Prof Thomas Pucadyil **Member**
Professor (Biology)
Indian Institute of Science Education
and Research (IISER)
Dr Homi Bhabha Road, Pashan
Pune - 411008

Prof Praveen Karanth **Member**
Professor and Chairperson
Centre for Ecological Sciences
Indian Institute of Science
Bengaluru 560012

Dr Vaishali Panjabi **Agency representative**
Scientist 'F', Department of Biotechnology
Ministry of Science & Technology
Block 2, 7th Floor, Room no 708
CGO Complex, Lodhi Road
New Delhi 110003

Dr Sauvik Maiti **Sister Laboratory**
CSIR-Institute of Genomics and Integrative Biology
Sukhdev Vihar
Mathura Road, New Delhi - 110020

Dr Lalita Goyal **DG's representative**
Senior Principal Scientist
Technology Management Directorate
Council of Scientific & Industrial Research
Vigyan Suchna Bhawan (CSIR-NIScPR Building)
14, Satsang Vihar Marg
New Delhi - 110067

Dr Vinay K. Nandicoori **Laboratory Director**
Director
CSIR-Centre for Cellular and Molecular Biology
Hyderabad

Management Council

Following is the composition of the Management Council of CCMB for the period 01.01.2024 to 31.12.2025 as approved under Rule-65 of the CSIR Rules 7 Regulations:

Dr Vinay K. Nandicoori **Chairman**
Director
CSIR-Centre for Cellular & Molecular Biology
Hyderabad

Dr D. Srinivas Reddy **Member**
Director
CSIR-Indian Institute of Chemical Technology
Hyderabad

Dr G Umapathy **Member**
Chief Scientist
CSIR-Centre for Cellular & Molecular Biology
Hyderabad

Dr A S Sreedhar **Member**
Chief Scientist
CSIR-Centre for Cellular & Molecular Biology
Hyderabad

Dr Sonal Nagarkar Jaiswal **Member**
Senior Scientist
CSIR-Centre for Cellular & Molecular Biology
Hyderabad

Dr Sravanti Vaidya **Member**
Principal Scientist
CSIR-Centre for Cellular and Molecular Biology
Hyderabad

Dr M..R Vishnu Priya **Member**
Chief Scientist
CSIR-Centre for Cellular and Molecular Biology
Hyderabad

Mr D.M. Nikhar **Member**
Principal Technical Officer
CSIR-Centre for Cellular and Molecular Biology
Hyderabad

Mr Kolla Ramesh **Member**
Controller of Finance & Accounts
CSIR-Centre for Cellular and Molecular Biology
Hyderabad

Mrs Sailaja Maddaly **Member-Secretary**
Senior Controller of Administration
CSIR-Centre for Cellular and Molecular Biology
Hyderabad

Director’s Office

The Director's office is responsible for central planning, co-ordination and execution of all activities at the Centre. This includes maintaining relationships with stakeholders interested in the Centre's development and collaborating with them.



From left to right: Lavanya, Lakshmi Rao, Vinay Nandicoori, Madhuri, Naveen, Srinath

Science Communication & Public Oureach

The Science Communication and Public Outreach team at CSIR-CCMB develops various ways to engage non-scientists with the scientific research at the institute. This includes developing stakeholder-specific content as well as platforms for engagement, in-person and online.



From left to right: Aditya Undru and Somdatta Karak

Planning Monitoring and Evaluation

Mandate of Planning Monitoring and Evaluation (PME) is to manage majorly all projects of CSIR-CCMB. Also to liaise between Director and research groups CSIR-HQ and other organizations. Primarily PME takes care to provide inputs of various projects like in-house, sponsored, collaborative, grant-in-aid and NMITLI projects. In addition, PME provides information to project audit agencies, parliamentary and RTI queries.

PME assists Director in preparation and collating institutional data for onward transmission to CSIR headquarters, survey agencies. PME also conducts various institutional programs and any other responsibility as advised by the Director from time to time.



Business Development

Business Development Group of CSIR-CCMB carries out various activities related to technical services, IPs and technology transfers. Technical services include diagnostics services (Molecular Diagnostics, Wildlife Forensics & Chromosomal Diagnostics) and various analytical services.

BDG coordinates with CSIR HQ for facilitating the research leads from CSIR-CCMB for patenting. The group also facilitates CSIR-CCMB's connect with industry for contract & collaborative research projects, technical services, tech transfers, trainings, etc.



From left to right, top row: K.Anitha, N Vijay Kiran Reddy, Archana Bharadwaj Siva, R Leela Kumari
Bottom row: M. Vinay, Divya Singh, B. Pavan Kumar, Md. Azmatullah Khan, Y V Subba Lakshmi

Administration

The Administration department handles all aspects of employee engagement, which includes Recruitment, Project Recruitment Induction, Training, Establishment matters, Salary and Wage Administration, Performance Management, Contracts Management, Legal/ vigilance and Disciplinary matters and complying with statutory laws, Grievance Handling and Resolution of Conflicts, Wellness Programs, Retirement and post retirement matters, handling technology systems like eoffice, eHRMS, AMS, PFMS, LCM etc. In addition, administration of CSIR-CCMB is responsible for management of facilities encompassing Medical services, Guest House, Transport, Security, Canteen etc. All the above activities are duly taken with active support of group of officers and other team members contributing immensely in seamless and effective handling of HR and administrative functions.



Finance & Accounts

The CSIR-CCMB Finance & Accounts Section is responsible for all financial matters i.e. Budget formulation, Budget execution and Budget reporting, Project Management, Generation of Annual Accounts, Maintaining proper books of accounts and other relevant records. The CCMB works in a computerized environment using a web-based Government-wide platform called Public Financial Management System (PFMS) for managing its payment and accounting functions.



From left to right: M Vishnu Yadav, Ashish, G Sateesh Kumar, Ranjeet Kumar, D Sankar, Kolla Ramesh (COFA),K Ramakrishna, Imran Khan, M Ashok Kumar, B Jaswanth Sainath Reddy, K Vineet Sai, Y Sadashiva, J Latha (SO), VVL Prasanna, G Anuradha, M Madhavi, M Manoj, T Sudhakar

Stores & Purchase

Stores and Purchase Division looks after the entire process of Indenting, Procurement, Storage and regular issues of all the Consumables, Chemicals and Equipments for CSIR-CCMB.

Apart from the regular procurements it also caters to the procurement of high value equipments. In recent past equipments like Ultra High Resolution Field Emission Biological Scanning Electron Microscope; Multichannel High Speed Super Resolution Imaging System;Consumables for Genome Sequencing; Supply and Installation of -86^0 C Single door upright ultra low temperature deep freezers etc., has been successfully done.

All the works at Stores and Purchase are carried out as a team work to facilitate the R & D efforts of CSIR-CCMB.



Security

Security staff ensures safety of all the members of this esteemed organization through preventive and corrective methods in liaison with various other law enforcing agencies such as Police, IB, etc. They control entry & exit points of the institute, provide security cover during VVIP visits and international seminars etc. They are trained in disaster management and emergency preparedness to meet any uneventuality. They take care of crowd management and attend to all other security related issues that arise from time to time.

Guest House

CSIR-CCMB maintains a well furnished guest house inside the main campus. The guest house has 28 rooms and 2 suites, used for visiting scientists from India and abroad as well as for other guests. The guest house also arranges special lunches and dinners for official meetings and during seminars and workshops.The main aim of the guest house is to provide a comfortable and homely stay in CSIR-CCMB.

Canteen Services

The CSIR-CCMB Canteen provides food for CCMB staff, students, contract staff and visitors. We serve breakfast, lunch, dinner and high tea. We have Canteens at three different campuses - CCMB main campus, LaCONES, CCMB Annexe-I and iHUB, CCMB Annexe-II. All canteens are operated with Canteen Smart Card System making it the first canteen in CSIR labs to operate in cashless mode. Canteen has also Online Advance Booking application for Breakfast, Lunch and Dinner. From this application Canteen users can see the menu and they can book their meals up to 7 days in advance. Canteen users can also do online recharge of their cards from this application.

