ANNUAL REPORT

2022-23

CSIR-CCMB

CENTRE FOR CELLULAR AND MOLECULAR BIOLOGY,
HYDERABAD

CONTENTS

DIRECTOR'S FOREWORD

Vinay Kumar Nandicoori, Director, CSIR-CCMB

वार्षिक रिपोर्ट 2022-23 की प्रस्तावना लिखना सौभाग्य की बात है। हमारे प्रधानमंत्री श्री नरेंद्र मोदी जी ने कहा है कि "विज्ञान में, विफलता जैसी कोई चीज़ नहीं होती। केवल प्रयोग और प्रयास होते हैं।"

सीसीएमबी एक विशिष्ट संस्थान है, जहां हम कोशिकीय, आणविक और संरचनात्मक जीवविज्ञान, पारिस्थितिकी, पशु एवं पौधे संरक्षण के मूलभूत पहलुओं पर काम करते हैं। सीसीएमबी की स्थापना होने के 46 वर्षों के बाद आज हम कहाँ खड़े हैं? विज्ञान और प्रौद्योगिकी में सीसीएमबी के योगदान पर गर्व करने के हमारे पास कई कारण है। सीसीएमबी अपने उच्च-गुणवत्ता वाले बुनियादी अनुसंधान और महत्वपूर्ण अनुप्रयोग-उन्मुख अनुसंधान जैसे डीएनए फ़िंगरप्रिंटिंग, बेहतर सांबा मसूरी चावल, वन्यजीव निदान और माउस डियर को पुन: प्रस्तुत करने पर लैंकॉन्स (LaCONES) और कोविड -19 महामारी के दौरान सीसीएमबी अपने काम के लिए जाना जाता है। भारत में कुछ संस्थान दुर्लभ बीमारियों के लिए नैदानिक सेवाएँ प्रदान करते हैं; हम उनमें से एक हैं। एक खास बात यह है कि सीसीएमबी ही एकमात्र ऐसा संस्थान है जो डायग्नोस्टिक और वन्यजीव डायग्नोस्टिक सेवाएँ प्रदान करता है। केवल तीन सीएसआईआर संस्थान ही ऐसे हैं जिनके पास इन्क्यूबेशन सेंटर है। अटल इनक्यूबेशन सेंटर के साथ हम उनमें से एक हैं। एक साल पहले फ्रंटलाइन में श्री आर.रामचंद्रन द्वारा प्रकाशित वैज्ञानिक यात्रा में मील के पत्थर के माध्यम से भारत की उल्लेखनीय प्रगति पर नज़र रखने पर एक लेख प्रकाशित हुआ था। लेख में उजागर किए गए हमारे शोध क्षेत्र से संबंधित नौ महत्वपूर्ण पहलुओं में से एक उल्लेखनीय स्तंभ, 1988 में सीसीएमबी के डॉ. लालजी सिंह की प्रयोगशाला द्वारा डीएनए फिंगरप्रिंटिंग तकनीक का विकास था।

दूसरी प्रमुख उपलब्धि, 1997 में "शांता बायोटेक्निक्स, जो स्वतंत्र रिसर्च फैसिलिटी के बनने तक एक निजी कंपनी सीसीएमबी से संचालित होती थी, ने भारत के पहले पुनः संयोजक स्वास्थ्य उत्पाद, शानवैक-बी नाम की हेपेटाइटिस बी वैक्सीन को बनाया था।

हमारे संस्थान के पास मजबूत आउटरीच गतिविधियाँ हैं, जिनमें ओपन डे, यंग इनोवेटर प्रोग्राम और कौशल विकास कार्यक्रम शामिल हैं, जो देश के किसी भी संस्थान द्वारा प्रदान की जाने वाली सर्वश्रेष्ठ गतिविधियों में से हैं। दो वर्षों के अंतराल के बाद, हमने 26 सितंबर 2022 को ओपन डे के लिए अपने दरवाजे खोल दिए, जिसे हमने इस वर्ष भी जारी रखा। इसमें लगभग 7000 विद्यार्थियों ने भाग लिया। हमने कॉलेज के छात्रों के लिए 28 फरवरी 2023 को इसे फिर से आयोजित किया, जिसमें लगभग 800 छात्रों ने भाग लिया। यह देश भर के कई स्कूल और कॉलेज के छात्रों द्वारा किए जाने वाले अन्य नियमित दौरों से अलग हटकर किया गया। मैं छात्रों, कर्मचारियों और सीसीएमबी की पूरी आउटरीच टीम के प्रयासों को धन्यवाद देना चाहता हूँ। उनके प्रयासों से ऐसे आयोजनों का आयोजन सहज नजर आता है।

पिछले वर्ष चार नए वैज्ञानिक सीसीएमबी में शामिल हुए, उनके नाम हैं- संतोष चौहान, ईश्वर्या वेंकटेश, रविकुमार रेड्डी और वेंकट महेश नितला। दूसरी तरफ कई सेवानिवृत्त हो गए हैं। हम संस्थान के प्रति उनकी निष्ठा, समर्पण और योगदान के लिए उन सभी को धन्यवाद देते हैं। हमारे यहाँ से हर वर्ष लगभग 150-180 प्रकाशन होते हैं। इस वर्ष, हमारे प्रकाशनों में पीएनएएस (PNAS) में चार, ईएमबीओ जे (EMBO J) में एक, ईलाइफ (eLife) में दो, एमबायो (mBio) में एक और सम्मानित सोसायटी पत्रिकाओं में कुछ शोध पत्र शामिल हैं। मैं हमारे संकाय सदस्यों और छात्रों की कुछ उपलब्धियों पर प्रकाश डालना चाहूंगा। डॉ. चांडक को NASI-काउंसिल प्रो. वी. पी. शर्मा मेमोरियल लेक्चर अवार्ड 2022 के लिए चुना गया है। डॉ. चौहान को NASI-स्कोपस यंग साइंटिस्ट अवार्ड 2022 से सम्मानित किया गया है और इंडियन एकेडमी ऑफ साइंसेज (IASc)-2023 का फेलो चुना गया है। डॉ. चट्टोपाध्याय को सोसायटी फॉर न्यूरोकेमिस्ट्री, इंडिया (एसएनसीआई) का अध्यक्ष चुना गया है। इसके अलावा, 20 से अधिक छात्रों को विभिन्न राष्ट्रीय/अंतर्राष्ट्रीय सम्मेलनों में सर्वश्रेष्ठ पोस्टर, यात्रा और सर्वश्रेष्ठ व्याख्यान का पुरस्कार प्राप्त हुए हैं ।

भविष्य की कुछ चुनौतियाँ भी हैं जिनसे हमें सावधान रहना चाहिए। व्यक्तिगत रूप से संचालित बुनियादी अनुसंधान परियोजनाओं के लिए वित्त पोषण पहले की तुलना में कम है। हमारा ध्यान कई प्रतिभागियों के साथ सामाजिक रूप से लाभकारी मिशन परियोजनाओं की ओर बढ़ रहा है। वन हेल्थ वाली परियोजनाओं पर जोर दिया जा रहा है। यद्यपि हम अत्याधुनिक शोध परियोजनाओं को पूरा करने के लिए अपना सर्वश्रेष्ठ प्रयास कर रहे हैं, प्रयास का एक हिस्सा निश्चित उद्देश्य के साथ कार्यक्रम परियोजनाओं की ओर निर्देशित किया जाना चाहिए। हालाँकि सीसीएमबी में हमारा बुनियादी ढांचा उत्कृष्ट है, हमें इसे देश में सर्वश्रेष्ठ बनाने पर काम करना चाहिए। जबकि सीसीएमबी का एक गौरवशाली अतीत रहा है, उच्च गुणवत्ता वाले विज्ञान और सामाजिक प्रासंगिकता वाले विज्ञान पर ध्यान केंद्रित करना अत्यंत महत्वपूर्ण है।

It is a privilege to write the foreword for the Annual Report 2022-23. Our Prime Minister, Shri Narendra Modi, stated, "*In science, there is no such thing as failure. There are only experiments and efforts*".

CCMB is a unique Institute where we work on fundamental aspects of cellular, molecular and structural biology, ecology, and animal and plant conservation. Where do we stand today after 46 years of CCMB's existence? We have every reason to be proud of CCMB's contribution to science and technology. CCMB is known for its high-quality basic research and important application-oriented research, such as DNA fingerprinting, Improved Samba Mashuri rice, wildlife diagnostics and LaCONES' work on reintroducing mouse deer, and CCMB's work during the COVID-19 pandemic. Few institutes in India offer diagnostic services for rare diseases; we are among them. What is unique is that CCMB is the only Institute offering diagnostic and wildlife diagnostic services. There are only three CSIR Institutes that have an incubation centre. With the presence of the Atal Incubation Centre, we are one among them.There was an article published in Frontline a year ago on tracking India's remarkable progress through milestones in its scientific journey written by Shri R. Ramachandran. Among the nine important facets relevant to our area of research highlighted in the article, one of the milestones mentioned was the development of DNA fingerprinting technology by Dr. Lalji Singh's lab at CCMB in 1988. Another was the launch of India's first recombinant health product, the hepatitis B vaccine named Shanvac-B, in 1997 by "Shantha Biotechnics, a private company that operated from CCMB until an independent research facility was built.

Our institute has strong outreach activities, including Open Day, Young Innovator's Program and Skill Development Programs, among the best offered by any Institute in the country. After a gap of two years, we threw open our doors for the Open Day on 26th September 2022, which we continued this year too. Almost 7000 students attended it. We did this again on 28th February 2023 for the college students, attended by around 800 students. This is, in addition to the other routine visits by many school and college students nationwide. I want to acknowledge the efforts of the students, staff and the whole outreach organisation team of CCMB for their efforts. Due to their efforts, the organisation of such events appears seamless.

Four new Scientists joined CCMB in the past year. They are Santosh Chauhan, Ishwariya Venkatesh, Ravikumar Reddi and Venkata Mahesh Nitla. On the other hand, many have superannuated. We thank them all for their dedication, contributions, and loyal services to the institute. We average around 150-180 publications a year. This year, our publications include four manuscripts in PNAS, one in EMBO J, two in eLife, one in mBio and quite a few in respected Society journals. I would like to highlight a few achievements of our faculty and students. Dr. Chandak has been selected for the NASI-Council Prof. V. P. Sharma Memorial Lecture Award 2022. Dr. Chauhan has been awarded the NASI-SCOPUS Young Scientist Award 2022 and elected Fellow of the Indian Academy of Sciences (IASc)-2023. Dr. Chattopadhyay has been elected president of the Society for Neurochemistry, India (SNCI). In addition, more than 20 students got the best poster, travel, or oration awards at various national/ international conferences.

There are also a few future challenges that we must be mindful of. The funding for individually driven basic research projects is lower than it used to be. The focus is shifting towards societally beneficial mission projects with multiple participants. There is an emphasis on projects addressing One Health. While we continue to do our best to carry out cutting-edge research projects, a part of the effort should be directed towards program projects with a definitive objective. While our infrastructure at CCMB is excellent, we must work on making it the best in the country. While CCMB has a strong past glory, it is crucial to continue focusing on high-quality science and science that has societal relevance.

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

1.1A
Research Summaries

AJAY GAUR

Conservation Genetics of Endangered Indian Species

From left to right: Akshar, Ajay Gaur, O. V. Padmalatha

Research interests

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

Recent publications

- Vipin, Tirupathi Rao Golla, Vinita Sharma, B. Kesav Kumar, Ajay Gaur (2022) Kleptoparasitic interaction between Snow Leopard *Panthera uncia* and Red Fox Vulpes vulpes suggested by circumstantial evidence in Pin Valley National Park, India. ***Journal of Threatened Taxa*** 14: 21928–21935.
- Tirupathi Rao Golla, Laura Tensen, Vipin, Kesav Kumar, Satish Kumar, Ajay Gaur (2023) Neutral and adaptive genetic variation in Indian snow leopards, *Panthera uncia*. ***Current Science*** 125: 204-209.

Our lab focuses on the development and application of molecular markers in conservation genetics of endangered species. We use non-invasive sampling protocols and develop species–specific DNA markers to investigate the genetic structure of existing populations. Bears are a prominent case where conflicting gene trees and an ambiguous fossil record make interpretation of their evolutionary history difficult. The sloth bear (*Melursus ursinus*) is a large wide-ranging carnivore species endemic to the Indian subcontinent. In the recent country-wide census of large carnivores and their prey species, sloth bears were found to have the most widely recorded distribution of any large carnivore in the Central India and Eastern Ghats landscapes. However, their distribution has gradually decreased and become patchy due to habitat loss, fragmentation and human-sloth bear conflicts. Additionally, poaching, trade of body parts and capture of live cubs for entertainment threatens them. 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 sloth bear's genetic diversity is distributed in its habitat. Our knowledge of non-invasive DNA based methods provides a significant scope of studying large carnivores in the Eastern Ghats to describe their population structure and existing level of genetic diversity. We initiated genetic studies in sloth bear by generating partial sequences of four conserved mitochondrial genes. Sequences of different bear species of family Ursidae were used for phylogenetic comparison. Preliminary data analysis of study samples of sloth bear gives promising insight into the phylogenetic position of this important species within its family and give a base platform for further research and studies to build up effective conservation strategies.

AMITABHA CHATTOPADHYAY

Membrane and Receptor Biology

From left to right: K. Venkatalaxmi, Saptadipa Basak, Subhashree Shubhrasmita Sahu, Amitabha Chattopdahyay, Ashwani Sharma, Akrati Bhat, Aditi Moharana, Abhishek Kumar

Research Interests

- Interaction of membrane lipids and actin cytoskeleton with G protein-coupled receptors (GPCRs): Implications in health and disease
- Role of membrane lipids in the endocytosis and intracellular trafficking of GPCRs, and the entry of pathogens into host cells

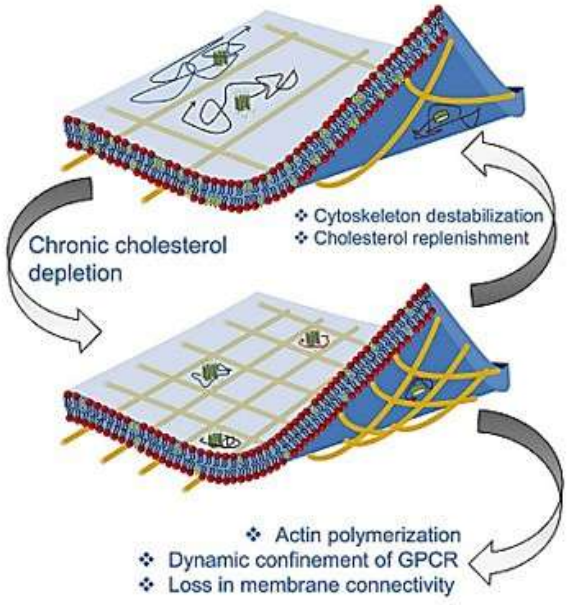
Selected recent publications

- Dutta A, Sarkar P, Shrivastava S, Chattopadhyay A (2022) Effect of Hypoxia on the Function of the Human Serotonin1A Receptor. ***ACS Chemical Neuroscience*** 13: 1456-1466.
- Sarkar P, Kumar GA, Shrivastava S, Chattopadhyay A (2022) Chronic Cholesterol Depletion Increases F-actin Levels and Induces Cytoskeletal Reorganization via a Dual Mechanism. ***The Journal of Lipid Research*** 63: 100206.
- Shrivastava S, Ror P, Chattopadhyay A (2022) Effect of Local Anesthetics on Dipole Potential of Different Phase Membranes: A Fluorescence Study. ***The Journal of Membrane Biology*** 255: 363-369.
- Shahi G, Kumar M, Khandelwal NK, Baneerjee A, Sarkar P, Kumari S, Esquivel BD, Chauhan N, Chattopadhyay A, White TC, Gaur NA, Singh A, Prasad R (2022) Inositol phosphoryl transferase, Ipt1, is a critical determinant of azole resistance and virulence phenotypes in Candida glabrata. ***Journal of Fungi*** 8: 651.
- Sarkar P, Chattopadhyay A (2022) Membrane Dipole Potential: An Emerging Approach to Explore Membrane Organization and Function. ***The Journal of Physical Chemistry B*** 126: 4415-4430.
- Sarkar P, Bhat A, Chattopadhyay A (2022) Lysine 101 in the CRAC Motif in Transmembrane Helix 2 Confers Cholesterol-induced Thermal Stability to the Serotonin1A Receptor. ***The Journal of Membrane Biology*** 255: 739-746.
- Shrivastava S, Sarkar P, Preira P, Salomé L, Chattopadhyay A (2022) Cholesterol-dependent Dynamics of the Serotonin1A Receptor utilizing Single Particle Tracking: Analysis of Diffusion Modes. ***The Journal of Physical Chemistry B*** 126:6682-6690
- Mohole M, Sengupta D, Chattopadhyay A (2022) Synergistic and Competitive Lipid Interactions in the Serotonin1A Receptor Microenvironment. ***ACS Chemical Neuroscience*** 13: 3403-3415.

- Kumar A, Sarkar P, Chattopadhyay A (2023) Metabolic Depletion of Sphingolipids Inhibits Agonist-induced Endocytosis of the Serotonin1A Receptor. ***Traffic*** 24: 95-107.
- Chattopadhyay A, Sharma A (2023) Smith-Lemli-Opitz Syndrome: A Pathophysiological Manifestation of The Bloch Hypothesis. ***Frontiers in Molecular Biosciences*** 10: 1120373.
- Shrivastava S, Paila YD, Chattopadhyay A (2023) Role of Cholesterol and its Biosynthetic Precursors on Membrane Organization and Dynamics: A Fluorescence Approach. ***The Journal of Membrane Biology*** 256: 189-197.

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 explore interactions of membrane lipids (such as cholesterol and sphingolipids) with GPCRs and its implications in health and disease. We employ a judicious combination of biophysical, biochemical, cell biological and molecular dynamics simulation approaches for this. We have shown that GPCR-cholesterol interaction is important for ligand binding, G-protein coupling, downstream signaling, oligomerization, endocytosis and trafficking 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 have recently identified certain regions (such as CRAC motifs) of the serotonin-1A receptor that are crucial for sensing altered membrane cholesterol levels. GPCRs orchestrate a multitude of physiological processes within cells, which are maintained within stringent spatiotemporal regimes. Endocytosis is an important regulatory feature of GPCR signaling that involves the internalization and sequestration of receptors from the plasma membrane into endosomes. The detailed mechanism of endocytosis and trafficking of GPCRs is not well understood. Importantly, dysregulated GPCR trafficking has been associated with several pathophysiological conditions, and exploring the mechanistic details of endocytosis and trafficking of GPCRs therefore assumes relevance. We explore the effects of altered membrane lipid composition and actin cytoskeleton on GPCR endocytosis and trafficking.

Interestingly, we recently reported that chronic cholesterol depletion using statins leads to significant polymerization of the actin cytoskeleton. Further, we explored the effect of reorganization of the actin cytoskeleton on dynamics of serotonin-1A receptor under cholesterol-depleted condition. A salient feature of our findings is that actin plays a crucial role in modulating receptor diffusion in cholesterol-depleted cells.



A schematic representation showing free diffusion of GPCRs under normal cholesterol levels and confined diffusion upon cholesterol depletion. Chronic cholesterol depletion using statins leads to extensive polymerization of the actin cytoskeleton (shown as orange rod-like structures) and leads to compartmentalization of membranes. As a result, receptor lateral diffusion becomes confined within these actin-induced domains.

ANANT B PATEL

Brain Energy Metabolism in Neurological and Psychiatric Disorders

From left to right: Bhargirdhar, Akila, Bedaballi, Anant, Vimala, Chaynita, Pranshi, Varadarajan

Research interests

- Development of multinuclear NMR spectroscopy and stable ^{13}C isotope (glucose and acetate) techniques to study neurometabolism
- Neurotransmitter energetics in neurodegenerative and psychiatric disorders

Recent publications

- Adusmilli M, Sarath Babu N, Varadarajan KS, Idris MM, Patel AB (2022) 1H-[13C]-NMR investigation of brain energy metabolism in zebrafish: Impact of acute ethanol. ***Journal of Magnetic Resonance Open*** 10–11: 100030.
- Sarawagi A, Bhat BA, Sinha S, Iyer H, Patel AB, Kumar A (2022) Astroglial Pathology in Major Depressive Disorders: Metabolic and Molecular Aspects in Glial Biology. ***The Biology of Glial Cells: Recent Advances*** 293-321.
- Sudhakar R, Dontamala S, Bingi TC, Gorde S, Panda A, Rizvi Z, Reddy GS, Kaswan S, Bhattacharjee M, Kumar D, Nivya MA, Mesipogu RR, Varadarajan KS, Patel AB, Gupta D, Harshan KK, Tallapaka KK, Sijwali PS (2022) A comparative study of antibody response, virus neutralization efficiency & metabolites in SARS-CoV-2-infected adults & children. ***Indian Journal of Medical Research*** 156: 659-668.
- Varadarajan KS, Bagga P, Ramesh A, Chagani AK, Patel AB (2023) Chronic Lead Exposure Disrupts Neurometabolic Activity in Mouse Brain: An ex vivo 1H-[13C]-NMR Study. ***Neurotoxicology*** 94:117-125.

Electroconvulsive therapy (ECT) is a rapid and the most effective treatment for drug-resistant depressive disorder. The major aim of the study was to assess the impact of ECT on neurometabolites homeostasis and neurometabolic activity at different times post-Electro convulsive shock (ECS). Two months old C57BL6 mice were divided into two groups: A. ECS Group, and B. Sham Group. Mice under isoflurane anesthesia received a single ECS via corneal electrodes, while controls did not receive the shock. Mice were administered either [1,6 -$^{13}C_2$] glucose or [2 -^{13}C] acetate after 3.5, 15, and 60 min of the shock. The ^{13}C labeling of neurometabolites was measured in ^{1}H-[^{13}C]-NMR spectra of brain tissue extracts.

There was an increase in the concentrations of gamma-aminobutyric acid (GABA), alanine, lactate, and choline in PFC in the 3.5 min ECS group of mice when compared with sham, and restored to normal levels at 60 min post-ECS. Moreover, the $^{13}C_2$ labeling of Ala-C3 and Lac-C3 from [1,6 -^{13}C]glucose was increased in the 3.5 min ECS group of mice. In contrast, Glu-C4, GABA-C2, Gln-C4, Asp-C3, and Glu-C3 labeling was reduced. Additionally,^{13}C labeling of amino acids from [2-^{13}C]acetate was reduced in the 3.5 min ECS group. These data indicate a decrease in the cerebral metabolic rate of glucose oxidation in neurons and astroglia in the ECS group of mice. These data provide evidence for the functional nature of astrocytes, and the coupling between neuronal and astroglial metabolic activity. Moreover, the findings indicate an uncoupling of anaerobic glucose metabolism (+111%) and oxidative phosphorylation (-43%) in the early time period of ECS mice. There was a strong correlation (R^2=0.93) between GABAergic and glutamatergic neurometabolic activity, further validating the hypothesis that inhibitory and excitatory neuronal activity increased together with brain activity.

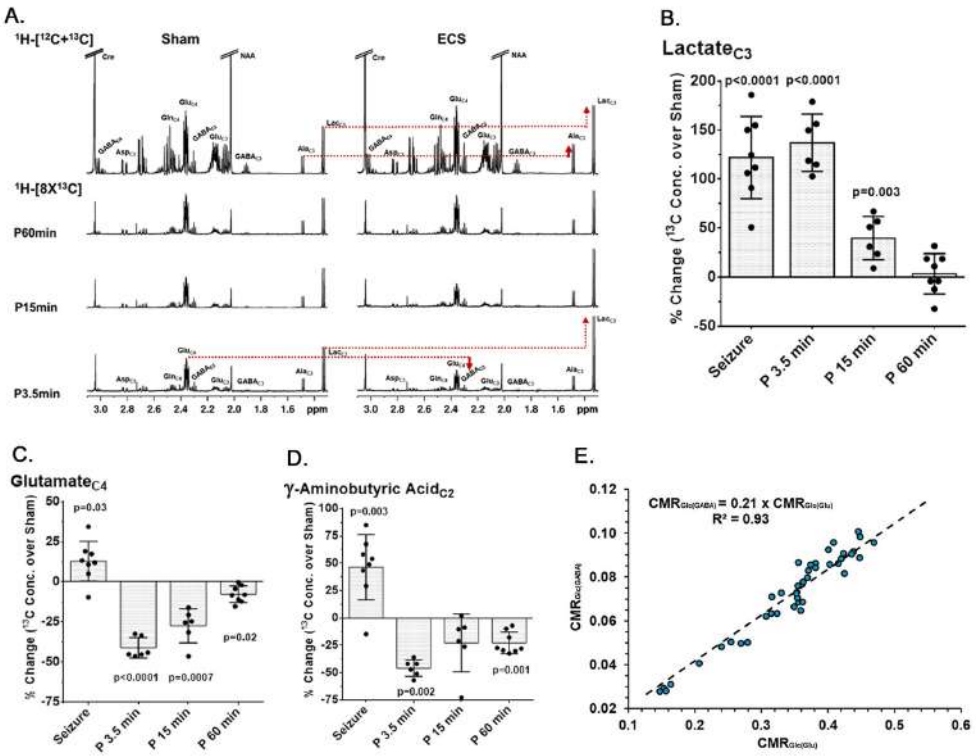


Fig: I. Impact of ECS on Neuronal metabolic activity in the prefrontal cortex (PFC): A. [^{13}C]-NMR spectra depicting ^{13}C labeling of PFC amino acids from [1,6-$^{13}C_2$]glucose after ECS. The spectra in the upper panel represent total metabolites in the Sham (left) and ECS (right) group, while the lower panel depict ^{13}C labeled metabolites at different time after ECS. The relative change in the labeling of B. Lactate-C3, C. Glutamate-C4, and D. GABA-C2 in the PFC of ECS mice when compared with sham mice during, and after 3.5, 15, and 60 min of ECS. E. Correlation between rates of glucose oxidation in GABAergic (CMR-Glc(GABA)), and glutamatergic (CMR-Glc(Glu)) neurons. Mice were infused with [1,6-$^{13}C_2$]glucose for 2 min, and the concentrations of ^{13}C-labeled metabolites were measured in PFC extracts using ^{1}H-[^{13}C]-NMR spectroscopy. Abbreviations: Ala-C3, alanine-C3; Asp-C3, aspartate-C3, Cre: creatine; GABA-C2, gamma-aminobutyric acid-C2; GABA-C4, gamma-aminobutyric acid-C4; Glu-C4, glutamate-C4; Glu-C3, glutamate-C3; Gln-C4, glutamine-C4; GPC, glycerol-phosphocholine; LacC3, lactate-C3; NAA, N-acetyl aspartate; P3.5min, P15min, and P60min refers to time after the start of [1,6-$^{13}C_2$]glucose infusion after ECS.

ARVIND KUMAR

Epigenetics & Neuropsychiatric Disorders

From left to right: Unis Ahmad Bhat, Arvind Kumar, Arpan Mukhoti, Sachin Singh, Aditya Undru, Pratishtha Wadnerkar, Bedaballi Dey, Devika Mahimkar, Ashutosh Kumar, Supraja Acharya, Shailaja Pathak, Annapoorna PK

Research interests

- Molecular mechanisms, particularly dysregulation of epigenetic and transcription regulatory mechanisms underlying etiology of neuropsychiatric disorders such as mood and cognitive disorders, using animal models
- Discovery of markers & biomarkers; Pre-clinical studies on potential small molecules for CNS drug discovery

Recent publications

- Bhat UA, Arun Kumar S, Chakravarty S, Patel AB, Kumar A (2023) Differential Effects of Chronic Ethanol Use on Mouse Neuronal and Astroglial Metabolic Activity. ***Neurochemical Research*** 48: 2580-2594.

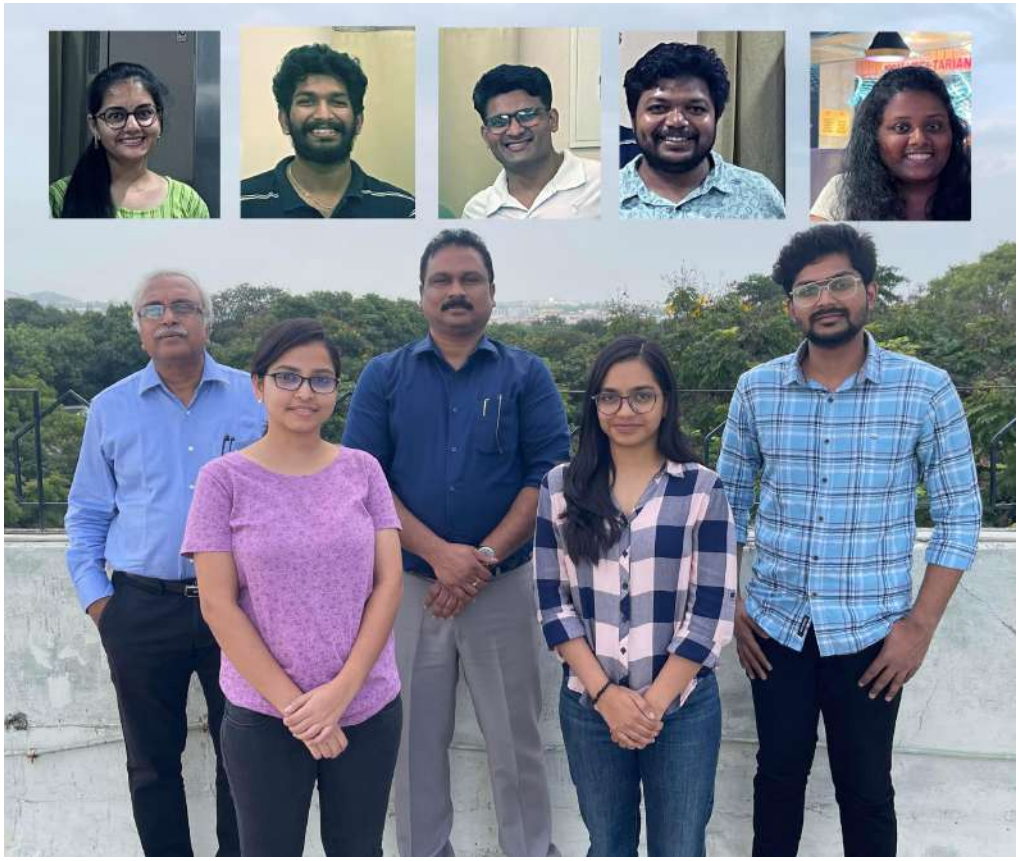
Lifestyle change involving high calorie diet, sedentary life and/or persistent stress has been linked to the onset of metabolic disorders (MeD). A cluster of associated disorders lead to Metabolic Syndrome (MetS), which comprises impaired fasting glucose, abdominal obesity, dyslipidemia and hypertension. MeD & MeS are risk factors for not only cardiovascular but cerebrovascular diseases too, which in the long run cause neurological and psychiatric disorders. MeD & MeS cases are rising worldwide but the molecular mechanisms underlying induced cerebrovascular perturbations and neuropsychiatric disorders, such as mild cognitive impairment, depression and related mood disorders using relevant animal models has not been investigated in detail. Using i) Lepr db/db, a genetic mouse model of MeS and ii) a high fructose diet (HFr diet) induced MeD mouse model, we tried to uncover the underlying neurometabolic and molecular mechanisms.

To investigate the underlying neuronal and astroglial metabolic changes in the Lepr db/db brain, infusion of either [2,4-$^{13}C_2$]-hydroxybutyrate ([2,4-$^{13}C_2$]BHB) or [2-^{13}C]acetate was performed, followed by the measurements of ^{13}C labelled amino acids in cortical tissue extracts, by ^{1}H-[^{13}C]-NMR Spectroscopy. MeS was found to be associated with impaired neurometabolic (glutamatergic) activity in Lepr db/db mice. Additionally, the increase in acetate oxidation together with an upregulation of inflammatory cytokines (Il6, Tnfα, NfkB) and inflammasome (Nlrp3,4), suggested heightened inflammatory conditions in the db/db mouse brain.

C57bl/6 mice on the HFr diet failed to develop hyperglycemia even after a year, unlike our rat model where 8-weeks was sufficient. However, these mice developed some components of MeD: hypercholesterolemia, hyperlipidemia, reduced lean mass and body weight, which appear to induce accelerated aging. Interestingly, just a brief exposure to chronic mild stress could induce insulin tolerance and mood & cognitive disorder phenotype, and transcriptomic analysis on the prefrontal cortical region suggested increased neuroinflammatory markers and attenuated neurotrophic, vasculogenic, neurometabolic, synaptic transmission and neuroplastic markers.

A S SREEDHAR

Stress Biology and Molecular Medicine



From left to right, top row: Akshita Kulshrestha, Vishaka Aravind V, Shrikant P. Dharasakar, Shubham Sonwani, Sneha Fernando
Bottom row: Khanderao Paithankar, Prateekshya Das, Amere Subbarao Sreedhar, Priyadarshini Singh, Harshvardhan Jana Janagarajan

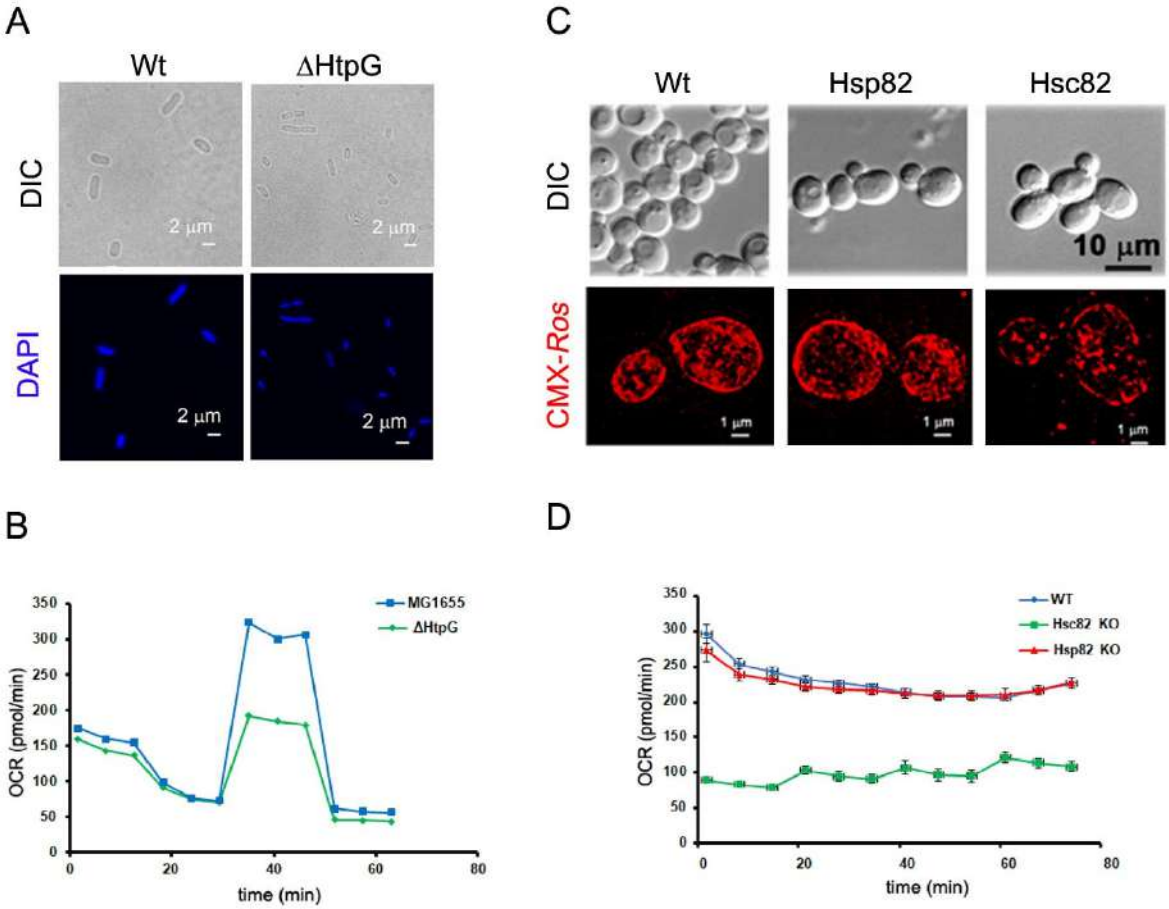
Research interests

- Understanding the stress response and its implications in disease biology
- Regulation of metabolic plasticity in cancer cells
- Epigenetic regulation of cancer
- Understanding the mechanism of acquired multidrug resistance in cancer
- Cancer EMT in phenotypic variability and disease progression

Recent publications

- Dharaskar SP, Amere Subbarao S (2023) The mitochondrial chaperone TRAP-1 regulates the glutamine metabolism in tumor cells. ***Mitochondrion*** 69: 159-170.
- Kanugovi Vijayavittal A, Kumar P, Sugunan S, Joseph C, Devaki B, Paithankar K, Amere Subbarao S (2022) Heat shock transcription factor HSF2 modulates the autophagy response through the BTG2-SOD2 axis. ***Biochemical and Biophysical Research Communications (BBRC)*** 600: 44-50.

Cancer emerges from genetic and epigenetic mechanisms and is considered an adaptive disease. Heat shock proteins function as molecular chaperones and are implicated in cellular adaptations. Among them, the Hsp90 chaperone contributes to the conformational maturation and functional stabilisation of mutated gene products and, hence, is considered a cancer chaperone. Our laboratory understands the roles of Hsp90 and its isoforms in cancer adaptations leading to disease progression and develops novel antitumor strategies that irreversibly target cancer. We demonstrated that Hsp90 is involved in oncogene addiction and transformation, facilitating tumour cell proliferation and metastasis. Hsp90 also contributes to epigenetic reprogramming and acquired multidrug resistance of cancer, while its mitochondrial homologue, TRAP-1, is engaged in metabolic rewiring. We demonstrated that TRAP-1 facilitates glutamine metabolism by grossly influencing mitochondrial functions, primarily oxidative phosphorylation (OXPHOS). Since mitochondria have descended from bacteria through endosymbiosis, we extended our studies and found that the bacterial homologue, HtpG, and baker's yeast homologue, Hsc82, exhibited similar functions to TRAP-1. Examining the knockouts (KO) for HtpG, Hsc82, and Hsp82 indicated that there are gross alterations in the cell (in the case of bacteria) and mitochondrial organisation (in the case of yeast) and metabolic pathways, suggesting that Hsp90 forms and their functions are evolutionarily conserved across species. We are presently working on understanding the role of these chaperones in maintaining mitochondrial integrity, cellular metabolism, and anti-apoptotic processes. On the other hand, we study the role of these chaperones in chemotherapy-induced phenotypic variability, altered epigenetic landscape, and disease aggression in preclinical models.



FA. Comparison of wild type (MG1655) and ΔHtpG E.coli cell morphology. The nucleus is stained with DAPI. B. Comparison of Oxygen Consumption Rate (OCR) between wild type and ΔHtpG *E.coli*. C. Comparison of wild type and Hsp82 and Hsc82 knockout (KO) *Saccharomyces cerevisiae* cell morphology. The mitochondria are stained with CMX-Ros. D. Comparison of OCR between wild type and KO cells. DIC: differential imaging contrast. Images A and B were captured using a scanning confocal imaging microscope (63X magnification). Images C and D were captured using the Elyra SIM2 Apotome (100x magnification). Wt: Wild type; DIC: Differential Interference Contrast; DAPI: 4′,6-diamidino-2-phenylindole; CMX-Ros: Mitotracker Red.

B KIRAN KUMAR

Niche and micro environment following cellular injuries

From left to right, front row: Renuga Devi, Jessie Thomas, Dr. B Kiran Kumar, Nehal Goyal, Khyathi Ratna
Back row: Mohammed Ghalib, Yash Rajendra Parekh, Hariharan, Gayathri

Research interests

To understand the factors which influence the cell or tissue recovery or regeneration following injury and possible therapeutic interventions using molecules and also use of stem cells for regeneration and restoration of dysfunctional cells/damaged tissues using *in vitro* and *in vivo* models

Recent publications

- Singh V, Chameettachal S, Venuganti A, Parekh Y, Prasad D, Sahoo A, Bokara K, Pati F, Basu S (2022) A biomimetic hydrogel-based therapeutic approach for preventing corneal scarring. ***Investigative Ophthalmology & Visual Science*** 63: 2638-2638.
- Singh VK, Kethiri AR, Venuganti A, Sahoo A, Salman M, Bokara K, Basu S, Singh V (2022) Assessment of epithelial restoration using limbal allograft transplantation in rabbit model with persistent corneal epithelial defect. ***Investigative Ophthalmology & Visual Science*** 63: 3231-A0266.
- Chauhan M, Bhardwaj VK, Kumar A, Kumar V, Kumar P, Enayathullah MG, Thomas J, George J, Kumar BK, Purohit R, Kumar A, Kumar S (2022) Theafavin 3-gallate inhibits the main protease (Mpro) of SARS-CoV-2 and reduces its count *in vitro*. ***Scientific Reports*** 12: 13146.
- Pandit SK, Chauhan P, Sinhamahapatra A, Parekh Y, Enayathullah MG, Bokara KK, Kumar A (2022) Covid -19 repellent cloth. ***Frontiers in Chemical. Engineering, Sec. Surface and Interface Engineering*** doi: doi.org/10.3389/fceng.2022.1066184.

Dry eye disease (DED) is an emerging global health concern with meibomian gland dysfunction (MGD) being the most common subtype of DED. Despite being quite prevalent, the pathophysiological mechanisms governing MGD are poorly understood. Animal models for MGD can be a valuable resource to advance our understanding of this entity and explore novel diagnostic and therapeutic modalities. Although a lot of literature on rodent MGD models exists, a comprehensive review on rabbit animal models is lacking. Rabbits offer a great advantage over other animals as models for studying both DED and MGD. Rabbits have a widely exposed ocular surface and meibomian gland anatomy comparable with humans, which makes performing dry eye diagnostic tests possible using clinically validated imaging platforms. The existing MGD models in rabbits can broadly be classifed as pharmacologically induced and surgically induced models. Most models show keratinization of the meibomian gland orifce with plugging as the fnal common pathway for developing MGD. Thus, understanding the advantages and disadvantages of each rabbit MGD model can help researchers choose the appropriate experimental plan based on the objective of the study. In the review in Indian Journal of Opthamology, we discuss the comparative anatomy of the meibomian glands in humans and rabbits, various rabbit models of MGD, translational applications, unmet needs, and future directions in developing MGD models in rabbits. Dry eye disease (DED) is an emerging health issue affecting people worldwide. There have been rapid advances in the development of novel molecules and targeted therapies for the treatment of DED in the recent past. For testing and optimizing these therapies, it is necessary to have reliable experimental animal models of DED. One such approach is the use of benzalkonium chloride (BAC). Several BAC-induced DED models of rabbits and mice have been described in literature. BAC induces high levels of proinflammatory cytokines in the cornea and conjunctiva, along with epithelial cell apoptosis and reduction of mucins, which leads to tear film.

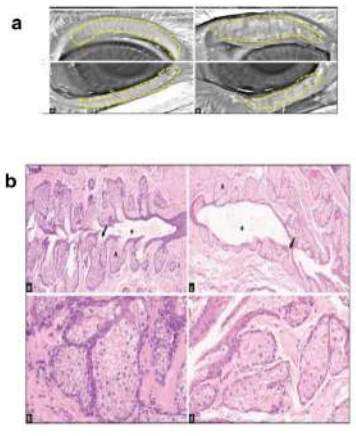


Figure 1

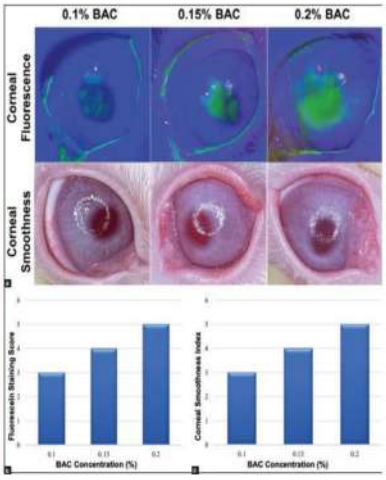


Figure 2

Fig 1: (a) Meibomian gland imaging in rabbits. (a) Meibography images of normal upper and lower eye lid of rabbit depicting shorter and more numerous glands in rabbits; Left, top to bottom (b) Meibography images of upper and lower eye lid of meibomian gland dysfunction of rabbit following intraductal cauterization of the MG orifces; right, top to bottom.
(b) Histopathological characteristics of meibomian gland postintraductal cauterization. (a) Photomicrograph of an 11 month old rabbit showing a normal central duct (asterix), ductules (one way arrow), and secretory acini (arrow head) of normal meibomian gland (MG) (H and E; 10 × original magnifcation). (b) Magnified image of normal MG acini of rabbit (H and E; 40 × original magnification). (c) Postintraductal electrocauterization: Photomicrograph shows markedly dilated central duct (asterix), dilated and shortened ductules (one way arrow) with reduction in size of secretory acini (arrow head) of electro cauterized gland (H and E; 10 × original magnification). (d) Shrunken and increased number of acini post electrocautery. (H and E; 40 × original magnification)

Figure 2: Clinical imaging and scoring after 2 weeks of BAC administration. Columns 1–3 comprise corneas instilled with 0.1%, 0.15%, and 0.2% BAC, respectively. (a) First row shows the slit lamp images of corneas after fluorescein staining, while the second row shows the corneal smoothness images. Graphs represent the (b) fluorescein staining score and (c) corneal smoothness index. BAC = benzalkonium chloride

DHANANJAY CHATURVEDI

In vivo Muscle Repair and Maintenance

From left to right, background: Sarasij Pal, Dhananjay Chaturvedi, Shashank MS, Kanthi MP, Swaraj Ranjan Paul
Foreground: Megha Menon and Thanishta Kumar

Research interests

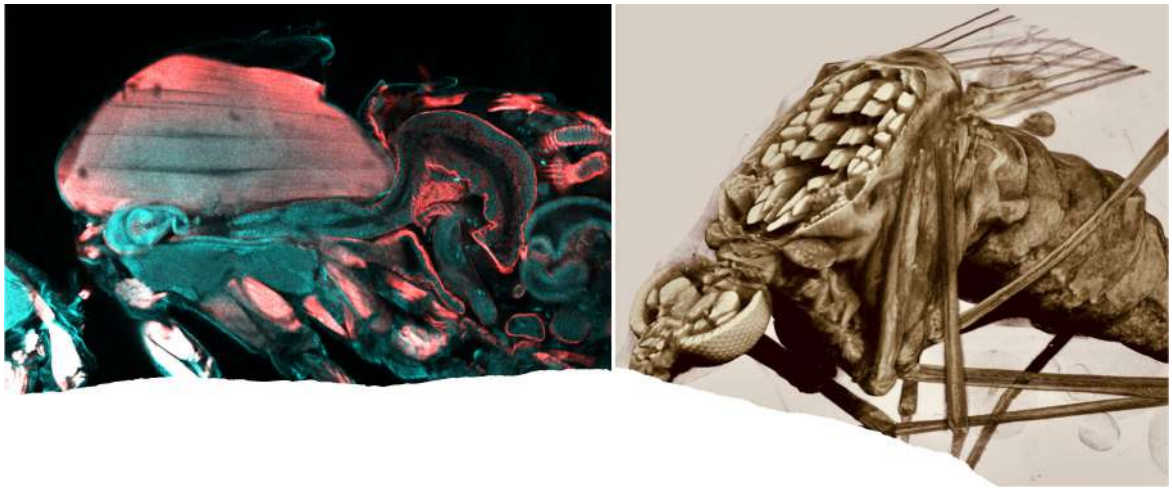
- *In vivo* muscle maintenance and homeostasis
- Insect anatomy

Skeletal muscles, the kinds that we rely on for movement of limbs and body have fascinating form and functions. They differ from most other cells in the body by virtue of being contractile syncytia. We are interested in understanding *in vivo* principles underlying their repair and homeostasis.