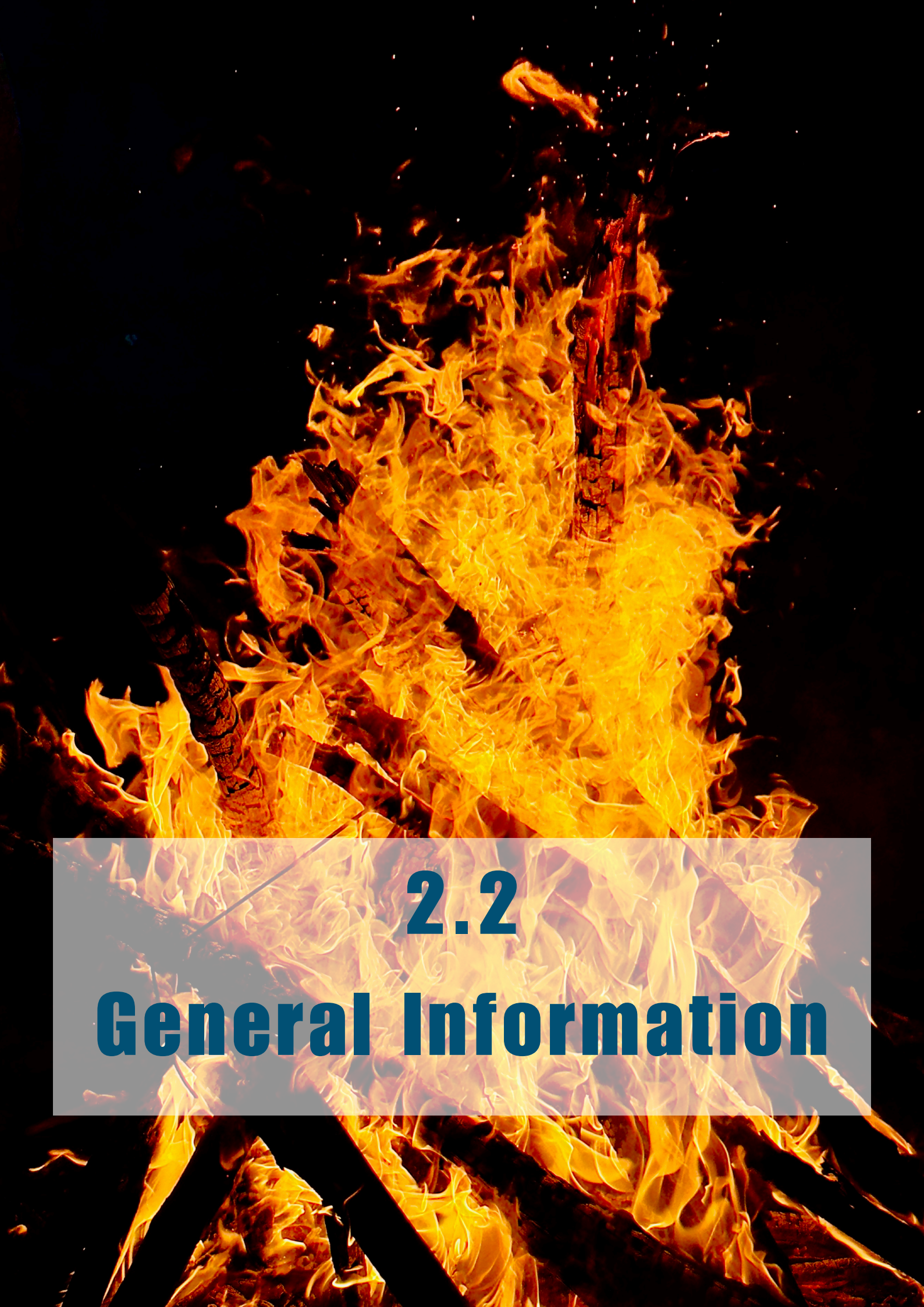
There are four food outlets of CSIR-CCMB Canteen in the main campus. These are Baithak, Ahlaad, Samvaad and Kiosk. They serve North Indian, South Indian, Continental and Chinese food. They serve 1000 people during the day and through various meals. They also have an in-house bakery and make all bakery products like bread, cookies, veg. puffs, cakes, pastries, pizza, etc. They also serve hot beverages 24/7 which is touchless, cashless and unmanned. Apart from regular dinner, they also cater to conferences, seminars, and symposia conducted by CSIR-CCMB.

They serve breakfast, lunch, dinner and high tea everyday for around fifty people in LaCONES Canteen, CCMB Annexe -I. They serve lunch and high tea for 100 people in iHUB Canteen, CCMB Annexe-II daily.

Medical Services

CSIR-CCMB Health center is catering the medical needs of employees, pensioners, and their dependants, students. Also visiting faculty/guest house inmates. Available facilities are: 1) Out Patient Service Allopathy (Modern medicine) and Ayurvedic. 2) Diagnostic service (Bio-Chemistry, Haematology, Clinical Pathology), ECG, 3) Pharmacy, and 4) Physiotherapy.





2.2
General Information



2.2 A List of Publications

- Chilukoti, N; Pavuluri, S; Kumar, S(2024).Differential expression of keratin and keratin associated proteins are linked with hair loss condition in spontaneously mutated inbred mice.BIOCHEMICAL AND BIOPHYSICAL RESEARCH COMMUNICATIONS.0006-291X.10.1016/j.bbrc.2024.151032.
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2.2 B List of Patents

Patents Granted in 2024-25

1. A rapid, low cost process for the preparation of SERS substrate and SERS substrate prepared thereby. Amit Asthana, Mohan Rao Chintalagiri, Saurabh Kumar Srivastava, Gopi Suresh Oggu.NFNO:0071NF2018/AU; Filing Date: 22-12-2020; Application No.: 2019292332; Grant Date: 05-09-2024; Patent No.: 2019292332.
2. Kit for detecting melanoma. Srivastava Avinash, Mishra Rakesh Kumar; NFNO:0186NF2018/EP; Filing Date: 26-07-2021; Application No.: 20744302.9; Grant Date: 06-11-2024; Patent No.: 3914726.

Patents Granted in 2024-25

1. A nanoformulation for therapeutic use. Santosh Chauhan, Kautilya Kumar Jena, Kollori Dhar, Ishwariya Venkatesh, Bokara Kiran Kumar, Aravind Kumar Rengan, Rohan Khadilkar . NFNO: 0135NF2024/IN; Filing Date: 16-07-2024; Application No.:. 202411054279.
2. Primers and Kit for the Detection of Restricted Materials obtained from Pantholops hodgsonii. Karthikeyan Vasudevan, Harika Segu, Gayathri Sreedharan, Naveen Kumar Chandrakumaran, Mubashir Majid. NFNO: 0175NF2024/IN; Filing Date: 16-08-2024; Application No.:. 202411062427.

2.2 C Awards & Honors

Research Staff

Amitabha Chattopadhyay

- Editor-in-Chief position of The Journal of Membrane Biology, a well-known and reputed journal in the area of membrane biophysics and membrane biology.

G Umapathy

- Delivered the Dr P Kutumbiah Memorial Endowment Lecture at the University of Madras.

Megha Kumar

- Awarded the Prime Minister Early Career Research Grant from Anusandhan National Research Foundation (ANRF).
- Board Member of the Indian Society of Developmental Biologists.

K Thangaraj

- Awarded the CSIR-Bhatnagar Fellowship.

Rajan Sankaranarayanan

- Awarded the Prof N Srinivasan Memorial Lecture Award-2023 by the Bioinformatics and Drug Discovery Society.

Deepa Selvi Rani

- Won the International Best Researcher Award from the International Science, Technology & Research Awards Congress 2024 for her work on cardiomyopathy.

Raghunand Tirumalai

- Elected Fellow of the Telangana Academy of Sciences.

Santosh Chauhan

- Elected as the INSA fellow for his work on autophagy and inflammatory pathways.

Students and Postdoctoral Fellows

CCMB ALUMNUS ARAVINDA PENMATSA was awarded the Rashtriya Vigyan Puraskar (Vigyan Yuva). He did his PhD with Rajan Sankaranarayanan and Yogendra Sharma at CCMB. He is currently, leading a research group studying structural biology of integral membrane proteins at IISc, Bangalore.

A S Priti

- SERB travel award to attend CILIA 2024 organized by EMBO in Ireland

Aditi

- Best oral presentation prize at the 11th International Toxinology meeting – Venoms and Toxins 2024 at Oxford, UK. She spoke on the evolution of scolopendrid centipede venoms

Ajay Sarawagi

- Best poster prize at the 11th Annual Meeting of the International Society for Magnetic Resonance in Medicine-Indian Chapter 2025 at IIT Hyderabad.

Akila Ramesh

- Best poster prize at the 11th Annual Meeting of the International Society for Magnetic Resonance in Medicine-Indian Chapter 2025 at IIT Hyderabad.
- Awarded Magna cum Laude for her oral presentation and second prize for her poster at the International Society for Magnetic Resonance in Medicine meeting in Singapore.

Alagu Sankareswaran

- Special Recognition Award for his oral presentation at the 9th International Diabetes Summit at Pune.
- SERB travel grant to attend the American Society for Human Genetics (ASHG) Annual Meeting- 2024 in Colorado, USA (Nov' 2024)

Avni Blotra

- Young Researcher Award at the 5th Science Conclave cum-National Biomedical Research Competition 2024 held at AIIMS New Delhi.
- Best poster award at the OMICS Technologies in Agriculture and Human Health conference at the Indian Institute of Chemical Technology.

Chaynita Dashora

- Best oral talk and the daily MRI quiz prizes at the 11th Annual Meeting of the International Society for Magnetic Resonance in Medicine-Indian Chapter 2025 at IIT Hyderabad.

Dixit Tandel

- SERB Travel Grant to attend the Keystone Symposium themed on Positive Strand RNA Viruses: Interdisciplinary Advances in Virology, Pathogenesis, Immunology and Technology Development at Killarney, Ireland

Gopi Krishnan

- Travel grant from the FSBI Symposium 2024 on Advancing fish ecology, management and forecasting through omics in Bilbao, Spain.

Katha Sanyal

- Best poster award at the Indian Academy of Neuroscience conference at NIMHANS, Bengaluru.

Korak Chakraborty

- Best poster award at the EMBO meeting - Host and pathogen heterogeneity in tuberculosis, at CCMB.

Koushick Venkatesh

- Best oral presentation prize at the 12th RNA Group Meeting at IIT, Guwahati

Manisha Ray

- Secured travel grant from International Symposium of Microbial Ecology and DST-SERB to participate in the 19th edition of the symposium at Cape Town, South Africa.

Manojkumar Kumaran

- IAN travel award at the Indian Academy of Neuroscience conference at NIMHANS, Bengaluru.

Md Jamaloddin

- Best poster award at the Emerging Trends in Food Processing Technologies for Food Security and Safety at CSIR-Indian Institute of Chemical Technology, Hyderabad.

Mukul JS

- Best poster prize at the 12th RNA Group Meeting at IIT, Guwahati.

Nikunj Tandel

- SOMA Young Scientist Award at 17th International Conference of Medical Arthropodology on Malaria and other Vector-borne & Zoonotic Diseases: Current Challenges and Opportunities in Public and Veterinary Health organized by P.G. Department of Zoology, Khalsa College, Amritsar, Punjab in association with Society of Medical Arthropodology

Pooja Gupta

- Best poster award at the 16th Annual Meeting of Proteomics Society, India and International Conference on Integrated Omics Approaches for Decoding Biological Research.
- Third prize in oral presentation at HySci 2024, held at IIT Hyderabad.

Pradeep Kumar

- KV Rao Scientific Society Research Award 2023-24 in Life Sciences for his work on chiral proofreading and aldehyde stress tolerance in land plants.

Prateekshya Das

- Best poster award at the international conference Intra- and Intercellular Regulatory Systems 2024 at University of Hyderabad.

Pratheusa Machha

- ASHG travel award to attend the American Society for Human Genetics (ASHG) Annual Meeting- 2024 in Colorado, USA

Priyadarshini Sanyal

- Best poster award at the EMBO meeting - Host and pathogen heterogeneity in tuberculosis, at CCMB.

Priyadarshini Singh

- Best poster award at the "Cancer NEXT 2024" held at Nizam Institute of Medical Sciences, Hyderabad, conducted by Federation of Asian Biotech Associations and Bharath Advanced Therapeutics.

Rutuja Pendharkar

- John Miller award at the Indian Academy of Neuroscience conference 2024 at NIMHANS, Bengaluru.

Shalini Vidyadharan

- Daily MRI quiz prize at the 11th Annual Meeting of the International Society for Magnetic Resonance in Medicine-Indian Chapter 2025 at IIT Hyderabad.

Sohail Rafik Mansuri

- Young Scientist Award at the 49th Annual Meeting of the Indian Society of Human Genetics held at NIMHANS, Bengaluru.

Sohini Ghosh

- Best poster prize at the 11th Annual Meeting of the International Society for Magnetic Resonance in Medicine-Indian Chapter 2025 at IIT Hyderabad.

Soumya Kundu

- First prize in oral presentation at HySci 2024, IIT Hyderabad.

Srinivas Reddy

- Best poster award at the 32nd National Congress on Parasitology, jointly organized by the Indian Institute of Science Education and Research (IISER) Pune, CSIR-National Chemical Laboratory and Savitribai Phule Pune University in association with the Indian Society for Parasitology.

S**umit Paliwal**

- Third prize in oral presentation at Sickle Cell Disease: Advances in Management and Prevention Conference held at ICMR-CRMCH, Chandrapur.

Tuhina Prasad

- Best poster award at the 5th Indian Zebrafish Investigators Meeting (IZIM) 2024 at Institute of Life Sciences, Bhubaneswar, jointly organized by CSIR-CCMB, Institute of Life Sciences and Agharkar Research Institute.

Vishal Sah

- Secured the EMBO and SERB travel grants and presenting his work on immune mechanisms against viruses at the Cell Bio 2024, a joint conference organised by American Society for Cell Biology and European Molecular Biology Organization at San Diego.

Yashwant Singh Panwar

- Outstanding student poster presentation award at the 10th World Congress of Herpetology in Kuching, Borneo. His travel was supported by the GARD24 (2024 Global Amphibian and Reptile Disease Conference) travel award.

Yogita Kapoor

- One of the 7 participants to get EMBL EMBO travel fellowship and one of the 5 to get the best poster award at the EMBO symposium (March 2025)
- Attended the EMBO BacNet conference 2024 in Spain with the EMBO registration waiver and CSIR travel grant. She spoke of her work on identifying and delineating the roles of novel DivIVA domain containing proteins of mycobacteria in cell division.
- Received the MITACS Graduate Research Award that allowed her do part of her PhD work at VIDO-InterVac, Canada.

2.2 D Conferences & Symposia

Workshop on Muscle Development and Diseases

The muscle scientists of CCMB led the Muscling through Species and Treating Diseases workshop from November 4th to 7th, 2024, to talk of the cutting edge tools and urgent questions being addressed in the field.

Laboratory Leadership for Group Leaders

One question that early career researchers struggle with, is how to transition from being an all-doing postdoctoral fellow to an effective lab leader, leading a team of people with diverse capabilities. Seeking solutions, 36 life science researchers leading research groups in different science institutions of India came to CCMB to participate in EMBO's Laboratory Leadership for Group Leaders course from November 11th to 21st, 2024.

6TH Autophagy India Network Meeting

The 6th Autophagy India Network meeting from January 20th to 22nd, 2025, brought together about 100 researchers and students studying the biology of autophagy from leading laboratories across the country, to CCMB. The meeting aimed to advance exceptional research in autophagy and cell biology within India by fostering collaborative scientific efforts.

EMBO Meeting on Host and Pathogen Heterogeneity in Tuberculosis

- Amid the public health discussions on tuberculosis, understanding the biology of this long malady of humankind still takes a backseat. The EMBO workshop at CCMB on Host and Pathogen Heterogeneity in TB aimed to bring our focus to the underlying biology of the disease. They helped us understand the multi-faceted nature of the disease.

- More than 200 tuberculosis researchers, many of them PhD students and postdoctoral fellows, came together for the EMBO meeting at CCMB from February 9th to 12th, 2025. The meeting brought in experts in the molecular and cell biology to evolution of Mycobacterium tuberculosis (Mtb) to human immunology, to broadly discuss the complexities of TB.

Seminar of CCSEA on Laboratory Animal Welfare Ethics

One-day seminar on Laboratory animal welfare ethics conducted by Ministry of Fisheries, Animal Husbandry and Dairying, Department of Animal Husbandry and Dairying, hosted by CSIR-CCMB was held on March 27, 2025. The event was attended by over 200 participants including researchers, veterinarians, pharmacists, etc.

2.2 E MoUs & Agreements

- NATIONAL CENTRE FOR BIOLOGICAL SCIENCES, BENGALURU (NCBS): An Addendum - III to the existing MoU signed on the 21st day of September, 2021- Consortium of R&D research and clinical institutions to advance pathogen genomics to track SARC-CoV-2 Variants and accelerate bioinformatics and global data sharing as a part of philanthropic financial support from the Rockefeller foundation for the project "COVID-19".
  April 03, 2024 - May 31, 2025

- ASHOKA UNIVERSITY, SONIPAT, HARYANA: An Addendum – II to the existing MoU signed on the 25th October 2022 -A consortium of R&D research and clinical institutions to advance pathogen genomics surveillance to track various,SARS-CoV-2 variants and accelerate bioinformatics and global data sharing as a part of philantropic financial support from the Rockefeller foundation for the project "COVID-19"
  April 12, 2024 - May 31, 2025

- PASTEUR INSTITUTE, MEGHALAYA : An Addendum – I to the existing MoU signed 16th day of December 2022 -A consortium of R&D research and clinical institutions to advance pathogen genomics surveillance to track various,SARS-CoV-2 variants and accelerate bioinformatics and global data sharing as a part of philantropic financial support from the Rockefeller foundation for the project "COVID-19"
  April 26, 2024 - May 31, 2025

- L V Prasad Eye Institute (LVPEI), HYDERABAD : An Addendum – I to the existing MoU signed 20th day of December 2022 -A consortium of R&D research and clinical institutions to advance pathogen genomics surveillance to track various,SARS-CoV-2 variants and accelerate bioinformatics and global data sharing as a part of philantropic financial support from the Rockefeller foundation for the project "COVID-19"
  April 26, 2024 - May 31, 2025

- AIIMS BIBINAGAR: An Addendum – I to the existing MoU signed 2 day of December 2022 -A consortium of R&D research and clinical institutions to advance pathogen genomics surveillance to track various,SARS-CoV-2 variants and accelerate bioinformatics and global data sharing as a part of philantropic financial support from the Rockefeller foundation for the project "COVID-19" .
  April 26, 2024 - May 31, 2025

- CENTRE FOR CELLULAR AND MOLECULAR PLATFORM (C-CAMP) ,Bangalore: An Addendum – I to the existing MoU signed on 15th December 2023 -A consortium of R&D research and clinical institutions to advance pathogen genomics surveillance to track various,SARS-CoV-2 variants and accelerate bioinformatics and global data sharing as a part of philantropic financial support from the Rockefeller foundation for the project "COVID-19"
  April 26, 2024 - May 31, 2025