As muscles accumulate damage and age, they are repaired by group of stem cells with markedly different properties called satellite cells. In vertebrates, molecular properties and behaviours have been investigated through a valuable reductionist approach for several decades, aimed to decouple the role of individual cues that muscles receive. We attempt to study their behaviour and contribution to muscle repair in an *in vivo* setting that integrates all the cues ranging from nutrition, immune signals and the physical environment.

Such an approach may provide insights that may further not only our conceptual understanding of cellular behaviour but impact therapy of injury and dystrophic conditions. With this aim we leverage the power of *Drosophila* genetics to vary conditions at a cellular and molecular level to make definitive substantive observations.

Even as muscles function without major injury, we ask if cellular processes operate uniformly over the length of a muscle syncytium at can be hundreds of microns long. Our findings suggest that there may be specific cytological processes that operate non uniformly over the length of a muscle cell and that their disruption can cause dystrophy like conditions. Such fundamental granular detail may inform treatment of similar conditions at a later date.



To the left, in a slice of a fruit fly, we show Dorsal Longitudinal Muscles (orange) in the thorax through immunofluorescence. To right we show a slice through a CT scan of an adult *Anopheles* mosquito.

DIVYA TEJ SOWPATI

Bioinformatics, Big Data, Algorithms in Biology

From left to right, Standing: Sofia, Arvind, Onkar, Saketh, Payel, Kiran, Akshay, Tej, Victor, Malini, Nitesh, Priyanka, Wasim, Shruti
Sitting: Reuben, Sree, Priya, Anukrati, Pratheusa, Ramya

Research interests

- Genetic variation in Indian populations
- Single cell genomics
- Algorithms in big data analysis
- DNA methylation

Recent publications

- Kemp SA, Cheng MTK, Hamilton WL, Kamelian K, Indian SARS-CoV-2 Genomics Consortium (INSACOG), Singh S, Rakshit P, Agrawal A, Illingworth CJR, Gupta RK (2022) Transmission of B.1.617.2 Delta variant between vaccinated healthcare workers. ***Scientific Reports*** 12: 10492.
- Tandel D, Sah V, Singh NK, Potharaju PS, Gupta D, Shrivastava S, Sowpati DT, Harshan HK (2022) SARS-CoV-2 Variant Delta Potently Suppresses Innate Immune Response and Evades Interferon-Activated Antiviral Responses in Human Colon Epithelial Cells. ***Microbiology Spectrum*** 10: e01604-22.
- Sureka R, Avvaru AK, Sowpati DT, Pathak RU, Mishra RK (2022) Structural and developmental dynamics of Matrix associated regions in Drosophila melanogaster genome. ***BMC Genomics*** 23: 725.
- Munigela A, Sowpati DT, Sasikala M, Banu S, Siva AB, Kumar VJ, Nutalapati C, Vishnubhotla R, Kulkarni A, Mukherjee P, Zaveri L, Rao GV, Tallapaka KB, Reddy DN, CCMB COVID-19 Team, AIG Hospitals COVID-19 Vaccine Study Team (2022) Clinical outcomes in individuals hospitalized with SARS-CoV-2 Delta variant (B.1.617.2) who had been vaccinated with Covishield (ChAdOx1) and Covaxin (BBV-152). ***IJID Regions*** 104-110.
- Singha B, Behera D, Khan MZ, Singh NK, Sowpati DT, Gopal B, Nandicoori VK (2023) The unique N-terminal region of Mycobacterium tuberculosis Sigma Factor A (σA) plays a dominant role in the essential function of this protein. ***Journal of Biological Chemistry*** 299: 102933.

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.

GHANSHYAM SWARUP

Molecular Mechanism of Neurodegreneration caused by Mutations in Optineurin

From Left to Right: Ghanshyam Swarup, Swetha Medchalmi

Research interests

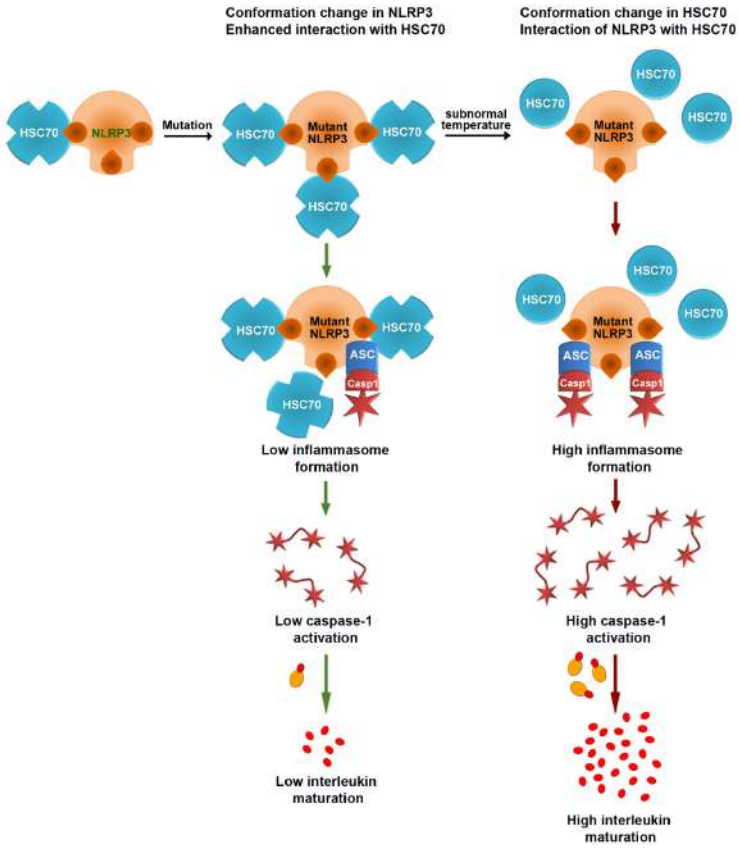
- To explore the functions of the protein optineurin, and how mutations alter its functions to cause neurodegenerative diseases
- To understand signalling by cytoplasmic immune receptors NLRC4 and NLRP3, and how mutations alter this signalling to cause autoinflammatory syndromes

Recent publications

- Moharir SC, Raghawan AK, Ramaswamy R, Swarup G (2022) Autophagy-independent cytoprotection by optineurin from toxicity of aggregates formed by mutant huntingtin and mutant ataxin-3. ***The Journal of Biological Chemistry*** 171: 555-565.
- Moharir SC, Swarup G (2022) Optineurin deficiency induces patchy hair loss but it is not sufficient to cause amyotrophic lateral sclerosis in mice. ***Biochimica et Biophysica Acta (BBA) - Molecular Basis of Disease*** 1868: 166470.
- Raghawan AK, Radha V, Swarup G (2022) HSC70 as a sensor of low temperature: role in cold-triggered autoinflammatory disorders. ***FEBS Journal*** 289: 8037-8049.
- Moharir SC, Sirohi K, Swarup G (2023) Regulation of transferrin receptor trafficking by optineurin and its disease-associated mutants. ***Progress in Molecular Biology and Translational Science*** 194: 67-78.
- Raghawan AK, Ramaswamy R, Swarup G (2023) Cold-induced loss of interaction with HSC70 triggers inflammasome activity of familial cold autoinflammatory syndrome-causing mutants of NLRP3. ***Biochemical and Biophysical Research Communications*** 641: 42-49.

Optineurin/OPTN polymorphism, M98K is associated with normal tension glaucoma in certain populations including Indian. We hypothesized that M98K-OPTN may sensitize retinal ganglion cells to various types of stress. To test this hypothesis, stable clones of a retinal cell line, 661W, expressing either wild-type (WT)-OPTN or M98K-OPTN were generated, and examined for their survival under various stress conditions. Our results show that M98K-OPTN sensitizes retinal cells to TNFα and ER stress-induced cell death. We also show that M98K-OPTN alters ER stress response signalling, which possibly enhances the sensitivity of retinal cells to ER stress. Our results provide support to the hypothesis that M98K-OPTN may cooperate with other genetic or environmental factors to cause retinal ganglion cell death associated with glaucoma.

Several gain-of function mutations of cytoplasmic immune receptor NLRP3 cause hereditary disorder of cold-induced hyper-inflammation known as familial cold autoinflammatory syndrome-1 (FCAS1). Although, caspase-1 activation and downstream interleukin-1β / interleukin-18 maturation are common effectors in pathophysiology of this disorder, molecular mechanisms of how exposure to subnormal temperature triggers mutant NLRP3-inflammsome activity is not understood. Our results suggest that interaction with HSC70 suppresses inflammasome formation by FCAS-causing NLRP3 mutants at physiological temperature, and loss of this inhibitory association at subnormal temperature causes aggravated inflammasome formation and caspase-1 activation leading to interleukin-1β maturation (Fig 1). These results provide evidence for HSC70 being a cold-sensor and a temperature-dependent regulator of inflammatory signaling by FCAS-causing NLRP3 mutants.



A model showing proposed mechanism of regulation of FCAS (Familial cold auto-inflammatory syndrome) -causing mutants of NLRP3 by HSC70 in a temperature-dependent manner. Wild-type NLRP3 interacts with HSC70 and this interaction is increased by FCAS-causing mutations of NLRP3. It is proposed that FCAS-causing mutations induce a conformational change in NLRP3 that exposes HSC70-binding sites resulting in enhanced interaction of these mutants with HSC70. This interaction with HSC70 keeps the activity of NLRP3 mutants suppressed. Upon exposure to subnormal temperature, HSC70 undergoes a conformational change resulting in loss of binding to the NLRP3 mutants. This leads to enhanced inflammasome formation and caspase-1 activation by the mutants, resulting in enhanced cytokine maturation and release. Our results provide evidence for HSC70 being a cold-sensor and a temperature-dependent regulator of inflammatory signaling by FCAS-causing NLRP3 mutants.

GIRIRAJ RATAN CHANDAK

Genomic Research on Complex Diseases

From left to right, front row: Seema Bhaskar, PSKDB Punyasri
Second row: P Vaidehi, Nahid Anjum, Meenal Meshram, Sowmya Mekala, Sumit Paliwal
Third row: Alagu Sankareswaran, Shagufta Tasneem, Sohail Rafik Mansuri, Jukanti Akshitha
Last row - Swati Bayyana, Jandhyala Vyshnavi, Archana D, Giriraj Ratan Chandak, Dimple Lavanuru, Aditya Naman Soni

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 causality.

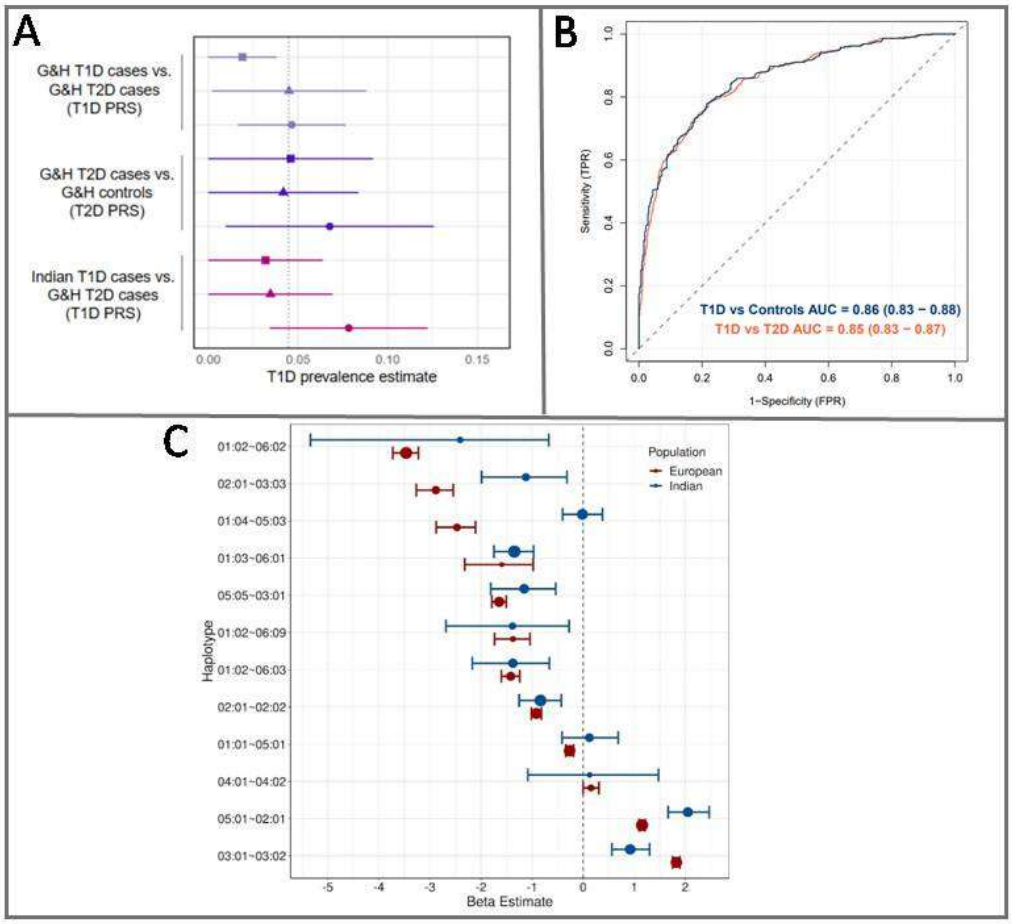
Recent publications

- Loh M, et al. (2022) Identification of genetic effects underlying type 2 diabetes in South Asian and European populations. ***Communications Biology*** 5: 329.
- Dave K, Kaur L, Sundrani D, Sharma P, Bayyana S, Mehendale S, Randhir K, Chandak GR, Joshi S (2022) Association of placental fatty acid desaturase 2 (FADS2) methylation with maternal fatty acid levels in women with preeclampsia. ***Prostaglandins, Leukotrienes and Essential Fatty Acids*** 184: 102472.
- Ramdas S, et. al. (2022) A multi-layer functional genomic analysis to understand noncoding genetic variation in lipids. ***The American Journal of Human Genetics*** 109: 1366– 1387.
- Lad H, Naskar S, Punyasri Pasupuleti SKDB, Nahrel R, Sihare P, Chandak GR, Patra PK (2022) Evaluation of pharmacological efficacy and safety of hydroxyurea in sickle cell disease: Study of a pediatric cohort from Chhattisgarh, India. ***Pediatric Hematology and Oncology*** 40: 395-406.
- Yengo L, et. al. (2022) A saturated map of common genetic variants associated with human height. ***Nature*** 610: 704-712.
- Masson E, et. al. (2022) The PRSS3P2 and TRY7 deletion copy number variant modifies risk for chronic pancreatitis. ***Pancreatology*** 23: 48-56.
- Kanoni S, et. al. (2022) Implicating genes, pleiotropy, and sexual dimorphism at blood lipid loci through multi-ancestry meta-analysis. ***Genome Biology*** 23: 268.

- Kaur L, Sundrani D, Dave K, Randhir K, Mehendale S, Bayyana S, Kalyanaraman K, Chandak GR, Joshi S (2023) Hypoxia Inducible Factors (HIF1α and HIF3α) are differentially methylated in preeclampsia placentae and are associated with birth outcomes. ***Molecular and Cellular Biochemistry*** 478: 2309–2318.
- Khare SP, Madhok A, Patta I, Sukla KK, Wagh VV, Kunte PS, Raut D, Bhat D, Kumaran K, Fall C, Tatu U, Chandak GR, Yajnik CS, Galande S (2023) Differential expression of genes influencing mitotic processes in cord blood mononuclear cells after a pre-conceptional micronutrient-based randomised controlled trial: Pune Rural Intervention in Young Adolescents (PRIYA). ***Journal of Developmental Origins of Health and Disease*** 14: 437-448.

India is the diabetes capital of the world. A correct diagnosis of the two major subtypes, type 1 (T1D) and type 2 (T2D) is important as the optimal treatment differs. But it is challenging due to overlapping symptoms, particularly in South Asians. We investigated the utility of the earlier developed 9-SNP polygenic risk score (PRS1) in South Asians using ancestry-optimised PRS1 in East London Genes & Health cohort. We observed a prevalence of ~6% T1D in the group with ambiguous diagnosis and correctly diagnosed 4.5% of previously diagnosed T2D as having T1D, confirming the utility of PRS1 in robust diagnosis.

Subsequently, we generated a 67-SNP PRS (PRS2) using the imputed high-throughput genomic data on 593 T1D, 1116 T2D and 317 control subjects and assessed its power of classification using Area Under Curve (AUC) of Receiver Operator Characteristic (ROC) curve. Although the PRS2 was better discriminative of T1D and T2D but still lower power compared to the Europeans (AUC: 0.86 vs 0.93; P<0.001).Genetic variants in the Human Leukocyte Antigen (HLA) locus are known to strongly contribute to T1D risk. Association analysis of this region showed directional consistency for the reported HLA DQA1~DQB1 haplotypes between Indians and Europeans but the effect sizes were significantly different. The protective DQ haplotype 01:03~06:01 had higher frequency in Indians (~20%) compared to Europeans (~1%), whereas the most frequent European DQ haplotype 01:02~06:02 (15%) was present in only 1.5% Indians. The haplotype 05:01~02:01 had twice the effect size in Indians (2.05 [1.67–2.48], $P=1.37x10^{-23}$) than in Europeans (1.16 [1.10-1.25], $P<2.2x10^{-16}$) whereas an inverse relationship for 03:01~03:02 was noted (Indians=0.92 [0.56-1.30], $P=9.6x10^{-7}$; Europeans=1.83 [1.76-1.90], $P<2.2x10^{-16}$). Our results highlight the power of polygenic risk scores in robust diagnosis of diabetes, the need to capture HLA genetic diversity in Indians and overall importance of ethnicity in genetic association studies.



Discrimination and robust diagnosis of Diabetes subtypes
A: Estimates of misclassification rates in the groups with ambiguous diagnosis in the ELGH cohort. The point type indicates the statistical methods used for estimation (Circle – Earth mover's Distance, Triangle – Kernel density estimation, Square – Means methods).
B: Comparison of the discrimination ability of T1D PRS2 in classifying T1D from T2D and Controls from India.
C: Comparison of the effect size of HLADQ haplotypes associated with T1D in Indians and Europeans.
(T1D, type 1 diabetes; T2D, type 2 diabetes; PRS, polygenic risk score; ELGH (GH), East London Genes and Health cohort)

G UMAPATHY

Understanding Species Extinction and Conservation Physiology

From left to right: Anusha Kiran, Vinay Teja, Rihil Wagh, Neel Ganguly, Vinod Kumar, Aamer Khan, G. Umapathy, Shahid Hameed, S. Manu, Manisha Ray, Gopi Krishnan and Jaya Ranga

Research interests

- Understanding species' extinction in human-dominated landscapes
- Conservation physiology
- Environmental DNA and genomics in Biodiversity conservation

Recent publications

- Iyer P, Kumar V, Reddy M, Umapathy G (2022) Impacts of Livestock Grazing on Fecal Glucocorticoid Levels and Gastrointestinal Parasite Prevalence in Blue Sheep in Spiti Valley, Western Himalayas. ***Journal of Endocrinology and Reproduction*** 26: 43-51.
- Ray M, Umapathy G (2022) Environmental DNA as a tool for biodiversity monitoring in aquatic ecosystems – a review. ***Journal of Threatened Taxa*** 14: 21102–21116.
- Trivedi M, Sree DK, Biswas J, Umapathy G (2022) Genetic Diversity and Population Structure in Western Hoolock (*Hoolock hoolock*) Gibbons in India. ***International Journal of Primatology*** 44: 1–5.
- Prabhakaran GK, Sunkara M, Raghavan R, Umapathy G (2022) Development of a species-specific qPCR assay for the detection of invasive African sharptooth catfish (*Clarias gariepinus*) using environmental DNA. ***Biological Invasions*** 25: 975–982.
- Kumar V, Manu S, Caroline K, Sekhar A, Mamta SK, Sandeep M, Wasimuddin, Senthilkumaran B, Umapathy G Discovery of 16-Androstenes (Androstenone and Androstenol), Their Synthesis Pathway, and Possible Role in Reproduction of Mouse Deer (*Moschiola indica*). ***Cells*** 11: 3837.

Successful breeding of mouse deer

Captive breeding has become an important tool for conserving threatened species and its success depends on the survival of species through self-sustaining populations.

Mouse deer is a primitive deer which plays a crucial role in the forest ecosystem as a key seed disperser and forms significant prey for both small and large predators. Despite its significance, little is known about this species' mating behavior and reproductive physiology in both the wild and captivity. As a part of the conservation breeding and species recovery program, a breeding program of mouse deer was started by the Nehru Zoological Park, Hyderabad in collaboration with CCMB to breed them in captivity and release them into the wild.

This program began with six founder individuals and bred successfully into 450 individuals within 10 years. Most of the captive bred individuals have been introduced into the wild.

Discovery of 16-Androstene pheromones in mouse deer

We discovered 16-androstenes pheromone in mouse deer during captive breeding program and examined the molecular characteristics, their synthesis pathway, and functional role of these compounds in reproduction. *CYP17A1* and *CYB5* genes were cloned and expressed in HEK-293, COS-7 cell lines and gonads of mouse deer to investigate *CYP17A1* gene's andien-β-synthase activity towards synthesis of 16-androstenes in mouse deer. Results showed that mouse deer's *CYP17A1* gene possesses andien-β-synthase activity and could transform pregnenolone into 5,16-androstadien-3β-ol. The expression of *CYP17A1* gene was upregulated in the testis and ovary, compared to other tissues in mouse deer. Significantly elevated androstenone and estrogens were recorded prior to delivery and postpartum estrus / mating in mouse deer and weak correlations between fecal androstenone and estrogens/ androgens in mouse deer during breeding season. The findings suggest that androstenone play a role in the reproductive activities of mouse deer. The knowledge can be used for captive breeding programs of mouse deer in India.

A captive bred mouse deer at the Nehru Zoological Park, Hyderabad

HITENDRA K PATEL

Plant-Pathogen Interactions and Plant Breeding

From left to right, first row: Hitendra Patel, Raju Madnala, Kranthi Brahma, Vinoth Kumar, Bipin Kumar, Kamal Kumar Malukani
Second row: Md. Jamaloddin, Rajkanwar Nathawat, Vishnu NM, Komal Awalellu, Gokulan CG, Anjana Sharma
Third row: Rennya PR, Deepak Niranjan, Apoorva Masade, Gattu Niranjan, Mitadru Mukherjee, Praveen Kumar Nayak
Fourth row: Maliha A, Nazia Khatoon, Devika Talwar, Jagati Rajasri Anjali, Nisha Sao

Research interests

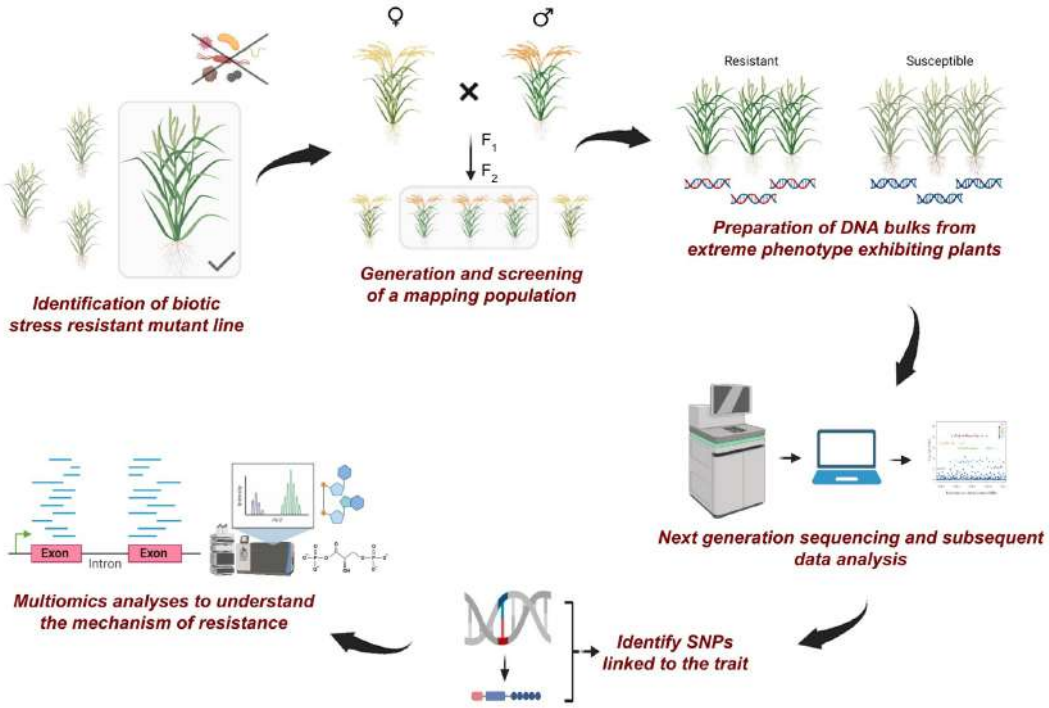
- Rice functional genomics
- Molecular plant-microbe interactions
- Marker-assisted selection

Recent publications

- Gandra J, Patel HK, Kumar SA, Doma M, Deepthi Y, Bhalothia P, Jalaja N, Chimakurthy J, Polavarapu R, Katam R, Suravajhala P, Kavi Kishor PB (2022) Metabolomic and proteomic signature of Gloriosa superba leaves treated with mercuric chloride and phenylalanine, a precursor of colchicine alkaloid. ***Industrial Crops and Products*** 178: 114557.
- Deb S, Gokulan CG, Nathawat R, Patel HK, Sonti RV (2022) Suppression of XopQ-XopX-induced immune responses of rice by the type III effector XopG. ***Molecular Plant Pathology*** 23: 634-648
- Nathawat R, Maku RV, Patel HK, Sankaranarayanan R, Sonti RV (2022) Role of the FnIII domain associated with a cell wall-degrading enzyme cellobiosidase of *Xanthomonas oryzae* pv. *oryzae*. ***Molecular Plant Pathology*** 23: 1011-1021.
- Rekha G, Kumar VA, Gokulan CG, Koushik MBVN, Prasanna BL, Kulkarni S, Aleena D, Harika G, Hajira SK, Pranathi K, Punniakoti E, Kale RR, Kumar TD, Ayyappa D, Anila M, Sinha P, Manohara KK, Padmavathi G, Subba Rao LV, Laha GS, Srinivas Prasad MS, Fiyaz RA, Suneetha K, Balachandran SM, Patel HK, Sonti RV, Senguttuvel P, Sundaram RM (2022) DRR Dhan 58, a Seedling Stage Salinity Tolerant NIL of Improved Samba Mahsuri Shows Superior Performance in Multi-location Trials. ***Rice (N Y)*** 15: 45.
- Rana R, Madhavan VN, Saroha T, Bansal K, Kaur A, Sonti RV, Patel HK, Patil PB (2022) *Xanthomonas indica* sp. nov., a Novel Member of Non-Pathogenic *Xanthomonas* Community from Healthy Rice Seeds. ***Current Microbiology*** 79: 304.

Our current rice research program includes the development of newer rice varieties for several important agronomic traits. Rice crops are susceptible to many biotic and abiotic stresses. The biotic stresses that we are trying to address include bacterial blight [BB; caused by a bacterial pathogen *Xanthomonas oryzae* pv. *oryzae* (*Xoo*)], sheath blight (ShB; caused by a fungal pathogen *Rhizoctonia solani*), and yellow stem borer (YSB; an insect pest of rice). In collaboration with the ICAR-Indian Institute of Rice Research (ICAR-IIRR), we have screened the EMS mutagenized population of Samba Mahsuri rice for several important agronomic traits and identified a few mutant lines that show the desired important agronomic traits including enhanced tolerance to biotic (BB, ShB and YSB) and abiotic (Lodging) stresses, early maturation and higher yield. Using functional genomics approach, transcriptome and metabolome analyses we have characterized a few selected mutants that show the desired agronomic traits. We have identified candidate genomic loci that might be associated with enhanced tolerance phenotype to above-mentioned biotic and abiotic stresses and agronomic traits. We are further validating the association of these markers/candidate regions with the desired trait of interest.

In parallel, we are also involved in plant-pathogen interaction studies using rice-*Xoo* and rice-*R. solani* as model systems. Plant-pathogen interaction is governed by multi-layered functions from both the host and the pathogen side. Plants possess an active basal immunity as well as pathogen-induced immunity that works to keep pathogens at bay. On the other hand, pathogens use various virulence factors for their pathogenesis. For successful pathogenicity, pathogens rely on manipulation of various host susceptibility factors. Through transcriptomics studies, we have identified candidate host susceptibility genes, and we are further validating the roles of candidate genes in rice susceptibility to *Xoo* and *R. solani* using a multiplexed CRISPR-Cas9 genome editing approach.



Workflow for the characterization of rice mutant lines

IMRAN SIDDIQI

Plant Reproductive Biology

From left to right, standing: Kaladhar Bethoju, Survi Mahesh, Imran Siddiqi, Vishakha Bharadwaj, Aswan Nalli, Chandan Kumar, Avinash Singh, Keith Frank, Bhaskar
Seated: Anand Singh, Sai Kiran, Sivakumar Prakash, Jayeshkumar Davda, Ginkuntla Saikiran, Arkasaradhi Gope

Research interests

Our laboratory works on understanding the control of meiosis and germ cell formation 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.

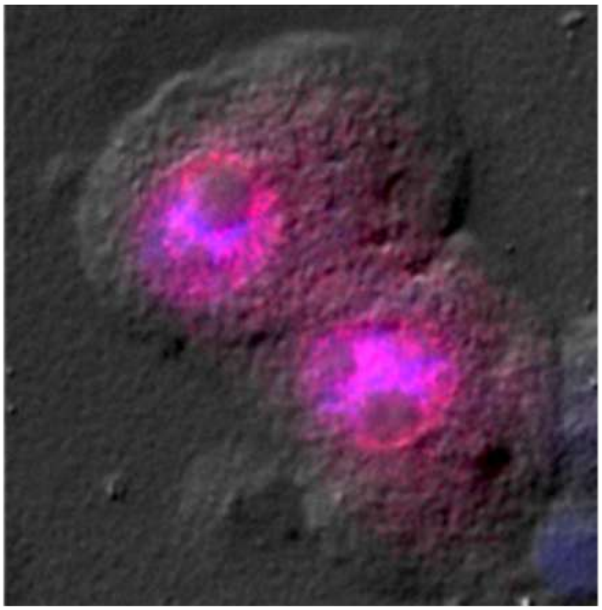
Recent publications

- Singh DK, Gamboa RS, Singh AK, Walkemeier B, Van Leene J, De Jaeger G, Siddiqi I, Guerois R, Crismani W, Mercier R (2023) The FANCC-FANCE-FANCF complex is evolutionarily conserved and regulates meiotic recombination. ***Nucleic Acids Research*** 51: 2516-2528.

We have studied the role of the *SHUKR* (*SKR*) gene in pollen development in Arabidopsis. SKR functions in meiosis to direct postmeiotic development of spores into pollen. This is an unexpected finding as the sporophyte (diploid) and gametophyte (haploid) form distinct generations in land plants and previous studies indicate gametophyte development to be controlled by genes that act in the gametophyte. We find instead that *SKR* acts in the sporophyte to control gametophyte development. The results reveal a new regulatory interface between the sporophyte and gametophyte.

In continuation of earlier work on the Arabidopsis *CDM1* gene in meiosis we have shown that *CDM1* expression is DNA damage inducible in vegetative cells, *CDM1* is required for genome integrity in male meiosis independent of SPO11-induced DNA double strand breaks, suggesting a role in regulation of premeiotic replication repair.

In collaboration with the laboratories of Raphael Mercier and Rajeev Kumar (INRA Versailles, France) we are studying the control of monopolar centromere orientation in meiosis and have identified 12 mutants mapped to 10 genes that affect monopolar orientation. The genes include components of the sister chromatid cohesion machinery as well as genes that encode components of the kinetochore. In a second collaborative project we have examined the contribution of the *FANCC*, *FANCE*, and *FANCF* genes in control of crossovers in meiosis by the interference insensitive Class II crossover pathway. The results support the hypothesis that *FANCC*, *FANCE*, and *FANCF* act additively with FANCM in reduction of Class II crossovers.



SKR expression in the nucleus of male meiocytes

ISHWARIYA VENKATESH

Regulation of Axon growth and Regeneration in the Mammalian Central Nervous System

From left to right: Manojkumar, Aastha Khiwani,Anisha Menon, Katha Sanyal, Sneha Manjunath, Ishwariya Venkatesh, Sanskruti Karwa, Shaik Shafiulla, Dhruva, Yogesh Sahu

Research interests

- Regulation of axon growth during nervous system development and regeneration

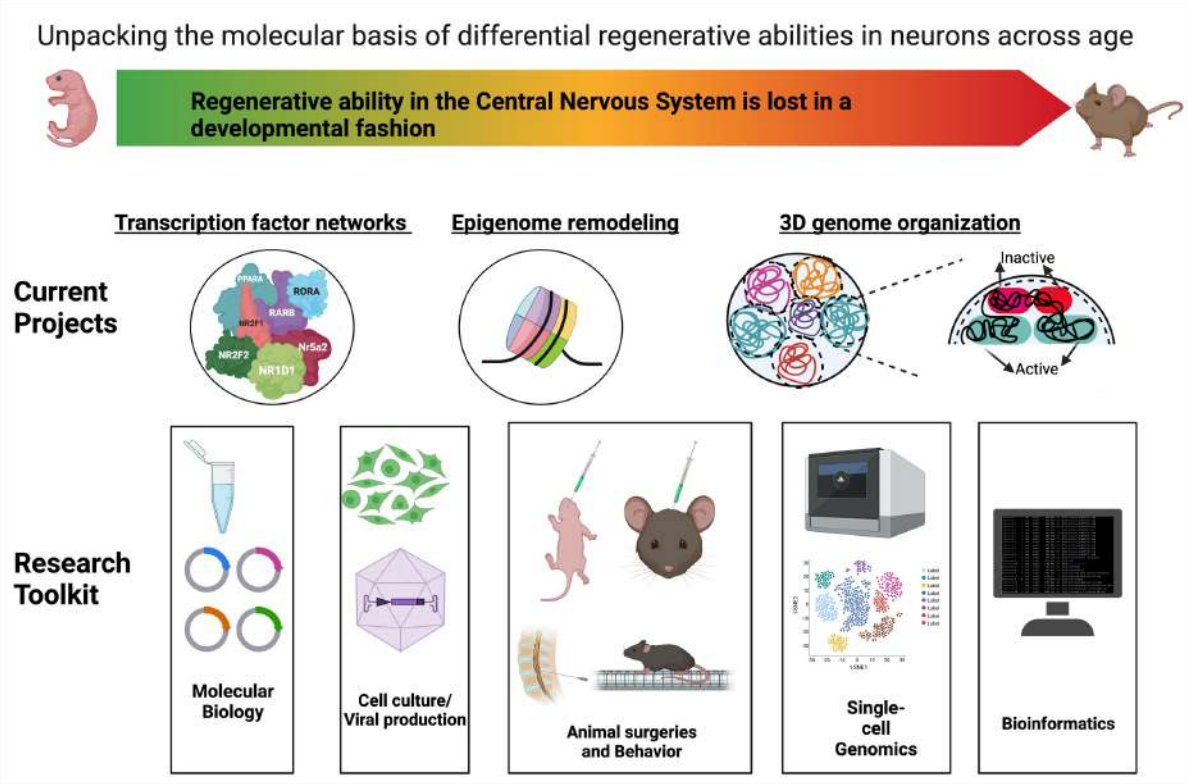
Our lab delves deep into the intricacies of axon growth, the long cables vital for neuron-to-neuron communication in the nervous system. During their early developmental phase, young neurons demonstrate a robust ability to regenerate and repair damaged axons. However, adult neurons are not as adept, often leading to irreversible damage in the nervous system.

Key Research Questions:

Why does regenerative capacity diminish as neurons mature?
What molecular pathways control developmental axon growth?
Do adult neurons require the reactivation of developmental mechanisms to achieve successful Central Nervous System (CNS) regeneration?
Can repair be coordinated through development-independent pathways?

To answer these pivotal questions, our research strategy combines:

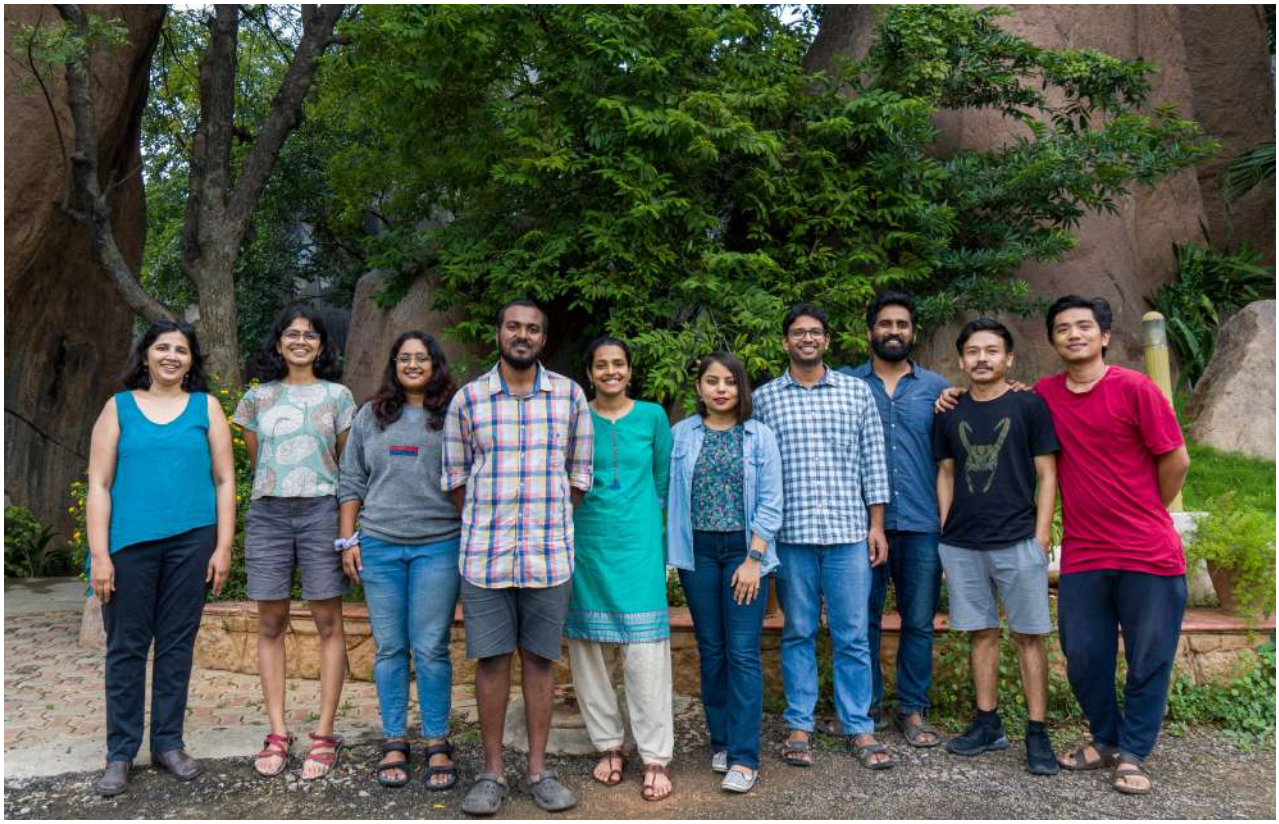
Bioinformatics: Analyzing large datasets for patterns and insights
Functional Genomics: Utilizing techniques such as Single-cell RNA-Seq, ATAC-Seq, Hi-C, and ChIP-Seq to explore the genome's functional elements
In vitro Assays: Monitoring growth dynamics under controlled conditions
In vivo Mouse Models: Studying injury and regenerative responses in a living organism
Behavioral Assessments: Evaluating the functional outcomes of neural injuries and regeneration



Schematic showing the lab's research overview, current projects, and techniques

JAHNAVI JOSHI

Systematics, Historical Biogeography & Diversification in the Tropical Forests



From left to right: Jahnavi, Maya, Payal, Pragyadeep, Bharti, Aditi, Mihir, Abhishek, Kaikho, Nehal

Research interests

- Systematic documentation of diversity in an integrative taxonomic approach in tropical Asian forests
- Examining the diversity, distribution, and assembly patterns and processes
- Macroecology & Macroevolution
- Biogeography
- Molecular Phylogenetics
- Soil Arthropods
- Tropical Forests

Recent publications

- Gopal A, Bharti DK, Page N, Dexter KG, Krishnamani R, Kumar A, Joshi J (2023) Range restricted old and young lineages show the southern Western Ghats to be both a museum and a cradle of diversity for woody plants. ***Proceedings of the Royal Society: Biological Sciences*** 290: 20222513.

1. Understanding the tempo and mode of diversification and their consequence for tropical biodiversity remains a key challenge as different taxa and regions exemplify distinct dynamics. We examined diversification rates and their drivers across 34 well-studied endemic lineages using birth-death models in Peninsular India (PI), one of the oldest regions of differentiation in the Oriental Realm. We showed that 18 lineages supported gradual diversification, indicating that the stability of the landscape was an important driver. Paleo temperature, Miocene aridification, monsoon intensification and existing species diversity explained non-uniform diversification patterns among 16 lineages. Speciation rates mainly drove the diversification and diversification rates were a major driver of differences in species diversity than clade ages for PI taxa. The importance of stability and regional biogeographic phylogenetic and geo-climatic history on the diversification dynamics among tropical landscapes was highlighted (Roy & Joshi, 2023, in prep).

2. We studied diverse freshwater arthropod assembly in rock pools on plateaus in the Western Ghats using Hierarchical Modeling of Species Communities approach. Environmental filtering was the dominant driver of community structure, where the pool-level covariates, explained greater variation (56.3%) in species occurrences rather than plateau-level covariates (climatic seasonality -33.7%). Spatial factors explained only 11% of the variation in species occurrences. The selected traits explained 22% variation in species' responses, with body size responding to the abiotic covariates at both spatial scales. Our results highlight the importance of habitat-level factors and the key role of evolutionary processes in shaping diversity in highly seasonal habitats (Kulkarni et al, 2023).