- PUNE KNOWLEDGE CLUSTER FOUNDATION (PKCF) IUCAA, Maharashtra :An Addendum – II is being executed to the existing MoA signed on the 25th day of October, 2022-A consortium of R&D research and clinical institutions to advance pathogen genomics surveillance to track various,SARS-CoV-2 variants and accelerate bioinformatics and global data sharing as a part of philantropic financial support from Rockefeller foundation for the project "COVID-19"
  April 26, 2024 - May 31, 2025

- APOLLO HOSPITALS, HYDERABAD: A collaboration to work towards testing exosome formulations/ therapeutics prepared and developed from various biological sources by AHERF.
  April 30, 2024 - April 29, 2027

- ICAR-INDIAN INSTITUTE OF RICE RESEARCH (IIRR), MAGSTIK PVT. LTD., AND AGRINNOVATE INDIA LTD: Licensing of Technology titled "Improved Samba Mahsuri".
  May 06, 2024 - May 05, 2029

- RICH (Research and Innovation Circle of Hyderabad) Hyderabad : A collaboration for "Scholarship and Mentorship Programme for Women in STEM education and careers"
  June 01, 2024 - May 31, 2029

- RAINBOW CHILDREN HOSPITAL, HYDERABAD: A collaboration to delve into the realm of neurology research.
  June 21, 2024 - June 20, 2029

- ZEROHARM SCIENCES PRIVATE LIMITED, HYDERABAD: A commercial agreement for Technology/Know-how licensing of the “panel of microRNAs useful for screening and detection of types, grades and stages of Human Breast cancer”
  June 24, 2024 - June 23, 2037

- INTERNATIONAL CENTRE FOR GENETIC ENGINEERING AND BIOTECHNOLOGY (ICGEB) NEW DELHI : A Collaboration for conduct a surveillance of dengue virus and other arboviruses in the Aedes sp. mosquitoes and waste water samples in Delhi, as a part of convening a consortium of R&D research and clinical Institutions to advance pathogen genomics and global data sharing as a part of philanthropic financially support from the Rockefeller Foundation titled Alliance for pathogen Surveillance Innovations- India (APSI-India)- phase 2.
  July 18,2024 - May 31, 2025

- CHHATTISGARH INSTITUTE OF MEDICAL SCIENCES (CIMS): A collaboration for working together on genetic screening, carrier detection, clinical and genetic counselling for Sickle Cell Anemia patients.
  July 24, 2024 - July 23, 2029

- ALL INDIA INSTITUTE OF MEDICAL SCIENCES (AIIMS) Nagpur, Maharashtra: A collaboration to work together on genetic screening, carrier detection, clinical and genetic counselling for SCA patients.
  August 03, 2024 - August 22, 2027

- ARIHANT MULTISPECIALITY HOSPITAL (AMH) NAGPUR, MAHARASHTRA: A collaboration to work together on genetic screening, carrier detection, clinical and genetic counselling for SCA patients.
  August 31, 2024 - August 30, 2027

- ARTPARK-I-Hub for Robotics and Autonomous Systems Innovation Foundation, also called AI and Robotics Technology Park (ARTPARK) Bangalore: Alliance for Pathogen Surveillance Innovations-APSI-Data storage and analysis of genomic data of environmental samples for different pathogens including but not limited to SARS-CoV-2, Dengue and AMR.
  September 17, 2024 - September 16, 2029

- AIG Hospitals, Hyderabad: A collaboration for undertaking “Joint Genome Research in Human Health and Disease (Rare Diseases, Complex Metabolic Diseases, Infectious Diseases, etc.) and further, generate reference genomic data wherever necessary".
  September 20, 2024 - September 19, 2029

- NCBS TIFR : Joint Research
  October 7, 2024 – October 6, 2027

- ALL INDIA INSTITUTE OF MEDICAL SCIENCES (AIIMS), BHOPAL: A collaboration for working together to extend the benefits of genetic screening, carrier detection, clinical and genetic counselling for SCA patients.
  October 25, 2024 - October 24, 2027

- Pt. Deendayal Upadhyay Memorial Health Sciences and Ayush University (DDUMHS& AU) Raipur, Chhattisgarh: A collaboration for working together to extend the benefits of genetic screening, carrier detection, clinical and genetic counselling for SCA patients in the state of Chhattisgarh.
  October 30, 2024 - October 29, 2027

- Directorate of Medical Education (DME) Raipur, Chhattisgarh: A collaboration for working together to extend the benefits of genetic screening, carrier detection, clinical and genetic counselling for SCA patients in the state of Chhattisgarh.
  October 30, 2024 - October 29, 2027

- LIGHTENING LIVES LLP HYDERABAD: A collaboration for working together to develop a technology for the detection of sickle cell anemia/ sickle cell disease (SCA/SCD) and also in possession of research infrastructure and reagents for validation of diagnostics kits for SCA.
  December 12, 2024 - December 11, 2029

- PUNE KNOWLEDGE CLUSTER FOUNDATION (PKCF) IUCAA, Maharashtra: An Addendum – III is being executed to the existing MoA signed on the 25th day of October, 2022-A consortium of R&D research and clinical institutions to advance pathogen genomics surveillance to track various, SARS-CoV-2 variants and accelerate bioinformatics and global data sharing as a part of philantropic financial support from the Rockefeller foundation for the project for the project initially titled as "COVID-19".
  December 13, 2024 - May 31, 2025

- ALL INDIA INSTITUTE OF MEDICAL SCIENCES (AIIMS), NEW DELHI: A collaboration s involving academic, research, product, process and human resource development which will have a profound social and economic impact for our country.
  December 17,2024 - December 16, 2029

- ZEROHARM SCIENCES PRIVATE LIMITED, Telangana, Hyderabad: An Addendum – I to the existing MoU signed on 24th June 2024 -A commercial agreement for technology/know-how licensing of the “panel of microRNAs useful for screening and detection of types, grades and stages of Human Breast cancer”.
  January 09, 2025 - June 23, 2037

- District Collectorate Nandurbar, Maharashtra (DCNM) Maharashtra: A collaboration for working together to extend the benefits of genetic screening, carrier detection, clinical and genetic counselling for Sickle Cell Anemia (SCA) patients.
  January 27,2025 - January 26, 2028

- PUNE KNOWLEDGE CLUSTER FOUNDATION (PKCF) IUCAA, Pune, Maharashtra: An Addendum – III is being executed to the existing MoA signed on the 25th day of October, 2022-A consortium of R&D research and clinical institutions to advance pathogen genomics surveillance to track various, SARS-CoV-2 variants and accelerate bioinformatics and global data sharing as a part of philantropic financial support from the Rockefeller foundation for the project “COVID-19".
  January 30, 2025 - May 31, 2025

- CENTRE FOR CELLULAR AND MOLECULAR PLATFORM (C-CAMP), Bengaluru: An Addendum – II to the existing MoU signed on 15th December 2023 -A consortium of R&D research and clinical institutions to advance pathogen genomics surveillance to track various, SARS-CoV-2 variants and accelerate bioinformatics and global data sharing as a part of philantropic financial support from the Rockefeller foundation for the project “COVID-19".
  January 30, 2025 - May 31, 2025

- INCOIS : Long-term collaboration for promotion of research in cutting areas such as Environmental DNA (e DNA) and its applications in Marine Ecological applied research including Species Specific habitat suitability studies, Linking ocean productivity to fisheries potential, Jelly fish and Algal bloom advisory research, Outreach and Capacity Building and other mutually identified area.
  February 3, 2025 - February 2,2030

- THE ICGA FOUNDATION, Pune, Maharashtra: A collaboration to create a comprehensive database of molecular profiles of different cancers in Indian population.
  February 4, 2025 - February 3,2030

- NANDANKANAN ZOOLOGICAL PARK, Odisha: An agreement for conservation of the biological samples in the “National Wildlife Genetic Resource Bank’ at LaCONES in CSIR-CCMB, submitted by Nandankanan Zoo.
  February 4,2025 - ongoing

- NATIONAL CENTRE FOR BIOLOGICAL SCIENCES (NCBS) Bangalore: An Addendum - IV to the existing MoU signed on the 21st day of September, 2021- A Consortium of R&D research and clinical institutions to advance pathogen genomics to track SARC-CoV-2 Variants and accelerate bioinformatics and global data sharing as a part of philanthropic financial support from the Rockefeller foundation for the project "COVID-19".
  February 12, 2025 - May 31,2025

- TATA STEEL FOUNDATION & National Health Mission (NHM) Jharkhand: A collaboration to implement a Sickle Cell Anemia Screening Program in East Singhbhum, West Singhbhum and Saraikela- Kharsawan districts with the aim to screen, identify carriers and affected individuals and families, provide appropriate counselling and provide treatment to symptomatic individuals, and attempt to develop a community-based sickle cell registry over a period of one year.
  March 11, 2025 - March 10, 2026

- VELUX STIFTUNG, ZURICH: A grant for investigating dysregulated immune mechanisms in chronic ocular SJS.
  March 21,2025 - January 31, 2029