JANESH KUMAR

Investigations into architecture and mechanisms of glutamate receptor signaling complexes in the central nervous system

From left to right: Sanjay, Ithaya, Aswini, Somnath, Mukund, Geeth, Janesh, Swathi, Saurav, Rajesh

Research interests

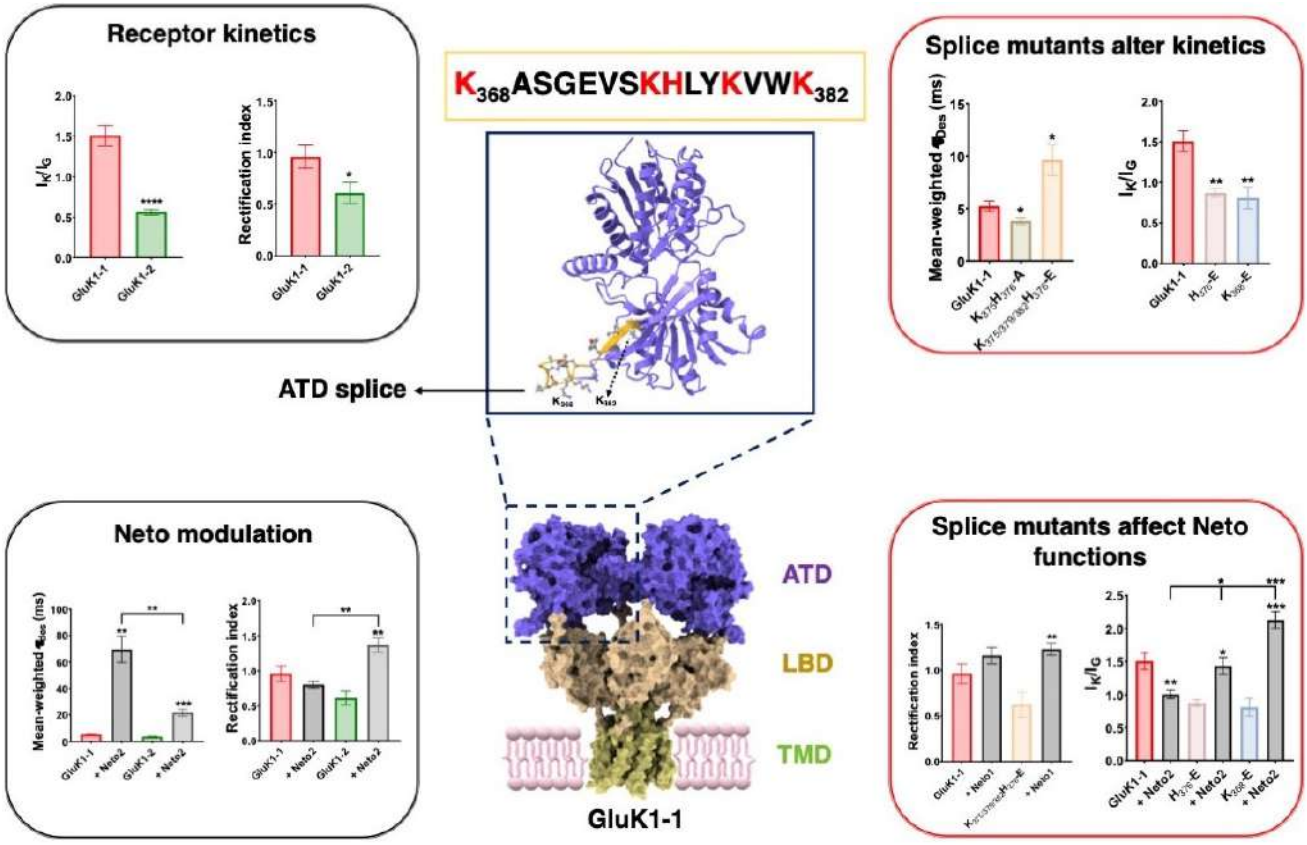
- Ionotropic glutamate receptors
- Membrane proteins
- Structural biology
- Cryo-EM

Recent publications

- Kumar J (2022) Ionotropic glutamate delta receptors: The enigma has finally begun to unravel. ***Neuropharmacology*** 207: 108944.
- Dhingra S, Yadav J, Kumar J (2022) Structure, Function, and Regulation of the Kainate Receptor. ***Subcellular Biochemistry*** 99: 317-350.

Functional Implications of the Exon 9 Splice Insert in GluK1 Receptors

Kainate receptors are key modulators of synaptic transmission and plasticity in the central nervous system. Different kainate receptor isoforms with distinct spatiotemporal expression have been identified in the brain. The GluK1-1 splice variant receptors, which are abundant in the adult brain, have extra fifteen amino acids inserted in the amino-terminal domain (ATD) of the receptor resulting from alternative splicing of exon 9. However, the functional implications of this post-transcriptional modification are not yet clear. We employed a multi-pronged approach using cryogenic electron microscopy, electrophysiology, and other biophysical and biochemical tools to understand the structural and functional impact of this splice insert in the extracellular domain of GluK1 receptors. Our study reveals that the splice insert alters the key gating properties of GluK1 receptors and their modulation by the cognate auxiliary Neuropilin and tolloid-like (Neto) proteins 1 and 2. Mutational analysis identified the role of key splice residues that influence receptor properties and their modulation. Furthermore, cryoEM structure of the variant shows that the presence of exon 9 in GluK1 does not affect the receptor architecture or domain arrangement in the desensitized state. Our study, thus, provides the first detailed structural and functional characterization of GluK1-1a receptors, highlighting the role of the splice insert in modulating receptor properties and their modulation.



Splice insert influences GluK1 receptor properties and its modulation by Neto proteins. Summary figure highlights the role of 15 amino acids inserted into amino terminal domain of GluK1 receptors. Splice residues not only influence the key gating properties of these receptors but also affect its modulation by auxiliary Neto 1 and Neto2 proteins. Mutational analysis identified K368, K375, H376, and K382 as key splice residues.

JYOTSNA DHAWAN

Molecular programs of quiescence in adult stem cells and skeletal muscle regeneration

From left to right, top row: Jyotsna Dhawan, Debarya Saha, Swetha Sunder, Bottom row: AS Priti, Ananga Ghosh, Kartik Jatwani

Research interests

- Control of cellular quiescence and its relationship to stem cell function
- Adult stem cells and skeletal muscle regeneration
- Epigenetic, transcriptional and post-transcriptional mechanisms in quiescence
- Secreted and mechanical signals in control of cell fate

Recent publications

- Atmakuru, P S and Dhawan J (2023) Opinion: The cilium-centrosome axis in coupling cell cycle exit and cell fate. ***Journal of Cell Science*** 136: jcs260454.
- Rumman M and J Dhawan (2022) PTPRU, a quiescence-induced receptor tyrosine phosphatase negatively regulates osteogenic differentiation of human mesenchymal stem cells. ***Biochemical and Biophysical Research Communications*** 636:41-49.
- Yao G, Dhawan J and Barr AR (2022) Cellular dormancy—State determination and plasticity. ***Frontiers in Cell and Developmental Biology*** 10:984347 (Editorial for Special Section on Cellular Dormancy).

Tissue-resident stem cells persist in adult mammalian tissues by entering a state of reversible quiescence/G0, which permits their reactivation to participate in repair and regeneration. We are particularly interested in the regulation of G0 in adult muscle stem cells (MuSC), but also investigate broader mechanisms coupling the cell cycle and cell fate in other stem cells. Three recent studies are summarized below:

A quiescence-induced receptor phosphatase PTPRU in hMSC fate decisions

Using reversibly quiescent hMSC which mirror the osteogenic cell fate preference of hMSC in vivo (Rumman et al, 2018, Stem Cell Res), we identified a receptor-type protein tyrosine phosphatase U to be induced in G0. Using RNAi, we uncovered a role for PTPRU in mediating the fate-changes seen in hMSC quiescence (Rumman and Dhawan, 2022) (Fig 1).

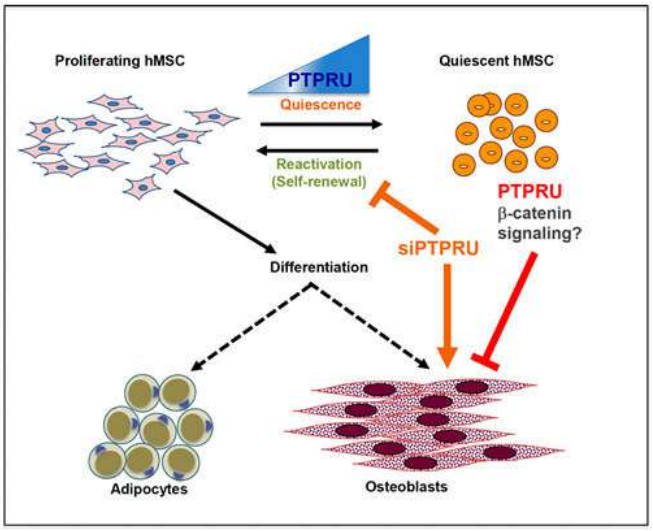
The biology of exosome signaling in quiescent muscle cells

Intercellular signaling via small extracellular vesicles (sEV/exosomes) is emerging as an important mechanism in homeostasis, regeneration and disease, but the roles of sEV derived from muscle cells are poorly defined. In a culture model of physiologically relevant muscle cell states, we have explored stage-specific regulation of secretory rates, proteomic profiles (Fig 2), as well as signaling capabilities (Devan, Ghosh et al submitted). We are now working towards understanding stage-specific exosomal signaling cross talk which may influence cell fate.

Modelling a role for the cilium-centrosome axis in myogenic cell fate

The centrosome establishes polarity, maintains chromosome integrity and faithful segregation by forming a bipolar spindle in mitotic cells, but reorganizes and extends the primary cilium upon cell cycle exit. The intrinsic asymmetry of the cilium-centrosome axis regulates signaling, translation, and metabolism, and may contribute directly to cell fate decisions by controlling localization of proteins and mRNAs (Fig 3). Delineating these mechanisms will help to identify therapeutic nodes for ciliopathies (Atmakuru and Dhawan 2023).

1.



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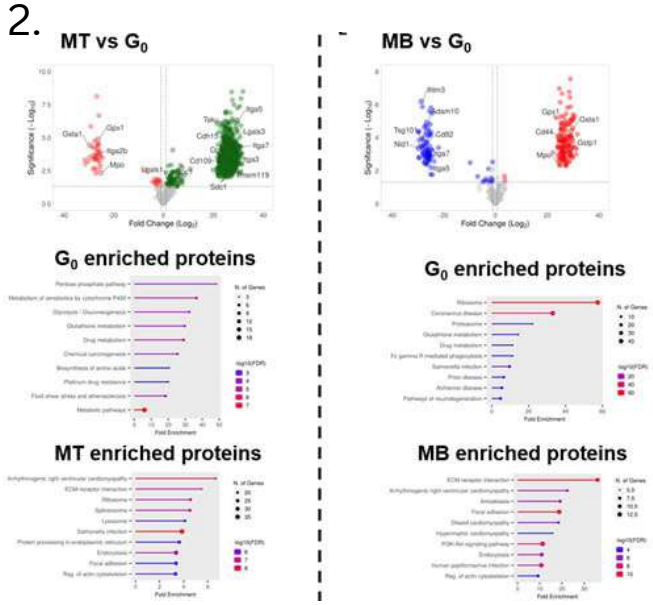

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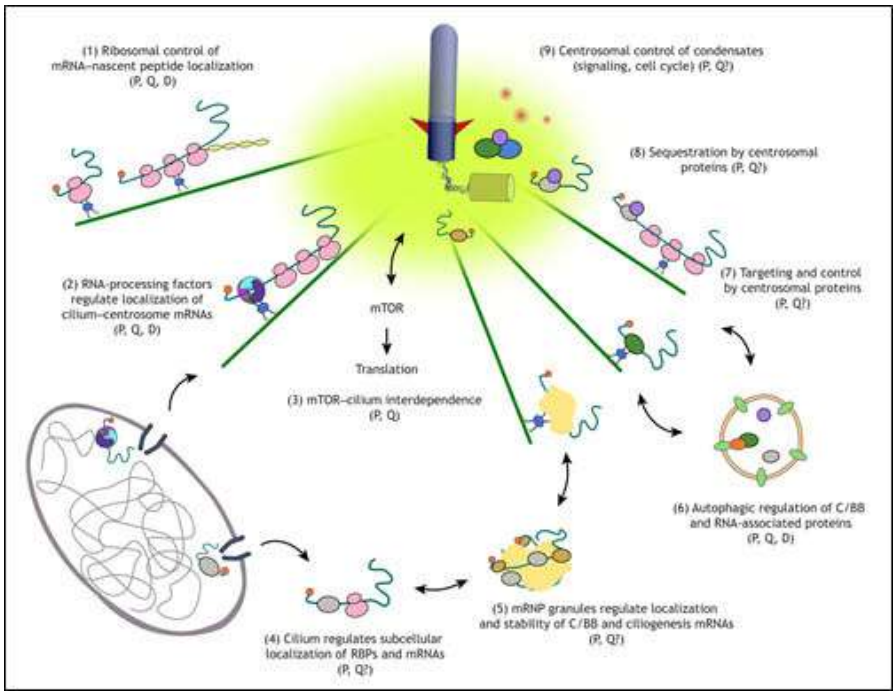


1. Schematic showing how PTPRU preserves self-renewal, maintains reversibility of the cell cycle arrest and suppresses expression of osteogenic lineage genes, potentially via effects on Wnt/b-catenin signaling. Enhanced stem cell properties and altered cell fate potential of post-quiescent hMSCs in vitro mimics their function in vivo, and may be mediated in part by PTPRU. (Credit: M. Rumman).

2. Proteomic profiling of purified exosomes from proliferating myoblasts (Mb), quiescent myoblasts (G0) and differentiated myotubes (Mt). Volcano plots depicting the distinct gene ontologies enrichment in a cell state specific manner, suggesting distinct signaling functions of exosomes from a single cell type in different cell states (Credit: Pallavi TR and Ananga Ghosh).

3. Adult stem cells traverse proliferation (P), reversible quiescence (Q) and irreversible differentiation (D) to maintain tissue homeostasis and regeneration. Fate choices are influenced by asymmetry of cellular components. The model integrates roles for the cilium-centrosome axis in coordinating RNP transport, translation at subcellular locations and formation of condensates. (Credit: Priti Atmakuru).

KARTHIKEYAN VASUDEVAN

Ecology and Conservation of Endangered Species

From left to right: Naveen C, Mubashir Dar, Shibi Muralidhar, Yashwant Singh, Karthikeyan Vasudevan, Gayathri Sreedharan, Avni Blotra, Swapnil Kiran, Aakash M
(Lab members not in the picture: Sambasiva Rao, Harika Katakam and Alka Sahu)

Research Interests

Our lab focuses on three main areas:

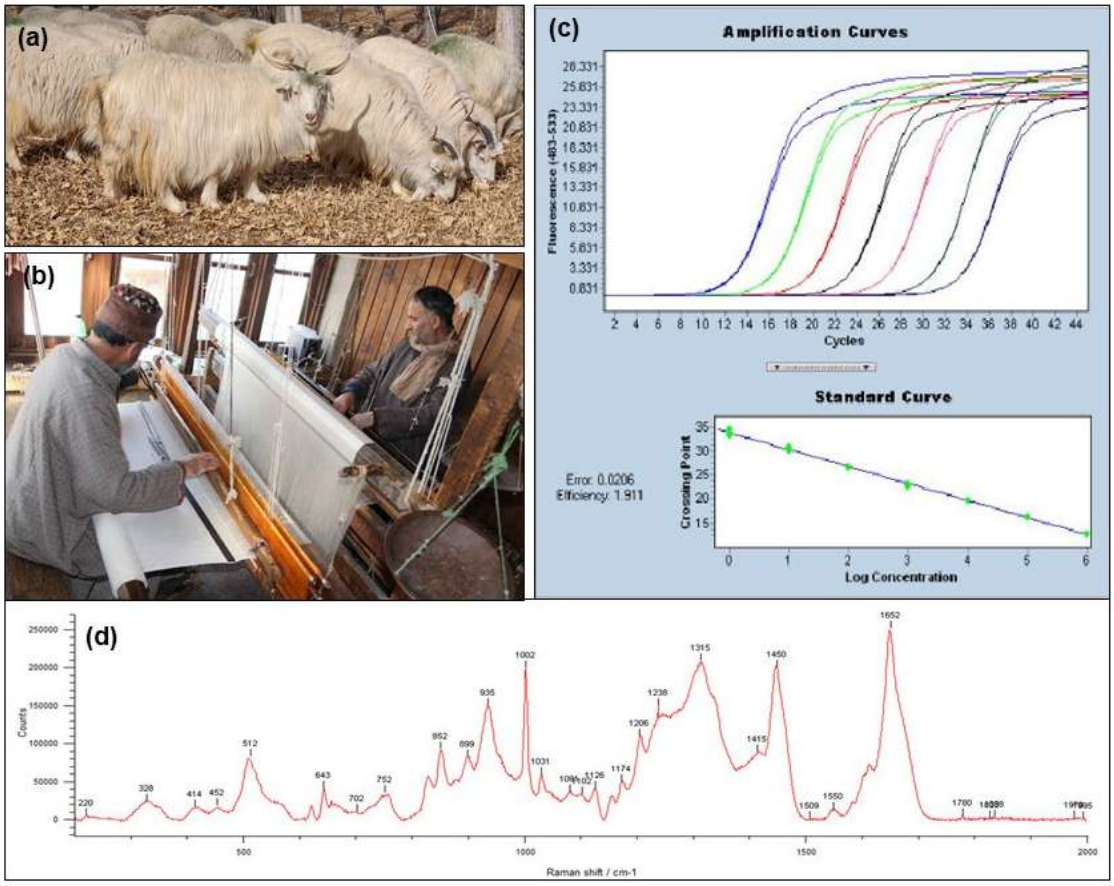
- Disease ecology - understanding dynamics of chytridiomycosis in amphibian populations
- Conservation biology - developing technologies\platforms that would help in conservation of endangered species
- Toxinology of venoms - understanding envenomation in humans by snakes and address human-snake conflict

Recent publications

- Bhatia S, Blotra A, Vasudevan K (2022) Evaluating antivenom efficacy against *Echis carinatus* venoms-Screening for i*n vitro* alternatives. ***Toxins*** 14: 481.
- Komanduri KPK, Sreedharan G, Vasudevan K (2023) Abundance and composition of forest-dwelling anurans in cashew plantations in a tropical semi-evergreen forest landscape. ***Biotropica*** 55: 594-604.
- Raj P, Vasudevan K, Agarwal RK, Dutta SK, Sahoo G, Mahapatra S, Sharma R, Janani J, Kar NB, Dubois A (2023) Larval morphology of selected anuran species from India. ***Alytes*** 39-40: 1-140.

1. Chytridiomycosis is the leading cause for rapid amphibian declines globally. The fungal pathogen *Batrachochytrium dendrobatidis* (Bd) causes chytridiomycosis. We monitored frog populations in five seasonal streams in the Tillari Conservation Reserve (TCR), Maharashtra from 2018 to 2022. We measured the load Bd in frogs, asked whether infection intensity affected frog survival, and whether infections are cleared/reduced. We uniquely tagged all anurans in five streams in TCR using Passive Integrated Transponder (PIT) tags, in two seasons annually. Skin swabs were collected and disease states were determined by qPCR. Pathogen growth was mapped to understand the fate of infected frogs. 74.6% of frogs had moderate levels of infection. Some cleared infections, some regained infection and others maintain high infection. We additionally collected skin swab samples from 1911 to 2020 from museums in Kolkata and Mumbai, and analyses of these samples are underway.

2. The Tibetan antelope or chiru (*Pantholops hodgsonii*) belongs to the subfamily *Caprinae*. It is also called Chiru, and it is found in Changthang wildlife sanctuary located in Ladakh, Jammu and Kashmir, and it is a protected species. It is exploited for the finest quality wool, commonly known as shahtoosh. The use of this fiber is illegal. Sometimes pashmina shawls made from pashmina goat get confiscated by customs. Since these products originate from India, it has brought attention to the existing monitoring mechanism. We aimed to develop a protocol that unambiguously assigns fiber samples used in weaving industry to belong to *Pantholops hodgsonii*. We employed Raman spectroscopy to identify animal fibers. We also isolated DNA from animal fibers, and developed novel *Pantholops hodgsonii*-specific qPCR primers. Finally, we validated the methods and provide a protocol that is reproducible for testing of animal fiber samples that includes raw fiber, yarn and woven material.



a. Pashmina goat reared in Upshi farm, Ladakh; b. Tradition weaving of pashmina fabric in Srinagar, Kashmir; c. Melt curve for shahtoosh obtained using qPCR primers; d. Raman spectra of Pashmina at 0.5% laser power using 785 nm laser and 500 accumulations

KRISHNAN H HARSHAN

Host-Virus Interactions: Molecular Perspectives

From left to right: Poojitha Sai Potharaju, Pooja Ravicanti, Vishal Sah, Dixit Tandel, Divya Gupta, Debasmita Basu, Prangya Parmita Sahoo, Krishnan H Harshan, Sandip Das Adhikary, Mohan Singh Moodu, Amit Kumar, Rajesh Pragada, Rose Emmanuela Prakash, and Aswathi Chandran

Research interests

- RNA viruses
- Host-Virus interaction
- Innate immune response
- RLR pathway
- SARS-CoV-2
- Dengue
- Antiviral therapeutics

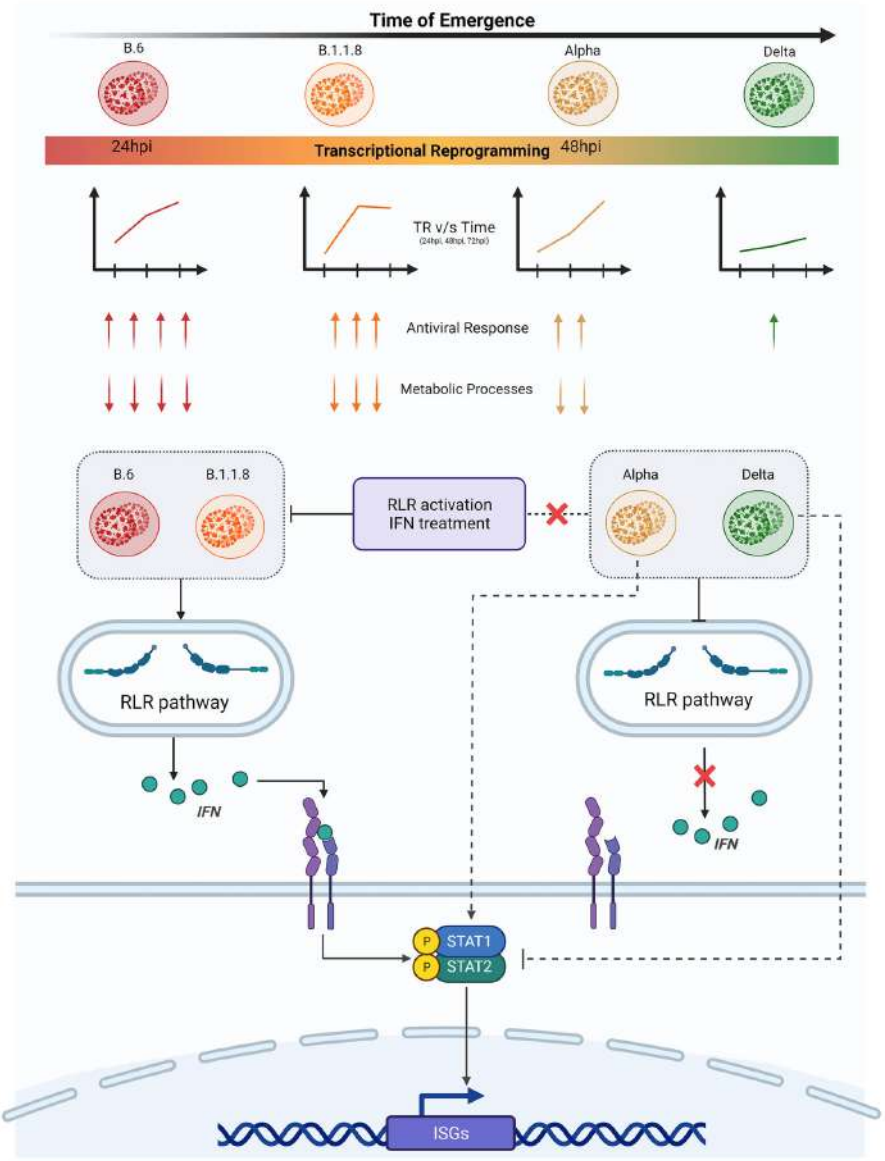
Recent publications

- Bhatt AN, Kumar A, Rai Y, Kumari N, Vedagiri N, Harshan KH, Kumar CV, Chandna S (2022) Glycolytic inhibitor 2-deoxy-d-glucose attenuates SARS-CoV-2 multiplication in host cells and weakens the infective potential of progeny virions. ***Life Sciences*** 295: 120411.
- Moharir SC, Chandra TS, Goel A, Thakur B, Tandel D, Mahesh SR, Vodapalli A, Bhalla GS, Kumar D, Naruka DS, Kumar A, Tuli A, Suravaram S, Bingi TC, Srinivas M, Mesipogu R, Reddy K, Khosla S, Harshan KH, Tallapaka KB, Mishra RK (2022) Detection of SARS-CoV-2 in the air in Indian hospitals and houses of COVID-19 patients. ***Journal of Aerosol Science*** 164: 106002.
- Tandel D, Sah V, Singh NK, Potharaju PS, Gupta D,, Shrivastava S, Sowpati DT, Harshan KH (2022) SARS-CoV-2 Variant Delta Potently Suppresses Innate Immune Response and Evades Interferon-Activated Antiviral Responses in Human Colon Epithelial Cells. ***Microbiology Spectrum*** 10: e0160422.
- Sudhakar R, Dontamala S, Bingi T, Gorde S, Panda A, Rizvi Z, Reddy GS, Kaswan S, Bhattacharjee M, Kumar D, Nivya MA, Mesipogu R, Varadarajan K, Patel A, Gupta D, Harshan KH, Tallapaka KB, Sijwali P (2022) ***Indian Journal of Medical Research*** 156: 659–668.
- Parthasarathy H, Tandel D, Siddiqui AH, Harshan KH (2023) Metformin suppresses SARS-CoV-2 in cell culture. ***Virus Research*** 323: 199010.
- Roy SS, Sharma S, Rizvi ZA, Sinha D, Gupta D, Rophina M, Sehgal P, Sadhu S, Tripathy MR, Samal S, Maiti S, Scaria V, Sivasubbu S, Awasthi A, Harshan KH, Jain S, Chowdhury S (2023) G4-binding drugs, chlorpromazine and prochlorperazine, repurposed against COVID-19 infection in hamsters. ***Frontiers in Molecular Biosciences*** 10: 1133123.

Our lab continues to investigate innate antiviral mechanisms that cells employ to counter RNA viral infections. We have been investigating how SARS-CoV-2 variants have been interacting with and manipulating the host innate immune response. Viruses generally learn to co-exist with the host during the process of its evolution. It is expected that SARS-CoV-2 would also evolve to co-exist in humans by trading-off its virulence for longer persistence causing milder disease. Clinically, the fatality associated with COVID-19 has been declining due to vaccination and pre-infections, but Delta variant caused the most severe disease and fatality across several parts of the world. Our study identified an evolving trend of SARS-CoV-2 variants where the variants emerged during early parts of the pandemic causing more robust innate immune response while the lately emerged variant Delta showed features of suppression of the response. The features that Delta has acquired could have strongly influenced the distinct pathophysiology associated with its infection. How these changed associations with the host influences the long-term evolution of the virus and the disease outcome would be keenly studied in understanding the process of viral evolution.

We also demonstrated that a popular anti-diabetic drug, metformin, has very strong anti-SARS-CoV-2 effects in cell culture models. The effect, reproducible in multiple cell lines, appears to be directed through AMPK, a key kinase complex that promotes catabolism in response to low ATP/AMP ratios in the cell. This study indicated that SARS-CoV-2 prefers anabolic state and is in agreement with previous reports of viral inhibition following the use of glycolytic inhibitors.

Additionally, through our collaboration with industry partner, VINS Bioproducts, we have developed an equine based antibody against SARS-CoV-2 and it is undergoing Phase-II clinical trials.



Delta variant has gained highly advanced control over the innate immune response and suppresses host responses effectively. The variants emerged during the early part of COVID-19 trigger moderate immune response by 24 h and robust response by 48 h post-infection. This was evident by the activation of RLR pathway that was further substantiated by transcriptome data. However, Alpha suppresses RLR pathway effectively, but failed to suppress STAT1 phosphorylation, possibly through IFN-independent mechanism. This was reflected in the late surge of transcriptional activities in Alpha infection. Delta has been the most advanced in suppressing not just innate immune response, but host response in general. Delta suppressed RLR pathway, IFN production and STAT1 phosphorylation, and this was reflected in the modest, steady response from the infected cells throughout the infection period. SARS-CoV-2 variants used in this study were presented based on their time of emergence from left to right with B.6 being the earliest and Delta being the most recent of them. The color of the variant virus particle shown in the schematic directly correlates with degree of transcriptional reprogramming by variants presented in graphical depiction below individual variants. The color intensity of the rectangular bar represents transcriptional reprogramming and control over host immune response by individual variant. Red represents elevated TR and strong activation of immune response while green represents lenient TR and greater control over host responses. Two of the GO enriched terms were presented with arrows. The numbers of arrows represent the potency of activation or inhibition, where up arrows indicate up-regulation of DEGs involved while down arrows indicate down-regulation. The variants studied here broadly fall under two groups based on the regulation of RLR pathway components and their response to activated innate immune responses (RLR activation by Poly I:C and JAK-STAT activation by IFN treatment). B.6 and B.1.1.8 activated RLR signalling followed by IFN secretion and ISGs expression via JAK-STAT axis. RLR and JAK-STAT signaling remain suppressed in Delta infection. Uniquely Alpha follows non-canonical mode of STAT activation without any detectable expression of IFNs.

KUMARASWAMY REGALLA

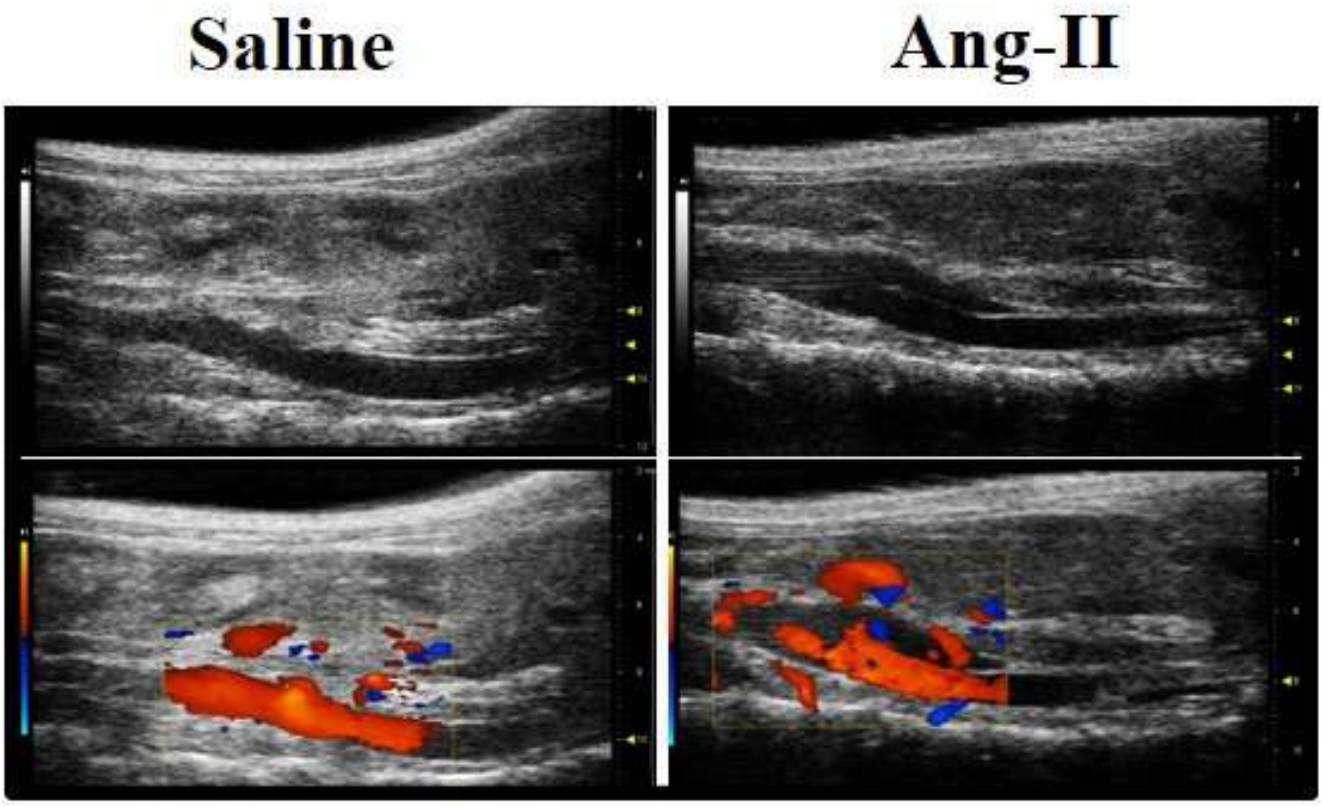
Cardiovascular Biology

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

K THANGARAJ

Evolutionary and Medical Genetics

From left to right: Lomus Kumar, V. Purushotham , Narmadha, G. Mala, Nipa Basak, Pratheusa Machha, S. Deepa Selvi Rani, K. Thangaraj, Rajan Kumar Jha, Jaydeep Aravindbhai Badarukhiya, Sagnik Dhar,D.V.S. Sudhakar, Sunil Kumar Tripathi, Haneef Sunitha Kundur, Nitin C. Tupperwar, Agyeya Pratap, Jagamohan Chhatai

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 - cardiovascular diseases, mitochondrial disorders, male infertility and sex determination

Selected recent publications

- Sudhakar DVS, Phanindranath R, Jaishankar S, Ramani A, Kalamkar KP, Kumar U, Pawar AD, Dada R, Singh R, Gupta NJ, Deenadayal M, Tolani AD, Sharma Y, Anand A, Gopalakrishnan J, Thangaraj K (2023) Exome sequencing and functional analyses revealed *CETN1* variants leads to impaired cell division and male fertility. ***Human Molecular Genetics*** 32: 533-542.
- Basnet R, Rai N, Tamang R, Awasthi NP, Pradhan I, Parajuli P, Kashyap D, Reddy AG, Chaubey G, Das Manandhar K, Shrestha TR, Thangaraj K (2023) The matrilineal ancestry of Nepali populations. ***Human Genetics*** 142: 167-180.
- Prasada KS, Chakrabarty S, Jayaram P, Mallya S, Thangaraj K, Singh KK, Satyamoorthy K (2023) Severe acute respiratory syndrome coronaviruses contributing to mitochondrial dysfunction: Implications for post-COVID complications. ***Mitochondrion*** 69: 43-56.
- Nashi S, Polavarapu K, Bardhan M, Anjanappa RM, Preethish-Kumar V, Vengalil S, Padmanabha H, Geetha TS, Prathyusha PV, Ramprasad V, Joshi A, Chawla T, Unnikrishnan G, Sharma P, Huddar A, Uppilli B, Thomas A, Baskar D, Mathew S, Menon D, Arunachal G, Faruq M, Thangaraj K, Nalini A (2023) Genotype-phenotype correlation and natural history study of dysferlinopathy: a single-centre experience from India. ***Neurogenetics*** 24: 43-53.
- Chimata P, Kashyap DK, Sairam T, Ganesh A, Thangaraj K, Purushottam M, Viswanath B, Jain S, Dhandapany PS. (2022) Generation of a new human induced pluripotent stem cell (hiPSC) line from a South Asian Indian with a MYBPC3Δ25bp variant. ***Stem Cell Research*** 65: 102978
- Patankar A, Sudhakar DVS, Gajbhiye R, Surve S, Thangaraj K, Parte P (2022) Proteomic and genetic dissection of testis-specific histone 2B in infertile men reveals its contribution to meiosis and sperm motility. ***F & S Science*** 3: 322-330.

- Jain PK, Jayappa S, Sairam T, Mittal A, Paul S, Rao VJ, Chittora H, Kashyap DK, Palakodeti D, Thangaraj K, Shenthar J, Koranchery R, Rajendran R, Alireza H, Mohanan KS, Rathinavel A, Dhandapany PS (2022) Ribosomal protein S6 kinase beta-1 gene variants cause hypertrophic cardiomyopathy. ***Journal of Medical Genetics*** 59: 984-992.
- Sehrawat JS, Agrawal S, Sankhyan D, Singh M, Kumar S, Prakash S, Rajpal R, Chaubey G, Thangaraj K, Rai N (2022) Pinpointing the Geographic Origin of 165-Year-Old Human Skeletal Remains Found in Punjab, India: Evidence From Mitochondrial DNA and Stable Isotope Analysis. ***Frontiers in Genetics*** 13: 813934.
- Singh PP, Suravajhala P, Basu Mallick C, Tamang R, Rai AK, Machha P, Singh R, Pathak A, Mishra VN, Shrivastava P, Singh KK, Thangaraj K, Chaubey G (2022) COVID-19: Impact on linguistic and genetic isolates of India. ***Genes & Immunity*** 23: 47-50.

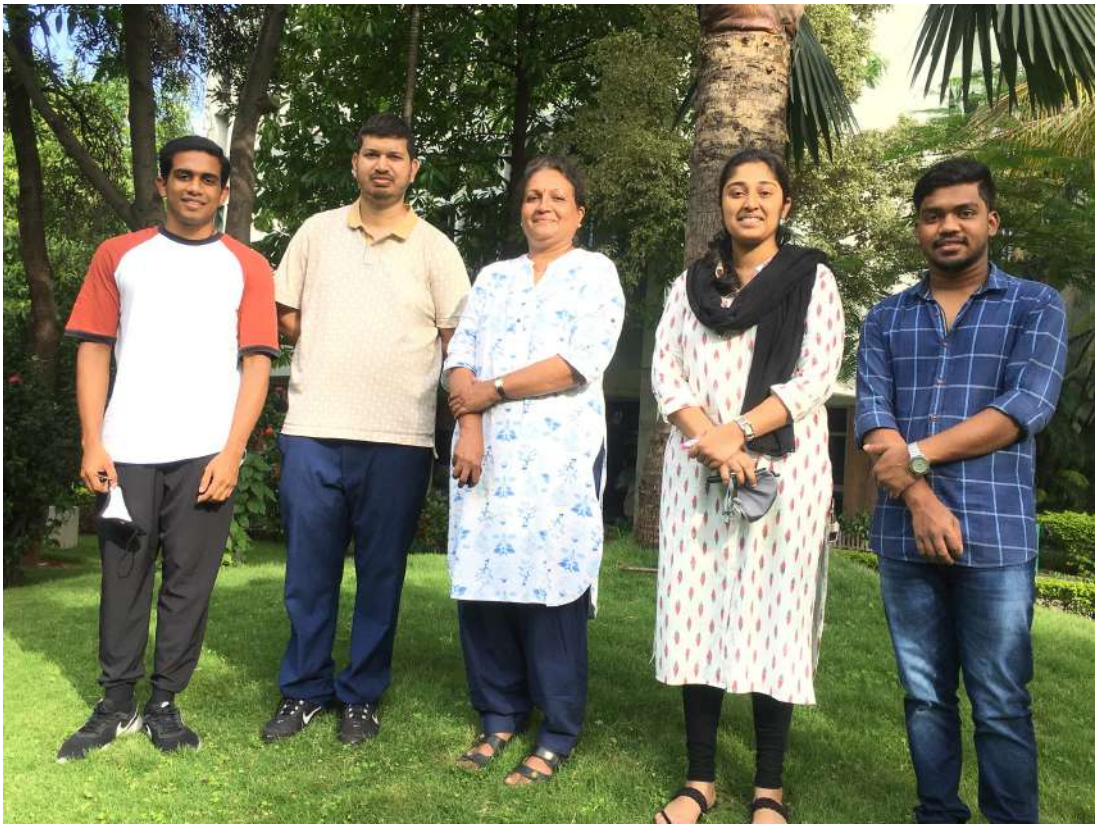
The Pattanam, an archaeological site located in the Ernakulam District of Kerala is part of the ancient port city of Muziris. Pattanam has witnessed multi-disciplinary archaeological investigations. The genetic evidence supporting the impact of multiple cultures or their admixing is still missing for this important archaeological site of South India. Hence, we tried to infer the genetic composition of the skeletal remains (Figure) excavated from the site in a broader context of South Asian and worldwide maternal affinity. We observed a high frequency of West Eurasian mitochondrial haplogroups (T, JT, and HV) and South Asian-specific haplogroups (M2a, M3a, R5, and M6). This study confirms that people belonging to multiple cultural and linguistic backgrounds have migrated, probably settled, and eventually died on the South-western coast of India (*Genes,* 2023).

Morbidity and mortality rates associated with cardiovascular disease are very high in South Asia. The thick cardiac filament b-myosin heavy chain (*b-MYH7*) is one of the major sarcomere genes. Nevertheless, very limited studies have been conducted on the *b-MYH7* gene among Indian cardiomyopathy patients. Hence, the disease has remained poorly understood in India. Therefore, we undertook a comprehensive study of *b-MYH7* in Indian patients with dilated cardiomyopathy (DCM). We detected numerous novel, and rare mutations in the *b-MYH7* gene (8.0%). We further demonstrated that how each mutant (missense) has uniquely disrupts a critical network of non-bonding interactions at the mutation site and may contribute to development of dilated cardiomyopathy (*Can. J. Cardiol. Open*, 2022).

Human skeletal remains recovered from excavations at trench of Pattanam site

LEKHA DINESH KUMAR

Wnt Signalling, Cancer, and Biomarker Discovery



From left to right: Rohan, P, Rohitesh Gupta, Lekha Dinesh Kumar, Aisha Shigna, Ankit Kumar

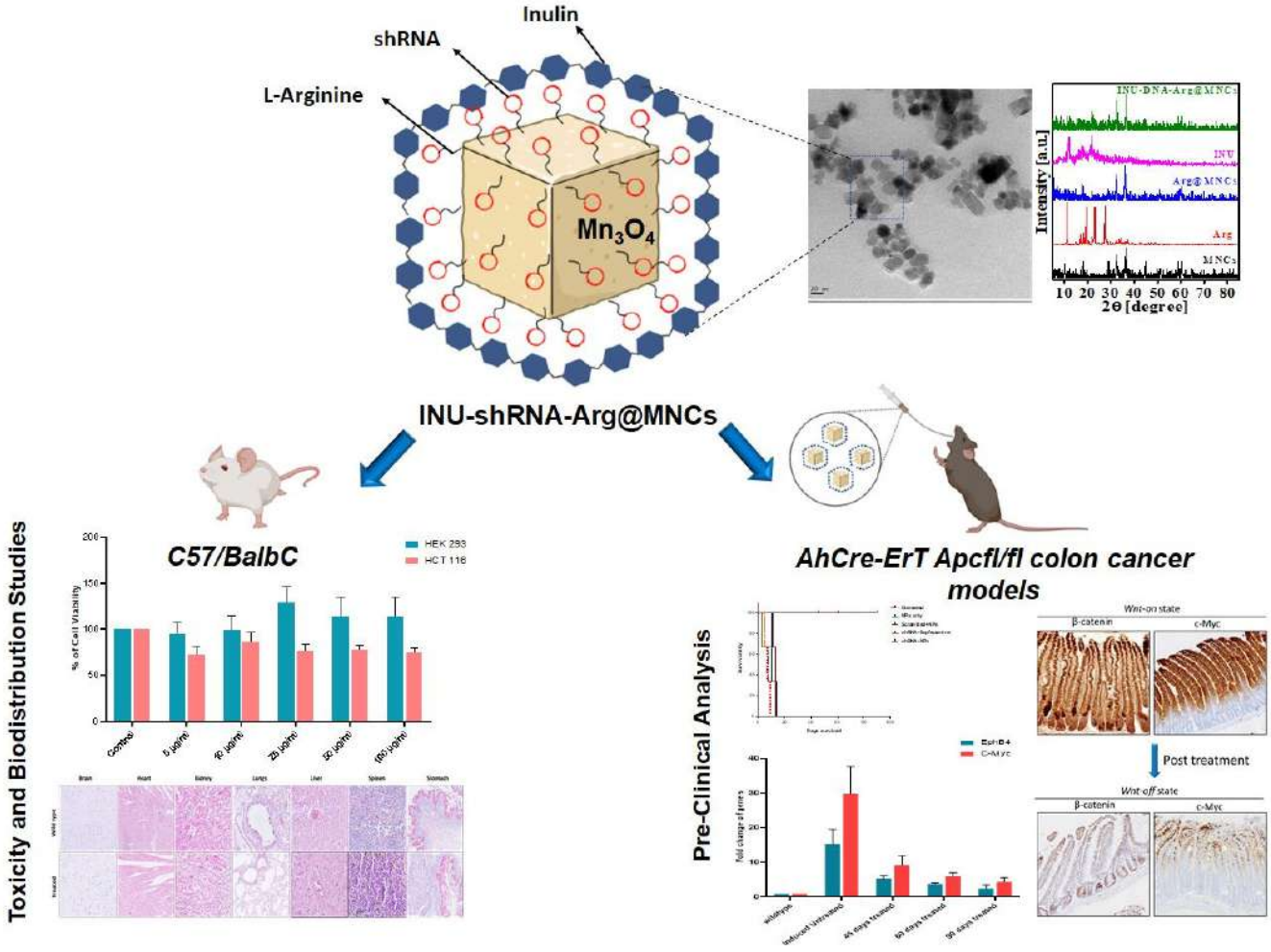
Research interests

- Role of Wnt deregulators in the initiation and progression of colon cancer
- Discovery of biodrug and its targeted delivery using RNA interference and nanotechnology
- Biomarker discovery in breast cancer
- Mechanisms of drug resistance

Recent publications

- Byroju VV, Nadukkandy AS, Cordani M, Dinesh Kumar L (2023). Retinoblastoma: present scenario and future challenges. ***Cell Communication and Signaling*** 21: 226.
- Aisha Shigna Nadukkandy, Eshani Ganjoo, Ankit Singh, Dinesh Kumar L (2022). Tracing New Landscapes in the Arena of Nanoparticle-Based Cancer Immunotherapy. ***Frontiers in Nanotechnology*** https://doi.org/10.3389/fnano.2022.911063
- Kumar A, Singam A, Swaminathan G, Killi N, Tangudu NK, Jose J, Gundloori Vn R, Dinesh Kumar L (2022). Combinatorial therapy using RNAi and curcumin nano-architectures regresses tumors in breast and colon cancer models. ***Nanoscale*** 14(2): 492–505.
- Kourani K, Jain P, Kumar A, Jangid AK, Swaminathan G, Durgempudi VR, Jose J, Reddy R, Pooja D, Kulhari H, Dinesh Kumar L (2022). Inulin coated Mn3O4 nanocuboids coupled with RNA interference reverse intestinal tumorigenesis in Apc knockout murine colon cancer models. ***Nanomedicine: nanotechnology, biology, and medicine*** 40: 102504.

The major challenges in achieving targeted gene silencing *in vivo* include the stability of RNA molecules, accumulation into pharmacological levels, and site-specific targeting of the tumor. We report the use of inulin for coating the arginine stabilized manganese oxide nanocuboids (MNCs) for oral delivery of EphB4 shRNA to the gut. Furthermore, bio-distribution analysis exhibited site-specific targeting in the intestines, improved pharmacokinetic properties, and faster elimination from the system without cytotoxicity. To evaluate the therapeutic possibility and effectiveness of this multimodal bio-drug, it was orally delivered to Apc knockout colon cancer mice models. Persistent and efficient delivery of bio-drug was demonstrated by the knockdown of target genes and increased median survival in the treated cohorts. This promising utility of RNAi-nanotechnology approach advocates the use of bio-drug in an effort to replace chemo-drugs as the future of cancer therapeutics.



Inulin-coated Mn3O4 nanocuboids conjugated with Ephb4 (INU-shRNA- Arg@MNCs) have been established to combat colorectal cancer in Apc knockout murine systems. The unique pH-responsive property of inulin, good MRI contrast, non-toxicity, improved tissue accumulation and faster elimination makes INU-shRNA-Arg@MNCs an ideal multimodal nano-carrier for colon drug delivery. Efficient knockdown of target genes that led to a reversal of Wnt deregulated crypt progenitor type to near normal state increased median survival in the treated cohorts compared to control cohorts of mice.

MANDAR V DESHMUKH

Molecular Basis of Evolutionary Divergence in RNAi Initiation

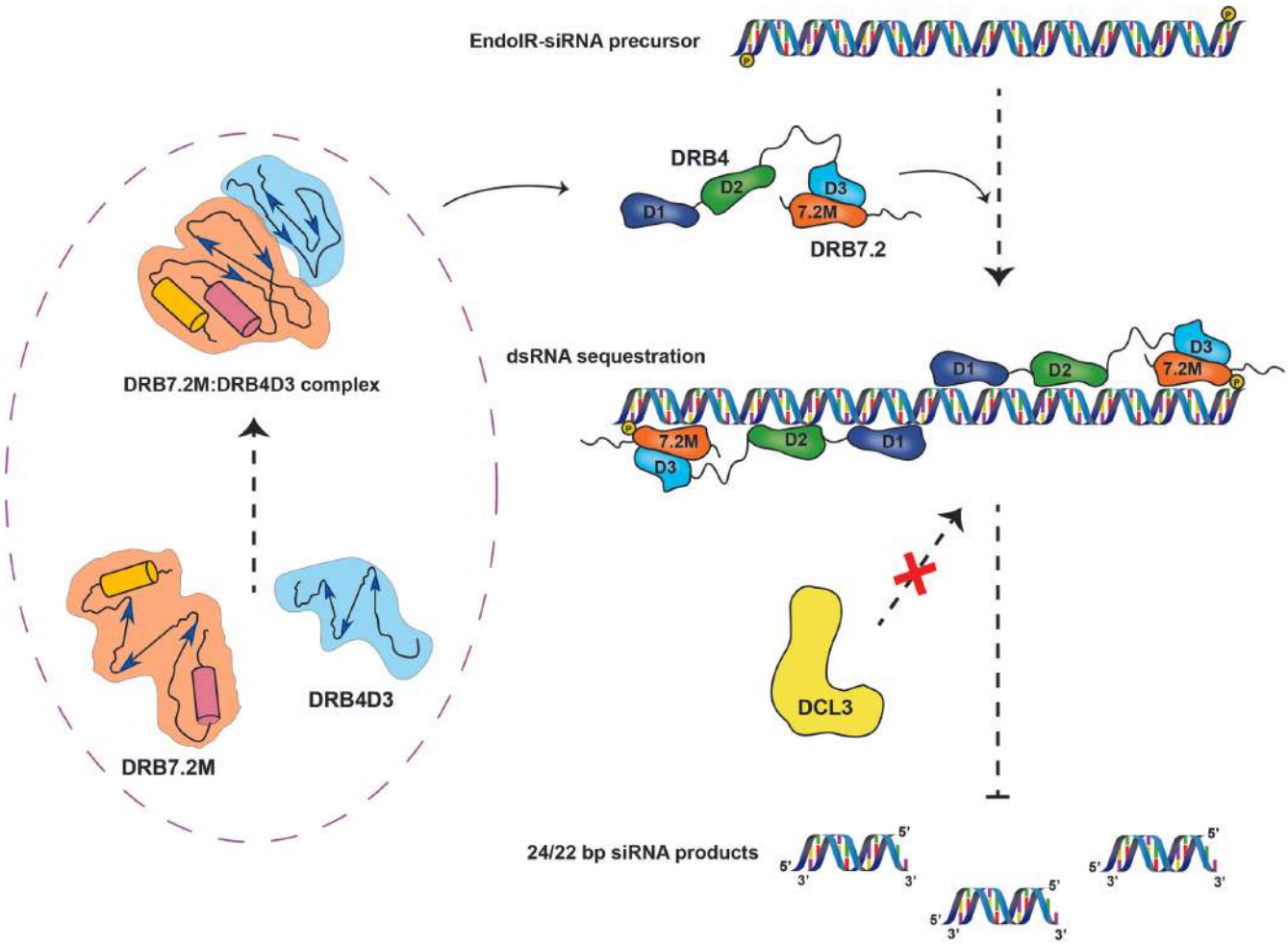
From left to right, top to bottom (clockwise): Mandar V Deshmukh, Sneha Paturi, Jaydeep Paul, Debadutta Patra, Ramdas Aute, Priti Chanda Behera, Supriti Das, Neelam Waghela, Phanindranath Regur, and K. Joy
Background: 600 MHz NMR Spectrometer and organisms that help us do our science

Research interests

We explore the role of RNA-binding gene regulatory proteins by studying the structure, inter-domain orientations, and dynamics to decipher the initiation of the non-coding RNA-mediated gene regulation in various species. These studies extend our understanding of one of the fundamental biological processes that are vital in infection, cancer, and development.

The RNAi pathway depends on a complex between Dicer, the initiator dsRNA, and a dsRNA-binding protein (dsRBP). In response to evolutionary selection pressure and developmental requirements, higher eukaryotes have developed an adaptable RNAi-based gene regulation pathway triggered by non-coding RNA. The evolutionary divergence in the RNAi pathway appears as custom-made alterations in Dicer and dsRBP domain architecture and recruitment of uneven numbers of Dicers and dsRBP. We hypothesize that RNAi initiation is a convoluted dynamic process tailored for evolutionary advantages to organisms.

During this year, we explored the mechanism of the DRB7.2:DRB4 mediated endogenous inverted-repeat dsRNA sequestering in plants. Noncoding transcribable inverted repeat sequences are vital in genome stability, regulation of transposable elements, mutations, and diseases in eukaryotes. In vascular plants, dsRNA Binding Proteins (dsRBPs), DRB7.2 and DRB4, inhibit Dicer-like-protein 3 (DCL3) to stall endogenous inverted-repeat dsRNA (endo-IR dsRNA) mediated gene silencing. As dsRBPs assist Dicers, the inhibition of DCL3 by a dsRBP complex is quite enigmatic. Here, we explore how the DRB7.2:DRB4 complex sequesters substrate dsRNA of DCL3 using a structure-based mechanistic approach. Intriguingly, the crucial first step of endo-IR dsRNA sequestration is the folding upon binding of interacting domains of DRB7.2 (DRB7.2M) and DRB4 (DRB4D3). Next, we establish that DRB7.2 simultaneously interacts with DRB4, substrate dsRNA, and ssRNA, whereas DRB4 contributes towards enhancement in the affinity of the complex with dsRNA, impairing DCL3 mediated cleavage of endo-IR dsRNA precursors. The novel fold adopted by DRB4D3 implies plants organize tasi/siRNA initiation complex formed by DCL4:DRB4 diversely from Animalia.



Proposed model for the dsRNA sequestration mechanism by DRB7.2 and DRB4 complex

MANJULA REDDY

Bacterial Cell Wall Synthesis and its Regulation

From left to right (Top row): Manjula Reddy, Balaji Venkataraman, Moneca Kaul, Nilanjan Som, Shambhavi Garde (Middle row): Bhargavi Krishna Sree, Raj Bahadur, Vaidehi Rajguru, Suraj Meher (Bottom row): Debnita Mongal, Krishna Chaitanya, Stuti Chatterjee, GSN Reddy, Meher Fatima

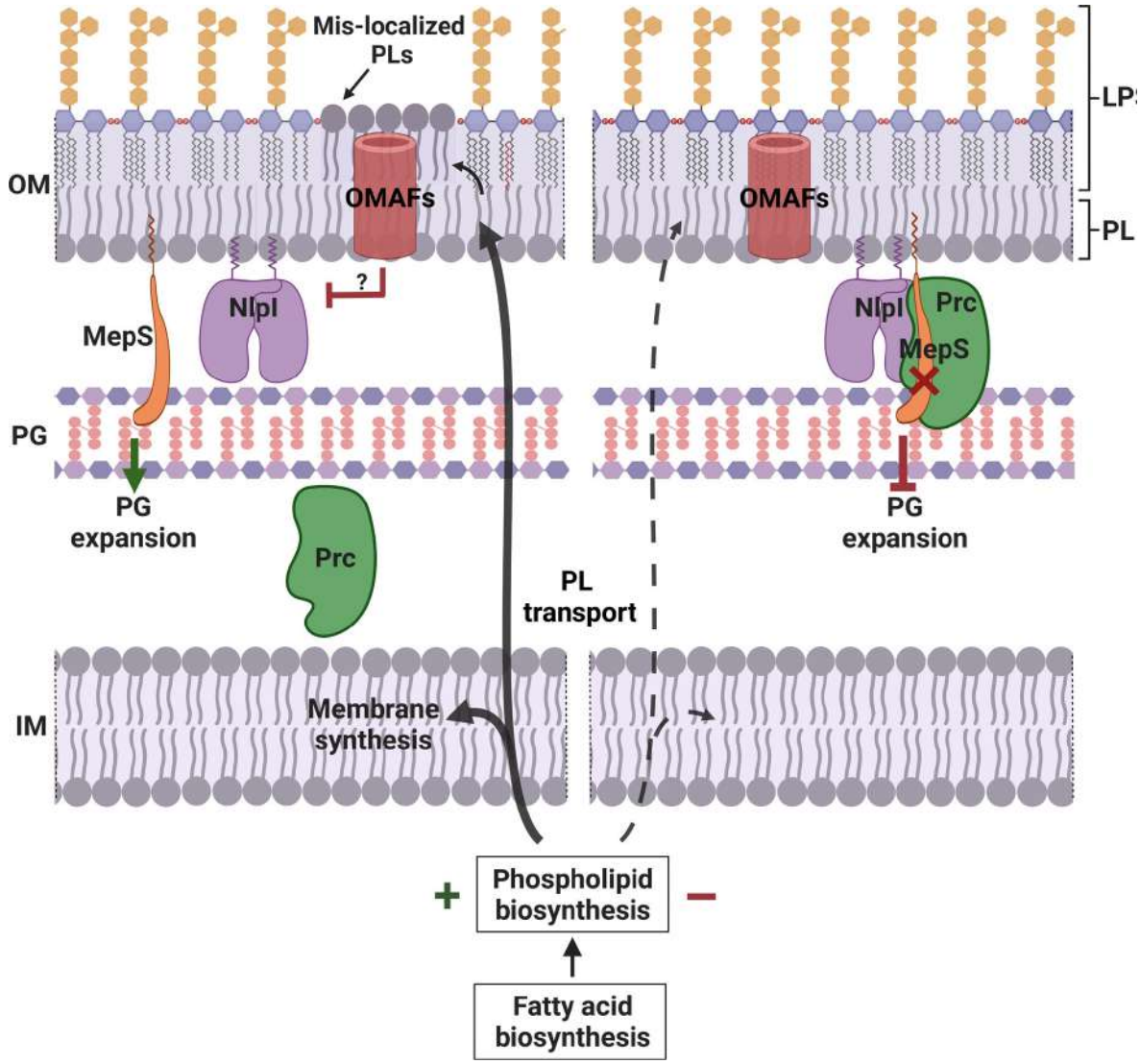
Research interests

- Deciphering the mechanisms of bacterial cell wall expansion
- Understanding the bacterial peptidoglycan growth and remodeling

Recent publications

- Chodisetti P, Bahadur R, Amrutha RN, Reddy M (2022) A LytM-factor, ActS functions in two distinctive peptidoglycan hydrolytic pathways in *Escherichia coli*. ***Frontiers in Microbiology*** 13: 913949.
- Nallamotu KC, Bahadur R, Kaul M, Reddy M (2022) Peptidoglycan Remodeling by an L,D-Transpeptidase, LdtD during Cold Shock in *Escherichia coli*. ***Journal of Bacteriology*** 205: e0038222.

Gram-negative bacterial cell walls including that of *E. coli* are made up of three layers. The innermost layer, the cytoplasmic or inner membrane (IM) encloses the cytosol and is made up of phospholipids (PL). A net-like large, elastic polymer, the peptidoglycan (PG) sacculus totally encases the IM and protects cells from turgor and also confers shape to the bacteria. The outermost layer is an asymmetric bilayered lipid membrane which is made up of lipopolysaccharides (LPS) in the outer leaflet and PLs in the inner leaflet. During the cell cycle, all these three layers of the cell envelope are expected to grow concomitantly; however, it is not known how it occurs. We previously demonstrated that enzymatic cleavage of PG peptide crosslinks is an essential step for PG expansion during bacterial growth. Three redundantly essential PG endopeptidases, MepS, MepM and MepH, were identified as the mediators of PG elongation. Further, we earlier discovered that stability of MepS is governed by a periplasmic adaptor-protease system (NlpI-Prc). Here, we show that the cross-link specific hydrolase MepS couples the expansion of PG sacculus with that of PL synthesis in the Gram-negative model bacterium, *E. coli*. Using genetic and biochemical approaches, we showed that the cellular availability of fatty acid (FA) or PL alters the post-translational stability of MepS by modulating the proteolytic activity NlpI-Prc towards MepS. In summary, this study showed the existence of a molecular crosstalk that enables coordinated expansion of the PG sacculus with that of membrane synthesis for balanced cell-envelope biogenesis.



Model depicting the coordinated growth of bacterial cell envelope components (Reference: Som and Reddy, PNAS, 2023)

MEGHA KUMAR

Cell and Developmental Biology

From left to right: Advait Gokhale, Tuhina Prasad, Megha Kumar, Sharada Iyer, Amisha Jain

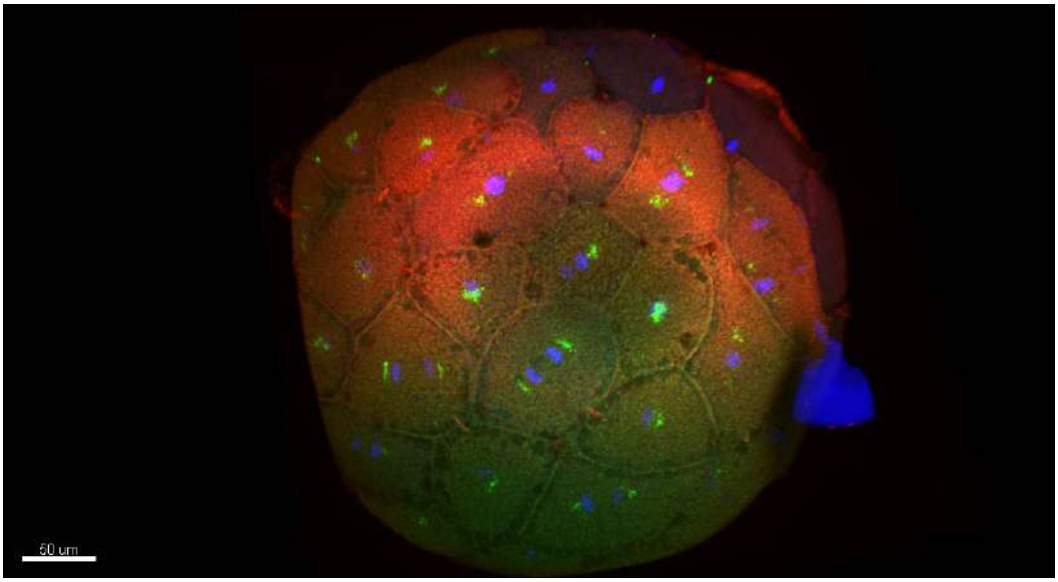
Research interests

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.

Recent publications

- Prasad T, Iyer S, Chatterjee S, Kumar M (2023) *In vivo* models to study neurogenesis and associated neurodevelopmental disorders-Microcephaly and autism spectrum disorder. ***WIREs Mechanisms of Disease*** 15: e1603.

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 proteins during cell division. Our preliminary results indicate that centrosomal genes are required for proper spindle orientation, resulting in correct specification of cell fate and normal tissue architecture during early embryonic development. Additionally, 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.



Sum projection confocal image of a 2.5-hour-old zebrafish embryo showing early mitoses. The embryonic blastomeres show DNA (blue), spindle pole (green), and microtubules (red).

MEGHNA KRISHNADAS

Community and Functional Ecology

From left to right: Mustaqeem, Athulya, Meghna, Tejaswini, Shubham, Souparna, Rishiddh, Vinayak, Peddiraju (sitting last)

Research interests

Our lab seeks to understand the processes that help maintain diversity in ecological communities, especially in the context of global environmental change. We work with plant communities, applying fundamental ecological theory to evaluate what processes act in which way to filter species in a habitat or mediate coexistence of competing species. To this end, we combine observational data with experiments in the field (*in-situ*) and greenhouse (*ex-situ*) with advanced statistical and predictive models.

Recent publications

- Krishnadas M (2022) Rainfall affects interactions between plant neighbours. ***Nature*** 615: 39-40 (invited commentary).
- Krishnadas M (2022) Climate and forest loss interactively restructure trait composition across a human-modified landscape. ***Ecology and Evolution*** 12: e9361.
- Krishnan A, Osuri AM, Krishnadas M (2022) Small mammals reduce distance dependence and increase seed predation risk in tropical rainforest fragments. ***Biotropica*** 54: 1428-1439.

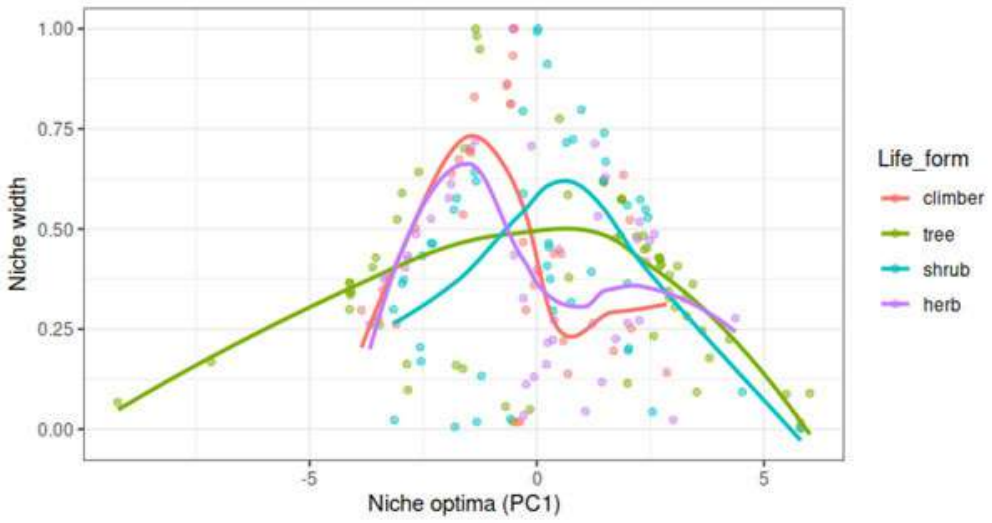
Our work encompassed the following objectives:

- Large-scale climate gradients and species distributions in a tropical dry ecosystem.
- The role of traits in mediating species distributions across environmental gradients.
- Biotic interactions across abiotic gradients.

Towards the first objective, postdoctoral fellow Dr. Souparna Chakravarthy analysed how climate explains species distributions of trees, shrubs, and herbs across the Eastern Ghats. He is following this up with an analysis of community assembly based on signals from taxonomic and phylogenetic diversity of the three life forms.

The second objective is a collaborative project with University of Bayreuth, funded by DBT-DFG Indo-German fundamental research grant. This work focuses on environmental gradients at smaller spatial scales, specifically light and water availability across a tropical humid forest, to relate plant distribution and performance to a suite of 16 functional traits. This includes hard-to-measure ecophysiological traits related to light- and water-use efficiency to draw a mechanistic link between ecological function and outcome. We are also analyzing how intraspecific trait variation explains distribution of tree species in a try tropical ecosystem (SERB Start-up Research Grant). Also, we have set up a new project via the CSIR MLP Eastern Ghats Project to understand how invasive plant species (Lantana camara) alter trait-mediated assembly of trees in a tropical dry ecosystem.

For the third objective, PhD students Rishiddh and Vinayak (and interns from IISER Trivandrum, IISER Tirupati, and Pondicherry University) conducted arduous field work. Rishiddh is testing whether seedling chemistry explains interspecific variation in insect herbivory. Vinayak wrapped up a project to test whether microbially-mediated coexistence of two plant species changes with abiotic context. He is also analyzing how abiotic conditions influence the soil microbiome of plant species. New PhD student Shubham is developing an idea to test whether root traits of seedlings correlate with their microbial composition and exudation patterns to dig deeper into plant strategies below-ground



Across the Eastern Ghats, communities in warmer, drier regions tend to consist of species preferring warm, dry climate but have lower niche width suggesting species specialized to these regions while more generalist species tend to form communities in the intermediate climatic conditions. PC1 represents the first axis of a Principal Component Analysis to characterize climate variation across all plots: larger values indicate warmer, drier sites. X-axis shows the mean niche optima of species found in a site and Y-axis shows the corresponding mean niche width. Larger values of X-axis suggest that species in that site on average have their peak occurrence at warm, dry conditions.

M M IDRIS

Bio-mechanisms of Regeneration

From left to right: Gayatri Devraj, PV Anusha, Anushka Arvind, Mohammed Idris

Research interests

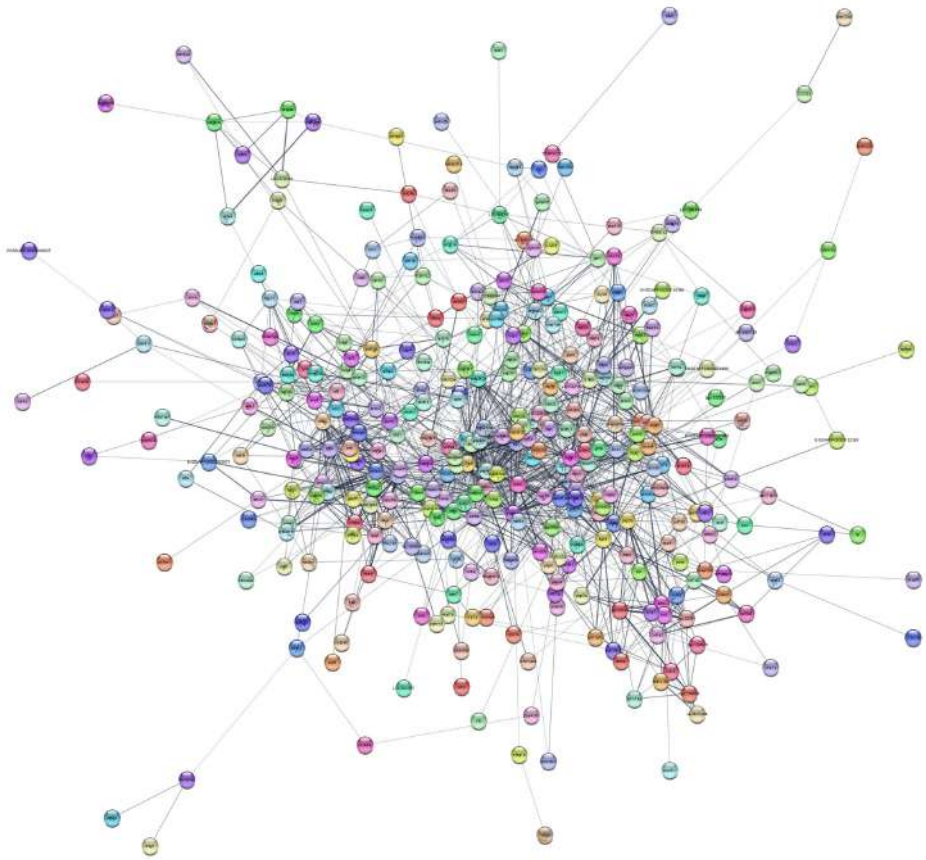
- Understanding the biomechanism of wound healing and regeneration in alternate model animals
- Development of primary reference standards for biologics and identifying impurities in biologics (supported by IPC)

Recent publications

- Banu S, Nagaraj R, Idris MM (2022) Defensins: Therapeutic molecules with potential to treat SARS-CoV-2 infection. ***Indian Journal of Medical Research*** 155: 83–85.
- Idris MM, Banu S, Siva AB, Nagaraj R (2022) Down regulation of defensin genes during SARS-CoV-2 infection. ***Acta Virologica*** 66: 249-253.
- Banu S, Nagaraj R, Idris MM (2023) A proteomic perspective and involvement of cytokines in SARS-CoV-2 infection. ***PLoS One*** 18: e0279998.

Our group works on understanding the intricate molecular and genetic mechanism that underlie tissue and organ regeneration in alternate model animals like zebrafish, geckos, ascidians and echinoderms. This exploration into the biomolecular intricacies of regeneration is profoundly significant, as it holds the potential to transform non-regenerative systems into regenerative ones, offering new avenues for therapeutic applications and healing. Epimorphic regeneration of zebrafish caudal fin tissue is complex and complete. Our group has established several hundreds of genes and proteins and their post translational modifications such as phosphorylation to be associated with regeneration, involving high-throughput transcriptomics and iTRAQ based quantitative proteomics analyses. Out study on network and pathway analyses have unveiled the central roles of cell cycle control, nervous system development, and cellular growth and proliferation pathways in the regeneration process. This study has provided a comprehensive understanding of the dynamic gene and protein changes that occur during tissue regeneration. Furthermore, our research extends to the examination of the impact of small molecules on regeneration. We recognize that low molecular weight micromolecules have been widely used without a deep understanding of their effects on biological processes. To address this gap, we are investigating the physiological, behavioral, and molecular changes induced by these molecules during epimorphic regeneration in zebrafish caudal fin tissue.

In addition to our work on regeneration, our team is actively engaged in developing primary reference standards for biopharmaceuticals, creating monographs, and establishing DNA barcodes for medicinal plants in accordance with the requirements of the Indian Pharmacopeia Commission.



Network pathway associated with zebrafish caudal fin regeneration based on differentially expressed genes/proteins.

MUKESH LODHA

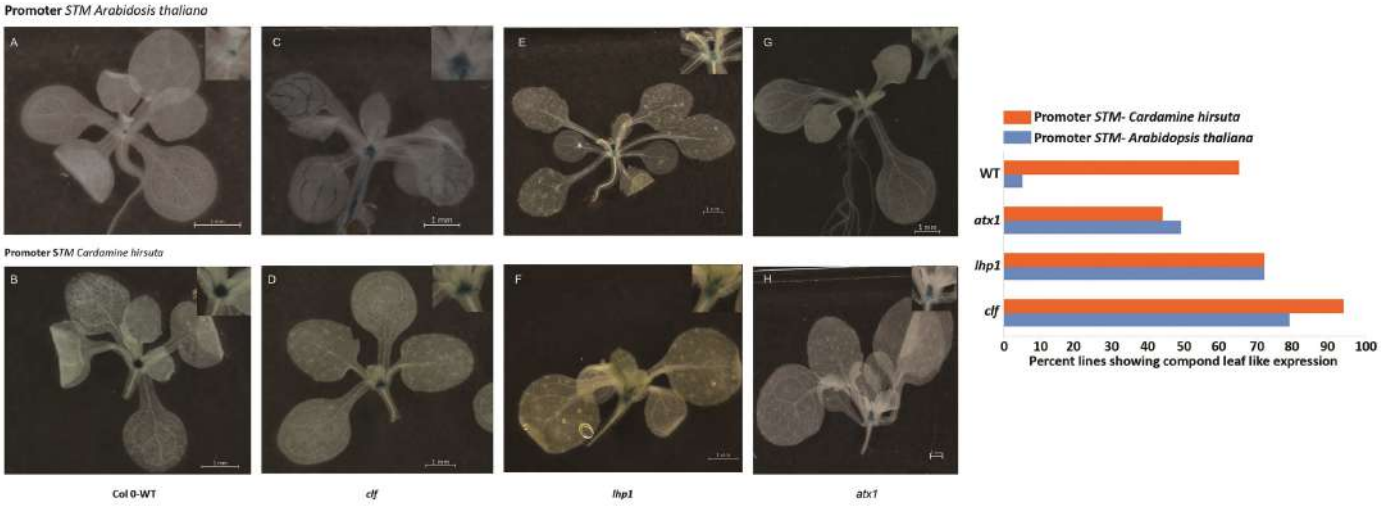
Mechanism of Epigenetic Inheritance in Plants

From left to right: Mukesh Lodha, Akanksha Garhewal, Preethi Jampala, Sai Deep

Research interests

- Plant Epigenetics
- Developmental Biology
- Flowering Time
- Polycomb
- Trithorax

Epigenetic information is heritable during mitotic and/meiotic cell divisions but it is not encoded in the genetic material. It is stable in the absence of initial trigger. Our group is using important developmental regulators, SHOOT MERISTEMLESS (STM) and FLOWERING LOCUS C (FLC), as tools to understand epigenetic regulation in plants. STM and FLC are important transcription factors. STM plays an important role in shoot meristem stem cell homeostasis and in determining leaf complexity. In both simple and compound leaf species STM is expressed in the shoot apical meristem and is down-regulated in leaf primordia. In simple leaf species like *Arabidopsis* this down-regulation is maintained throughout the leaf development where as in compound leaf species like *Cardamine hirsuta*, tomato and potato, STM down regulation occurs in leaf primordial but is not maintained. We have identified the cis regulatory element which recruits Polycomb in the proximal promoter of *Arabidopsis* STM and Trithorax complex in the distal part of the *Arabidopsis* STM promoter. It turned out that in simple leaf species Polycomb and Trithorax recruiting elements forms a repressive loop which prevents regaining of STM expression in developing leaves. In compound leaf species repressive loop is diminished; as a result, STM regains expression and transform developing leaf into a compound one. FLC is a repressor of flowering. Vernalization (prolonged cold) transcriptionally represses FLC which is maintained in the subsequent warmer period, allowing flowering. We are using natural variations in vernalization response of *Arabidopsis* accessions to understand epigenetic mechanism of FLC regulation.



Expression pattern of simple leaf species (*Arabidopsis thaliana*) and compound leaf species (*Cardamine hirsuta*) STM in wild type (A&B), Polycomb mutants (C, D, E &F), Trithorax mutant (G &H). Bar graph shows percentage of transgenic lines showing compound leaf species like pattern.

N NAGESH

Structure and Interaction of G-Quadruplex DNA

From left to right: Sindhuja, Sowjanya, Ira Bhatnagar, Narayana Nagesh, C B Tripura Sundari, Truptimayee, Afna Safia, Arushi

Research interests

- G-quadruplex DNA interaction with macromolecules and small synthetic molecules. Studies to stabilize them under *in vitro* conditions.
- Synthesis and biological studies on small molecules, developed for cancer cure and antimicrobial activities
- Synthesis of small molecules that has specific interaction with biological markers, leading to their specific identification

Recent publications

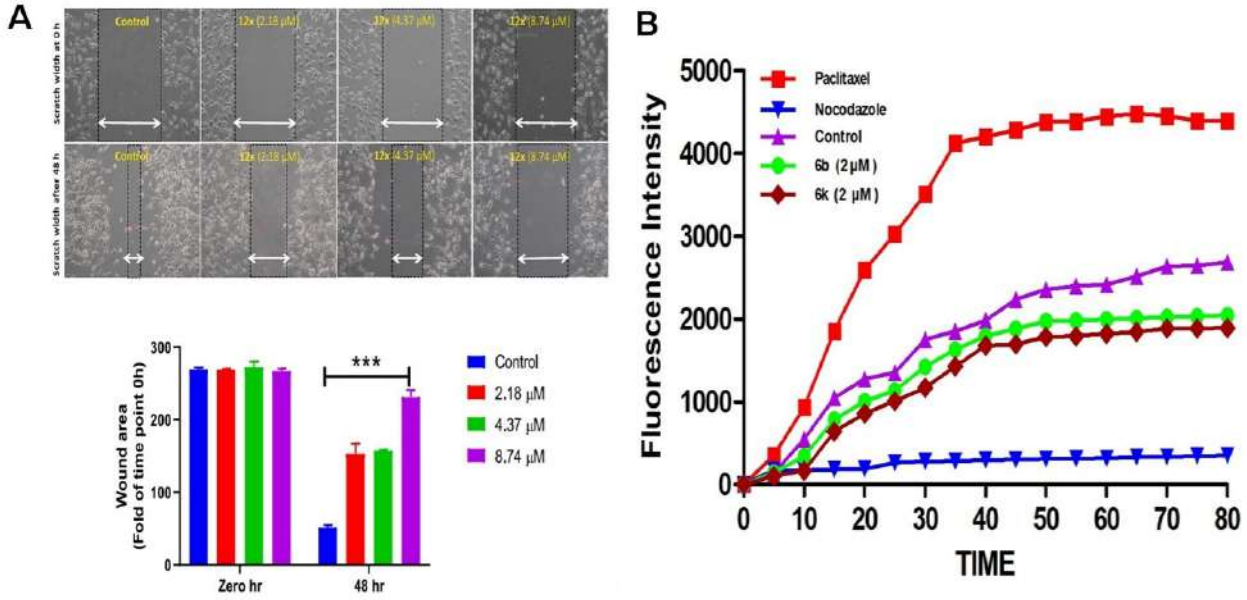
- Debnath S, Nair RR, Ghosh R, Kiranmai G, Radhakishan N, Nagesh N, Chatterjee PB (2022) A unique water soluble probe for measuring the cardiac marker homocysteine and its clinical validation. ***Chemical Communications*** 58: 9210-9213.
- Kadagathur M, Patra S, Devabattula G, George J, Phanindranath R, Shaikh AS, Sigalapallia DK, Godugu C, Nagesh N, Tangellamudi ND, Shankaraiaha N (2022) Design, synthesis of DNA-interactive 4-thiazolidinone-based indolo-/ pyrroloazepinone conjugates as potential cytotoxic and topoisomerase I inhibitors. ***European Journal of Medicinal Chemistry*** 238:114465
- Laxmikeshav K, Rahman Z, Mahale A, Gurukkala Valapil D, Sharma P, George J, Phanindranath R, Dandekar MP, Kulkarni OP, Nagesh N, Shankaraiah N (2023) Benzimidazole derivatives as tubulin polymerization inhibitors: Design, synthesis and *in vitro* cytotoxicity studies. ***Bioorganic & Medicinal Chemistry Letters*** 96: 129494.
- Laxmikeshav K, Sayali M, Devabattula G, Valapil DG, Mahale A, Sharma P, George J, Phanindranath R, Godugu C, Kulkarni OP, Nagesh N, Shankaraiah N (2023) Triazolo-linked benzimidazoles as tubulin polymerization inhibitors and DNA intercalators: Design, synthesis, cytotoxicity, and docking studies. ***Archiv der Pharmazie*** 356: e2200449.

- Laxmikeshav K, Sharma P, Palepu M, Sharma P, Mahale A, George J, Phanindranath P, Dandekar MP, Kulkarni OP, Nagesh N, Shankaraiahah N (2023) Benzimidazole based *bis*-carboxamide derivatives as promising cytotoxic agents: Design, synthesis, *in silico* and tubulin polymerization inhibition. ***Journal of Molecular Structure*** 1271: 134078.
- Soni JP, Reddy GN, Rahman Z, Sharma A, Spandana A, Phanindranath R, Dandekar MP, Nagesh N, Shankaraiah N (2023) Synthesis and cytotoxicity evaluation of DNA-interactive β-carboline indolyl-3-glyoxamide derivatives: Topo-II inhibition and in silico modelling studies. ***Bioorganic Chemistry*** 131: 106313.

G-quadruplex DNA structures are known to have role in oncology. I am interested in various biochemical and biophysical aspects of G-quadruplex DNA and its interaction with macromolecules/small synthetic molecules. I studied the role of non-metallic cations in G-quadruplex stabilization. Stability of G-quadruplex DNA has a major role in cancer cure. My group is the first one to initiate the use of non-metallic cations to stabilize G-quadruplex DNA and understand its role in oncology. G-quadruplex formation and stabilization are the two major aspects, important to understand cancer progression. Studies on G-quadruplex DNA formation, stabilization and its structure has applications in oncology, structural biology and in the field of pharmacology.

Besides studying the G-quadruplex aspects, I am also interested in knowing the role of structurally modified synthetic small molecules in enhancing the anticancer property and induce apoptosis among cancer cells. Using combinatorial chemistry methods, we have synthesized several small molecules and tested for their ability to induce apoptosis among cancer cells. Their efficiency was assayed using modern biological techniques.

Our team has successfully developed a synthetic small molecule that specifically interacts with Homocysteine and Cysteine. Further we have designed an aptamer for HCV detection, carbohydrate antigen 125. Besides this, we have initiated mRNA vaccine platform to combat viral infections that may affect future generations.



A. Wound healing assay for finding the potential of synthetic molecules affecting cancer cell proliferation.
B. Tubulin Polymerization Inhibition assay of synthetic molecules that show anticancer activity.

PAVITHRA L CHAVALI

Cellular and Developmental Biology

From left to right: Denna David, Tejas Borkar, Pavithra Chavali, Aswathy Krishnan, Dhruvkumar Shakyawar, Sourav Ganguli

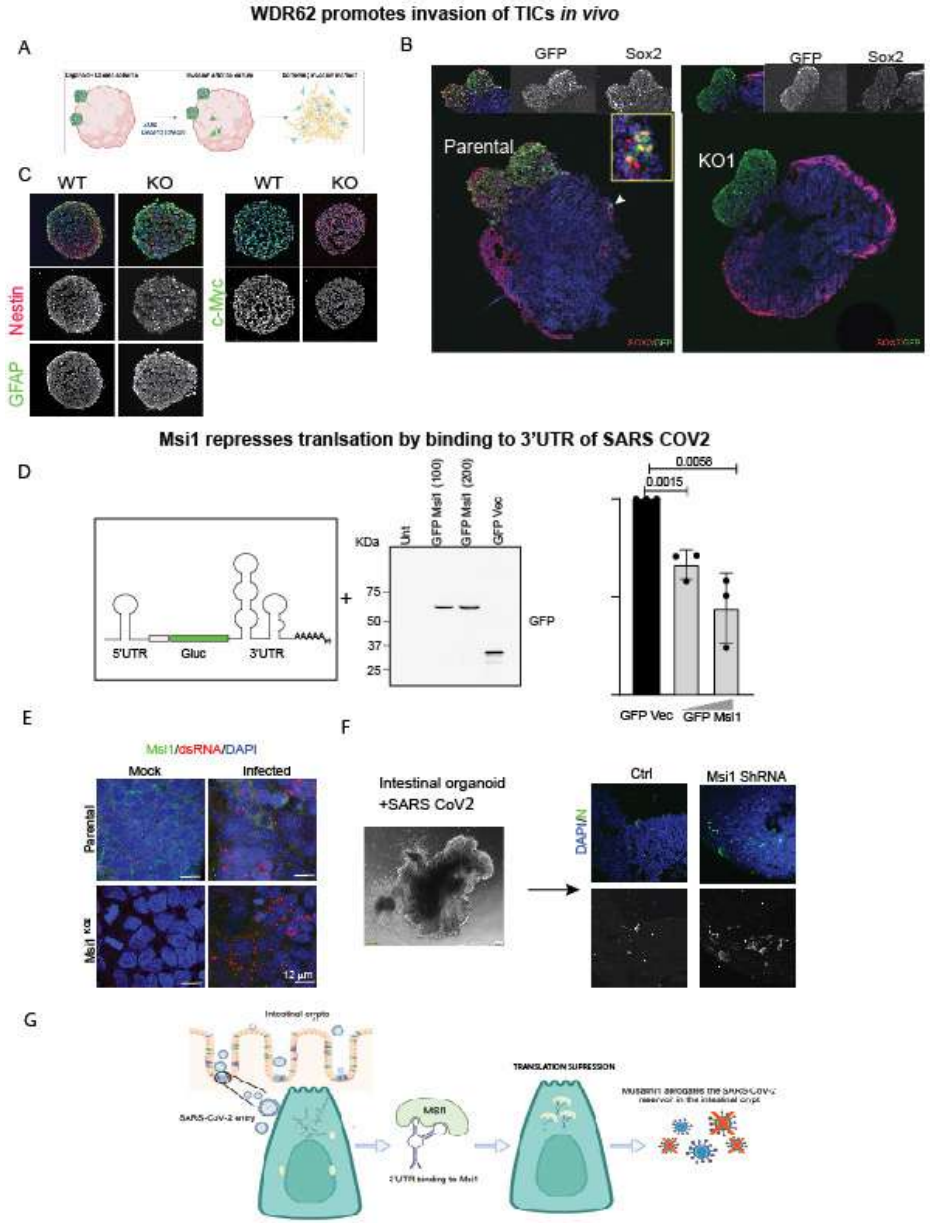
Research interests

- Developmental mechanisms exploited in diseases and infections
- Use of stem cells and 3D organoids as a model for disease progression

Recent publications

- Parvatam S, Chavali PL (2022) Organs-on-a-Chip in Preclinical Studies. ***Microfluidics and Multi Organs on Chip*** 557–588.

There is mounting evidence that genes that regulate early embryonic development are involved in diseases like cancer and that infectious organisms exploit these genes to survive. In this regard, our team investigates the functions of a subset of crucial microcephaly (MCPH) genes, whose absence results in a small brain phenotype in humans. Unknown biological processes underlie these genes' intriguing roles in both malignancies and infections. Delineating the roles of such crucial MCPH genes in neural development and figuring out whether the same pathways are used or disturbed in cancers and other illnesses are the aims of research in our lab. Our research over the previous year has uncovered the molecular aetiology of two of these developmental genes: *WDR62* in glioma and *Musashi1* in SARS CoV-2 infections.



A. Schema depicting coculture of wild type organoids with reporter tagged tumor spheres generated from control or WDR62 KO cells B. Immunostaining of sections of GliCor showing invasion in wild type tumour spheres. Inset shows presence of Sox2 positive TICs in wild type only. C. Immunostaining of tumor spheres from wild type and WDR62 KOs depicting loss of Myc, Nestin and increase in GFAP in WDR62 KOs. D. Gaussia reporter assay depicting significant decrease in translation of SARS CoV-2 mini gene by transfecting increasing amounts of Msi1. E. Immunofluorescence assay of control and Msi1 KO Caco2 cells depicting increase in dsRNA staining in Msi KOs. F. Intestinal organoids treated with or with out Msi1 shRNA were infected with SARS CoV-2 and sectioned and stained for Nucleocapsod protein (green). G. Model depicting Msi1 mediated translational repression of SARS CoV-2

P CHANDRA SHEKAR

Early Embryonic Development in Mouse

From left to right (Standing): Srishti Joshi, Purinima Sialasree, Akshay Kumawat, Narmata, Niharika Tiwary, Altamash, P. Chandra Shekar, Pratham Tanotra, Elarani Mahjee, Debabrata Jana. (Sitting): M. Karthik, Kankipati Teja Shyam

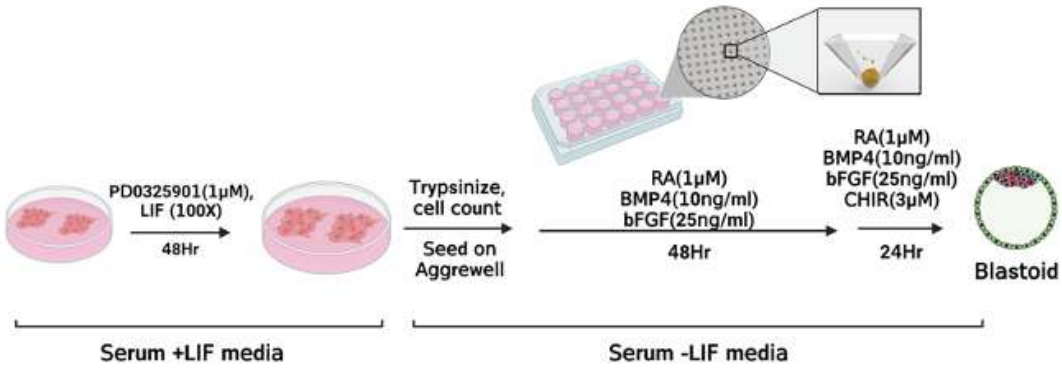
Research interests

- Understanding cell fate choice based on transcription factor modulation in pluripotent state. Studying the molecular mechanisms of pluripotency state transition and self-organisation of cell types from preimplantation embryonic stages to embryo like structures

Recent publications

- Kale HT, Rajpurohit RS, Jana D, Vishnu VV, Srivastava M, Mourya PR, Srinivas G, Shekar PC (2022) A NANOG-pERK reciprocal regulatory circuit regulates Nanog autoregulation and ERK signaling dynamics. ***EMBO Reports*** 23: e54421.