- BANNERUGHATTA BIOLOGICAL PARK BENGALURU (BBP) Bengaluru: A collaboration for preserving genetic diversity of species and supporting for conservation breeding by preserving the samples in the "NATIONAL WILDLIFE GENETIC RESOURCE BANK" at the Laboratory for the conservation of Endangered Species (LaCONES) in CSIR-CCMB.
  April 21, 2025 - April 20, 2030

2.2 F Invited Talks

PROF MARTIN LOWE
University of Manchester, UK
Understanding the mechanisms underlying secretory trafficking and immune receptor signaling

PROF KESHAV K. SINGH
University of Alabama at Birmingham, USA
Keeping the power on for healthy longevity

DR ANITA CHANDRAN
Editor, Nature Communications
Navigating the Publishing Landscape at Nature Communications

DR PRAMOD K. JANGIR
Biozentrum, University of Basel, Switzerland
Evolutionary factors driving resistance to a last-resort antibiotic

DR K SHANMUGHA RAJAN
Weizmann Institute of Science,
Rehovot, Israel
Decoding the atomic structure and molecular mechanisms of non-coding RNA mediated translational regulation in eukaryotes and vector-borne pathogens

PROF RAVINDER REDDY
Director of the Center for Advanced Metabolic Imaging in Precision Medicine, University of Pennsylvania, USA
Multinuclear metabolic imaging in neurodegenerative diseases

PROF L S SHASHIDHARA
Director, NCBS, Bangalore
Founder`s day Lecture : From Fly Genetics to Cancer Genomics

DR SUDIPTA TUNG
Ashoka University
Ecological and evolutionary response to environmental variation

PROF JAYANTA HALDAR
Antimicrobial Research Laboratory, New Chemistry Unit and School of Advanced Materials, Jawaharlal Nehru Centre for Advanced Scientific Research, Bangalore
Targeting the cell envelope: A versatile antibacterial strategy

PROF UPENDER MANNE
Director, Translational Anatomic Pathology Section, Co-Director, the UAB Tissue Biorepository, Senior Scientist, O`Neal Comprehensive Cancer Center, University of Alabama at Birmingham
Population-Based Integrative Approaches in Translational Cancer Research

PROF T P VELAVAN
Institute of Tropical Medicine, Tubingen, Germany
Battling infectious diseases in Southeast Asia and sub-Saharan Africa

PROF BENJAMIN WHITE
Chief, section on Neural Function NIH-National Institute of Mental Health, USA
From Cells to Circuits: Tools for Identifying the Neural Substrates of Behavior

PROF CHRISTOPHE D`ENFERT
Institut Pasteur, Paris
Candida albicans genome diversity: mechanisms and consequences

DR GREGORY EDGECOMBE
London, UK
Fossils, molecules and arthropods

PROF VINOD KUMAR PAUL
Hon'ble Member (Health), NITI Aayog, New Delhi
CCMB Foundation Day Lecture : India's COVID-19 vaccine journey and imperatives for future pandemic preparedness

DR AMAR DEEP
Department of Cellular and Molecular Medicine, University of California, San Diego, USA
Molecular and Mechanistic Insights into the Microbial Immune Systems

DR SRIKAR KRISHNA
Yale School of Medicine, USA
Measuring the functional impact of 5`UTR variants in human disease

DR PRASHANT PRADHAN
University of Texas Southwestern Medical Center, USA.
Regulation of transcription by biomolecular condensates

PROF SOMNATH DUTTA
Molecular Biophysics Unit, IISc, Bengaluru
Decoding Toxin-Membrane Interactions: Structural perspective from Cryo-EM studies

DR AREEJIT SAMAL
Professor, The Institute of Mathematical Sciences (iMSc), Chennai
Linking exposome and health by leveraging computational data-driven approaches

DR T N C VIDYA
JNCASR, Bengaluru
Associations and agonism among male Asian elephants

DR NAGARAJU DHANYASI
Jeff Lichtman`s lab, Harvard University, USA
Developmental connectomics in the cerebellum

DR PUJA BANERJEE
Department of Chemistry, University of Chicago, Illinois, USA
Deciphering the mechanism of HIV-1 Assembly and Maturation

DR PRAVEEN VEMULA
inStem, Bangalore
Developing Chemical Technologies for Solving Unmet Clinical Needs

PROF SUSHANT KUMAR
Assistant Professor, Department of Medical Biophysics, University of Toronto
Building computational toolboxes for cancer prevention and precision oncology

DR GOPINATH VISWANATHAN
Department of Molecular Genetics and Microbiology, Duke University School of Medicine, USA
Decoding Macrophage and Neutrophil Dynamics During TB Infection

DR NITYA RAMKUMAR
Duke University School of Medicine, USA
Design principles of epidermal morphogenesis

DR SIDDHARTH KULKARNI
IISER, Trivandrum
Role of whole genome duplications in evolutionary success

DR DHANANJAY BAMBAH MUKKU
University of California San Diego, USA
Ontogeny, Execution and Evolution of Rodent Social Behaviors

DR PADMINI SALGAME
Professor, Department of Medicine,Rutgers - New Jersey Medical School, USA
Uncovering bacterial and host interactions driving heterogeneity in M. tuberculosis transmissibility

DR SRIDHAR DHARMAPURI
Senior Food Safety and Nutrition Officer, Food and Agriculture Organization of the United Nations, Regional Office for Asia and the Pacific, Bangkok, Thailand
Building food safety systems in the Asia-Pacific Region

DR MAINAK BOSE
European Molecular Biology Laboratory (EMBL), Heidelberg, Germany
Functional regulation of RNA-protein condensates in the Drosophila germline

DR STEPHEN G. MATTHEWS
Canada Research Chair in Early Development and Health, University of Toronto & Senior Scientist, Lunenfeld-Tanenbaum Research Institute, Toronto, Canada.
The Environment and the Developing Brain: A Complex and Continuing Conversation

DR STEPHEN J. LYE
Executive Director, Alliance for Human Development Sr Investigator, Lunenfeld-Tanenbaum Research Institute, Toronto Professor, Departments of Obstetrics and Gynaecology, University of Toronto
Preterm Labour: Mechanisms, Diagnostics and Therapeutics

DR DHANANJAY HUILGOL
Department of Neurobiology, Duke University School of Medicine, North Carolina, USA
Generating neuronal diversity in the cerebral cortex

MR JAILABDEEN
Project Manager, Gharial Ecology Project, Morena
Investigating communication in gharial using acoustic and olfactory signals

PROF CHRISTIAN GRIESINGER
Director at the Max Planck Institute for Multidisciplinary Sciences, Gottingen, Germany
Fast protein dynamics and small molecules triggering transmembrane signaling and interfering with aggregation important in neurodegeneration

DR SOMDATTA SINHA
INSA Honorary Senior Scientist, IISER Kolkata & Adjunct Professor, IISER Mohali
Computational Analysis of Genomes - a Physics-based approach

DR SOMDATTA SINHA
INSA Honorary Senior Scientist, IISER Kolkata & Adjunct Professor, IISER Mohali
Modelling in Ecology

DR SUROJIT SURAL
Department of Biological Sciences, Howard Hughes Medical Institute, Columbia University, New York, USA
Starvation modulates interoceptive signals from the gut to remodel feeding behavior

DR SAYAN BHATTACHARJEE
CUIMC/Columbia University, New York, USA
Capturing Short-lived Intermediates in Ribosome Recycling Through Time-Resolved Cryo-EM, spanning 10-1000 milliseconds

DR TRIDIB MAHATA
Department of Clinical Microbiology and Immunology, School of Medicine, Tel Aviv University, Israel
Investigate phage-bacteria interactions to explore novel bacterial immune systems and phage-derived antimicrobials

DR KRITIKA M GARG
Ramalingaswami Fellow, Centre for Interdisciplinary Archaeological Research, Department of Biology, Ashoka University, Haryana
Species response to fluctuating climate

DR S SUBRAMANIAN
University of Minnesota Medical School, USA
Colorectal Cancer Immune Resistance and Novel Therapeutic Strategies

DR SHEKHAR C. MANDE
Distinguished Professor, Bioinformatics Centre, Savitribai Phule Pune University, Pune
History of Biomedical Sciences in India

MR SHUBHAM SINGH
Sloan Kettering Institute, MSKCC, New York, USA. (Intl PhD Graduate student at IISER, Pune)
Mapping the biosynthesis of BMP, a key phospholipid enabling lipid degradation in the lysosomes

DR APARNA LAJMI
University of Haifa, Israel
Understanding trait evolution in an ecological context

2.2 G Events

Independence Day

CCMB celebrated 78th Independence day on August 15, 2024. Dr. Vinay Nandicoori, Director, CCMB, hoisted the flag and distributed prizes and certificates to staff and students who won prizes in various competitions conducted by CSIR-CCMB staff club on the occasion of Independence day.

37th Foundation Day

Dr N Kalaiselvi, DG, CSIR inaugurated the PM Bhargava Auditorium at CSIR-CCMB on the eve of its 37th Foundation Day, 25 Nov, 2024. The spacious complex has a 300-seater auditorium, 100-seater lecture hall and two, 25-seater rooms.



The Foundation Day lecture was delivered by Prof. Vinod K Paul, Hon'ble Member-Health, NITI Aayog delivered the Foundation Day lecture on "India's COVID-19 vaccine journey and imperatives for future pandemic preparedness" discussing the strengths of India's science and technology ecosystem in tackling the country's healthcare needs, as demonstrated during the COVID-19 pandemic. CSIR-CCMB students performed as part of the cultural event.

Republic Day

On the occasion of Republic day on January 26, 2025, Dr. Vinay K Nandicoori, Director, CCMB, unfurled the National flag followed by address by the Chief guest, Dr Geetha Nagasree, Oncologist, CARE Hospitals, Hyderabad.

CCMB's 2nd Alumni Reunion

On February 21, 2025, CCMB 2nd Alumni Reunion was held wherein the present and past students came together to inspire and imagine the future of life scientists together, while the more experienced helped the younger ones navigate through the uncertainties.





9th Founder's Day

In remembrance of the Founder-Director Dr Pushpa M Bhargava, staff and students of CSIR-CCMB celebrate his birthday February 22nd as 'CCMB Founder's Day'. The proceedings include Sci-Setu, a CCMB student's led programme, wherein CCMB alumni are invited to share their journey of success with the PhD students of CCMB. Our alumni, Dr Suvendra Kumar Ray spoke about "Post CCMB career in research and teaching" and Dr Puneeta Arora spokes about "Innovations: Research to patents".

Prof L. Shashishara, Director, NCBS, distinguished guest for the day, delivered the keynote address on "From Fly genetics to cancer genomics". In cultural program, Canopy theatre presented a Theatrical production.



2.2 H Science Outreach & Popularization Programs

Anu leaned back in her chair, flipping shut the thick CCMB annual report with a dramatic sigh.
"I tried, Ravi. I really did. But somewhere between DNA replication and zebrafish brains, I lost the plot."
Ravi laughed. "Same here. These scientists live in a different universe. But I wonder... do they do anything to explain this stuff to, you know, people like us?"
"Actually, yes," Anu said, pointing back to the Outreach section. "They don't keep their science locked away. Look at this. They literally open their doors."

Open Day

7000+ visitors, mostly school and college students and educators came to CSIR-CCMB to celebrate science with us on CCMB Open Day on 26 Sept. From fun games to art corner to interactive exhibits and live experiments, we had something for all.



"Seven thousand people in a research institute? That's wild," Ravi said.

"And that's just one day," Anu replied. "They also run study tours throughout the year. School and college groups come in from across Telangana and other states to see real labs in action."

Study Tours

In 2024–25, around 4000 students took part across the year, guided by researchers who explained tools, experiments and discoveries.

Milo CCMB

CCMB's engagement does not stop at tours. Programs like Milo CCMB give students of the CCMB staff an immersive lab experience. After a lecture, the students take a tour of the campus and do various activities.



"Amazing!" Ravi nodded. "It's not just a tour. They let them live it."

Young Innovators Program

The Young Innovators Program continues to draw bright young minds from schools across Hyderabad and beyond. After an inaugural talk and a selection test, a group of students is invited to CCMB for a week of intensive lab work and interactions with scientists. They explore different areas of research through carefully designed experiments and discussions.



Teacher Visits

Teachers are a key part of this picture too. Through teacher visits and workshops, CCMB trains educators from government schools to use interactive genetics modules in their classrooms, bridging the gap between cutting edge science and everyday teaching.

Wildlife Week Celebrations

LaCONES, CCMB's wildlife research centre, hosts its own signature events. During Wildlife Week, children participated in a treasure hunt and painting competition that encouraged them to think about biodiversity in the Western Ghats.



Ravi flipped the page. "So that's everything they do inside the campus. But do they go out and talk to people elsewhere too?"

"They do," Anu replied. "In fact, they've taken science to some very interesting places this year."



National Science Day

At Vigyan Vaibhav 2025, organized by the Defence Research and Development Laboratory in Hyderabad, CCMB presented the biology of genetic and infectious diseases to aerospace and defence researchers, professionals and enthusiasts. The sessions invited participants from other disciplines to engage with biology and explore how understanding diseases connects to the larger goal of safeguarding health.



Vijnana Bharati's Shastra Pratibha

CCMB hosted students from grades 6 to 12 from various schools in the UAE as part of Vijnana Bharati's Shastra Pratibha program. The visiting students toured CCMB's facilities and interacted with scientists, asking questions about sustainability, genetic engineering and the future of research in India. Their curiosity and enthusiasm turned the visit into a lively exchange between cultures and generations.



Gene-Health Connect

The Gene-Health Connect mobile science exhibition continued its journey through Andhra Pradesh this year. The bus visited educational institutions and community spaces covering more than 2 lakh visiors across the state since its launch.



India International Science Festival

CCMB also participated in the India International Science Festival. This national level event brought together institutions, students and the general public from across the country. CCMB's stall highlighted its research areas and outreach activities, and scientists interacted with a wide audience ranging from school students to policymakers. It was an opportunity to showcase science from Hyderabad on a national platform.



"That's smart," Ravi said. "But what about people who can't come to these events?"

"They've thought of that too," Anu said, tapping the next section. "They also share their science through stories, zines and online content."

SciTales

SciTales is CCMB's dedicated popular science website. It hosts stories written by students and researchers, as well as interactive content. Over the past few years, it has grown into a rich archive that connects CCMB's science with diverse audiences online. This year, it continued to feature stories that brought out the human side of research and explained complex concepts in accessible ways.

Zines

Another medium through which CCMB shares its science is zines. These are short, illustrated booklets that can be printed or read digitally. Each zine focuses on a scientific idea or a researcher's journey, using simple language and engaging visuals. They are shared with schools, colleges and other organizations, often serving as conversation starters in classrooms and public events.







"They also collaborated with artists, organisations and festivals," Anu added. "Some of these were pretty unique."

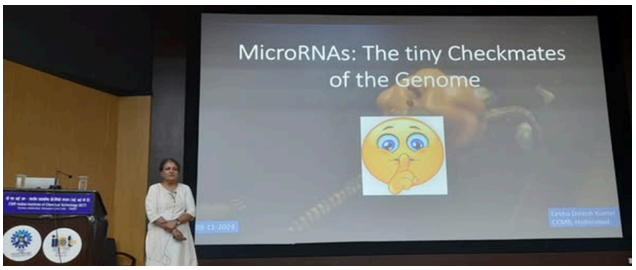
Urban Sketchers Hyderabad at CCMB

Urban Sketchers Hyderabad visited CCMB to spend a day sketching science spaces. Artists observed labs, corridors and common areas, and translated their impressions into sketches. The visit resulted in a vibrant set of artworks that captured the atmosphere of a working research institute from fresh perspectives.



Public Lecture on 2024 Nobel Prize for Medicine

Lekha Dinesh Kumar delivered a public lecture at CCMB on the role of microRNAs in cellular function. The talk drew a diverse audience, including students, teachers and members of the public. Through an engaging session, she highlighted recent findings in the field and connected them to broader questions about human history.



"That sounds like the kind of talk that makes you rethink what you know," Ravi said, as he read the summary.

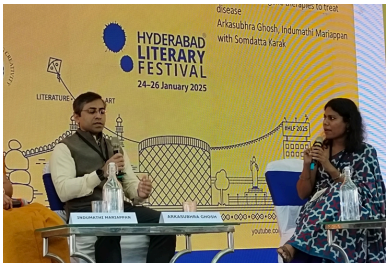
Royal Society for Chemistry

CCMB collaborated with the Royal Society for Chemistry to host a program that brought high school teachers to the institute for a workshop. The event also featured our game of Climaze played by the teachers.



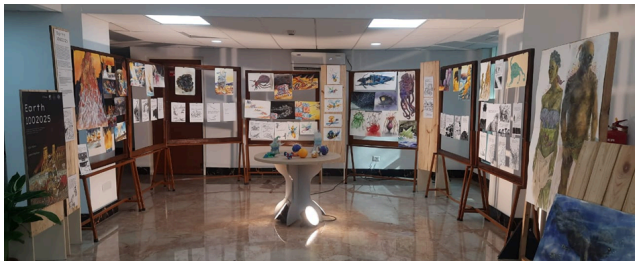
Hyderabad Literary Festival (HLF)

CCMB participated in the Hyderabad Literary Festival as part of the Science and the City stream. Scientists and students engaged with festival attendees through discussions, activities and exhibits including puzzles and stories in collaboration with Story Box.



Earth 1002025

CCMB hosted Earth 1002025, a speculative art exhibition by IIT Gandhinagar artists Argha Manna and Suman Chaudhuri, imagining life on Earth a million years from now. By bringing art and science together, CCMB encouraged visitors to think about evolution, extinction and the future. The exhibition was later hosted at TIFR Hyderabad as well.





Ravi leaned back, impressed. "I didn't realize outreach could be this varied. It's not just lab visits, it is conversations, collaborations and creativity."

"Exactly," Anu smiled. "Science doesn't stay behind their walls. It travels, connects and grows."