Embryonic stem cells are derived from the pluripotent epiblast. The epiblast of the blastocyst is formed after the differentiation of the trophectoderm. The epiblast and the pluripotent stem cells generally lack the potential to differentiate into cells of the trophectoderm layer. In recent years Human pluripotent stem cells and epiblast have been shown to differentiate to trophectoderm however such a differentiation potential is considered to be limited to humans but not to other mammalian models like mice. In pursuit of understanding the basis for this difference, we discovered a novel culture condition by which we the mouse epiblast as well as the pluripotent stem cells could be readily differentiated to trophectoderm. We could derive stem cells of trophectoderm (trophoblast stem cells (TSCs)). The TSCs had transcriptome and DNA methylation patterns similar to the TSC from the embryos. These TSCs successfully contributed to the chimeric blastocyst and were exclusively localised to the TE compartment. When the chimeric blastocyst was implanted they divided and differentiated to efficiently contribute to the placenta. Our results demonstrated that the mouse embryonic stem cells have the potential to differentiate to trophectoderm linage under appropriate culture conditions. We developed a culture method to generate blastocyst-like structures (blastoids) exclusively from mouse ESCs. The blastoids were composed of all three types of the cells of the blastocyst as shown by the single cell RNA Seq, further when transplanted into the mice the blastoids implanted and induced decidualisation and post-implantation development until gastrulation.



The schematic describing the generation of blastoids exclusively from mouse ESCs

PURAN SINGH SIJWALI

Roles of the Ubiquitin Proteasome System and Autophagy in Malaria Parasite Biology and Pathogenesis

From left to right (Row1): Kajal Pandey, Vishwagithe S.L., Somesh Gorde, R. Nandhakumaar
(Row 2): Pritam Das, Puran Singh Sijwali, G. Srinivas Reddy, Deepak Kumar
(Row 3): Anjana Vijayan, Pragati Patra, Manash Kumar Behera, Kanika Saxena
(Row 4): Nishu, Zeba Rizvi, Saloni Sakshi, Aniket Viswas

Research interests

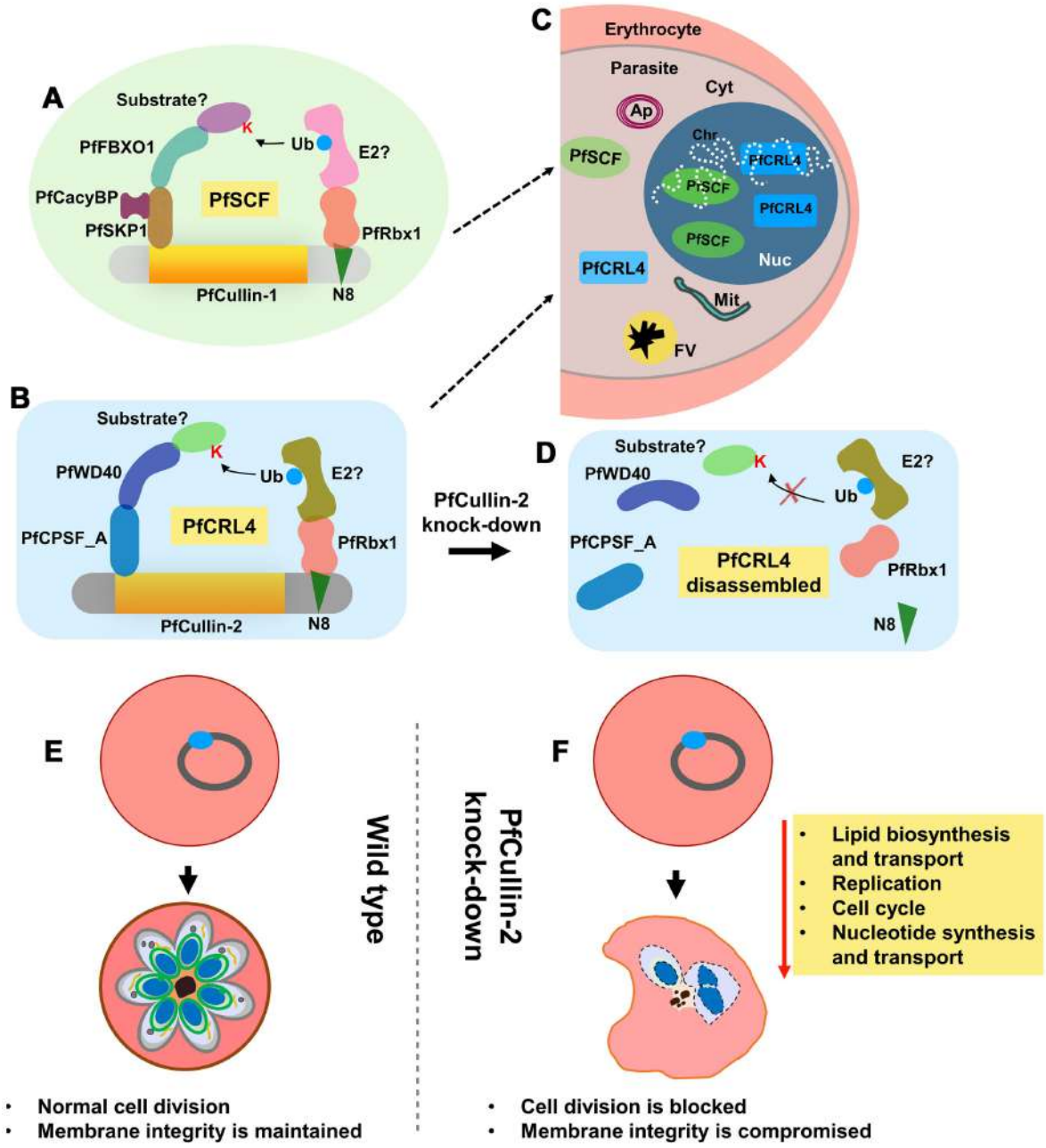
Ubiquitin proteasome system, Autophagy, Cullin-RING ubiquitin E3 ligases, DNA-protein crosslink repair, Plasmodium, Toxoplasma, Malaria, Toxoplasmosis, Proteases

Recent publications

- Sudhakar R, Adhikari N, Pamnani S, Panda A, Bhattacharjee M, Rizvi Z, Shehzad S, Gupta D, Sijwali PS (2022) Bazedoxifene, a Postmenopausal Drug, Acts as an Antimalarial and Inhibits Hemozoin Formation. ***Microbiology Spectrum*** 10: e02781-21.

Plasmodium species cause malaria in humans and several other vertebrates. A major necessity to identify new drug and vaccine targets for controlling/eliminating malaria is to better understand the parasite biology. My group is investigating autophagy and ubiquitin proteasome system of malaria parasites, which likely have roles in disposal and remodelling of parasite and host cellular contents.

Ubiquitination is essential for cellular homeostasis and regulation of several processes, including cell division and genome integrity. Ubiquitin E3 ligases determine substrate specificity for ubiquitination, and Cullin-RING ubiquitin E3 Ligases (CRLs) make the largest group among the ubiquitin E3 ligases. CRLs remain underappreciated in *Plasmodium* and related parasites. To investigate the CRLs of *P. falciparum,* we generated parasites expressing tagged cullin-1 (PfCullin-1), cullin-2 (PfCullin-2), Rbx1 (PfRbx1) and Skp1 (PfSkp1). PfCullin-1 and PfCullin-2 showed predominant expression in erythrocytic trophozoite and schizont stages, with nucleocytoplasmic localization and chromatin association, suggesting roles in these compartments. Immunoprecipitation, *in vitro* protein-protein interaction and ubiquitination assay confirmed the presence of a functional SCF (PfSCF), comprising of PfCullin-1, PfRbx1, PfSkp1, PfFBXO1 and calcyclin binding protein. Immunoprecipitation, sequence analysis and ubiquitination assay indicated that PfCullin-2 forms a functional human CRL4-like complex (PfCRL4), consisting of PfRbx1, cleavage and polyadenylation specific factor subunit_A and WD40 repeat proteins. PfCullin-2 knock-down significantly decreased asexual and sexual erythrocytic stage development. Several pathways, including DNA replication and protein degradation were dysregulated upon PfCullin-2-depletion, which likely reflects association of PfCRL4 with multiple pathways. PfCullin-2-depleted schizonts had poorly delimited merozoites and internal membraned structures, suggesting a role of PfCRL4 in maintaining membrane integrity. PfCullin-2-depleted parasites had significantly lower number of nuclei/parasite than the normal parasites, indicating a crucial role in cell division. Taken together, we have demonstrated the presence of functional CRLs in *P. falciparum*, with crucial roles for PfCRL4 in cell division and maintaining membrane integrity.



PfCullin-1 and PfCullin-2 serve as scaffolds for assembly of the indicated proteins into functional PfSCF (A) and PfCRL4 (B) ubiquitin E3 ligases, respectively. Both the complexes localize (C) to cytoplasm (Cyt) and nucleus (Nuc), and associate with chromatin (Chr), suggesting their roles in these compartments, including DNA-associated processes. Apicoplast (Ap), mitochondria (Mit) and food vacuole (FV) with haemozoin (black structure) are also shown in the parasite within the erythrocyte. PfCullin-2 knock-down at protein level would prevent assembly of the indicated subunits into functional PfCRL4 (D), thereby affecting the associated processes. Wild type asexual erythrocytic parasite developed normally from ring to multinucleate schizonts (E), whereas PfCullin-2 knock-down parasites exhibited downregulation of several key pathways, resulting in a block in cell division and compromised membrane integrity (F). Contrary to the wild type schizont that showed multiple nuclei with distinct outer membrane and intracellular membraned structures, the PfCullin-2 knock-down schizont had less number of nuclei and poorly demarcated membraned structures.

RAGHUNAND R TIRUMALAI

Physiology and Pathogenic Mechanisms of *Mycobacterium tuberculosis*

From left to right: Raghunand Tirumalai, Adhyeta Choudhuri, Muskan Gupta, Simran Sharma, Korak Chakraborty, Jennifer Albert, Ravi Prasad Mukku

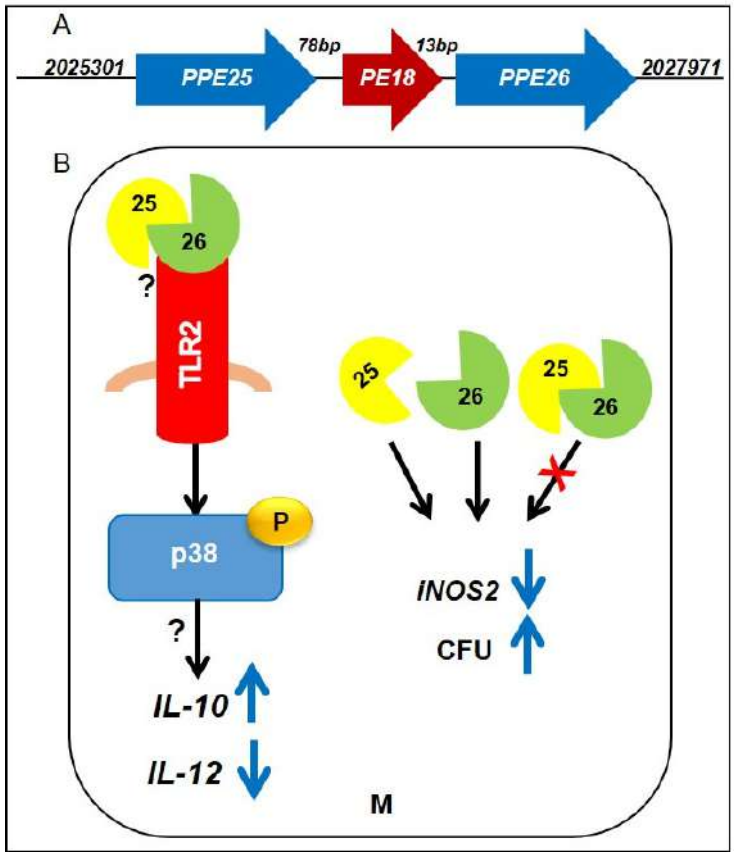
Research interests

Our group studies the physiology and pathogenic mechanisms of *Mycobacterium tuberculosis* (*M.tb*), the causative agent of human tuberculosis. Research in our laboratory is focussed towards:

- Studying immune evasion mechanisms of *M.tb*
- Identifying novel mechanisms of drug resistance
- Investigating the role of membrane associated factors in mycobacterial entry

Functional characterisation of the *PPE25 (Rv1787)- PE18 (Rv1788)- PPE26 (Rv1789)* gene cluster in immune evasion by *Mycobacterium tuberculosis*

M. tb encodes multiple virulence factors to subvert host immune responses. One such class of proteins is encoded by the multigenic PE_PPE family which accounts for 10% of its coding potential. A number of these genes occur in clusters, of which the *PPE25(Rv1787)-PE18(Rv1788)-PPE26(Rv1789)* locus alone, is organised in a PPE-PE-PPE arrangement. We establish here that this cluster is co-operonic in *M. tb*, and identify for the first time, PPE25::PPE26 as the sole interacting protein pair encoded by this cluster. Recombinant *M. smegmatis* strains expressing PPE25, PE18, and PPE26, exhibited enhanced survival in THP-1 macrophages, with infected cells displaying increased levels of the anti-inflammatory cytokine IL-10, and reduced levels of the pro-inflammatory cytokine IL-12. Macrophages infected with recombinant *M. smegmatis* expressing PPE26 showed increased phosphorylation of the MAP kinase p38, consistent with the known TLR2 binding activity of PPE26. In contrast to strains expressing the individual cluster genes, the recombinant expressing the entire PPE25-PE18-PPE26 operon showed no change in intra-macrophage CFUs, suggestive of an inhibitory role for the PPE25::PPE26 complex in CFU enhancement. Taken together, our findings implicate the PPE25-PE18-PPE26 cluster in playing an immune evasion role in the pathophysiology of *M. tb* (Figure) (Manuscript in revision).



A) Schematic showing the genomic organisation of the *PPE25-PE18-PPE26* region of the *M. tb* genome. (B) Model depicting the immunomodulatory role of PPE25/PPE26. M - Macrophage

RAJAN SANKARANARAYANAN

Structural Biology

From left to right, standing: Sambhavi, Shobha, Sahar, Nikita, Jotin, Rukmini, Aravind, Rajkanwar, Sankaranarayanan, Akshay, Lalitha, Reshmika, Madhavi, Viola, Pujaita, Varsha, Biswajit, Ankit
Sitting: Priyadarshan, Dinesh, Mukul, Santosh, Mallesh, Sakshi, Bapin, Pradeep, Koushick, Suhail, Sudipta

Research interests

- Mechanistic basis and functional implications of chiral proofreading mechanisms in the cell that maintain high fidelity during translation of the genetic code
- Insights into lipid metabolite-producing enzymes : how cell fine-tunes lipid subspecies for cellular homeostasis and environmental adaptation

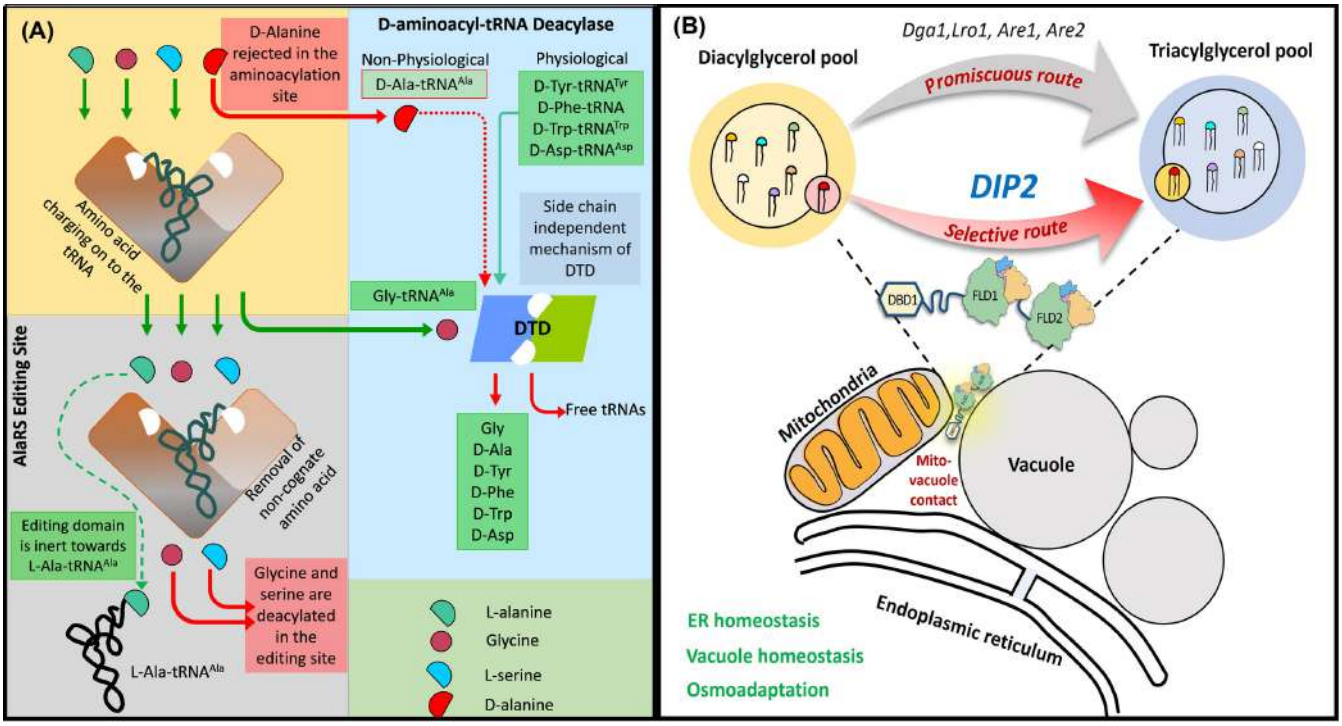
Recent publications

- Mondal S, Kinatukara P, Singh S, Shambhavi S, Patil GS, Dubey N, Singh SH, Pal B, Shekar PC, Kamat SS, Sankaranarayanan R (2022) DIP2 is a unique regulator of diacylglycerol lipid homeostasis in eukaryotes. ***eLife*** 11: e77665.

Homochirality of cellular proteome is attributed to the L-chiral bias of translation apparatus. Chiral specificity of enzymes was elegantly explained using the 'four-location' model by Koshland two decades ago. In accordance with the model, it was envisaged and noted that certain aminoacyl-tRNA synthetases (aaRS) that charge larger amino acids are porous to D-amino acids. However, the mechanistic basis of how other synthetases efficiently exclude the incoming D-amino acids remained elusive. By utilising alanyl-tRNA synthetase (AlaRS) that is responsible for charging the smallest L-amino acid, alanine, we showed the basis of D-alanine exclusion from the active site. In addition, we also provided the biochemical evidence of D-aminoacyl-tRNA deacylase (DTD) acting on smaller D-aa-tRNAs. Overall, this study substantiates how chiral fidelity is perpetuated during protein synthesis.

Diacylglycerols (DAGs) are a minor component of cell membranes, and are crucial for physiological processes like cell signalling and membrane trafficking in eukaryotes. Since DAGs are devoid of any chemical head groups, acyl chain-length variations have been proposed as the basis of functional diversity. Our study has identified an ancient Fatty-acyl-AMP-ligase (FAAL) domain-containing protein family, Disco-interacting protein 2 (DIP2), as a unique DAG regulator, which converts a specific subset of DAGs (C36:0, C36:1) to triacylglycerols (TAGs), and is exclusive of bulk DAG metabolism. We further show that the DAG regulation by DIP2 is conserved from yeast to mammals. We demonstrate that DIP2 localises to mitochondria-vacuole contact sites and is indispensable for maintaining vacuolar and endoplasmic reticulum homeostasis.

Thus, the study establishes DIP2 as a family of selective DAG regulators at spatiotemporal scale in the cellular milieu.



(A) Overall model showing the modus operandi of AlaRS and DTD.
(B) Model depicting the role of FAAL-like protein family, DIP2, in regulating subpopulation of diacylglycerol lipids to ensure cellular homeostasis.

RAKESH K MISHRA

Genome Organization and Epigenetic Regulation

From left to right, top row: Rakesh K. Mishra, Rashmi U. Pathak, Runa Hamid, K. Phanindhar, Ashish Bihani, Avvaru Akshay Kumar
Bottom row: Ravina Saini, Soujanya M. S, 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

Recent publications

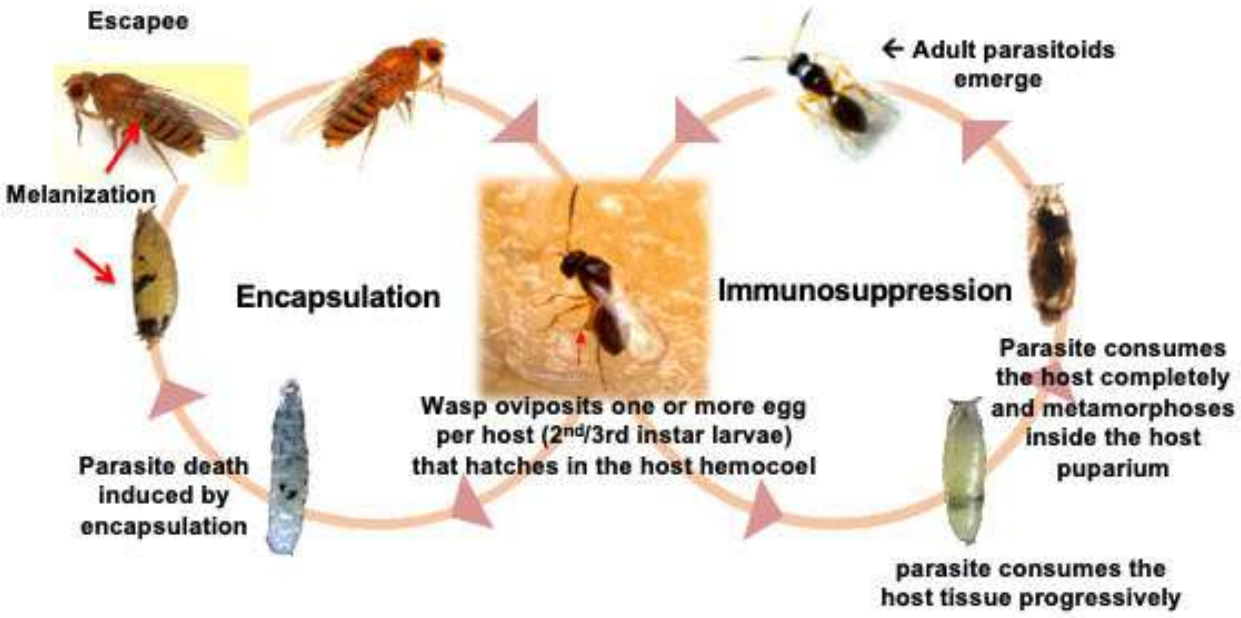
- Mamilla Soujanya, Ashish Bihani, Nikhil Hajirnis, Rashmi U Pathak, Rakesh K Mishra (2023) Nuclear architecture and the structural basis of mitotic memory. ***Chromosome Research*** 31(1): 8.
- Kundurthi Phanindhar and Rakesh K Mishra (2023) Auxin-inducible degron system: an efficient protein degradation tool to study protein function. ***BioTechniques*** 74(4): 186-198.
- Khera, H. K. and R. Mishra (2023) Nucleic Acid Based Testing (NABing): A Game Changer Technology for Public Health. ***Molecular Biotechnology*** doi: 10.1007/s12033-023-00870-4.
- Nikhil Hajirnis, Shubhanshu Pandey, Rakesh K. Mishra (2023) CRISPR/Cas9 and FLP-FRT mediated regulatory dissection of the BX-C of *Drosophila melanogaster*. ***Chromosome Research*** 31(1): 7.
- Shagufta Khan, Rakesh K. Mishra, Surabhi Srivastava (2023) Epigenetic regulation of cis-regulatory elements and transcription factors during development. Editor: Garima Singh In ***Translational Epigenetics, Perinatal and Developmental Epigenetics***, Academic Press, Volume 32, 71-113, ISBN 9780128217856, doi: 10.1016/B978-0-12-821785-6.00004-9.
- Rahul Sureka, Akshay Kumar Avvaru, Divya Tej Sowpati, Rashmi Upadhyay Pathak & Rakesh Kumar Mishra (2022) Structural and developmental dynamics of Matrix associated regions in Drosophila melanogaster genome. ***BMC Genomics*** 23.
- Manupati Hemalatha, Athmakuri Tharak, Harishankar Kopperi, Uday Kiran, C. G. Gokulan, Rakesh K. Mishra, S. Venkata Mohan (2022) Surveillance of SARS-CoV-2 genome fragment in urban, peri-urban and rural water bodies: a temporal and comparative analysis. ***Current Science*** 123: 987-994.

Our research activities are catered around the fundamental question of how information in encoded in genome that can lead to development of complex organisms from a single cell stage. One of the key features of this process is cell type packaging of the genome in order that genes not needed in a cell type are inaccessible to transcriptional machinery and the ones needed to be expressed are enabled with appropriate and efficient interactions of regulatory elements with the gene promoters. We aim to discover DNA elements involved in this process and explore the mechanisms that facilitate this process.

Some of our findings during the period of this report:

Identical DNA sequence can give distinct genetic output in distinct context. What is this second layer of information on the DNA sequence is an interesting unsolved question. We use abiotic stress (heat shock) and biotic stress (exposure to parasitic wasp) in *Drosophila* to explore the genetic and molecular basis of epigenetic mechanisms. We show that the transgenerational inheritance of both biotic and abiotic stress is exclusively through the male germ line. Furthermore, we observe that epigenetic factors (Polycomb group of genes) identified initially as the regulators of homeotic genes, have key role to play in transgenerational epigenetic inheritance.

Having established the paternal route of the epigenetic memory, we carried out extensive analysis of sperm sample for the proteomics, transcriptomics and DNA methylome of normal and stressed lineage. These molecular explorations further help in understanding the epigenetic memory of stress passed on to the generations.



Arms race between *Drosophila melanogaster* and *Leptopelina boulardi.* Our study shows that the host fly takes adaptive measures in escaping from infestation if subjected recurrently to the parasite wasp.

R NAGARAJ

Host-defense Antimicrobial Peptides; Activity and Developing Future Therapeutic Agents

R. Nagaraj

Research interests

- Biology of host-defense peptides

Recent publications

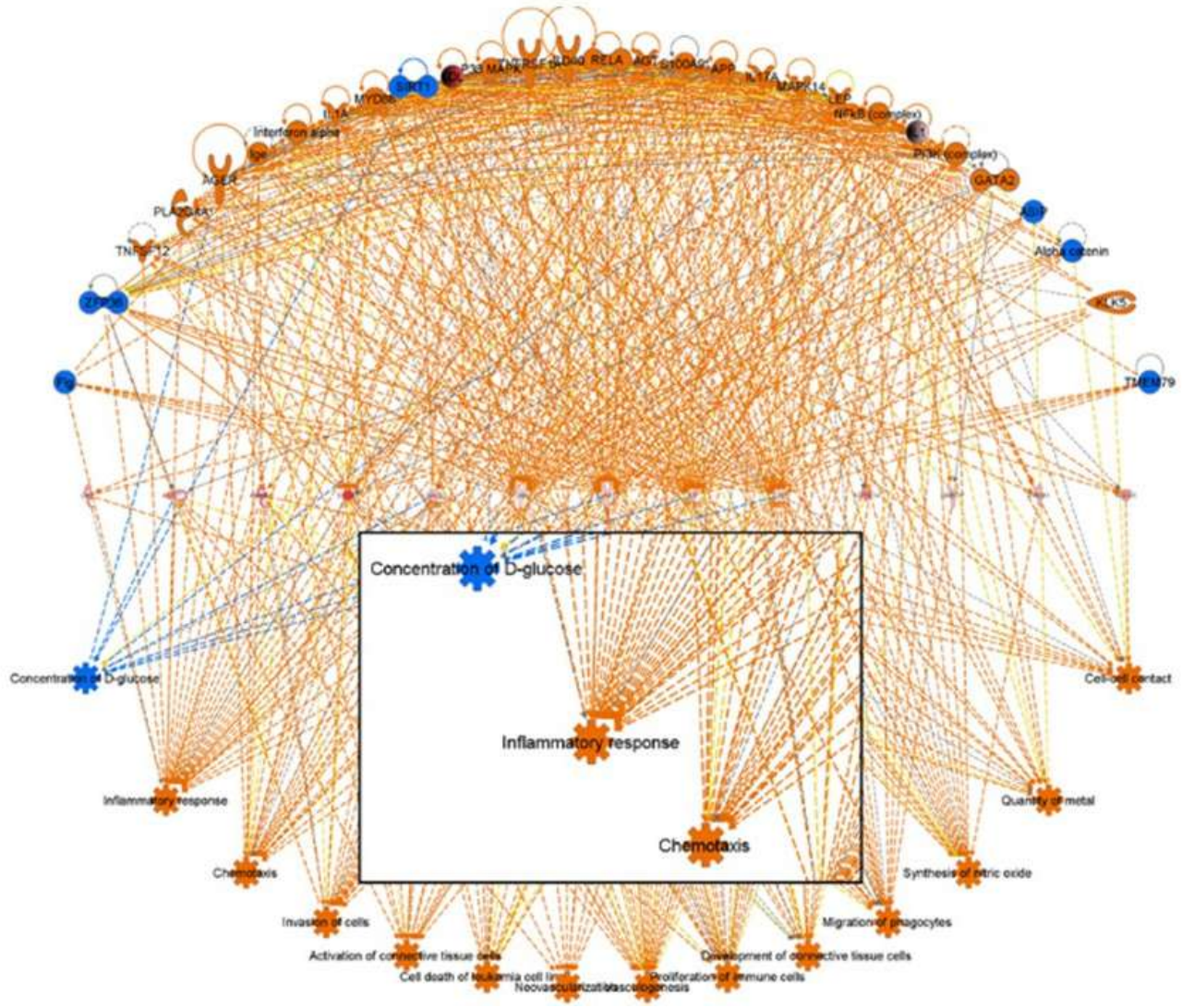
- Banu S, Nagaraj R, Idris MM (2022) Defensins: Therapeutic molecules with potential to treat SARS-CoV-2 infection. ***Indian Journal of Medical Research*** 155: 83–85.
- Idris MM, Banu S, Siva AB, Nagaraj R (2022) Down regulation of defensin genes during SARS-CoV-2 infection. ***Acta Virologica*** 66: 249-253.
- Banu S, Nagaraj R, Idris MM (2023) A proteomic perspective and involvement of cytokines in SARS-CoV-2 infection. ***PLoS One*** 18: e0279998.

In collaboration with Dr MM Idris' group

A. The symptoms caused by the coronavirus SARS-CoV-2 are highly variable among infected individuals and also appear to depend on the infecting strain. Responses by various populations may differ considerably. Hence, it is important to investigate protein and gene expression from patients from different geographical locations and ethnicity. By a combination of proteomics analysis, gene expression studies and blot array, we were able to detect several proteins related to inflammation and auto immunity such as histones and annexins and up regulated cytokines. Proteins which were found up-regulated were also up-regulated at the gene level. Clearly a multi-dimensional approach is necessary to obtain a complete picture on SARS-CoV-2 infection. Such an approach would facilitate therapeutic interventions.

B. Entry of SARS-CoV-2 into cells is initiated by binding of the spike protein S to human receptor ACE2 (ACE2) via a contiguous stretch of amino acids in the receptor-binding domain (RBD). We had earlier shown that melittin inhibits the activity of SARS-CoV-2 in cultured cells. Our *in silico* analysis indicates that melittin can associate with the ACE2 binding domain in RBDs of the first isolated strain characterized during the course of the pandemic. Analysis indicated that melittin residues interact with the residues of spike protein that are involved in interacting with the residues of ACE2.

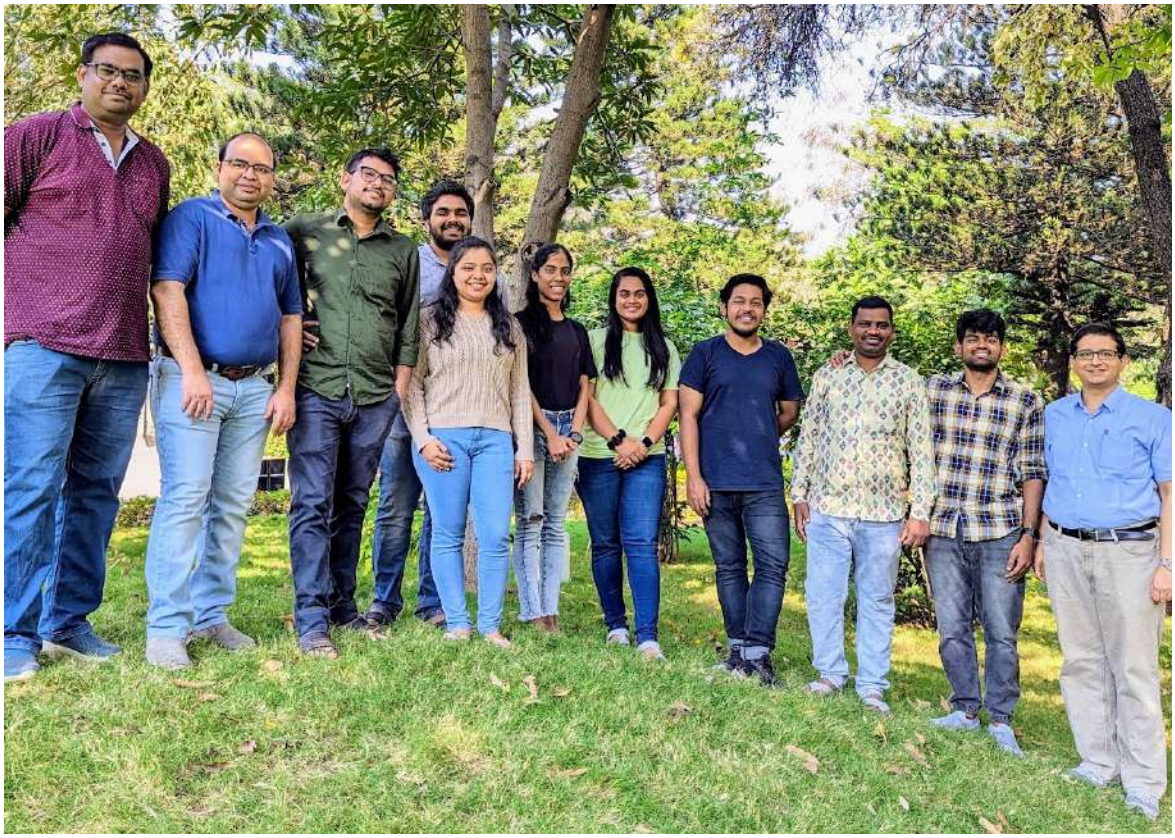
Banu S, Nagaraj R, Idris MM (2023) A proteomic perspective and involvement of cytokines in SARS-CoV-2 infection. PLoS ONE 18(1): e0279998. https://doi.org/10.1371/journal.
pone.0279998.



Network pathway analysis of the genes/proteins associated with infection in nasopharyngeal/oropharyngeal swab samples

SAIKAT CHOWDHURY

Structural Biology of Macromolecular Machinery



From left to right: Harikrishna Adicherla, Sandeep Shrivastava, Palash Kumar Seal, Pathri Achyutha Krishna, Madhvi Pokle, Kowshika Muniandi, Kaanuka Sai Kanapaneni, Rishav Mitra, Rajesh Palle, Justus Francis, Saikat Chowdhury

Research interests

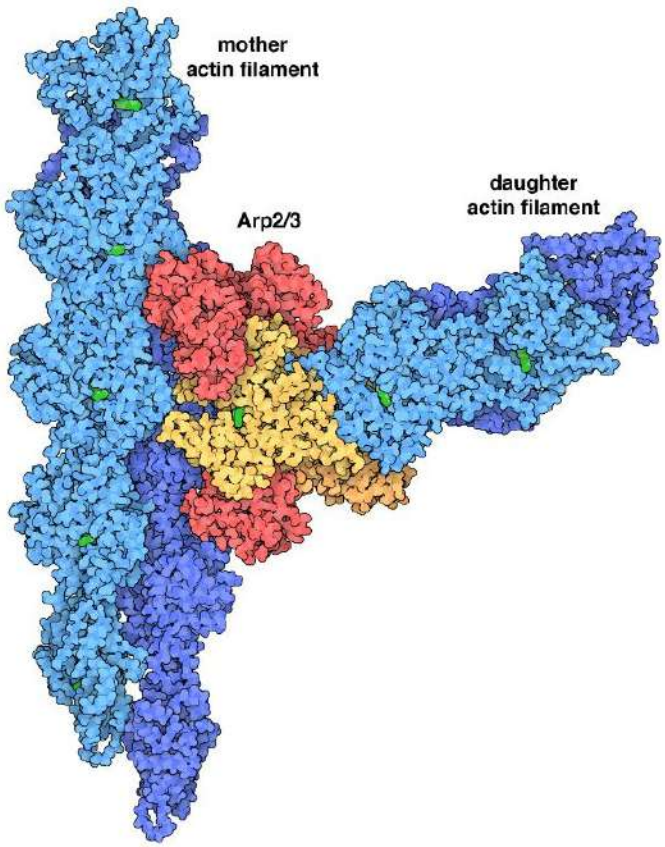
- Understanding the molecular basis of actin cytoskeletal nucleation by different nucleators in response to cellular signals or stimuli
- Unraveling the molecular mechanism of crosstalk between different cytoskeletal elements
- Developing methodologies to determine structures of dynamic macromolecular machinery by cryogenic electron microscopy

Recent publications

- Ding B, Narvaez-Ortiz HY, Singh Y, Hocky GM, Chowdhury S, Nolen BJ (2022) Structure of Arp2/3 complex at a branched actin filament junction resolved by single-particle cryo-electron microscopy. ***Proceedings of the National Academy of Sciences, USA*** 119: e2202723119.
- Ding B, Yang S, Schaks M, Liu Y, Brown AJ, Rottner K, Chowdhury S, Chen B (2022) Structures reveal a key mechanism of WAVE regulatory complex activation by Rac1 GTPase. ***Nature Communications*** 13: 5444.
- Yang S, Tang Y, Liu Y, Brown AJ, Schaks M, Ding B, Kramer DA, Mietkowska M, Ding L, Alekhina O, Billadeau DD, Chowdhury S, Wang J, Rottner K, Chen B (2022) ***Science Advances*** 8: eadd1412.

Forces required for various cellular functions like cell division, change in cellular morphology and cellular migration are provided by cytoskeletal assemblies. The broader goal of our research is to dissect the molecular mechanisms that regulate dynamic cytoskeletal elements and how different cytoskeletal networks work in unison in response to intracellular and extracellular stimuli. Ultimately, these will help us understand how deregulation of cytoskeletal networks can lead to different diseases.

Polymerizing actin filament networks provide forces harnessed by cells for many cellular processes. Precise regulation of actin filament dynamics is essential for these processes, and nucleation of new actin filaments is one of the most important actin regulatory steps because it allows cells to control precisely when and where actin networks assemble. Besides nucleation, the rate of filament growth and the length of polymerizing filaments are also regulated to harness the exact required forces necessary for these cellular functions. A molecular appreciation of how actin nucleators initiate actin filament polymerization and how regulators control length and rate of polymerizing filaments is critical for understanding cancer metastasis and number of neurological diseases. It is also unclear as to how different nucleators precisely regulate actin filament polymerization. Using structural, biophysical and cell biology methodologies we are trying to understand how molecules inside cells precisely regulate actin filament nucleation and how different cytoskeletal elements cross talk with each other. Besides these, our lab is also interested in understanding how different macromolecular machinery works in different types of cells and in different organisms. We are also working on novel electron microscopy data collection schemes and image processing for resolving various molecular machines of different sizes and complexity in action.



Arp2/3 complex mediated branched actin junction structure (PDB ID: 7TPT). Figure made by David Goodsell. This was highlighted as "Molecule of the Month" for November 2022 (https://pdb101.rcsb.org/motm/275).

SANTOSH CHAUHAN

Cell Biology, Host-Pathogen Interactions, Cancer Immunity, and Autoimmune Disorders

From left to right: Ravi Solanki, Sahidur Rehman, Soumya Kundu, Jagmohan Chhatai, Santosh Chauhan, Vennela Nampalli, Lopamudra Bhadra, Snigdha Chatterjee

Research interests

- Understanding the host cell autonomous defense systems against pathogens
- Crosstalk between autophagy and inflammation
- Identifying genes and mechanisms that are critical for cancer progression

Recent publications

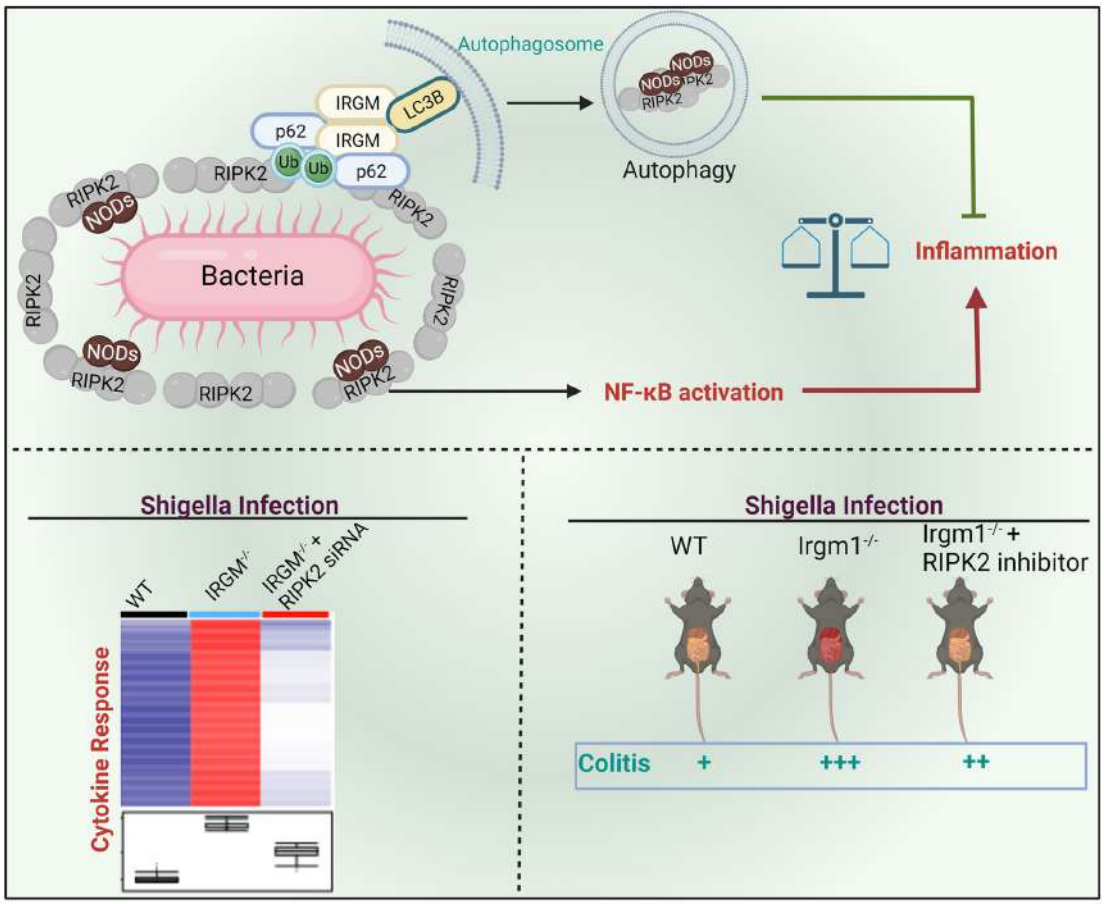
- Mehto S, Jena KK , Yadav R, Priyadarsini S, Samal P, Krishna S, Dhar K, Jain A, Chauhan NR, Murmu KC, Bal R, Sahu R, Jaiswal P, Sahoo BS, Patnaik S, Kufer TS, Rusten TE, Chauhan S, Prasad P, Chauhan S (2022) Selective autophagy of RIPosomes maintains innate immune homeostasis during bacterial infection. ***EMBO Journal*** 41: e111289.
- Mehto S, Kundu S, Chauhan S, Chauhan S (2023) RIPosomes are targets of IRGM-SQSTM1-dependent autophagy. ***Autophagy*** 19: 1045-1047.

The NOD1/2-RIPK2 is a key cytosolic signaling complex that activates NF-κB pro-inflammatory response against invading pathogens. However, uncontrolled NF-κB signaling can cause tissue damage leading to chronic diseases. The mechanisms by which the NODs-RIPK2-NF-κB innate immune axis is activated and resolved are poorly understood. In our study, we demonstrate that bacterial infection induces the formation of RIPK2 oligomers (RIPosomes) that are self-assembling entities recruited over the bacteria to induce NF-κB response (Fig).