2.2 I Media coverage



2.2 J Staff, Research Students, Project Staff

(As on 31.03.2025)

SCIENTIFIC RESEARCH GROUPS

A S Sreedhar Group

A S Sreedhar	Chief Scientist
Priyadarshini Singh	Ph.D. student
Prateekshya Das	Ph.D. student
Vivek Chaudhary	Ph.D. student
Nitesh Kumar Gupta	Ph.D. student
Ebin Philip Thompson	Proj. Research Scientist-I
Vishnupriya D	Project Associate-I
Jukanti Rakesh	Project Assistant-I
Dinesh Kumar Mohanta	Project Assistant-I

Ajay Gaur Group

Ajay Gaur	Senior Principal Scientist
Akshar	Project Associate-I
Stanley J B	Field Assistant

Anant B Patel Group

Anant B Patel	Chief Scientist
K S Varadarajan	Sr. Technical Officer (1)
Bedaballi Dey	Ph.D. student
Ajay Sarawagi	Ph.D. student
Chaynita Dashora	Ph.D. student
Akila Ramesh	Ph.D. student
Prajakta Pramod Biyani	Ph.D. student
Paila Vimala Kumari	Ph.D. student
Sohini Ghosh	Ph.D. student
Hilal Roshan S M	Ph.D. student
Arpan Mukhoti	Ph.D. student*
Devika D. Mahimkar	Ph.D. student*
Shalini	Project Associate-I
Pranshi Agrawal	Project Associate-I
Priya Patel	Project Associate-I
Zubair Ahmed	Project Associate-I

* co-guide upon superannuation of Dr. Arvind Kumar

**PhD student of Dr Arvind Kumar

B Kiran Kumar Group

B Kiran Kumar	Principal Scientist
Khyathi Ratna P	Project Associate-II
Renuga Devi M	Project Associate-I
Namdigalla Prashanth	Project Associate-I
Nandhakumaar R	Project Associate-I
Hemasri Kilaru	Project Associate-I
Sreenivasan K	Project Associate-I

Dhananjay Chaturvedi Group

Dhananjay Chaturvedi	Senior Scientist
Sarasij Pal	Ph.D. student
Ishita Kalshyan	Ph.D. student
Swaraj Ranjan Paul	Project Associate-I
Haritha S	Project Associate-I

Divya Tej Sowpati Group

Divya Tej Sowpati	Senior Scientist
Nitesh Kumar Singh	Sr. Technical Officer (1)
Sofia Banu	Ph.D. student
Onkar V. Kulkarni	Ph.D. student
Vinayak Prakash Saini	Ph.D. student*
Apuratha Pandian	Project Scientist-II
Partheusa Machha	Data Analyst
Sreelekshmi M S	Project Associate-II
Anukrati Sharma	Project Associate-I
Isha Choubey	Project Associate-I
Sudarsanam Sriram	Project Associate-I
Rhea Jana	Project Associate-I
Jayesh Jain	Project Associate-I
Pooja Tayade	Project Associate-I
Ankita Ramdas Punde	Project Associate-I
Abishek Kumar S	Project Associate-I
Nadigadda Shiva Sai	Web Developer
Sangepu Jyothi	Laboratory Assistant

** Joint student with Dr. K. Thangaraj

* Transferred student from Dr. Meghna Krishnadas lab

G Umapathy Group

G Umapathy	Chief Scientist
Vinod Kumar	Sr. Technical Officer (1)
Gopi Krishnan P	Ph.D. student
Manisha Ray	Ph.D. student
Krupa Vinay Teja P	Ph.D. student
G Anusha	Ph.D. student
Neeldeep Ganguly	Ph.D. student
Shubham	Ph.D. student
Siddharth S. Kulkarni	Ramanujan Fellow
Anuja Pandey	Project Associate-I
Reuben Jacob Mathew	Project Associate-I
Abhilasha S. Nair	Project Associate-I
Mamidala Srilakshmi	Project Associate-I
Rochitha Shree V R	Project Associate-I
Gayatri Divekar	Project JRF
Himanshu Kothari	Project JRF
Samuel Singh	Project JRF
Ram M S	Proj. Research Assoc.-III
Sonal Suman	Project SRF
Mohd Khalid Waheed	Proj. Technical Assistant
Pratiksha Goriwale	Proj. Technical Assistant

** Co-guide for Dr. Meghna Krishndas student

Hitendra Kumar Patel Group

Hitendra Kumar Patel	Senior Principal Scientist
Raju Madanala	Sr. Technical Officer (3)
Vinoth Kumar	Technician (1)
Komal Ashok Awalellu	Ph.D. student
Anjana Sharma	Ph.D. student
Praveen Kumar Nayak	Ph.D. student
Amita Rani Supriyo	Ph.D. student
Sarath Dev G P	Ph.D. student
Jamaloddin Mohd	Project Scientist-II
Rennya P R	Prl. Project Associate
R Kirtana	Proj. Research Assoc.-I
T Sreenivasa RS Sandeep	Senior Project Associate
Deepti Rao	Senior Project Associate
Molieswar J	Project Associate-I
Shashi Kiran	Project Associate-I
Deepika M	Project Associate-I
Sumedha C Prabhu	Project Associate-I
Preethi K P	Project Associate-I
Raihana Najla N	Project Associate-I
Erum Khan	Project Associate-I
Lokesh Choudhury	Project Associate-I
Daravath Swetha	Project Assistant-II
Mukka Ganesh Kumar	Project Assistant-II
Dheeraj Patel	Project Assistant-I
Hemsagar Patel	Field Assistant
Rupdhar Yadav	Field Assistant

Ishwariya Venkatesh Group

Ishwariya Venkatesh	Senior Scientist
Yogesh Sahu	Ph.D. student
Anisha S. Menon	Ph.D. student
Rutuja Arun Pendharkar	Ph.D. student
Shringika Soni	SERB-NPDF
Manojkumar K	Proj. Research Assoc.-II
Prakash C	Senior Project Associate
Konda Meghana	Project Associate-I
Kesireddy Dhruva Kumar	Project Associate-I
Katha Sanyal	Project Assistant

Jahnavi Joshi Group

Jahnavi Joshi	Senior Scientist
Aditi	Ph.D. student
Abhishek Gopal	Ph.D. student
Pragyadeep Roy	Ph.D. student
Rishiddh Jhaveri	Ph.D. student
Shalini Parmar	Project Scientist-I
Swathi Balakrishnan	Proj. Research Assoc.-I
Karunakar Majhi	Project Associate-I
Madhumithraa N R	Project Associate-I
Sudhanshu Kumar	Project Associate-I
Marwa Abdul Razak	Project JRF

Janesh Kumar Group

Janesh Kumar	Senior Principal Scientist
Sanjay Kumar Suman	Sr. Technical Officer (1)
Bhavya Kailash Dawath	Ph.D. student
Aswini Kumar Gupta	Ph.D. student
Sandip Das Adhikary	Ph.D. student
Shantanu Subhash Visal	Ph.D. student
Swathi P	Ph.D. student
Rahul Ramsinh Parmar	Ph.D. student
Somanath Baral	Ph.D. student
Mukund Sudharsan	SERB-NPDF

Rajesh Vinnakota	Proj. Research Assoc.-III
Ithayaraja	Proj. Research Assoc.-III
Sushree A. Mohapatra	Project Associate-II

Karthik Bharadwaj Group

Karthik Bharadwaj	Scientist
Haricharan Goud Nerella	Ph.D. student
Pranjal Verma	Ph.D. student
Chandreswara Raju K.	Project Scientist-I
Ramakanth Chirravuri V.	Project Scientist-I
Vanitha Shyamili	Project Scientist
Priyanka Garg	Senior Project Associate
R. Hema Sindhuja	Project Associate-II
Banda Lavanya	Project Associate-I
Rakshpal R. Bhagat	Project Associate-I
Sushmitha Raj Nitta	Project Associate-II
Biswadeep Singha	Senior Project Associate
Sathya Swetha Na	Project Associate-I
Shalini Kumari	Project Associate-I
Ramesh Dovari	Project Assistant-I
Esari Deepshikha	Field Assistant
Dibya Rana Saha Roy	Field Assistant
Mohammed Osed Annan	Field Assistant

Karthikeyan Vasudevan Group

Karthikeyan Vasudevan	Chief Scientist
B Sambasiva Rao	Senior Principal Scientist
S Harika	Sr. Technical Officer (1)
K Rajya Lakshmi	Sr. Technical Officer (1)
Avni Blotra	Ph.D. student
Alka Sahu	Ph.D. student
Yashwant Singh Panwar	Ph.D. student
Suchetana Gupta	Ph.D. student
Swapnil Kiran	Ph.D. student
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M Mohammed Idris Group

M Mohammed Idris	Senior Principal Scientist

Mandar V Deshmukh Group

Mandar V Deshmukh	Senior Principal Scientist
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Supriti Das	Ph.D. student
Nilam Waghela	Ph.D. student
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Manjula Reddy Group

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Suraj Kumar Meher	Ph.D. student
Vaidehi Mihir Rajguru	Ph.D. student
N. Krishna Chaitanya	Ph.D. student
Stuti Chatterjee	Ph.D. student
Debnita Mongal	Ph.D. student
Vishnu Vachana M.	Ph.D. student
Soma Banerjee	Ph.D. student
Loka Ram Prasad	Ph.D. student**
Pradyumna Swanand P.	Ph.D. student**

**co-guide

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P Anuradha Reddy Group

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P Chandra Shekar Group

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Puran Singh Sijwali Group

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Pragati Patra	Ph.D. student
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Rajan Sankaranarayanan	Outstanding Scientist
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Biswajit Pal	Senior Principal Scientist
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Shankhadeep Baksi	Project Associate-I
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Raghunand R Tirumalai Group

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Priyanka Pandey	Ph.D. student
Sachin Gupta	Ph.D. student
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Swasti Raychaudhuri Group

Swasti Raychaudhuri	Principal Scientist
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Aanchal	Ph.D. student
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Cheshta Agarwal	Ph.D. student
Gayathri S.	Ph.D. student
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Amit Chakraborty	Ph.D. student
Sutashree Nath	Ph.D. student
Bitan Rakshit	Ph.D. student
Asis Kumar Khuntia	Ph.D. student
Aruna Panda	Program Manager
N V Sanjeev Kumar	Project Scientist
Yogita Kapoor	Research Scientist
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CSIR BHATNAGAR FELLOWS

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J C BOSE FELLOWS

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Alagu Sankareswaran	Ph.D. student
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EMERITUS SCIENTISTS

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Manoj Kumar Balyan	Senior Scientist
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*Mentored by Dr Ghanshyam Swarup

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CCMB-Atal Incubation Centre

N Madhusudhana Rao	Chief Executive Officer
Ramjee Pallela	Chief Operating Officer
Ritika Marrampalli	Commun. Manager
Ashish Kumar Perukari	Manager – Technology & Innovations

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S Prashanth	Technician (2)
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M Rajeshwari	Multi Tasking Staff
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BSL 2/3 facility

Amit Kumar	Technical Officer

Diagnostics Facility

M K Kanakavalli	Sr. Technical Officer (2)

Drosophila Facility

V. Bharathi	Sr. Technical Officer (3)

Imaging Facility

Nandini Rangaraj	Chief Scientist
Nitla Venkata Mahesh	Scientist
G Srinivas	Sr. Technical Officer (2)
T. Avinash Raj	Sr. Technical Officer (2)
Suman Bhandari	Sr. Technical Officer (1)

Integrated Structural Biology Facility

Shiv Pratap Singh Yadav	Scientist
Ravi Kumar Reddi	Scientist
R Rukmini	Prl. Technical Officer
A Harikrishna	Sr. Technical Officer (3)
Sandeep Shrivastava	Sr. Technical Officer (2)
R Phanindranath	Sr. Technical Officer (2)
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Next Generation Sequencing Facility

Mohammad Jafurulla	Sr. Technical Officer (2)
A Sreenivas	Sr. Technical Officer (2)
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Proteomics Facility

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Y Kameshwari	Prl. Technical Officer
K Ranjith Kumar	Technical Assistant

Tissue Culture Facility

Zareena Begum	Prl. Technical Officer
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Wildlife Forensics Facility

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B Kranthi	Sr. Technical Officer (1)

Zebrafish Facility

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SUPPORT FACILITIES

Academic Cell

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S Madhuri	I/c Academic Cell
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S Ramya	AcSIR Executive Assistant

Business Development, Human Resources & Documentation Group

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Devidas M Nikhar	Senior Suptd. Engineer
Lingam Sridhar	Suptd. Engineer
B Vijaya Kumar	Suptd. Engineer
K Nagendrababu	Suptd. Engineer
A Varaprasada Rao	Suptd. Engineer
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Ch Ravindra Babu	Senior Technician (2)
M Tirumala Rao	Senior Technician (2)
A J Narsing Rao	Senior Technician (2)
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L Kumar	Technician (2)
Anirban Adhikari	Technician (2)
Mallikanti Srinu	Technician (2)
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K Nagabhushanam	Lab Assistant
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Aparna Kumari	Senior Scientist
Biswajit Roy	Scientist
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K Sambasiva Rao	Prl. Technical Officer
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A Syam Kumar	Sr. Technical Officer (2)
Sudatt T Tambe	Sr. Technical Officer (2)
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ADMINISTRATION & MANAGEMENT

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Administration

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Chandan Kumar	Administrative Officer
J Venu	I/c. Transport
Noopur Rani Prasad	Hindi Officer
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S Kanchanamala	Section Officer (G)
N C Vamshi Krishna	Section Officer (G)
M Vanisree	Principal Private Secretary
N K Naveen Kumar	Private Secretary
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T Rajani	Asst. Section Officer (G)
Ch Sridevi	Asst. Section Officer (G)
Ashok Kumar Swasani	Asst. Section Officer (G)
Sudhakar Palem	Asst. Section Officer (G)
Neha	Asst. Section Officer (G)
Praveen Kumar	Asst. Section Officer (G)
Pradeep	Asst. Section Officer (G)
Jyoti Yadav	Asst. Section Officer (G)
Ram Gopal	Asst. Section Officer (G)
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Salla Umamahesh	Jr. Secretariat Asst. (G)
S Sivanath	Jr. Secretariat Asst. (G)
Prathab P	Jr. Secretariat Asst. (G)
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K Krishnamacharyulu	Lab Assistant
Ch Chandrashekar	Lab Assistant
S Yadaiah	Lab Assistant
Savitri Luhura	Lab Assistant
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Ambe Naveen Kumar	Multi Tasking Staff
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Ashish	Asst. Section Officer (F&A)
Tulasi Vinoothna	Asst. Section Officer (F&A)
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K L Kavitha	Private Secretary
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A Mahesh	Sr. Technical Officer (1)

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C V Tirumala Rao	Senior Security Officer*

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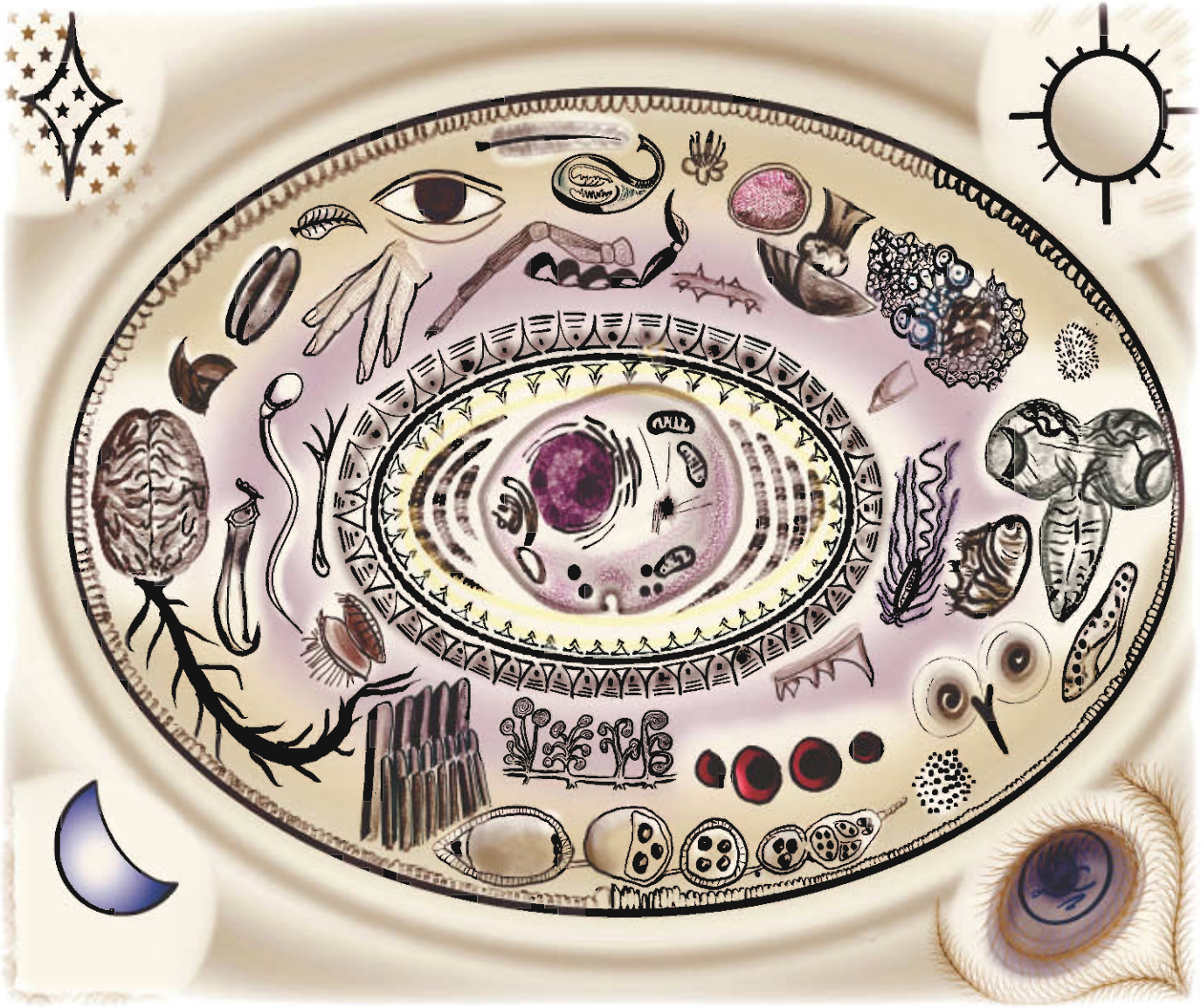

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