Next, we show that autophagy proteins, IRGM and p62/SQSTM1 physically interact with NODs, RIPK2, and RIPosomes to execute their selective autophagy and limit the NF-κB activation (Fig). IRGM suppresses multiple RIPK2-dependent pro-inflammatory programs induced by *Shigella* and *Salmonella* (Fig). Consistently, the therapeutic inhibition of RIPK2 ameliorates *Shigella* infection- and DSS-induced gut inflammation in Irgm1 KO mice. Thus, this study identifies a unique mechanism where the innate immune proteins and autophagy machinery are recruited together over the bacteria for defense and maintaining immune homeostasis.

Implications:

This study delineates new cell-autonomous mechanisms of NODs-RIPK2-dependent pro-inflammatory response and its resolution by selective autophagy. Further, our study also suggests that inhibition of RIPK2 could be a good therapeutic strategy for suppression of gut inflammation associated with IRGM depletion, a risk factor in the progression of Crohn's disease.



Bacterial infection induces RIPosomes (RIPK2 oligomers) formation that are recruited to the bacteria to enhance the NF-κB response. In order to maintain innate immune homeostasis, RIPosomes undergo selective autophagy mediated by autophagy proteins, IRGM, and p62/SQSTM1. IRGM suppresses *Shigella* and *Salmonella*-induced RIPK2-dependent NF-κB and interferon responses. RIPK2 inhibition using GSK583 ameliorates shigellosis- and DSS-induced gut inflammation in Irgm1-KO mice.

SANTOSH KUMAR

Receptor Signalling and Immune Response

From left to right: Niladri, Sitanshu, Blessie, Ketaki, Aleena, Apoorva, Ajmal, Santosh, Swagat

Research interests

- Understanding the principles of immunoreceptor signaling, using the tools of *in vitro* reconstitution, fluorescence imaging, and cellular biochemistry
- Understanding the T cell and NK cell responses in human diseases, using the tools of single cell sequencing, genomics, and cellular biochemistry

Recent publications

- Sarangi SK, Lande KM, Kumar S (2023) KIR signaling is regulated by electrostatic interaction of its cytosolic tail with the plasma membrane despite being neutral polyampholyte. ***Proceedings of the National Academy of Sciences, USA*** 120: e2212987120.

Natural killer (NK) cells express an array of receptors on their surface that can activate them for cytotoxicity and secretion. The activation of human NK cells is tightly controlled by class I major histocompatibility complex (MHC-I)-specific inhibitory receptors expressed on their surface. Inhibitory receptor signals upon tyrosine phosphorylation in immunoreceptor tyrosine-based inhibitory motifs (ITIM) present in its cytosolic tail. Boosting NK cell cytotoxicity by dampening inhibitory signaling is a promising strategy in cancer immunotherapy. Further, ITIM-bearing receptors perform many other biological functions. My lab is interested in signaling by the inhibitory killer-cell immunoglobulin-like receptor (KIR) that recognizes the MHC-I molecule HLA-C on other cells. KIR blocks NK cell activation and paradoxically maintains NK cells in a state of proper responsiveness. Therefore, KIR blockade has not been effective in cancer therapy, underscoring the need of deeper understanding of KIR signaling. We recently found that KIR cytosolic tail interacts electrostatically with the plasma membrane. The interaction inserts ITIM-tyrosines in the lipid bilayer. Binding of KIR to HLA-C on target cell leads to dislodging of KIR tail from the plasma membrane at the NK-target synapses. Tail dislodging renders ITIM-tyrosines accessible, initiating KIR signaling at the synapses. Phosphorylated ITIMs recruit and activate the protein tyrosine phosphatase SHP-1. Protein tyrosine dephosphorylation by activated SHP-1 blocks NK cell activation. The SH2 domains of SHP-1 is seen to bind to lipids *in vitro*. We are working to understand roles of SHP-1 lipid binding in controlling SHP-1 function in NK cell inhibition. Through an unknown mechanism, inhibitory receptor recruits the protein tyrosine kinase c-Abl that phosphorylates the adaptor protein Crk. c-Abl is seen to bind to and phosphorylate SHP-1 during radiation-induced responses. We will, therefore, test roles of SHP-1 in c-Abl recruitment and function during inhibitory signaling.

SHRISH TIWARI

Sequence Analysis of Biomolecules

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

Research interests

- Bioinformatics
- NGS analyses, whole genome/transctiptome assembly, variation analyses
- Imroving rice quality by increasing yield, selecting for early maturation, pest resistance
- Functional analyses of noncoding RNAs
- Protein structure modeling, docking
- miRNAs associated with cancer

Recent publications

- Thummala SR, Guttikonda H, Tiwari S, Ramanan R, Baisakh N, Neelamraju S, Mangrauthia SK (2022) Whole-Genome Sequencing of KMR3 and *Oryza rufipogon*-Derived Introgression Line IL50-13 (Chinsurah Nona 2/Gosaba 6) Identifies Candidate Genes for High Yield and Salinity Tolerance in Rice. ***Frontiers in Plant Science*** 13: 810373.

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 that 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 in the process of sequencing *Aeluropus lagopoides*, which is a mangrove grass that secretes salt in its stems and leaves. We now have an assembly of *A. lagopoides* using the short reads, the long reads and the optical mapping data. We also have sequenced the RNA content of the plant and are in the process of annotating the genome by a combination of gene prediction programs and the long sequencing of RNA pooled from various tissues.

Aeluropus lagopoides, **a mangrove grass that accumulates salt on its leaves and stem**

SONAL NAGARKAR JAISWAL

Developmental Biology

From left to right: Sofia, Reshmi, Aishwarya, Andrea, Sonal, Rishad, Sachin, Priyanka, Nandan

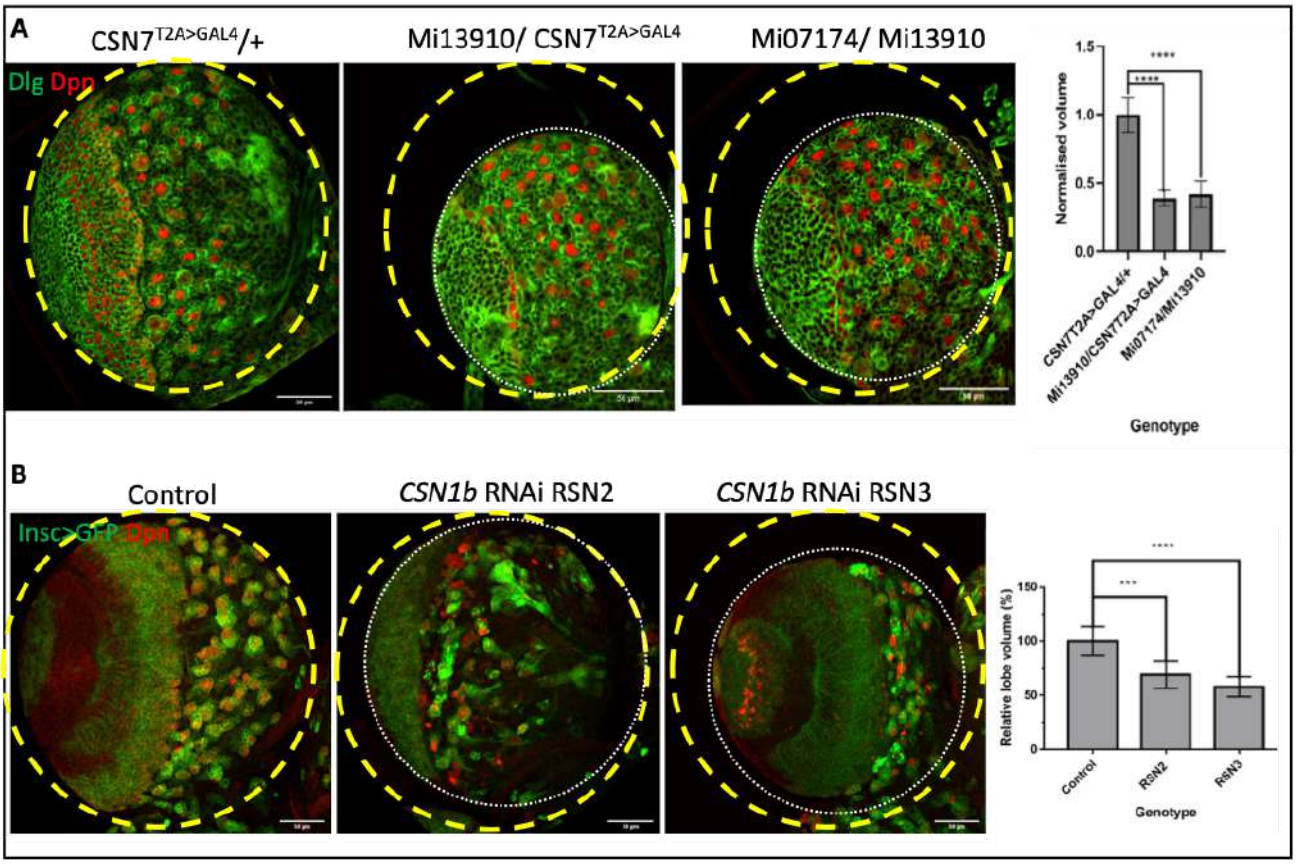
Research interests

- Neural stem cell maintenance during development and disease.
- Mitochondrial dynamics during development and disease.
- Vesicular trafficking

Recent publications

- Cheramangalam RN, Anand T, Pandey P, Balasubramanian D, Varghese R, Singhal N, Jaiswal SN, Jaiswal M (2023) Bendless is essential for PINK1-Park mediated Mitofusin degradation under mitochondrial stress caused by loss of *LRPPRC*. ***PLoS Genetics*** 19: e1010493.

Neural stem cells self-renew to maintain their pool, yet differentiate into enormous functionally and morphologically distinct neurons and glia. Proper regulation of self-renewal and differentiation has profound consequences in development and homeostasis. Decreased neurogenesis could lead to defects in brain development resulting in neurodevelopmental disorders like microcephaly, epilepsy and autism. On the other hand, an increase in self-renewal could lead to malignancies such as cancer. We are interested in identifying the mechanisms and the molecular players underlying neural stem cell self-renewal and differentiation. To study these processes, we use *Drosophila* developing brain and human neuronal stem cells as model systems. We utilize state of the art genome editing tools and a diverse set of cell and molecular biology approaches.



Loss of COP9 subunits CSN1b and CSN7 leads to a small brain phenotype. Larval brains (A) from controls (left) and CSN7 mutants (middle and right), brains are stained with anti-Dlg (green) and Dpn (red) antibodies .(B) controls (left) and CSN1b mutants (middle and right) exhibiting small brain phenotype. Brains are stained with anti-GFP antibody). Scale bar =50mm

SRIRAM VARAHAN

Cellular Metabolism, Microbial Genetics and Microbial Pathogenesis

From left to right: Sujatha, Nivedhitha R, Adishree M, Dhrumi Shah, Sriram Varahan, Ashwin Jiju, Sudharsan M, Riya Bhattacharjee, Nikita Rewatkar, Narasimha

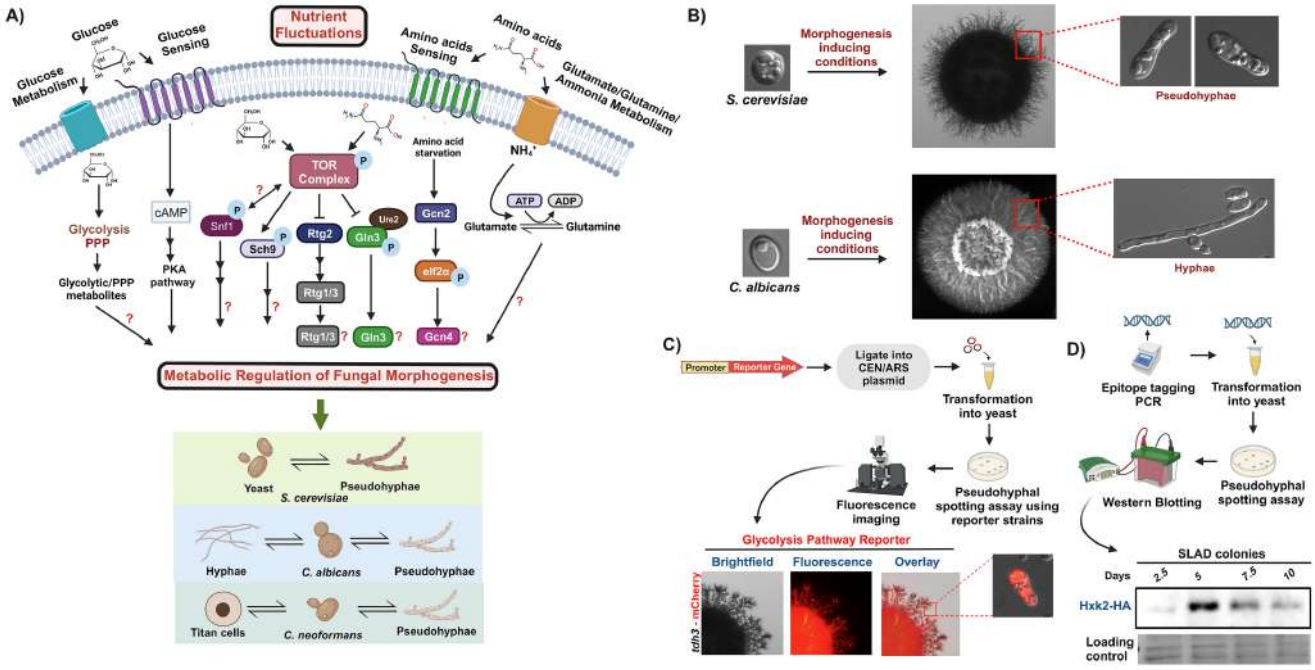
Research interests

- Metabolic basis of cell state transitions in microbial systems
- Emergence of phenotypic heterogeneity in clonal cell populations
- Metabolic regulation of fungal pathogenesis

Recent publications

- Varahan S (2023) Unity in Diversity: Interkingdom Polymicrobial Biofilms in Disease. ***Multispecies Biofilms: Technologically Advanced Methods to Study Microbial Communities*** pp.309-321 (Book chapter)

Fluctuations in nutrient availability are one of the most common challenges encountered by microorganisms. Microorganisms have a remarkable ability to reversibly transition to specialized cell states in response to changing nutrient levels and this allows them to develop into complex biofilm communities, colonize diverse niches and cause persistent infections in a variety of hosts. Current studies have largely focused on identifying genes/gene regulatory networks that control these cell state transitions. However, we lack a complete understanding of the driving metabolic processes behind such cellular decision-making events, and how they are regulated. Our research program aims to understand cell state transitions in the context of microbial community development and host pathogenesis from a metabolism perspective i.e. a molecules and processes based perspective, elucidating how specific metabolites, metabolic processes and metabolic switches drive cell state transitions in these processes. Fungi serve as excellent model systems to address this, as they exhibit a remarkable spectrum of cell state transitions in response to nutrient fluctuations. Our group employs simple fungal models (*Saccharomyces cerevisiae*), as well as pathogenic fungi (*Candida albicans* & *Cryptococcus neoformans*), to understand how conserved metabolic events regulates cell state transitions in response to nutrient fluctuations, and how this influences fungal pathogenesis.



Metabolic Regulation of Fungal Morphogenesis: Our lab is interested in understanding how conserved metabolic events regulate fungal morphogenesis specifically in the context of fungal biofilm development and host pathogenesis, using model fungi including *Saccharomyces cerevisiae* and pathogenic fungi including *Candida albicans* and *Cryptococcus neoformans* (A). In response to nutrient limitation, fungi undergo morphogenetic switching wherein yeast cells transition to pseudohyphal cells or hyphal cells, which are elongated in morphology and exhibit altered budding and cell polarity (B). Spatial distribution of mCherry fluorescence across a *S. cerevisiae* colony exhibiting pseudohyphal differentiation, indicating the transcriptional expression of glycolytic enzyme, glyceraldehyde-3-phosphate dehydrogenase (tdh3 reporter). Colonies containing the tdh3 activity reporter were spotted onto synthetic low ammonium (SLA) medium with 2% glucose. Colonies were allowed to develop for 10 days and were imaged using a high resolution epifluorescence and bright-field microscope (C). Temporal expression of the glycolytic enzyme, hexokinase (Hxk2) was monitored in *S. cerevisiae* colonies exhibiting pseudohyphal differentiation. Hxk2 was epitope tagged and Western blotting was performed to monitor its level as the colonies developed (D).

SWASTI RAYCHAUDHURI

Proteotoxicity in Age-related Diseases

From left to right: Harshit, Pooja, Pallavi, Neha, Alivelu, Swasti, Sristi, Shemin, Aanchal, and Suparna

Research interests

- Quality control of respiratory complex biogenesis
- Cause and consequences of spatiotemporal organization of protein inclusion bodies
- Plasma proteomics and metabolomics to identify biomarkers of Sickle Cell Anemia and chronic metabolic diseases including Cardiomyopathy and Diabetes

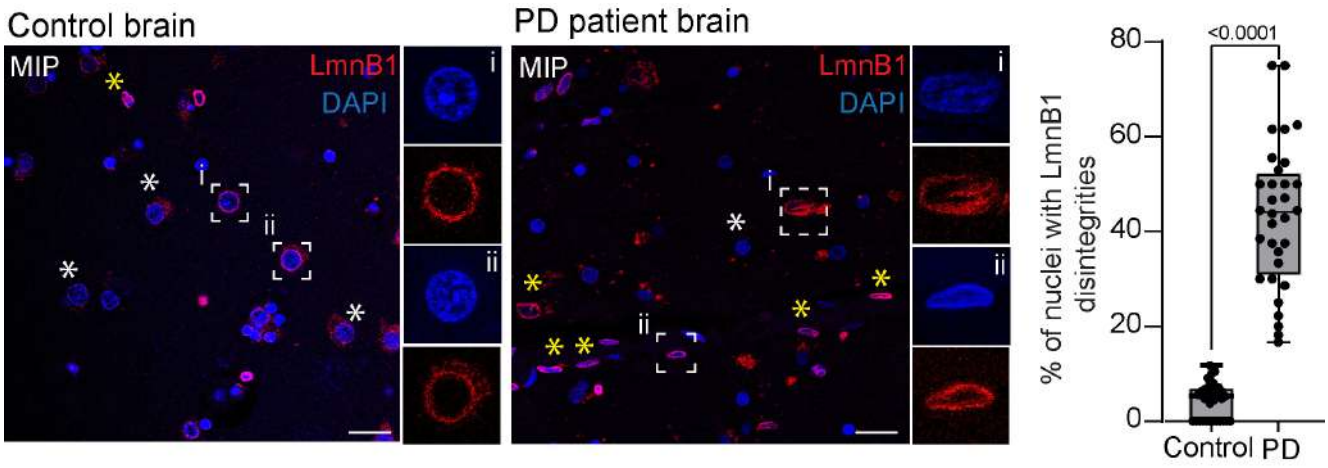
Recent publications

- Narayana Rao KB, Pandey P, Sarkar R, Ghosh A, Mansuri S, Ali M, Majumder P, Ranjith Kumar K, Ray A, Raychaudhuri S, Mapa K (2022) Stress Responses Elicited by Misfolded Proteins Targeted to Mitochondria. ***Journal of Molecular Biology*** 434: 167618.
- Polepalli S, Singh R, Naskar S, Pasupuleti Punyasri SKDB, Ranjith Kumar K, Kameshwari Y, Krishnakumari V, Bakthisaran R, Jain D, Chandak GR, Raychaudhuri S (2022) Rapid and Deep Plasma Proteomics workflows for robust identification and quantification of biomarkers of Sickle Cell Anaemia. ***Journal of Proteins and Proteomics*** 13: 205–218.

Respiratory complexes are multi-subunit protein complexes with the central function in aerobic energy metabolism. 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. Now, we figure out that the subunits of respiratory complexes display a mosaic pattern of amino acid sequence evolution. Sequences of the mitochondrial matrix subunits are conserved across eukaryotes. Subunits embedded into the mitochondrial inner membrane are conserved within eukaryotic kingdoms but diverged beyond. Our recent results suggest that lipid-interactions of inner membrane subunits shape up the evolution of eukaryotic respiratory complexes.

We also work with amyloid inclusions. Amyloidogenic proteins form fibrillar inclusion bodies which are hallmark of many age-related neurological diseases. The pathological role of amyloid fibrils has obscure views, from being the cause of the pathogenesis to being the inert-end products of protein-misfolding. We work with α-Synuclein which is an amyloidogenic protein associated with Parkinson's Disease (PD). The canonical pathological inclusions of α-Synuclein in PD are known as Lewy Bodies (LBs). We created models in primary neurons and cultured cells recapitulating LBs. Our results suggest that LBs are dump-yard of amyloidogenic α-Synuclein for eventual degradation. However, overgrown LBs deregulate cytoskeleton-nucleoskeleton connections at the perinucleus and damage the nuclear lamina. We find that perturbed nuclear lamina is directly associated with deregulated transcription of stress-chaperones in LB-containing aging neurons.

We also perform plasma proteomics of Sickle Cell Anaemia and involved in "Phenome India-CSIR Health Cohort Knowledgebase" project.



Maximum Intensity Projection (MIP) of a non-neurological disease (control) and Parkinson's disease (PD) patients' brain sections stained with LmnB1 antibody. Insets: Zoomed images of box-indicated locations. Scale bar- 20 µm. White asterisk – representative nuclei with unperturbed lamina; Yellow asterisk – nuclei with lamina disintegrities. The percentage of nuclei with lamina disintegrities among total LmnB1 positive nuclei per field of control brain and Parkinson's disease (PD) patients' brain sections were plotted.

T KARTHIK BHARADWAJ

Medical Genetics

Legend:
Top row: Chandreshwara Raju, Neha Singh, Suryanarayan Mishra, Sumedha, Amar; **Middle row**: Vidyadhari, Himashree, Karthik Bharadwaj, Lamuk Zaveri, Vasanth Kumar; **Bottom row**: Aman Suryan, Mahfuz Hasan, Priya

Research interests

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

Recent publications

- Moharir SC, Chandra TS, Goel A, Thakur B, Tandel D, Mahesh SR, Vodapalli A, Bhalla GS, Kumar D, Naruka DS, Kumar A, Tuli A, Suravaram S, Bingi TC, Srinivas M, Mesipogu R, Reddy K, Khosla S, Harshan KH, Tallapaka KB, Mishra RK (2022) Detection of SARS-CoV-2 in the air in Indian hospitals and houses of COVID-19 patients. ***Journal of Aerosol Science*** 164: 106002.
- Singh P, et. al. (2022) A machine learning-based approach to determine infection status in recipients of BBV152 (Covaxin) whole-virion inactivated SARS-CoV-2 vaccine for serological surveys. ***Computers in Biology and Medicine*** 146:105419.
- Nerakh G, Vineeth VS, Tallapaka KB, Nair L, Dalal A, Aggarwal S (2022) Microcephalic primordial dwarfism with predominant Meier-Gorlin phenotype, ichthyosis, and multiple joint deformities-Further expansion of DONSON Cell Cycle-opathy phenotypic spectrum. ***American Journal of Medical Genetics*** 188: 2139-2146

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* & *CHFR* genes. In addition, our lab is currently handling diverse projects like Genome India, Indian Breast Cancer Genome Atlas and various genomics-based infectious disease surveillance activities. As a crucial member of the INSACOG consortium, the team is involved in tracking the evolution and surveillance of the SARS-CoV2 virus in the country. In addition to sequencing the viral genome itself, the team pursues research on other aspects of COVID-19 including host immune response to SARS-CoV-2 infections, role of host genomic factors and SARS-CoV-2 reinfections. We have also initiated optical genome sequencing at CCMB during the last year. This technology is better than other available sequencing technologies for identification of genome-wide large structural and copy number variations, enabling us in diagnosis of certain rare genetic disorders and also in construction of accurate reference genomes.

VASANT SHINDE

Field and Scientific Archaeology

From left to right: P. Nagarjuna, Ganesh Bhongale, Vasundhara, Vasant Shinde, Niraj Rai, Garima Singh P. Syama, Divya Jyothi

Research interests

The major research interest of our group is centered on understanding the genesis of the basic sciences and technologies through archaeological sources.

- Understanding the ancient human existence, diet, health and migration by studying artifacts and ecofacts.
- Understanding the process of peopling of South Asia and cultural dispersal through archaeogenetic records.

A thorough examination of artefacts and ecofacts, which are tangible remnants or traces left by past civilizations, enables us to understand the complexities of ancient human societies, with a focus on their existence, dietary customs, health, and migration patterns. Artifacts include tools, pottery, works of art, architectural element, and any objects made by humans, providing valuable insights into technological advances, social structures and cultural practices. Whereas, ecofacts related to organic remains such as skeletons of human and animal and plant remains, including grains, help to understand ancient diets, health conditions and interactions with the environment. Studying these factors helps understand how ancient humans lived, food consumed, their environmental interaction, and migration from one region to another.

Genetic information from ancient DNA that has been retrieved from skeletal remains or artefacts can monitor data on the genetic and ancestry of ancient populations. We aimed to apprehend the origins, migration patterns, and contacts of early human populations in South Asia by way of inspecting DNA evidence from several archaeological sites. This method will assist to get a clearer view on number of cultures interacted, and modified over the years, adding to South Asia's sizeable cultural range. It contributes to a deeper knowledge of the historic and anthropological dynamics of the location by make-up plying crucial facts on migratory patterns, intercultural interactions, and the emergence of exclusive cultural capabilities.

Samples from Harappan cemeteries dated to 2500 BCE and Megalithic Burials dated to 1200 BCE have been collected systematically and their analysis may tell us on continuity, genetic mutation, etc.

Excavation of Harappan human skeletal remains at Rakhigarhi (C. 2500 BCE)

VEGESNA RADHA

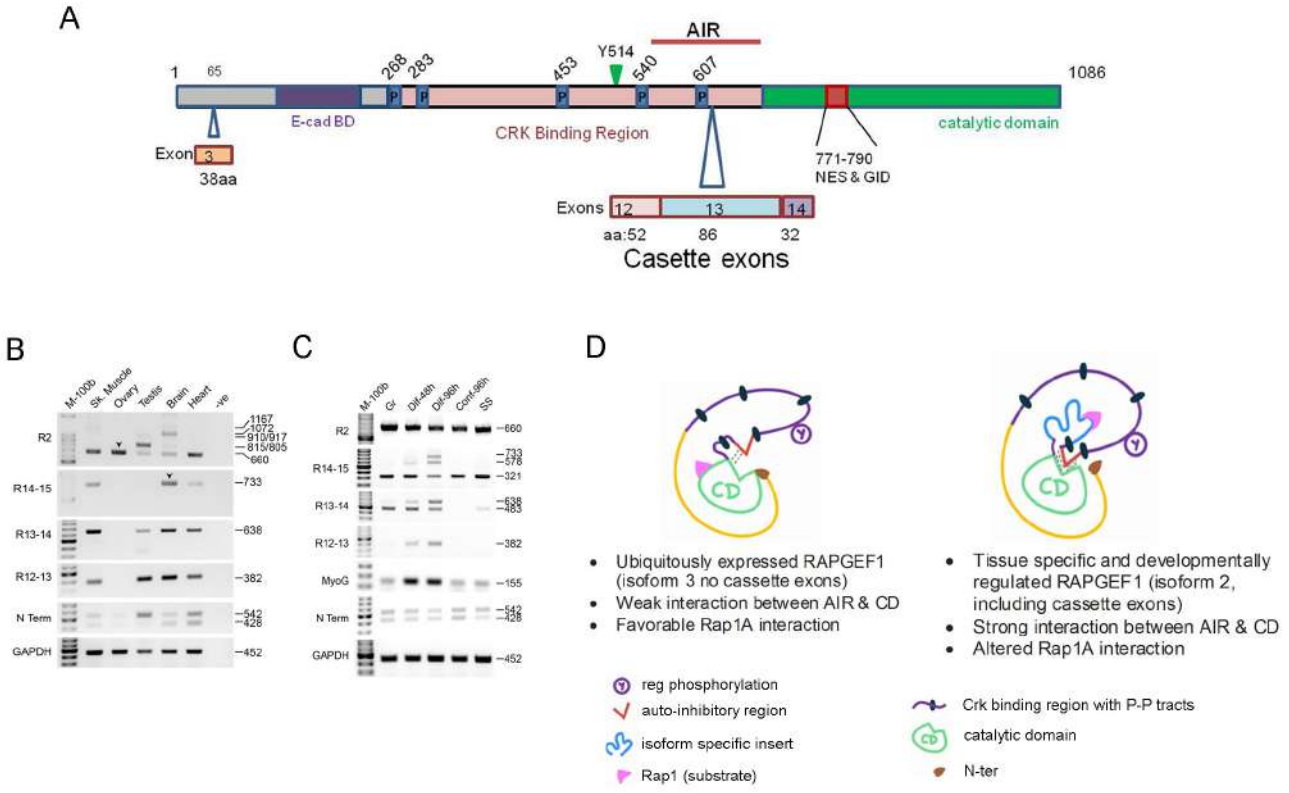
Signaling and Regulation of Cell Fate

From top left to bottom right: Vegesna Radha, K. Lavanya, Abhishek Goel, Niladri Koner G. Gowthaman

Research Interests

- Identifying and characterizing molecules that serve as master regulators of cell and tissue differentiation in vertebrates
- To understand how these fundamental processes are controlled, and how deregulation results in pathological situations

Work on understanding the regulation and function of RAPGEF1 (C3G) in vertebrate development was continued. L557P mutant fibroblasts were characterized and shown to differ from normal human fibroblasts in morphological features, adhesion properties, and expression of cell cycle control genes. iPSCs obtained from mutant fibroblasts were used to develop cortical organoids to examine if they were defective in early brain development. These organoids were more rounded, with smooth surface, features typical of lissencephaly, and showed delayed neural differentiation. Studies using the zebrafish model showed multiple defects in brain and eye development, as well as impaired body, fin, and tail development upon knockdown of Rapgef1 expressed from linkage group b. Early embryos showed supernumerary centrioles, and altered expression of developmental genes. Studies on splice variants of Mm RAPGEF1 identified the expression of previously un-annotated transcripts, and isoform switching as myocytes in culture were differentiated to myotubes (Figure panel B,C). Attempt was also made to understand properties of the splice variants of RAPGEF1. The cassette exons incorporated in some variants encode an intrinsically disordered, serine-rich polypeptide chain inserted in the protein interaction domain (Figure panel A). The presence of these additional amino acids alters intra-molecular interaction of the auto-inhibitory domain with the catalytic domain, and also inter-molecular interaction with its substrate Rap1 (Figure panel D). These studies identified for the first time alternate splicing as a novel means of regulating RAPGEF1 activity in various tissues, and during differentiation.



Development and tissue specific expression of novel C3G (RAPGEF1) transcripts that encode intrinsically disordered segments with regulatory functions

VENKAT CHALAMCHARLA

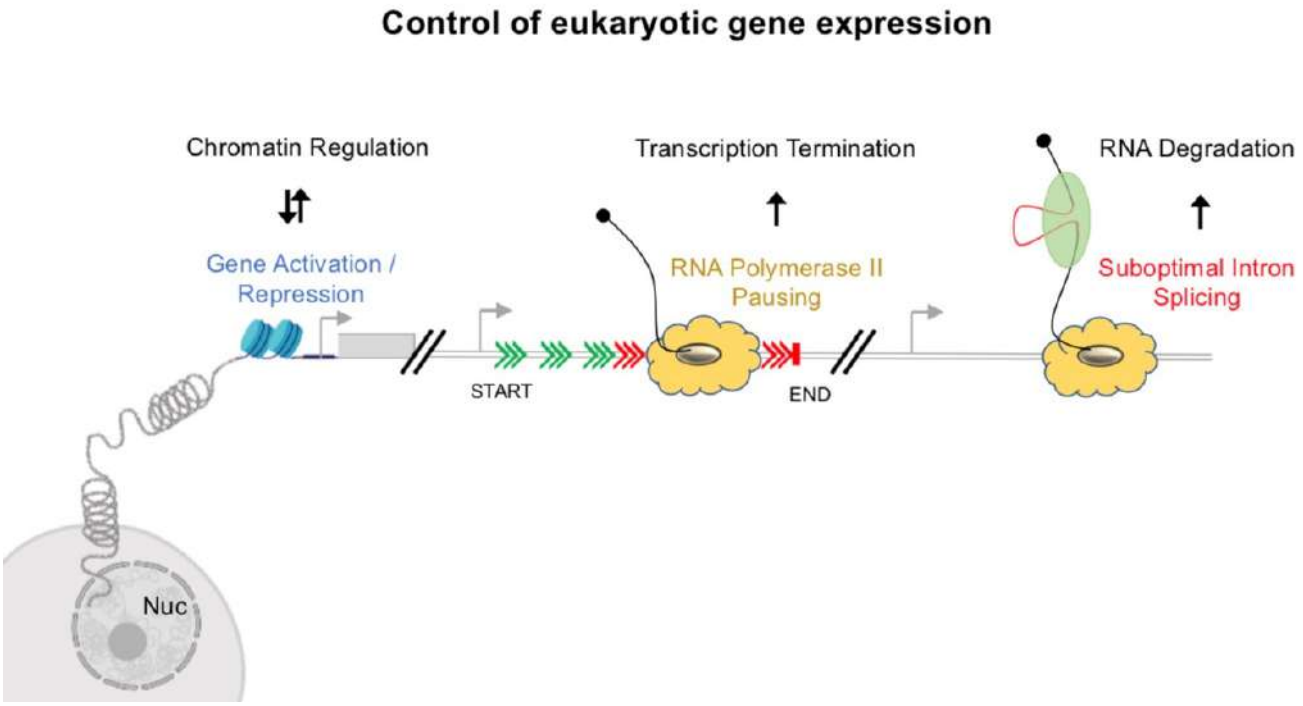
Transcription and Chromatin Regulation

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 model organism, 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.

VINAY K. NANDICOORI

Molecular & Cellular Biology, Bacterial Genetics

From left to right: Venkatesh L, Abhishek Saha, Baburam Nepali, Shreya VM, Yashasvi Bhat, Debatri Dutta, Yogita Kapoor, Vinay K. Nandicoori, Sutashree Nath, Priyadarshini Sanyal, Asis Kumar Khuntia, Purushotham Vodnala, Amit Chakraborty

Research interests

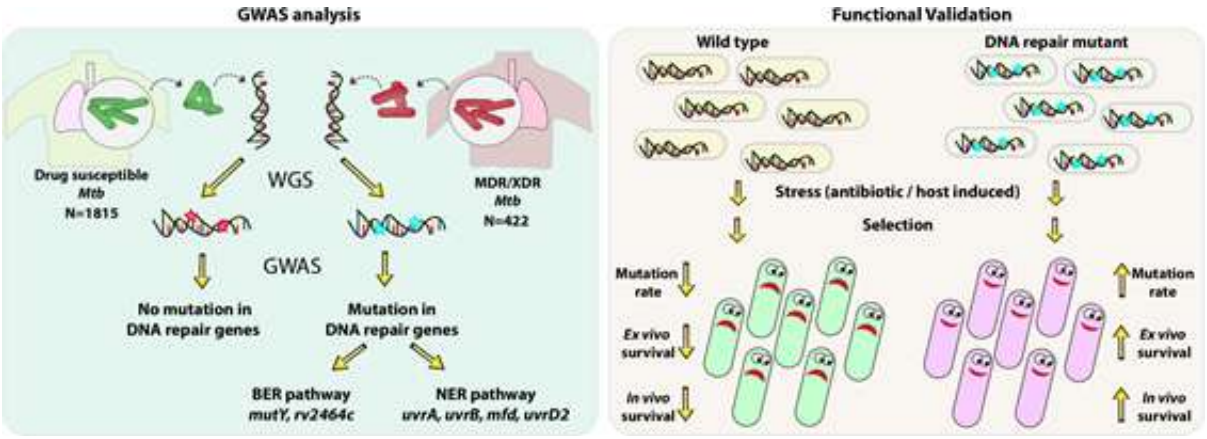
- Delineate the underlying mechanism via which **S**erine **T**hreonine **P**rotein **K**inases (STPKs) regulate multiple cellular processes in *Mycobacterium tuberculosis* (*Mtb*)
- Determine the function of transcription factors
- Elucidate novel mechanisms of evolution of drug resistance in *Mtb*
- Identify new possibilities for Host-**D**irected **T**herapy (HDT)

Recent publications

- Kumar S, Khan MZ, Khandelwal N, Chongtham C, Singha B, Dabla A, Behera D, Singh A, Gopal B, Arimbasseri GA, Kamat SS, Nandicoori VK (2022) *Mycobacterium tuberculosis* Transcription Factor EmbR Regulates the Expression of Key Virulence Factors That Aid in *Ex Vivo* and *In Vivo* Survival. ***mBio*** 13(3):e0383621.
- Naz S, Paritosh K, Sanyal P, Khan S, Singh Y, Varshney U, Nandicoori VK (2023) GWAS and functional studies suggest a role for altered DNA repair in the evolution of drug resistance in *Mycobacterium tuberculosis*. ***eLife*** 12: e75860.
- KNaz S, Dabral S, Kumar D, Nandicoori VK (2022) Protocol for *ex vivo* competition and sequencing of mycobacterium isolated from infected guinea pigs. ***STAR Protocols*** 3:101804.
- Gupta S, Arora A, Saini V, Mehta D, Khan MZ, Mishra DK, Yavvari PS, Singh A, Gupta SK, Srivastava A, Kumar Y, Verma V, Nandicoori VK, Bajaj A (2022) Hydrophobicity of Cholic Acid-Derived Amphiphiles Dictates the Antimicrobial Specificity. ***ACS Biomaterials Science & Engineering*** 8: 4996-5007.
- Salini S, Bhat SG, Naz S, Natesh R, Kumar RA, Nandicoori VK, Kurthkoti K (2022) The Error-Prone Polymerase DnaE2 Mediates the Evolution of Antibiotic Resistance in Persister Mycobacterial Cells. ***Antimicrobial Agents and Chemotherapy*** 66: e0177321.
- Soman S, Chattopadhyay S, Ram S, Nandicoori VK, Arimbasseri GA (2023) Codon optimality has minimal effect on determining translation efficiency in mycobacterium tuberculosis. ***Scientific Reports*** 13:415.
- Singha B, Behera D, Khan MZ, Singh NK, Sowpati DT, Gopal B, Nandicoori VK (2023) The unique N-terminal region of *Mycobacterium tuberculosis* sigma factor A plays a dominant role in the essential function of this protein. ***Journal of Biological Chemistry*** 299: 102933.

A role for altered DNA repair in the evolution of Drug resistance in *Mycobacterium tuberculosis* (*Mtb*)

The emergence of drug resistance in *Mtb* is alarming and demands in-depth knowledge for timely diagnosis. Prolonged treatment duration, high drug toxicity, and the expensive drug regimen pose a challenge for treating the MDR and XDR-TB. Despite well-known mechanisms of drug resistance, in 10-40% of the clinical isolates of *Mtb*, drug resistance cannot be determined by the mutations in the direct targets of antibiotics, implying the presence of hitherto unknown mechanisms that foster the development of resistance in *Mtb*. We performed genome-wide association analysis using 2237 clinical strains of *Mtb* to identify novel genetic factors that evoke drug resistance. In addition to the known direct targets, we identified for the first time, a strong association between mutations in DNA repair genes and the multidrug-resistant phenotype. To evaluate the impact of variants identified in the clinical samples in the evolution of drug resistance, we utilized knockouts and complemented strains in *Mycobacterium smegmatis* and *Mtb*. Results show that variant mutations compromised the functions of MutY and UvrB. MutY variant showed enhanced survival compared with wild-type (*Rv*) when the *Mtb* strains were subjected to multiple rounds of *ex vivo* antibiotic stress. In an *in vivo* guinea pig infection model, the MutY variant outcompeted the wild-type strain. We showed that novel variant mutations in the DNA repair genes collectively compromise their functions and contribute to better survival under antibiotic/host stress conditions.



1.1B
Research Facilities

Microscopes in the Advanced Microscopy and Imaging Facility

Light Sheet Microscope

Model: 3i Marianas

It is a Dual Inverted Selective Plane Illumination imaging microscope. It consists of two symmetrical optical paths for light sheet imaging. Two water immersion objectives perpendicular to each other are placed at 45 degrees above a sample mounted horizontally. A light sheet is projected onto the sample from one objective and the reflected light goes through the other objective and imaged using high speed, high resolution sCMOS cameras with large FOV. Three scanning objectives (10X, 20X and a 40X) and 405 nm, 488 nm, 561 nm and 640 nm lasers are available for fluorescence imaging.

The scanned sheet method used in light-sheet fluorescence microscopy with cleared tissue reduces phototoxicity, especially when scanning a large FOV at depth, allows 3D imaging and long term time lapse imaging at high spatial and temporal resolution. High scattering and absorption of opaque tissues limit the penetration of light into deep tissues. Some of the tissue optical clearing methods are refractive index matching via dissociation of collagen, de-lipidation, decalcification and dehydration to reduce scattering.

The post acquisition processing of data from the two optical paths are de-skewed to put back into geometrically correct position and computationally merged and de-convoluted to yield a 3D data set with isotropic resolution using Marianas reconstruction algorithms.

ISTED (Stimulated Emission Depletion) Super Resolution Microscope

Model: Leica TCS SP8 X 3D

In a stimulated- emission depletion (STED) microscope the system combines the normal excitation laser and a donut-shaped depletion laser with vortex (STED beam) of longer wavelength in the focal plane. The excited fluorophores that are exposed to the STED beam are instantaneously 'bleached' back to the ground state. Therefore, only molecules that are sitting in the centre of the STED beam are able to emit fluorescence. This physically narrows the PSF, therefore increasing resolution beyond the diffraction limit. The effective detected fluorescence emission, smaller than the diffraction-limited confocal volume, is collected with higher spatial (~40 nm) and axial (~100 nm) resolution. A broad range of suitable fluorophores can be imaged, enabled by the option of two different STED lasers (592 and 775 nm available) and the spectral flexibility of white light laser (WLL) for excitation.

Sample preparation: Samples must be prepared only on #1.5 or #1.5H glass coverslips, sample should be bright and photostable, avoid DAPI for counterstaining, Prolong Gold and Prolong Diamond anti-fade reagents are good options for mounting samples for STED.

Atomic Force Microscope (AFM)

Model: Nanonics Imaging Ltd (Multiview 1000)

Atomic force microscope (AFM) is a high-resolution scanning probe microscope. The probe is a cantilever with a 50-500 um long and 10 nm radius glass tip, mounted on a tuning fork with a resonance frequency of ~ 32.4 kHz. Normal force tuning fork technology with high Q factor phase feedback is used for imaging. It gives a topographic image of the sample surface. The height and distance profiles can be obtained from these images using WSxM 5.0 software. The diameter of spherical structures can also be measured using the height and distance profiles.

Samples that can be analyzed by AFM: Biological assemblies as diverse as multi subunit enzymes, viral capsids, bacteria, biofilms, nucleosomes, biological membrane components, protein aggregates, amyloids and organic/inorganic nanomaterials.

High Resolution Confocal Microscope with Airy Scan

Model: Zeiss LSM 880

It is a high resolution Confocal Microscope having both PMT and GaAsP detectors. The Airyscan microscope transforms a diffraction-limited, point-scanning confocal microscope into a super-resolution microscope using an array detector consisting of 32 hexagonal micro-lenses arranged in a circular disk, where each lens receives photons emitted from a small portion of an Airy disk and sends them through their individual optical fiber to a linear GaAsP detector array. Each detector element functions as a single very small pinhole of 0.2 AU. This enables highly efficient imaging by making use of all the photons collected by the objective. It has 405, 458, 476, 488, 514, 543, 594 and 633 nm laser lines. This microscope gives a resolution of ~140 nm laterally and ~400 nm axially. Time scan, Tile scan, FRET, FRAP and Linear unmixing can be done using this system using Zen software.

Confocal Microscope

Model: Leica TCS SP8

This is a classical inverted laser scanning Confocal Microscope. Confocal microscopes use point illumination and a spatial pinhole in an optically conjugate plane in front of the detector to eliminate out-of-focus signal and are used to optically slice thick samples (~50 µm). It provides direct, non-invasive, serial optical sectioning of intact, thick, living specimens with a minimum of sample preparation. Confocal microscope scans specimens in the XY- plane along with the Z-plane thus allowing data collection in 3D. It gives a resolution of ~200 nm laterally and ~ 500-800 nm axially.

It has two PMT detectors and additional two highly sensitive hybrid GaAsP detectors and receives illumination from multiple laser lines (405, 458, 476, 488, 514, 561, 594 and 633 nm). 2D analysis of multiple fluorescently-labelled samples combined with DIC, 3D reconstruction, kinetic analysis, spectral analysis, Fluorescence Recovery after Photo bleaching (FRAP) and Fluorescence Resonance Energy Transfer (FRET) can be carried out.

Confocal Microscope for Live Cell Imaging

Model: Olympus FV 3000

It is a live cell Laser Scanning Confocal Microscope for real-time imaging with solid state lasers and GaAsP detectors. It has 405, 445, 488, 514, 561, 594 and 640 nm excitation lasers.
It also has an additional chamber for maintaining samples at temperatures ranging from ambient to 40°C with continuous supply of air and CO2 for imaging live samples over long time periods. The offline cellSens software enables the users to process their data.

Raman Microscope and Raman Rapid Imaging

Model: RENISHAW InVia Raman Microscope

Raman spectroscopy is a non-destructive vibrational spectroscopic technique in which the sample is focused under a microscope (5x, 20x and 50x objectives) and illuminated with a monochromatic laser beam (532 nm, 633 nm and 785 nm lasers are available). From the resultant inelastic scattered light intensity, the Raman spectrum is obtained as a function of frequency shifts in the spectral range of 100 to 3200 cm-1 in this system. From the characteristic Raman frequencies, the chemical composition of a sample can be obtained.

Raman rapid imaging is done using Stream Line technique by acquiring data from different points on the sample to generate maps based on parameters of resulting spectra.

Samples that can be analyzed using Raman Microscope: Biofluids, fixed and live cells, thick tissue specimens, bacteria, plant materials, drugs, semiconductors, nanomaterials, proteins, organic and inorganic compounds.

Scanning Electron Microscope

Model: Hitachi S3400N

Scanning electron microscopy (SEM) uses a finely focused beam of electrons in order to produce a high resolution image of the surface structure of a sample by detecting the secondary electrons resulting from interactions of the electron beam with atoms at various depths within the sample.
Samples that can be analyzed using SEM: Bacteria, normal and tumor cells, nanomaterials, organic and inorganic materials, dental and bone implants among others.

Zeiss AxioZoom V16 Stereo Microscope with Apotome

A stereomicroscope directs light to each eye from two independent light paths. Because light from a single point on the specimen travels independently through two different paths to reach each eye, the specimen appears three dimensional. A stereo microscope has a lower magnification and also has a longer working distance.

Zeiss AxioZoom V16 Stereo Microscope with Apotome is a high resolution advanced Stereo fluorescence microscope using the structured illumination technique for optical sectioning of thicker samples to get high quality images.

Zeiss Axioimager Z2 with Apotome

It is a highly sophisticated Fluorescence Imaging system with Apotome and DIC attachment, a monochrome digital camera and a fully motorized microscope. The system is used to observe the biological specimens with fluorescence technique and acquires Z-sections at good resolution. The system works on structured illumination principle to get high quality images with improved signal to noise ratio and is capable of acquiring images on both DIC and fluorescence. The optical tomography technique uses optical grid for structured illumination.

Zeiss Axioimager Z2

This is an advanced fully motorized upright Fluorescence imaging Microscope for imaging both, black and white and colour images and also acquiring Z-sections. A colour camera for unstained samples and a monochrome digital camera for capturing images of fluorescent samples are the attachments which are also controlled by the inbuilt software.

Zeiss Axioplan 2 2

This is a universal manual upright fluorescence microscope model suitable for fluorescence, bright field, phase, DIC, dark field applications for research. The AxioVision software for capturing images with CCD camera has a number of features like capturing images both in black & white and colour, image export or import, enhancement, annotations, archiving and multi-channel acquisitions.

From left to right: Angothu Ramesh, Suman Bandari, Nandini Rangaraj, Chivukula Subbalakshmi, N. Ravindra Chakravarthi

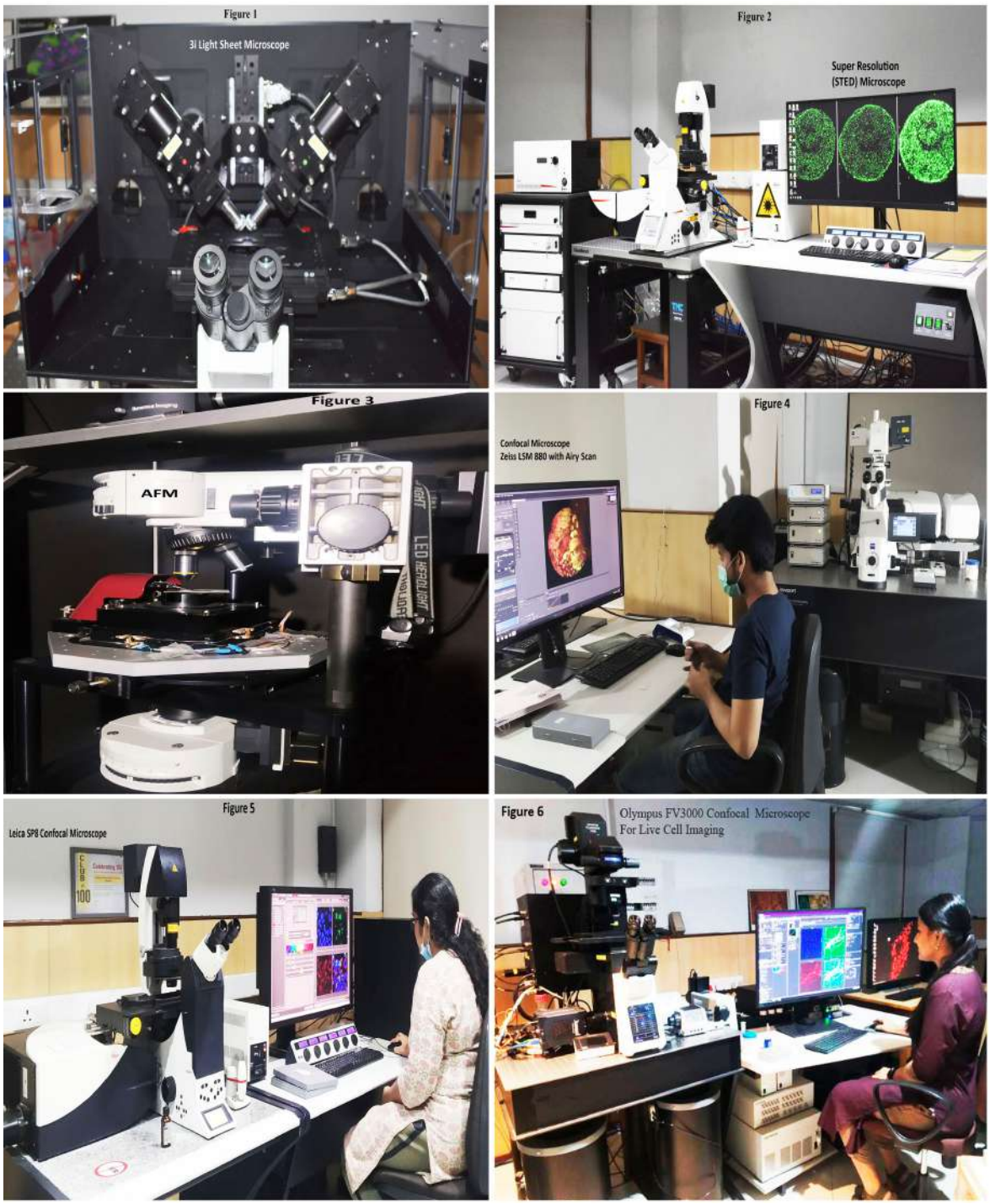


Figure 1: Light Sheet Microscope; Marianas 3i
Figure 2: Stimulation Emission Depletion Super Resolution Microscope; Leica TCS SP8 X 3D STED
Figure 3: Atomic Force Microscope; Nanonics Imaging Ltd (Multiview 1000)
Figure 4: High Resolution Confocal Microscope; Zeiss LSM 880 with Airy Scan
Figure 5: Confocal Microscope; Leica TCS SP8
Figure 6: Confocal Microscope for Live Cell Imaging; Olympus FV3000

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 in the year of 1999. Registration number is 20/GO/RBi/S/99/CPCSEA for the purpose of Research and Breeding of mice, rats, rabbits and hamsters for In-house purpose and commercial for trading purpose.

Main objective of animal house is to supply genetically defined various strains of mice, rats and rabbits to CCMB 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 PI(s) can raise the 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. Its a monitoring platform software to generate the data's of microbial, genetic monitoring with micro environmental parameters of animal rooms such as temperature and relative humidity.

CCMB AH 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. Animal facility maintains 62 strains of various inbred, out bred mice including different transgenic & knockout 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.

All animal rooms are environmentally controlled and monitored for temperature, humidity and automatic lighting system to control 12hrs /12hrs light and dark cycle. The Animal House team comprises of one veterinarian and 2 technical Officers, 4 trained technicians who are involved in breeding and maintenance of various lab animals and also providing technical support to a various ongoing research projects. The Total number projects approved for animal experimentation under Institutional Animal Ethical Committee(IAEC) in this year 2022-2023 is 123 projects.

CCMB animal house has various disease models of Transgenic and Knock-out mice around 42 strains are available in Animal house facility source from Jackson laboratory USA, Riken Institute Japan, Charles River USA, Cardiff University UK, National Cancer Institute USA, MMRC USA, St Jude Children's research hospital, USA

Number of animals supplied during this year are as follows:

Mice: 7689 **Rats: 108** **Hamsters: 48** **Rabbits: 42**

CCMB- IAEC [Institutional Animal Ethics Committee] Members visit to Animal House during Annual Inspection

BSL2/ BSL3

CCMB Biosafety facility has a BSL2 and a BSL3 laboratory. BSL2 laboratory is equipped to handle viral, bacterial, and parasitic organisms. The BSL3 laboratory has the capability to handle both viral and bacterial pathogens.

Animal Tissue Culture Facility

The centralized animal tissue culture facility of CCMB is one of the best in its class. We have a repository of a variety of cancerous and non cancerous cell lines from Human, Mouse and a few other mammals. We provide frozen and / or in-culture cell lines, media, serum, other reagents and plastic-ware for more than thirty plus research groups users in CCMB. A dedicated BSL2 facility is available that permits use of reagents/viruses/human primary cells requiring biosafety measures. The facility also houses modern instruments like Class I and Class II Biological safety cabinets, CO2 Incubators, inverted microscopes, cold storage, deep freezers and liquid nitrogen storage facility as well as FLoid cell imaging system, nucleofector for transfections and automated cell counters.

The facility has dedicated and experienced staff that has the expertise in maintenance of cell lines, stem cells, growth of organoids and primary cultures, cell fusions to produce monoclonal antibodies, transfections to establish stable clones and cryopreservation of cell, etc. Monoclonal antibodies are being raised against housekeeping genes and tagged proteins that can be regularly used for western hybridisation in house. Some of monoclonal antibodies raised against specific genes have been patented.

To detect cellular cross-contamination, molecular genotyping technique Short Tandem Repeat (STR) DNA genotyping of human and mouse cell lines is regularly done for authenticating the commonly used human and mouse cell lines. Apart from all this, a short-term training course is provided on Animal Cell Culture procedures for PhD students, faculty members and other researchers from within our institute as well as from universities/ institutes/ industry who are interested in learning cell culture techniques.

Facility Staff: Zareena Begum, B.V.V Pardhasaradhi, V.R. Sundareswaran, D. Parthasarthi, S. Easra, T. Dayakar

Histology Facility

Microscopic anatomy is an important technique for examining biological tissues. The histology facility in CSIR-CCMB is well equipped with modern instruments like cryomicrotome, paraffin microtome and wax embedding station. The facility provides services to numerous research projects for producing high quality tissue sections and staining for microscopy.

The various techniques and services provided are processing and sectioning of paraffin and frozen blocks of tissues. We have expert staff who helps in staining with special stains like Masson Trichrome, Van Gieson, Sirius Red and also routine staining like Hematoxylin & Eosin.

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

Facility Staff: Avinash Raj

Publications :

Long-term and non-invasive in vivo tracking of DiD dye-labeled human hepatic progenitors in chronic liver disease models

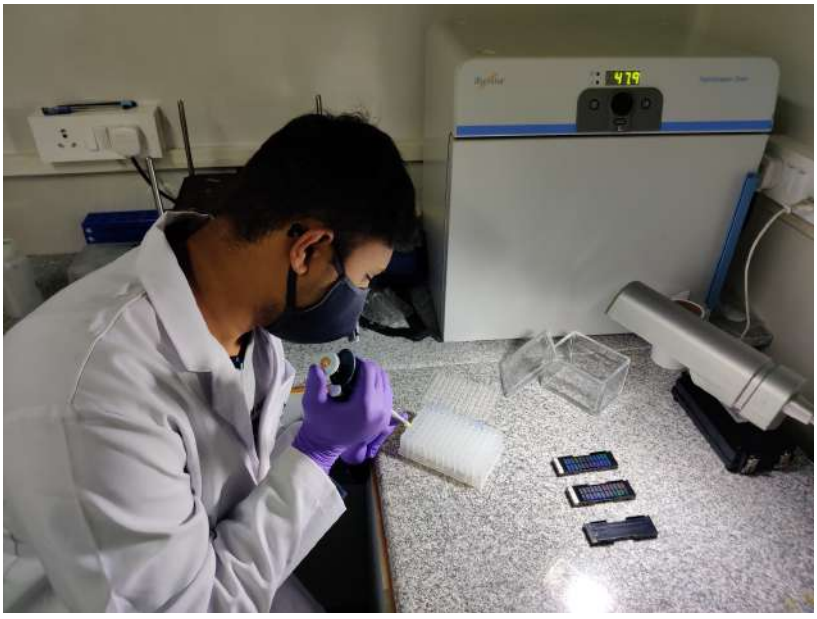
Chaturvedula Tripura, Srinivas Gunda, Sandeep Kumar Vishwakarma, Avinash Raj Thatipalli, Jedy Jose, Mahesh Kumar Jerald, Aleem Ahmed Khan, Gopal Pande

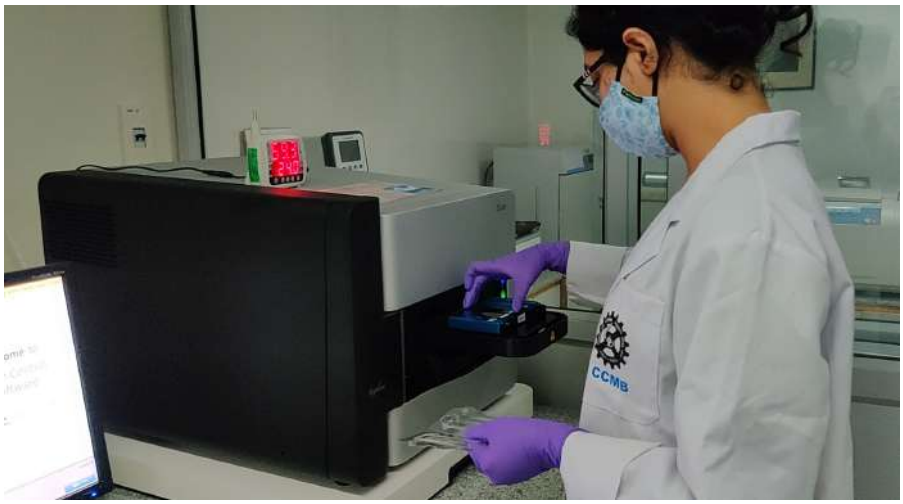
World J Hepatol. 2022 Oct 27; 14(10): 1884–1898

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.





Electron Microscopy Facility

The Electron Microscopy Facility (EM Facility) of CSIR-Centre for Cellular and Molecular Biology (CSIR-CCMB) is a state-of-the-art establishment dedicated towards revealing the otherwise unseen mysteries of the living world with scales spanning from organism level to atomic structures of building blocks of life. Since its inception, many users within CCMB, as well as external users from all over India have been using the facility. The external users range from academic institutions such as IIT Mumbai, IISc Bengaluru, IISER Pune, Osmania University, Hyderabad Central University etc., to R&D institutes such as CSIR-NCL Pune, CSIR-IMTECH Chandigarh, TIFR Hyderabad, Bose Institute Kolkata, NCCS Pune etc. Besides catering to academic and national institutes, our facility has been catering to the R&D activities of several pharmaceutical and biotechnology industries across the nation. The EM facility helped users to investigate important cellular physiological events such as cell signalling, neurotransmission, viral replication, drug delivery, developmental biology, host pathogen interactions, cell migration, contact sites of cellular organelles and stem cell biology. The facility houses sophisticated instruments for delicate sample preparation, and high-resolution imaging at unprecedented details. Information about these instruments are mentioned below.

1. Ultra-microtome Leica EM UC7 with FC7:
The acquisition of high-resolution images via a transmission electron microscope required exceptionally thin samples, enabling movement of electrons through the specimen. EM center hosts a Leica cryogenic ultra-microtome facilitating the meticulous preparation of consistently high-quality ultra-thin sections derived from biological specimens, both ambient and cryogenic temperatures, thus accommodating a diverse range of experimental conditions. The ultra-microtome empowers researchers to achieve section sizes as minute as 60 nm, thereby enabling the exploration of an array of applications, including immunogold labelling and investigations into host-pathogen interactions.

2. Thermo Scientific Vitrobot Mark IV:
The Vitrobot system is a sophisticated robotic apparatus specifically designed to streamline and automate the vitrification process, resulting in rapid, effortless, and consistently reproducible sample preparation. Vitrobot provides a remarkable degree of precision and adaptability to prepare electron microscopy grids at different temperatures and humidity during the plunge-freezing procedure.

3. Quorumtech New Gloqube plus:
A glow discharge system enables surface modification of transmission electron microscopy (TEM) grids, thereby facilitating the efficient loading of biological macromolecules to ensure successful imaging. The EM Centre has a glow discharge unit procured from Quorumtech, delivering a comprehensive suite of functionalities encompassing grid cleaning, hydrophilization, and surface modification. The system encompasses two distinct chambers, thereby offering researchers the flexibility to select between in-air or in-chemical vapor discharges, depending upon the desired surface charge optimization for proteins and nucleic acids.

4. Talos L120C Transmission Electron Microscope:
The Thermo Scientific Talos L120C, a cryogenic transmission electron microscope operating within the voltage range of 20-120 kV. The 120 kV TEM is equipped with a thermionic, LaB6 filament as an electron source and featuring a high-speed readout Ceta CMOS camera, this microscope facilitates the acquisition of exceptional imaging results. Primarily designed for the comprehensive characterization of biological entities such as cells, cell organelles, and polymers, both in two-dimensional and three-dimensional contexts, the Talos L120C TEM accommodates imaging at both ambient and cryogenic temperatures.

5. Talos Arctica Cryo-TEM:
The Thermo Scientific Talos Arctica is a cryogenic electron microscope works in the voltage range of 80-200 kV, featuring a Field Emission Gun as an electron source. This microscope showcases a sophisticated array of detection capabilities, encompassing the utilization of a Falcon IV direct electron detector and CetaD cameras, enabling the

determination of high-resolution structures. Additionally, the Talos Arctica encompasses a robotic autoloader system, accommodates up to 12 vitrified grids, thus facilitating high-throughput and automated imaging procedures through the utilization of the EPU software suite. The Thermo Scientific Constant Power C-TWIN objective lens provides a remarkable equilibrium between contrast and resolution for imaging studies. Leveraging its revolutionary cryo-based technology and inherent stability, the Talos Arctica is suitable for semi-automated applications, including single particle analysis, electron crystallography, and cryo-electron tomography.

The CSIR-CCMB's EM Facility is not only catering to the scientific requirements of the host institute, but also of several other institutes in the nation. In time to come its' contributions towards scientific breakthroughs will become apparent in the form of scientific publications in journal of repute and also in terms of product development and technological advancements from industrial users.

The EM facility operations are overseen by Mr. Harikrishna Adicherla, Mr. Sandeep Shrivastava, Dr. Ravikumar Reddi with faculty in charge Dr. Saikat Chowdhury. Further technical support to the Centre is provided by Mr. K Sanjeev Kumar and Mr. Amol Mandlik from CSIR-CCMB Instrumentation Division.

Publications from the Electron Microscopy facility:

1. Apte S, Bhutda S, Ghosh S, Sharma K, Barton TE, Dibyachintan S, Sahay O, Roy S, Sinha AR, Adicherla H, Rakshit J, Tang S, Datey A, Santra S, Joseph J, Sasidharan S, Hammer Schmidt S, Chakravortty D, Oggioni MR, Santra MK, Neill DR, Banerjee A. 2023, An innate pathogen sensing strategy involving ubiquitination of bacterial surface proteins. Sci Adv. 2023 Mar22;9(12):eade1851.

2. Ghosh S, Roy S, Baid N, Das U, Hajra D, Menon S, Sahil M, Shaw S, Rakshit S, Rajmani R, Adicherla H, Mondal J, Chakravortty D, Banerjee A. 2023, A host AAA-ATPase exhibits bacteriolytic activity for clearance of microbial infection. bioRxiv; 2023.07.18.549519, doi: https://doi.org/10.1101/2023.07.18.549519.

3. Bihani A, Avvaru AK, Mishra RK. 2023, Biochemical deconstruction and reconstruction of Nuclear Matrix reveals the layers of nuclear organization. bioRxiv 2023.01.28.525997; doi: https://doi.org/10.1101/2023.01.28.525997.

Left: Collage of photographs from various events at the CSIR-CCMB Electron Microscopy Centre along with all the available equipment and research infrastructures

Bottom: Staff members of the CSIR-CCMB Electron Microscopy Centre. Standing from left to right: K Sanjeev Kumar, Ravikumar Reddi, Harikrishna Adicherla, Sandeep Shrivastava and Amol Mandlik

Flow Cytometry

The FACS facility is used to measure the multi-parameters which are expressed by a single cell, multiple cells or particles on the basis their light scattering and fluorescence properties. The facility has been used in CCMB for the phenotypic analyses of different kinds of cell populations, as well as for high speed sterile sorting of cells for subsequent culturing or biochemical studies. The CCMB Flow Cytometry facility provides training to their students/project staff as well as support in designing and analysis of experiments to all CCMB investigators and to the local scientific community. The facility is used frequently by various research groups, such as Cell biology, Stem cell biology, and Infection biology research groups, and offers 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.

In addition, FACS facility at CCMB is concerned with further development and optimization of various aspects of the FACS SOPs, experiment related protocols and methodology. The facility also provides support to external users like R&D companies and Universities in their research work under CRTDH programme.

Facility staff: G. Srinivas

Recent additions/ improvements made to the facility:

Facility has two sophisticated advanced analyzers and two high-speed cell sorters. All the instruments are capable of multi-parametric analysis of cell populations.

a) Gallios analyzer has three lasers (405 nm, 488 nm, and 638nm) (2+5+3 configuration)

b) Fortessa analyzer has three lasers (488 nm, 561 nm, 640 nm) (2+5+3 configuration)

c) MoFlo XDP high speed sterile sorter (351 nm, 488 nm, 638 nm) (2+5+3 configuration)

d) BD FACS Aria Fusion High speed sterile cell sorter (405 nm, 488 nm, 561 nm, 638 nm) (6+2+4+3 configuration)

Involvement of the facility in internal & external use:

Facility staff provide complete training to their students and project staff to operate individually by the users. All of the analyzers can be booked and used by trained/authorized personnel at CCMB.

Top left: BD FACS Aria Fusion Sorter,
Top right: BC Gallios Analyser,
Bottom left: BC MoFlo XDP Sorter,
Bottom right: BD LSR Fortessa with HTS

Fly Lab

Drosophila melanogaster, the fruit fly is one of the most studied and highly tractable genetic model organisms due to its short-life cycle, low maintenance costs, conserved biology, and available powerful genetic toolbox. About 65% of the protein coding genes of *Drosophila* is conserved in human and from these genes about 75% are implicated in various diseases. Therefore, fly is effectively being used for studying basic biology as well as understanding molecular mechanisms underlying human diseases.

In CCMB, we have a very well established fly lab. We maintain about 2000 different fly strains. Among these, we have strains for ongoing research activities that include studies of body patterning, neural and muscle development, behavior, stress, longevity etc. We also have fly stains for *in-vivo* genome editing (CRISPR and MiMIC) and about 100 different tissue specific GAL4 driver lines. In addition, we maintain fly models for various human diseases including cancer, Parkinson's disease, Alzheimer's disease, muscular dystrophy and neurodevelopmental disorders such as microcephaly. These strains can very well be used for drug screening. The main fly lab is equipped with several stereomicroscopes for fly pushing, a fluorescent stereo microscope for transgenic larva/fly sorting, and an Axioplan.

In addition, we have a well-established injection facility, which is being used extensively by the research groups from CCMB. We also have a fully equipped behavior room with Drosophila Activity Monitoring (DAM) system, T-maze, an equipment used to study learning and memory, and set up for tracking larval locomotory behavior.

We have supporting facilities Nectar and embryo collection lab. Nectar supplies fly food in vials, bottles and embryo collection plates. This facility is equipped with an automatic fly food preparation and dispensing machine, hot plate with magnetic stirrers, cold cabinets, hot air oven and RO water system for fly food preparation. This facility also helps in cleaning and sterilizing the bottles & aluminum trays to prevent contamination. Whereas, the embryo collection room is a small nonstop fly reproduction center, which is designed for constant supply of fly embryos. This facility is equipped with large fly cages and collection plates to collect embryos for high throughput experiments.

We also provide service to other universities/institutes. Students and teaching staff from different national and international universities visit fly lab to get a hands on experience of *Drosophila melanogaster* culture and maintenance. Fly lab also provides flies to different colleges in the city for teaching purpose and various strains to other research institutes in India for research purpose.

Staff working in the facility:

Dr. V. Bharathi, Senior Technical officer
Srikanth, LTS worker
Krishna, LTS worker
Rani, LTS worker

High Performance Computing Facility

CCMB was one of the first institutes in the country to have a dedicated Bioinformatics wing, starting in the late 80s. The High Performance Computing Facility (HPCF) of CCMB provides infrastructure support for large scale genomic data analysis, docking, molecular simulations, modelling, and curation of biological databases.

In particular, the computing facility is extensively used for the following genomics applications:

- Whole genome/exome sequencing
- RNA Sequencing
- ChIP/Bisulfite Sequencing
- Single Cell Transcriptomics
- *de novo* Genome Assembly
- Metagenomics (including viral genome sequencing)

The facility infrastructure is mainly composed of two high performance computing clusters. The first one, called EpiHED, has a peak performance of over 5 TFLOPS, powered by more than 280 CPU cores and 4.5TB of shared RAM. The more recent Ramanujan cluster boasts a performance of >100 TFLOPS, with over 1300 CPU cores, 27000 GPU cores, and a total RAM of 14.3 TB. The GPU server nodes are used for processing Oxford Nanopore data, CryoEM data analysis, and training neural network models. Additional standalone servers offer flexibility and provide the computing power for non standard pipelines. CCMB also houses an on-premise hardware accelerated Bio-IT platform for genomic data analysis called DRAGEN. The storage needs are met by a centralized storage totalling to over 2PB. A further 2PB is currently envisaged to meet the large genomic data storage requirements.

The HPC facility mainly caters to various groups within CCMB to meet their data analysis needs. In particular, it is at the heart of large scale, multi institute projects of national importance such as the Genome India project, which aims to catalog genetic variation in 10000 healthy humans sampled from all over India, and the Indian Breast Cancer Genome Atlas, a consortium geared to dissect the molecular underpinnings of Breast Cancer in India using multi-omic technologies. In addition to these large projects, the HPC facility provides IT infrastructure to support collaborative analyses, as well as to drive analysis services provided by CCMB. The most prominent analysis service is our clinical diagnostics program, where whole exome or whole genome data of clinical samples is analyzed to understand the causative genetic variants underlying observed phenotypes.

Clockwise: Data Centre with Smart Aisle cooling, new Ramanujan HPC, EpiHED HPC

Next-Gen Sequencing (NGS) Facility

The Next Generation Sequencing (NGS) facility at CCMB boasts a range of state-of-the-art genomics equipment such as follows.

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.

Left image: From top left to bottom right: Illumina NovaSeq 6000, Oxford Nanopore GridION, MGISEQ 2000, Oxford Nanopore PromethION, Bionano Saphyr, Tecan liquid handler

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 two liquid handlers that enable fast, automated sample processing that minimize hands-on time as well as improve reproducibility.

The facility caters to all internal research groups of CCMB, and also plays a key role in successful implementation of large scale genomics projects of national importance such as the Genome India project, which aims to catalog genetic variation in Indian populations, and the Indian Breast Cancer Genome Atlas project, which is using a multi-omic approach to delineate the molecular signatures of breast cancers in Indians. The NGS facility was also pivotal for genomic surveillance of the COVID19 virus. As part of various consortia, data for more than 35,000 viral genomes was generated in this facility. Finally, sequencing is also offered as a service to other researchers and private companies.

Right image: From left to right: Sreenivas, Valli, Jyothi, Tej, Karthik, Jafurulla, Tulasi

Nuclear Magnetic Resonance (NMR) Facility

The 600 MHz narrow bore NMR facility was set up in 2009 to study biomolecular structure and function at the physiological condition in the solution. The facility consists of a 600 MHz narrow bore NMR spectrometer equipped with a cryogenically cooled probe. The enhanced sensitivity of the cryoprobe allows *de novo* 3D structure determination of relatively large proteins (MW > 25 kDa) and nucleic acids as well as their ligand-bound complexes at the physiological condition.

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*. Some of the important findings derived from the data generated by the facility are: (1) The solution structure of RDE-4 (*C. elegans*) elucidated structural modifications in both dsRBDs that were responsible for selecting the trigger dsRNA (2) Understanding the RNAi initiation in plants through the solution structure complemented with the structure-based activity assays of DRB4 (*A. thaliana*) (3) The solution structure of Crc (~32 kDa and presumably the largest solution structure derived by NMR from India) revealed its non-canonical RNA binding surface responsible for regulating the carbon catabolite repression process (4) Understanding the process of enantioselection to elucidate the mechanism of chiral proofreading during protein translation

Over the years, the 600 MHz NMR (Structural Biology) has become an integral part of CCMB's research activities and had immensely contributed to numerous projects including studies and design of thermostable Lipases, studies on antimicrobial peptides, to study the interaction of intracellular loops of GPCRs with membranes, structure-function relationship of key proteins in *P. falciparum* among others. The data generated by the 600 MHz NMR facility has been used in research articles published from CCMB in several internationally acclaimed scientific journals such as Proc. Natl. Acad. Sci. USA (2010), J. Mol. Biol. (2011), eLife (2013), Biochem. J. (2014), PLOS Biol. (2016), Nucl. Acids Res. (2017), and J. Magn. Res. Open (2022).

600 MHz NMR spectrometer equipped with a cryoprobe

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

Our instrument platforms include cutting-edge Orbitrap Exploris 240, Q-Exactive-HF, Q-Exactive, 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.

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, Sr. Technical Officer (3)
V Krishna kumari, Principal Technical Officer
B. Raman, Sr. Technical Officer (3)
K. Ranjith Kumar, Technical Assistant

Left image: i - JEOL Spiral TOF JMS-S300, ii - Thermo Scientific Orbitrap Exploris 240, iii - Thermo Scientific Q Exactive HF, iv - Thermo Scientific Q Exactive, v - Thermo Scientific Dionex Ultimate 3000

Right image: From left to right: B Raman, Y Kameswari, V Krishnakumari, K Ranjith Kumar, Swasti Raychaudhuri

Radioisotope Facility

Radioisotopes in India can be procured and handled only by the authorized users duly authorised by Radiological Safety Division (RSD), Atomic Energy Regulatory Board (AERB). This authorisation is based on the radiological safety status of the institution intending to establish a radioisotope laboratory. For this purpose it is mandatory that the plan of the radioisotope laboratory is approved by RSD from radiation safety stand point. The planning of the radioisotope laboratory depends upon the type of the radioactive material to be used, its physical form, activity and the type of experiments to be carried out using the radioactive materials, etc.

Based on the above, CCMB is accredited by AERB and classified as a Type II radioisotope facility. CCMB has more than 35 radiation workers, one radiological safety officer (RSO) and one license holder. The license holder is the head of the institute, that is the Director of CCMB. CCMB uses close to 30 mCi of ^{32}P labeled nucleotides and 10mCi of other radioisotopes like ^{14}C, ^{3}H, ^{35}S, etc.

CCMB uses the following radio isotope for labeling bio-molecules in various research projects:

Sl. no.	Isotope	Radioactivity group	Max activity to be handled (mCo/MBq)	Form	Type of operation with this isotope
1	^{3}H	Group IV	50/1850	Simple, organic biomolecule	Simple, wet enzymatic or non-enzymatic chemical reaction; no dry operation
2	^{14}C	Group III	5/185	Simple, organic biomolecule	Simple, wet enzymatic or non-enzymatic chemical reaction; no dry operation
3	^{45}Ca	Group II	5/185	Inorganic salt	Simple, wet enzymatic or non-enzymatic chemical reaction; no dry operation
4	^{51}Cr	Group III	10/370	Inorganic salt	Simple, wet enzymatic or non-enzymatic chemical reaction; no dry operation
5	^{125}I	Group III	10/370	Inorganic salt	Simple, wet enzymatic or non-enzymatic chemical reaction; no dry operation
6	^{32}P	Group III	100/3700	Simple, organic biomolecule	Simple, wet enzymatic or non-enzymatic chemical reaction; no dry operation
7	^{33}P	Group III	5/185	Simple, organic biomolecule	Simple, wet enzymatic or non-enzymatic chemical reaction; no dry operation
8	^{35}S	Group III	20/740	Simple, organic biomolecule	Simple, wet enzymatic or non-enzymatic chemical reaction; no dry operation
9	^{65}Zn	Group III	1/37	Simple, organic biomolecule	Simple, wet enzymatic or non-enzymatic chemical reaction; no dry operation

Layout and structure of the radioisotope facility

In order to handle radioactivity, special facilities are required to shield radiation emitted from sources, and to prevent contamination of the environment by the radioactive materials released during handling and processing. In Type II research laboratories the processed activities are medium to high, and, therefore, the requirements of shielded facilities and Personnel Monitoring Badges are mandatory.

The radioisotope facility contains 18 research labs and one radio-iodination lab to handle low level radiation measuring 25 sq m. The facility has one storage room having dedicated lockable freezers. The facility also equipped with preparation room, handling room, counting room, dilution and distribution room, auto-radiography room, separate low medium and high activity labs. The floors are covered with PVC and the walls with strippable paint. Work surface covered with smooth lining. The laboratory is equipped with foot-operated dustbins, pro-pipettes/remote pipettes (micro pipettes) , stainless steel sink, fume hood, fume hood with filter, glove box , face mask, surgical gloves, etc. The laboratory has monitoring instruments like G.M. Survey meter and contamination monitor.

Services offered by the radioisotope facility

1) Procuring regulatory documents from AERB and implementing
Every purchase of the radio isotope should go for the regulatory clearance from the competent authority from AERB. The competent authority AERB provides a No Objection Certificate after scrutinizing the institute's license, source purchased already and the type of the laboratory. The NOC is a vital document to procure radioactive source either from India or to import, without the NOC the supplier should not supply the radioactive source to its customer as per the IARP law. The central radio isotope facility does the service for almost 30 users of CCMB.

2) Radioactive waste disposal and waste management
Low level radioactive wastes are discharged through the sink; this includes liquid waste generated from DNA hybridization experiments, washing of un-reacted radioisotopes from various experiments. Medium and high active waste materials stored in the delay tanks are disposed after considerable reduction of the activity. The high and medium solid active waste material are stored and incinerated after considerable reduction of the activity.

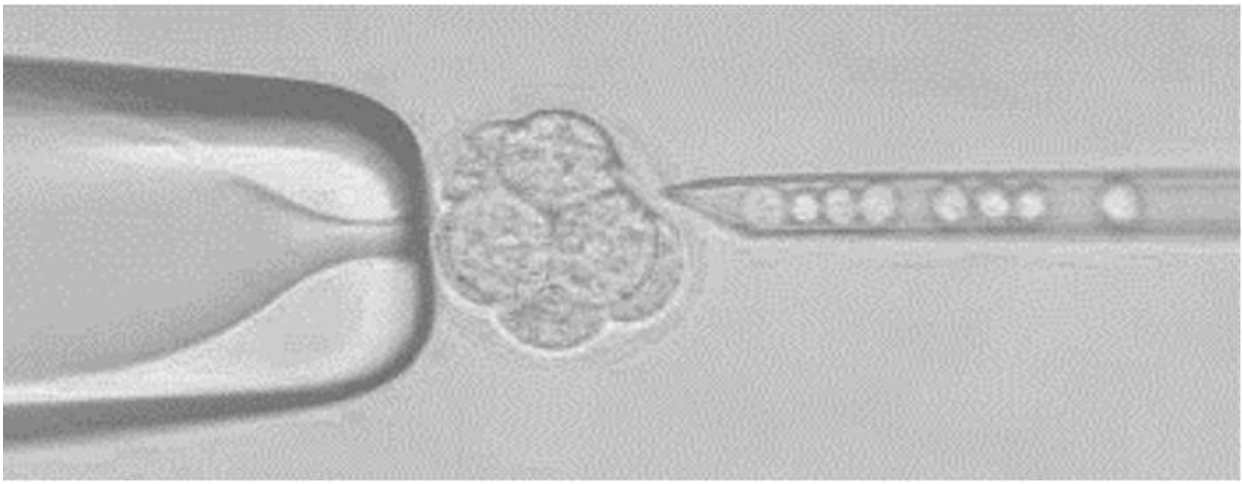
3) TLD service
As per the AERB and IARP mandate the occupational radioisotope workers should be periodically monitored for the radioactive exposure. CCMB radioisotope facility caters to nearly 30 radioisotope workers, and monitors their radiation exposure the exposure is monitored through TLD. The TLD service is outsourced from AERB approved laboratory. All the radioisotope users are provided with a TLD badge the absorbed dose is monitored every 90 days. If any radioisotope workers received the dose more than the IARP /AERB recommendations the radiation worker is advised to keep away from the radioactivity for 180 days.

4) Procurement , storage , distribution and reports to AERB
Following the AERB guidelines the facility procures ^{32}P labeled chemicals from the authorized agencies and store them in the dedicated storage room. The authorized users dispense the source according to their requirements, an usage log is maintained for audit by AERB. The CRIF report is sent to the AERB about the major spillage of radio isotope, loss of radioisotope, radioisotopic accidents, etc through the license holder of the institute the Director of CCMB.

Transgenic and Gene Knock Out Facility

The transgenic and gene knock out mice core facility was established to create, procure and maintain, Transgenic and gene knock out mice models. Gene targeting in embryonic stem cells, micromanipulation, survival surgeries are performed to generate Transgenic and gene knock out mice models. The facility generates transgenic animals by pronuclear injections into F1 embryos. The facility generates targeted ES cells lines, which are used in blastocyst injections experiments to generate gene knock mice models. The facility utilizes CRISPR editing to generate genome-edited mice. The facility supports many research groups in CCMB in generating Transgenic and knock-out 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. Students/ staff from various institutes like inStem, NCCS, NIAB have been trained.



Injection of genome-edited ES cells being injected to the 8 cell stage morula to generate chimeric mice

X-Ray Crystallography - SAXS & Crystallization

High Throughput (HT) Crystallization Facility

A state-of-the-art HT-Crystallization facility provides complete solution for crystallization of macromolecules. Three major components are: Alchemist for liquid handling, Mosquito and Oryx 4 for crystallization drop setting and two incubators (4°C and 20°C) for incubation and storage of crystallization plates. There are several microscopes, one of which has a polariser, for the inspection of plates for crystal growth. The facility is supported by dynamic light scattering(DLS), a useful tool to diagnose size distribution, stability, and aggregation state of macromolecules in solution prior to crystallization.

X-ray Crystallography Facility

The 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. 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.

Small Angle X-ray Scattering (SAXS)

X-ray facility is also equipped with Small Angle X-ray Scattering (SAXS) System for deciphering physical and structural features of macromolecules in solution. 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.

SAXS facility houses BioSAXS-2000 (Rigaku) with 2-D Kratky collimation, mounted on the existing left port of MicroMax™ 007 HF (Rigaku) Cu anode X-ray generator. 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.

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

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

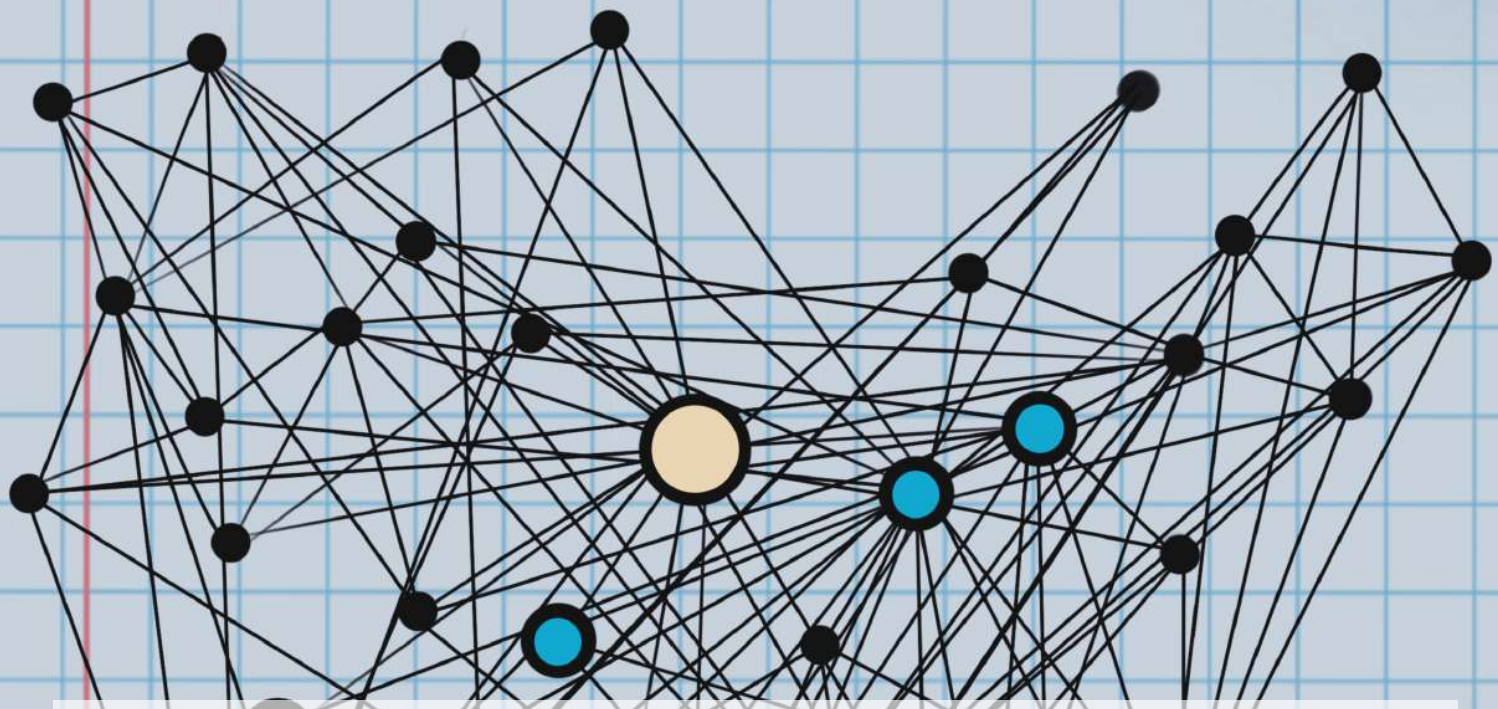
1) Robotic Systems: Automated crystallization: 1(a) Mosquito [TTP LabTech] Hanging Drop 1(b) Oryx 4 [Douglas Instruments] : Sitting Drop
2) Dynamic Light Scattering (DLS) [Nano Biochem Technology]
3) X-ray diffractometers [Rigaku] 3(a) MicroMax™ 007 HF Rotating Cu anode generator with mar345 IP detector 3(b) FR-E+DW SuperBright System with Cu / Cr anode generators having R-axis IV++ image plate detector
4) BioSAXS-2000[Rigaku] with 2-D Kratky collimation.

Zebrafish Facility

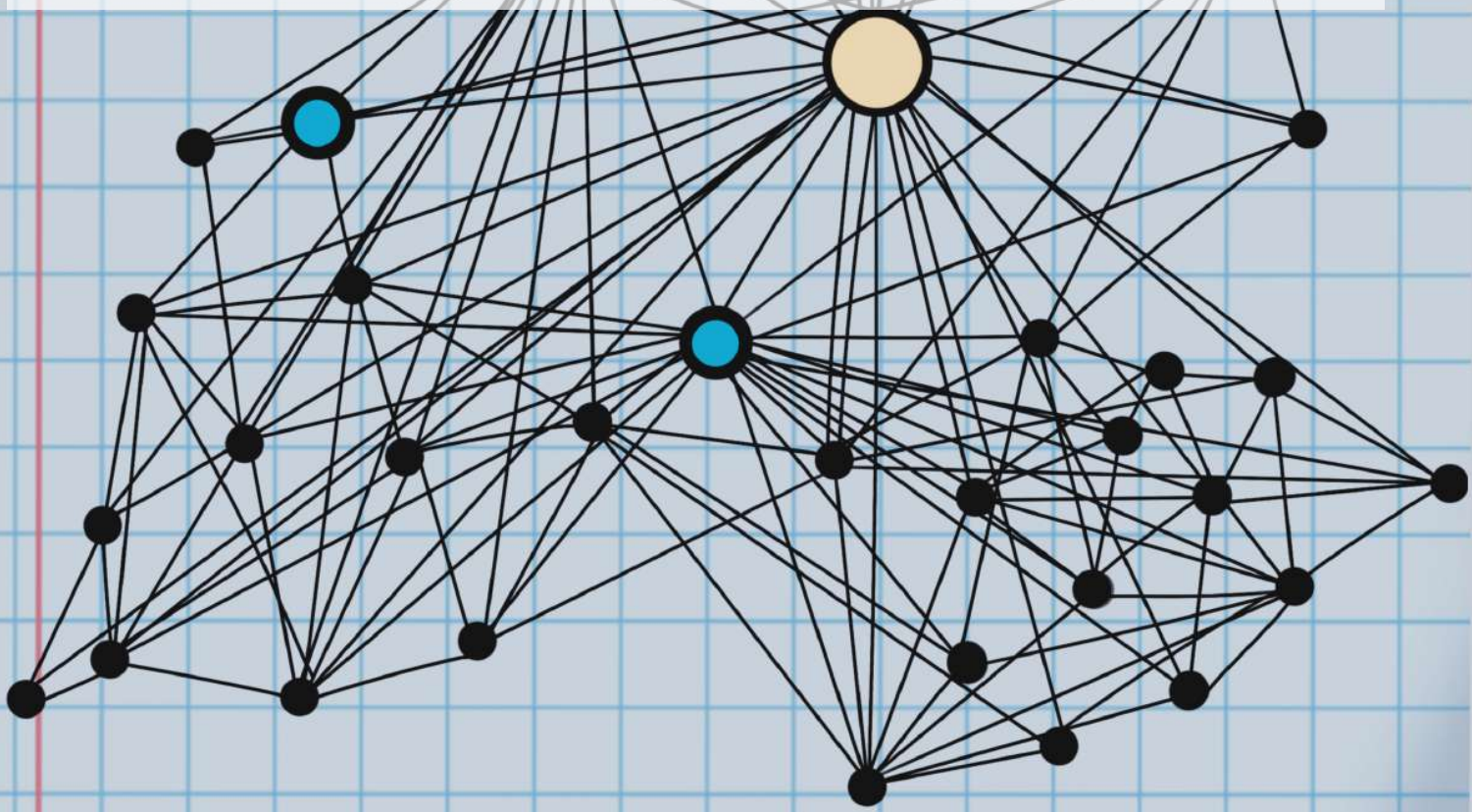
The zebrafish facility is equipped with housing zebrafish adults, transgenics, larvae, juveniles and adults. We also have large scale breeding & embryo collection capacities, live feed (artemia) hatching facility and water purification system to maintain the fish. The advanced automated standalone systems maintain transgenic lines for developmental biology, cell biology and behavioral studies. The facility also houses a high resolution microscopy and imaging system (Model M205 FA) that has motorized advanced stereofluorescence for multichannel fluorescence and bright-field imaging of entire zebrafish larvae and juveniles. The facility is also equipped with micromanipulation system and trained staff to help researchers generate transgenic fishes and perform genetic manipulations. A computer aided tracking system (Danio vision with ethovision software) is available to carry research on behavioural aspects of this vertebrate model.

WT Housing aquariums, behavior assays and microinjection system

From left to right: ML Arvind Swamy, G. Raju, G. Nagesh Babu



1.1c Research Resources



Instrumentation

CCMB has a strong and highly supportive Instrumentation group which takes care of the installation, maintenance and repair of scientific instruments in house without any maintenance contracts. The group provides technical help to the PI's for the procurement of equipment by way of framing technical specifications and making Technical Evaluation Reports of bids. Maintenance of UPS and audio-video projection systems is also taken care by the group. The group conducts training programs, on the usage of instruments with safety instructions, for the new research students during August every year and for other research staff throughout the year. The state of the art facilities are managed, maintained and run without much downtime due to support and services provided by the group. Further, the group carries out in-house design, development, modification and fabrication of instruments as and when needed and also provides technical advice to other institutes in the procurement and usage of scientific instruments. The group's contribution to symposia, seminars, workshops and other events are multifarious, particularly for audio-video and exhibition arrangements.

Instrumentation Facility/ Services for repair, maintenance, design of scientific equipment

From left to right, Front row: A. Syam Kumar, Dattatrya N G, N.R.Chkaravarthi, K.Sanjeev Kumar, Devender S, A. Ramesh, USTRB Bapiraju

Back Row:: Janardhan, Chetan K, Karthik,Sudatt T Tambe, Amil Mandlik, NAgaraj, A. Bala Murugan

Fine Biochemicals

CCMB's Fine Biochemicals facility maintains and stocks large number of biochemicals for the ongoing research activities of the laboratory. The facility has a walk-in freezer (-18°C to -20°C) and a cold room and, two deep freezers (-20°C & -80°C), for storage of chemicals as per the recommended storage conditions. However, the chemicals stable at room temperature are kept in a room (72 sq.mtrs plinth area) where temperature is maintained at 26-28°C. The stocks of fine biochemicals include amino acids, proteins, enzymes, purification kits and buffer reagents. In addition, stocks of restriction enzymes, antibodies, reagents necessary for purification and detection of recombinant proteins, reagents for DNA/protein gel electrophoresis, PCR, RT-PCR, DNA sequencing and synthesis and buffers, and gel electrophoresis. The requirement for these chemicals is monitored such that procurement is carried out on a regular basis, so as to maintain a constant level of supply. Requirement for these chemicals/enzymes is monitored with a help of software developed by CCMB IT Group such that procurement is carried out on regular basis so as to maintain a constant level of supply. Availability of various chemicals can be seen on CCMB intranet.

The fine biochemicals indented by all the scientists is first received by the facility, and issued to the corresponding groups, in addition, to the general chemicals maintained by this facility.

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 for scientific and other conventions, etc.

The services of this group span across the CCMB main campus at Habsiguda, LaCONES, CCMB Annex-1 at Attapur and Medical Biotechnology Complex, CCMB Annex-2 at Uppal.

Information Technology Group

The Information Technology group plays a major role in the creation and management of IT infrastructure to facilitate research works and collaborations. It prevents organisation's network and research data from cyber-attacks.

CSIR-CCMB have two data centres comprising of 7 smart racks and 4 server racks populated with 72 Tera Flops 42 nodes High Performance Computing clusters, 2 numbers of 300 TB SAN storages, usable 4 PB NAS and other high end servers. All these are managed by IT group to support computational research.

Organisation website, intranet site and other websites related to various services are maintained by IT department. The team also develops many online applications and tools to automate and manage Research facilities and administrative work for the lab. Applications were also developed as per the requirement of CSIR Head Quarters.

CSIR-CCMB is connected with 1 Gbps leased line link from NKN and redundant 100 Mbps leased line from BSNL. Ethernet backbone was recently upgraded to 10 Gb in CCMB and its Annex campuses LaCONES and MBT. New data centre and NGS facility are connected with 40 Gb uplink. Annex campuses are connected to the main campus through site-to-site VPN.

Other facilities like Surveillance camera system, Biometric Attendance system, Telephone, Fire alarm, Building Management System (BMS), Closed Circuit TV are also administered by IT group in all the 3 campuses.

From left to right: M Srinivas Rao, B Shiva Kumar, G Sai Krishna, Biswajit Roy, Sreekanth M, P Nagalinga Chary, P Radhakrishna Murthy, Sublari Balaraju, Geetha Thanu, K Sambasiva Rao, N Siva Rama Prasad, K Rama Chary, S Mahalingam, A Padmavathi, Aparna Kumari

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.

An inspection on Official work done in Hindi by CCMB was held by Hon'ble Members of the Parliament, second sub – committee on Official Language on 24 August 2022. CCMB successfully passed the inspection and was awarded with the award certificate.

Also, an inspection on Official work related to Rajbhaha was conducted by Regional Implementation Office, Bangalore, Ministry of Home Affairs, Govt. of India in the month of March 2023.

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 08 September 2022 to 21 September 2022, concluding the Valedictory function on 30th September, 2022. 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. Shri Rakesh Shukla, Scientist SG, Head CS, Department of Space, has been invited as Chief Guest for the function. Every year, we invite some eminent writer, poet or expert of a subject of general interest to deliver a popular lecture in Hindi. This helps our staff and Students to interact with such personalities and get benefited by listening to their valuable views.

This year, All India Rajbhasha Sammelan was held on 14 & 15 September 2022 in Surat,Gujrat. Shri Sudhanshu Kumar, Admin. Officer, Smt Noopur Rani Prasad, Hindi Officer & Smt. Savita Kumari, Jr. Hindi Translator represented CCMB in the meeting.

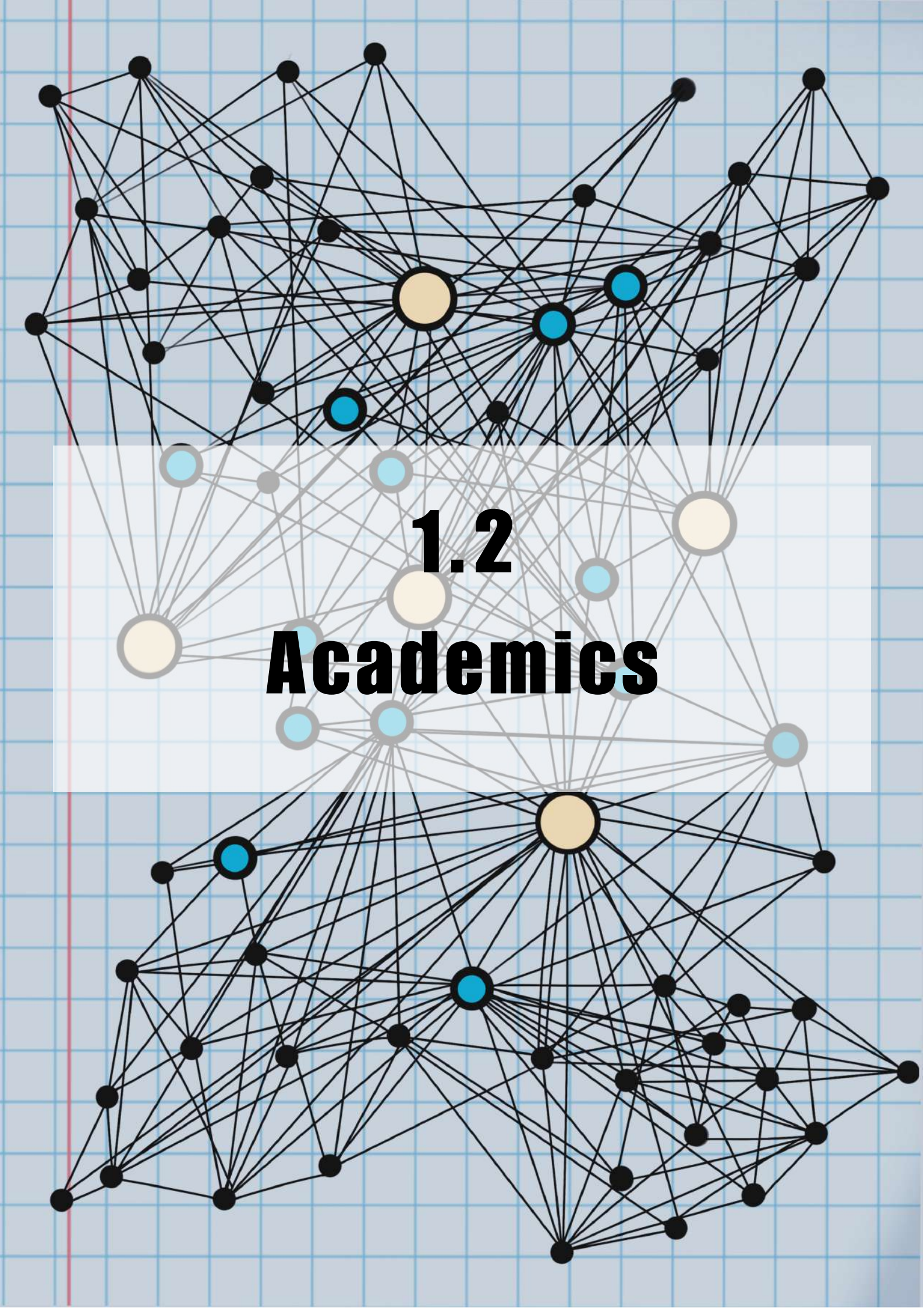
Under Hindi Teaching Scheme, 09 Staff were nominated for Prabodh, 03 for Pragya and 13 for Parangath. After passing the exam, trained staff contribute their efforts in implementation of Rajbhasha Rules and Polices in the Organisation.

The unit regularly conducts Hindi workshops for the staff and Officers for training and upliftment of progressive usage of Hindi in the organization. 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.

The Unit also conducts other activities, viz., inviting eminent speakers of various fields to deliver popular talks in Hindi for the benefit of staff and research students. The spectrum of topic includes Personality development, Space Technology, Geology, Management Skills, Classical Music etc., and they proved very useful for the staff to gain some basic knowledge in these areas.

The Rajbhasha Unit has a very good library consisting 3185 Hindi Books on various subjects viz., classic works of Hindi literature, science, translations and books of general interest, personality development, etc. This year 70 books have been added to this collection. Thus, the Rajbhasha unit takes care of CCMB in respect of implementation of Official Language as prescribed by GOI time to time.



1.2 Academics

1.2 A Academic Cell & PhD Program

CCMB-PhD program is run by Academic cell, which consists of two academic coordinators and an AcSIR Executive Assistant. This cell handles almost all the academic activities related to PhD students, including selection and recruitment of students, course work, lab allotment, Doctoral Advisory Committee (DAC) meetings, Comprehensive Exam, and PhD thesis submission. The Academic cell keeps records of the performance in course work, progress reports of the PhD work, and all AcSIR related documents. In case of JNU-CCMB PhD program, all administrative matters related to JNU committee are responsibility of a separate JNU-CCMB committee.

Selection of students for CSIR-CCMB PhD program happens in August and January every year. Eligible candidates are invited to apply and selected based on performance in a written test, followed by two rounds of interviews at CCMB. The students can apply through CCMB-AcSIR.

So far, CSIR-CCMB has produced 465 PhDs since its inception.This program targets students who intend to pursue research careers in interdisciplinary areas within or outside academia. Our main goal is to provide students a strong technical background, enhance their capacity for analytical thinking, and address new kinds of problems for the advancement of science and society.

In the year 2022-23, 10 students joined PhD program in August 2022 and 10 students in January 2023. As of March 2023, 146 PhD students are on roll, 22 of them gave their PhD colloquia and 4 students submitted PhD thesis. 21 students were awarded PhD degree from JNU/AcSIR during this year.

1.2 B PhDs Awarded

List of students awarded with PhD degrees during April 2022 to March 2023

Siddharth Bhatia
Understanding molecular and functional venom variation in geographically isolated *Echis carinatus* venoms (13-04-2022)
Guide: Dr. Karthikeyan Vasudevan

Vishnu Narayanan M
Studies on virulence factors of the rice pathogen *Xanthomonas oryzae pv. oryzae*. (11-05-2022)
Guide: Dr. Ramesh V Sonti

Kamakshi Dandu
Pyrogallol: A potential therapeutic agent for Retinoblastoma (12-07-2022)
Guide: Dr. Ch. Mohan Rao

Vishnu Vijay V
Molecular Insight into the fine control of core pluripotency factors in ES cells (13-07-2022)
Guide: Dr. P. Chandra Shekar

Nilanjan Som
Studies on bacterial peptidoglycan synthesis and its regulation (29-07-2022)
Guide: Dr. Manjula Reddy

Amrutha HC
Exploring the structural and functional insights of secretagogin, a calcium-binding protein (28-07-2022)
Guide: Dr. Yogendra Sharma

Nikhil Hajirnis
Genome organization and regulation of bithorax complex in *Drosophila melanogaster* (03-08-2022)
Guide: Dr. Rakesh K Mishra

Lomous Kumar
Genetic affinity among the populations of west coast India (12-09-2022)
Guide: Dr. K. Thangaraj

Akanksha Garhewal
Mechanism of epigenetic regulation in plants: Role of histone modifications and non-coding RNA (20-09-2022)
Guide: Dr. Mukesh Lodha

Ashish Bihani
Biochemical and genetic investigation of nuclear matrix (29-09-2022)
Guide: Dr. Rakesh K. Mishra

Deepak Kumar Kashyap
Identification and functional characterization of novel gene(s)/variants associated with cardiomyopathy (22-11-2022)
Guide: Dr. K. Thangaraj

Raj Bahadur
Function and regulation of peptidoglycan hydrolases in *Escherichia coli* K-12 (01-12-2022)
Guide: Dr. Manjula Reddy

Debarya Saha
Analysis of the regulatory mechanisms governing quiescence (13-12-2022)
Guide: Dr. Jyotsna Dhawan

Jaydeep Aravindbhai Badarukhiya
Rheumatic heart disease influence of genetic and immunological factors (14-12-2022)
*Guide: Dr. K. Thangara*j

Jotin Gogoi
Physiological and evolutionary insights into proofreading during translation of the genetic code (10-01-2023)
Guide: Dr. R. Sankaranarayanan

Haripriya Parthasarathy
Investigating the association between AMPK and stress response in regulation of eukaryotic protein translation (16-01-2023)
Guide: Dr. H.H. Krishnan

Frank Keith Max
Control of reproductive development in *Arabidopsis thaliana*: Role of the DYAD gene in meiotic-specific DNA methylation (27-01-2023)
Guide: Dr. Imran Siddiqi

Mihir Trivedi
Population genetics and phylogenetics of primate species in Northeast India with special emphasis on Hoolock gibbons (01-03-2023)
Guide: Dr. G. Umapathy

Divya Gupta
Identification of novel host factors in RNA virus infections (06-03-2023)
Guide: Dr. H.H. Krishnan

Mansi Srivastava
The metabolic control of mouse development (24-03-2023)
Guide: Dr. P. Chandra Shekar

Zeba Rizvi
Identification and characterization of CRLs of malaria parasite (28.03.2023)
Guide: Dr. Puran Singh Sijwali

1.2 C 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 only online (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 CCMB to complete a small research project towards their partial fulfilment of the academic degree. The program offers one-week lectures on good laboratory practices, bio-safety, research methodology, scientific writing, research ethics, recent research developments and career opportunities in life sciences. Student visits are organised to other annexes of CCMB as part of training. After completing their research, students must present a poster to the 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 2022 - 2023, 70 students were selected for their dissertation research training at CCMB.

Project-based Student Training Program (PBST)

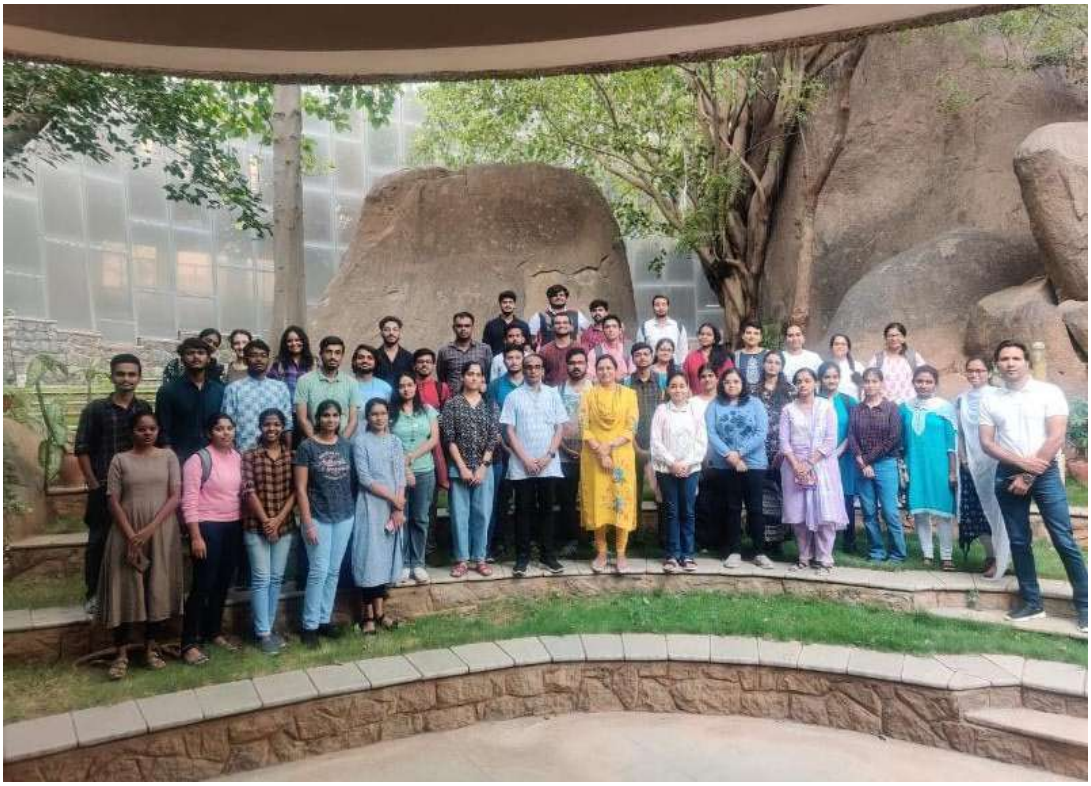
This program encourages students who have completed their studies in M.Sc/ M.Pharm/ M.Tech/ MD/ B.Pharm/ BDS/ B.Tech/ MBBS and would like to spend time learning and improving their laboratory skills. Unlike the dissertation research training program, students can choose their supervisor based on their research interest and take their consent to work in their laboratory for either six months or one-year duration, and 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, bio-safety, research methodology, scientific writing, and research ethics.

DRTP & PBST students during lecture series

Summer Training Program

The program is open to students from all branches of life science studying at any Indian University/College/Research Institute. However, the program is offered to students still pursuing their studies. M.Sc/ M.Tech students who completed at least two semesters, B.Tech/ B.Pharm students who completed six semesters, integrated B.Tech-M.Tech/ B.Sc-M.Sc students who completed eight semesters and MBBS/ BDS students in any year of their study can apply. The tenure is 60 days between May and 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. Each selected student will be assigned to a CCMB staff scientist who will mentor them to execute 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 mainly intends to give students real-time exposure/ hands-on experience in research. In 2023, we accommodated 43 students, which includes 7 Academy students.

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



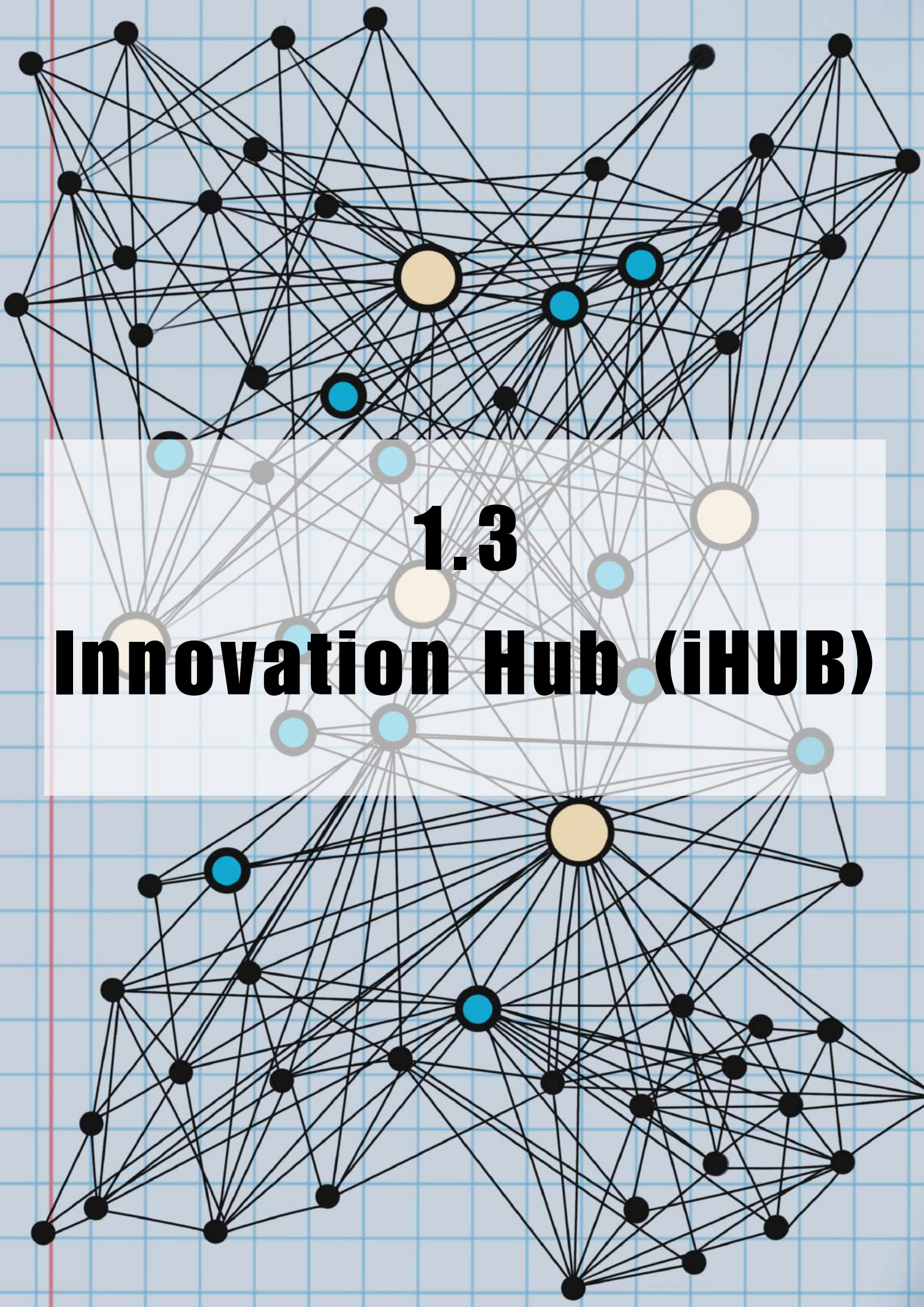
STP students during the LaCONES visit

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. This year as well, the Skilling Programs were continued and apart from the courses which have been offered in previous years, such as the Medical Student Research Training Program (MedSRT), Wildlife forensics, Cell biology, CRISPR technology, Recombinant DNA Technology (RECOMB), Proteomics (PROTEO), new sponsored training programs such as Rastriya Ayurveda Vidyapeeth, Ministry of AYUSH, GOI, sponsored AYUSH CME Training Program on "Identification of Medicinal and Herbal Plants using DNA-Based Barcode Analysis", DBT-TSCOST sponsored Skill Vigyan Faculty Training Program on "Basic Techniques in Genetics and Molecular Biology" , and WWF-TRAFFIC INDIA sponsored Workshop on "Wildlife Crime Scene Investigation and Evidence Collection" SBIF sponsored Sewage Surveillance training programs were introduced.

The training program for medical students- Medical Student Research Training Program (MedSRT) was held in December for 2 weeks and 20 medical students had participated in this. The purpose of MedSRT has been to create an orientation of Medical students (mostly in their 2nd and 3rd years) towards clinical research through lectures and hands-on trainings.

About 14 different trainings including sponsored, fee based and non fee based workshops, spanning from one day to 3 weeks benefitting around 212 candidates were held - in various advanced areas of CCMB expertise namely, Wildlife Forensics, Cell Biology, CRISPR technology, Recombinant DNA Technology, Proteomics, The ultimate aim of these programmes is to improve employability and career advancement (through reskilling/ upskilling) in the area of Life Sciences. Several entry-level skilling courses in Instrumentation, Laboratory Attendants, Animal Attendants, etc. are in the pipeline as well..



1.3
Innovation Hub (iHUB)

1.3 A Services

Consolidated Diagnostics Facility at iHUB

CSIR-CCMB has been running diagnostic services for the past two decades for the benefit of patients with rare genetic disorders. We offer both molecular and cytogenetic services including NGS based testing.They are now running in a centralized facility at the CSIR-CCMB, Annexe-II. Last year witnessed addition of several new diagnostic tests into our armamentarium including optical genome mapping for the diagnosis of Facioscapulohumeral dystrophy and to identify other genetic disorders caused by large structural variants in the genome. A total of 2023 patients from 1860 families have benefited from our testing services in the last financial year.

Molecular Diagnostics

Advances in molecular and cell biology have provided an understanding of the mechanisms of disease at molecular and genetic levels, which can now be translated into diagnostic, prognostic, and therapeutic applications in modern medicine. A number of genetic disorders are known to result from the defects in a single gene. Although rare in comparison to the infectious diseases, genetic disorders cause enormous misery since they are largely incurable and result in many cases, severe morbidity and mortality. In absence of specific treatments, molecular diagnosis, genetic screening for carrier detection, genetic counseling, pre-pregnancy testing, pre-implantation genetic diagnosis and prenatal diagnosis for these disorders becomes the best approach to prevent their transmission to next generation. The Molecular Diagnostics Facility, CSIR-CCMB, Hyderabad provides diagnostic services for about 30 such monogenic disorders. The facility provides DNA-based testing for a number of inherited and acquired genetic diseases including hemoglobinopathies, musculopathies, bleeding and clotting disorders and neurodegenerative diseases. The strategy is to identify the causal genetic defect in an individual, screen at risk members for carrier status, tracking inheritance of the genetic defect in the fetus by performing prenatal diagnosis on fetal samples (procured at appropriate stage of pregnancy through hospitals) and providing appropriate and timely genetic counseling. The major thrust of these diagnostic services is to provide reliable genetic testing services to the common man within a rapid turnaround time and at affordable rates.

The advent of NGS in to clinical practice has tremendously increased out potential to identify the molecular defect in a wide spectrum of genetic diseases. Exome sequencing enables us to screen ~20,000 genes at a go for pathogenic variants. The initiation of NGS diagnostic services is in line with our motto to provide quality, low-cost genetic diagnostics to the people of our country and at the same time aid in generation of data important for research and public health care.

Chromosomal Diagnostics

Chromosomal abnormalities are a group of genetic disorders due to microscopically detectable defects at the level of chromosomes. They are commonly implicated in mental retardation, congenital malformations, dysmorphic features, primary and secondary amenorrhea, bad obstetric history, infertility and neoplastic diseases. Cytogenetic evaluation of patients is helpful in the counseling the affected individuals and families and disease management. Prenatal diagnosis of chromosomal abnormalities in high-risk pregnancies helps in detecting chromosomal abnormalities in fetuses and aids in their genetic counseling and reproductive decision making. The state-of-the-art facility offers cytogenetic tests such as karyotyping (conventional-G banding techniques) and FISH (fluorescence in situ hybridization which includes probes using WCP and LSI, mFISH, mBAND, SKY), which involves investigation of genetic defects at the chromosome level.

Diagnostics team

Wildlife Diagnostics

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 LaCONES.

During the period (April 2022 – March 2023), a total of 235 wildlife crime cases were received for different analyses. The 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. 25 lakhs was generated towards the DNA analysis fee charges.

From left to right: O. V. Padmalatha, B. Kranthi, Swati Chauhan, Ajay Gaur, P. Anuradha Reddy, Deepanwita Purohit, Raghavendra Babu

1.3 B Atal Incubation Centre-CCMB

Five Years of Powering india's Bio-Economy

In the dynamic landscape of modern science and technology, innovation is the lifeblood of development. Atal Incubation Centre - Centre for Cellular and Molecular Biology (AIC-CCMB) stands tall as a shining testament to India's commitment to fostering innovation, entrepreneurship, and scientific excellence. Nestled at the crossroads of cutting-edge developmental and translational research, it serves as a nurturing ground for budding startups and MSMEs in the field of biotechnology and life sciences. AIC-CCMB provides a conducive environment for entrepreneurs, researchers, and innovators to collaborate, ideate, and develop their projects. With state-of-the-art infrastructure, mentorship programs, access to cutting-edge research facilities, and a network of industry experts, the centre equips startups with the tools they need to thrive in today's competitive landscape.

AIC-CCMB marked its 5-year anniversary in 2022, a testament to half a decade of fostering ground-breaking innovation in the field of life sciences. Over the years, we have witnessed remarkable discoveries, nurtured brilliant minds, and forged valuable collaborations. As we celebrate this milestone, we are inspired by our progress and are excited to continue driving advancements in healthcare and biotechnology for many years to come. We highlight some of our achievements over the past year in the pages to come.

Transformative Projects

mRNA Project

In May 2022, the team of scientists led by Dr. Madhusudhana Rao at AIC-CCMB announced the development of India's first indigenous mRNA vaccine technology for COVID-19. This technology was developed without any external scientific assistance and leverages mRNA technology which be used not only against COVID-19 but also for the prevention of several other infections. With rigorous testing underway and promising early results, this scientific achievement brings hope for safer and more effective weapons in the global fight against infectious diseases.

CoSI Lab

Conservation Science and Innovation Laboratory (CoSI-Lab) was inaugurated in September 2022, at the University of Kashmir at Kashmir University's Centre of Research for Development (CORD). The Himalayan range situated in the regions of Jammu & Kashmir and Ladakh boasts of a unique biodiversity and endemic wildlife population. This precious ecosystem is now facing dire threats from the surge in illegal wildlife practices, which in turn, jeopardize sustainable development in the region. Recognizing the urgent need to safeguard this ecological treasure, the Centre of Research Development at the University of Kashmir has embarked on a transformative initiative. With crucial support from the CSIR–CCMB, AIC-CCMB, and IKP Knowledge Park, a cutting-edge 'Conservation Science and Innovation Laboratory' (CoSI-Lab) has been established. Rural Electrification Corporation Foundation (RECF) has generously funded the establishment of this lab under its CSR initiative.

This visionary laboratory will serve a dual role, functioning as both a field office and a knowledge hub. At its core, the CoSI-Lab will be dedicated to testing and implementing innovative technologies. Additionally, it will provide invaluable transferable skill training and forensic diagnostic services, besides promoting technology based entrepreneurship in the region.

NIDHI PRAYAS

AIC-CCMB has taken a pioneering stride to use innovation as a tool to foster economic growth and societal progress by establishing the National

Initiative for Developing and Harnessing Innovations (NIDHI) PRAYAS Centre in 2023. This centre is aimed at nurturing start-ups and innovative ideas, facilitating the growth of promising start-ups and empowering young innovators to bridge the gap between ideas and successful businesses.

Through workshops, seminars, and networking events, the centre plans to attract budding entrepreneurs who are passionate about their concepts. Additionally, the centre will collaborate with educational institutions, research organizations, and industry experts to identify individuals with groundbreaking ideas. While ideation and early-stage development are crucial, true success lies in a start-up's ability to scale its operations and impact. The centre will provide a comprehensive support system of advanced laboratory access, specialized equipment, seed funding, grants, and access to a network of investors, industry partners, and market experts. So far, the NIDHI PRAYAS program has received more than 100 applications from aspiring entrepreneurs.

Highlights

HIGH 5: Celebrating Half a Decade of Empowering India's Bio-Economy

AIC-CCMB celebrated five years of excellence in the field of life sciences incubation with a gala event "HIGH 5". This event highlighted the achievements of the centre, its various programs and start-ups via informative stalls and interactions with incubated start-ups and program coordinators. The event was attended by a host of eminent scientists and government officials, including Secretary of the Department of Biotechnology, Government of India, Rajesh Gokhale, former DST secretary, T. Ramasami, CCMB Director, Vinay Kumar Nandicoori, former CCMB director and present Director of Tata Institute for Genetics and Society, Rakesh Mishra. Aasya Healthcare, Empiezo IT Solutions, Fastsense Innovations, Satyarx Pharma Innovations and Avyantra were recognised as some of the best startups incubated at AIC-CCMB. Several other companies such as Instashield, Consytel, Acrannolife, Waferchips, incuMed, Sirfbio, Huwel, RR Animal Healthcare, BioArtis, Zedblox, Althion Tech Innovations and Semantic Web India were awarded for their efforts in creating market-ready products.

Gran Tourismo: Catalyzing Student Innovations to Drive India's Bio-Economy

Team AIC-CCMB kicked off the new year with the innovation yatra 'Gran Tourismo: Catalyzing Student Innovations to Drive India's Bio-Economy", transversing five colleges across three districts of Telangana to encourage students in the fields of biotechnology, pharmacy and biology to dip their toes into entrepreneurship and innovation. The three-day tour was flagged off by Dr. Manjula Reddy, with opening statements from Dr. Madhusudhana Rao, CEO. AIC-CCMB team members interacted with students from SR Engineering College, NIT Warangal, Surabhi Institute of Medical Sciences, Government Degree College, Siddipet, BV Raju Institute of Technology and MLR Institute of Technology played fun games, spoke about their individual programs and conducted a pitch competition for budding innovators. Winning teams were awarded pre-incubation incentives, expert guidance & cash prizes, along with invitations to attend a pitch fest at AIC-CCMB on the occasion of National Startup Day.

National Startup Day

AIC-CCMB marked the occasion of National Startup Day with students from schools and colleges all over Telangana visiting the incubator to learn about entrepreneurial spirit. Students, including winners of the pitching competitions during the Gran Tourismo, participated in a pitch fest, competing for awards and cash prizes as they explained their innovative ideas in creative ways. Several incubated start-ups like Instashield, Neat Meatt and 30M Genomics were part of the Technology Showcase, where visitors learned about all the exciting products and work being done.

"Health-Hacks" Hackathon

In an effort to foster a culture of entrepreneurship and innovation with national significance, a national-level 36-hour hackathon was conducted in February 2023 named "Health-Hacks," in collaboration with SINE, IIT Bombay. 10 teams of innovators battling it out over 36 hours, coding furiously to present their solutions to a wide variety of challenges in fields like genomics, precision medicine and data visualization. This exhilarating bout was peppered with discussions, mentoring sessions and mock pitches. The winning teams not only received cash prizes but also invaluable mentorship, propelling them towards a future of entrepreneurial excellence. Winning thematic areas included wearable smart patches for early warning of diabetic complications, a no-code AI builder for medical imaging, a database for identifying medicines, app-based real-time screening for throat infections and a mental health illness predictive app.

Investing in the Future

Over the past five years, AIC-CCMB has raised and disbursed more than INR 5 crores to several start-ups through its various funding programs. This financial infusion has been instrumental in propelling the organization's mission and has supported many cutting-edge research initiatives, state-of-the-art laboratory facilities and support for promising startups.

Startup India Seed Fund Scheme

Startup India Seed Fund Scheme (SISFS) facilitated by Startup India aims to provide financial assistance to start-ups for proof-of-concept, prototype development, product trials, market entry and commercialization. This will enable these start-ups to graduate to a level where they will be able to raise investments from angel investors or venture capitalists or seek loans from commercial banks or financial institutions. The program has funded six young entrepreneurs who have created employment opportunities for more than 20 people:

Nidhi-Seed Support Scheme (SSS)

Nidhi-Seed Support Scheme (SSS) facilitated by NSTEDB provides financial funding to startups for proof of concept, prototype development, product trials, market entry and commercialization etc. The scheme also enables the incubators to widen their pipeline of startups and share the success of their startups which would also result in ensuring their long-term operational sustainability. So far, the program has funded 5 startups in HealthTech. The startups have successfully pivoted to the Revenue stage with a cumulative revenue of ~INR 3.5 crores in FY 23, raised follow-on funding of ~INR 5.5 crores, and been awarded ~5 IPR.

COVID-19 Technology Deployment (CoviTED)

In April 2021, Security Printing and Minting Corporation of India Limited (SPMCIL), a significant player in the financial and security sectors, pledged its first healthcare Corporate Social Responsibility (CSR) fund to AIC-CCMB to accelerate the deployment of technologies developed by start-ups.

As a CSR initiative, SPMCIL has provided pivotal support to the COVID-19 Technology Deployment (CoviTED) program, showcasing its dedication to social responsibility and community well-being.

CoviTeD is executed by selecting promising startups in pandemic-related technologies, immersing them in an accelerator program and supporting them with funding. Seven start-ups nurtured and supported by the CoviTeD program developed several products, ranging from diagnostic tools, digital health solutions, medical devices and other innovative technologies to combat the virus, mitigate its impact, and improve public health. Start-ups also received funding support through the CoviTeD acceleration program to help advance their technologies.

Immersion to Incubation: Programs at AIC-CCMB

Technology Incubation and Development of Entrepreneurs (TIDE 2.0)

Supported by the Ministry of Electronics and Information Technology (MeitY) is a program nurturing force for innovation and emerging technology-driven startups in the realm of Information and Communication Technology (ICT). Within this vibrant ecosystem, AIC-CCMB serves as a formidable ally to life sciences startups harnessing the power of IoT, Robotics, Data Analytics, Artificial Intelligence (AI), and Machine Learning (ML). Each TIDE 2.0 cohort supports four startups under the Entrepreneur-in-Residence (EiR) program and four through the Grant in Aid initiative, all for a period of one year. So far, TIDE 2.0 has driven forward 24 innovative startups in three cohorts. The current 3rd cohort began in October 2022 and includes 4 Entrepreneur-in-Residence (EiR) startups and four through the Grant in Aid startups like the previous cycles.

SPARSH Social Innovation Immersion Program (SIIP)

Biotechnology Industry Research Assistance Council (BIRAC), Government of India, initiated the Social Innovators in the Biotech Industry (SIIP) fellowship program to cultivate an entrepreneurial spirit among young graduates and professionals. Over the course of 18 months, the selected cohort of fellows, known as "Social Innovators," are tasked with identifying pressing needs and gaps within their communities and crafting socially impactful solutions, in the form of affordable products or services. AIC-CCMB is a Sparsh Centre currently engaging 4 fellows in Maternal and Child Health. The program involved immersion activities in clinical settings across a spectrum of locations, including Tier 1, 2, and 3 areas. Besides the fellowship, the innovators receive INR 5 lakh kick-start grants developing their prototypes. These talented individuals are also in the process of formalizing their startups and pursuing patent applications.

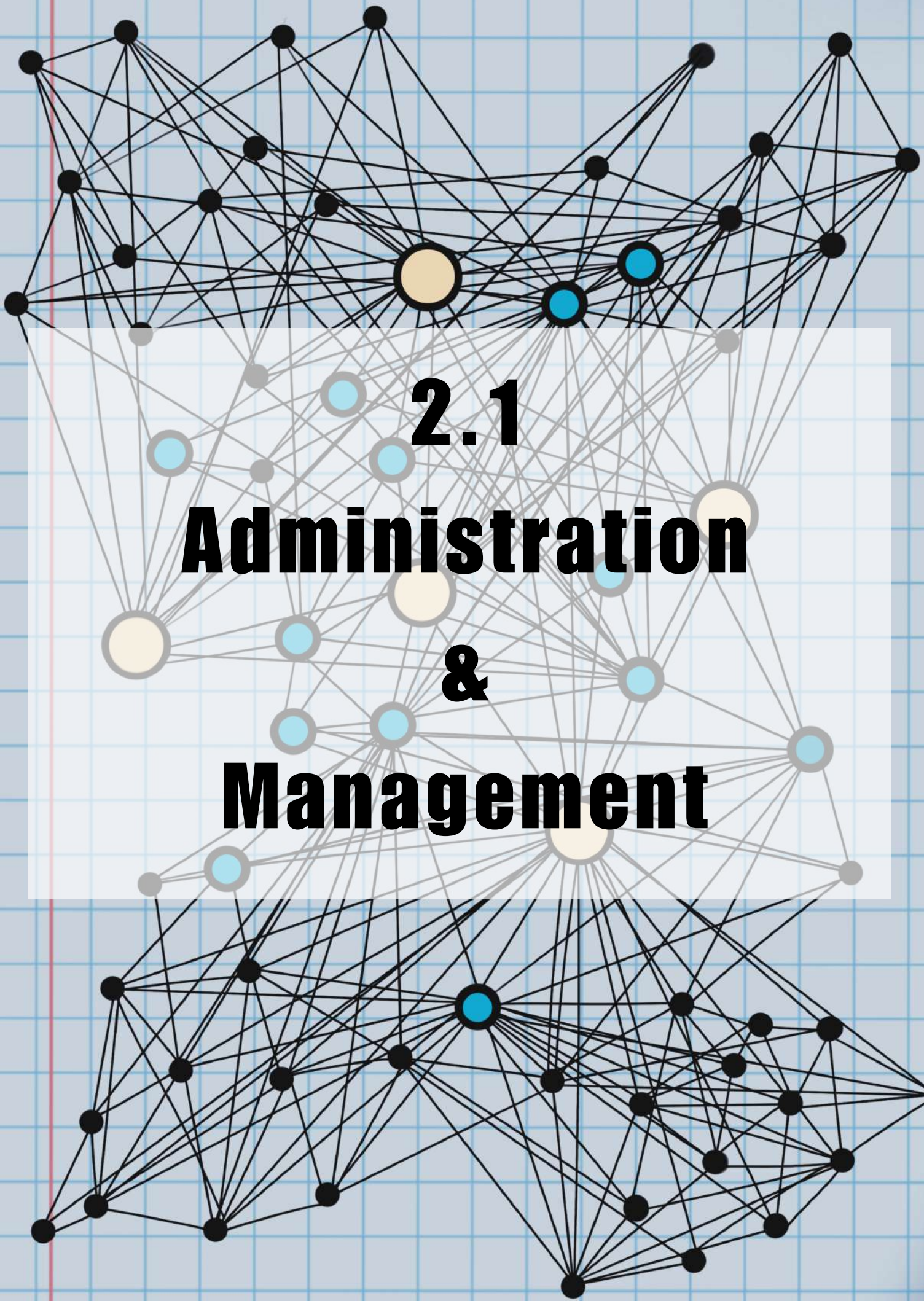
Centre for Predictive Human Model Systems

The Centre for Predictive Human Model Systems (CPHMS) is a scientific and policy think-tank that promotes the use and development of human-relevant methodologies, such as organoids, organ-on-chip, and computational tools in India. We do this through a wide range of outreach and awareness initiatives that champion the use of non-animal methodologies. Our educational initiative, Back to the Future! Virtual Labs, supported by the 3rd IndiaBioscience Outreach Grant focuses on showcasing cutting-edge & new technologies being used in biological research. We launched an interactive, open-access Microphysiological Systems Database to showcase information from all researchers across the country working on alternate animal methods and techniques. CPHMS publishes a quarterly newsletter focusing on the latest advances in this field of research and conducts a monthly webinar series featuring eminent Indian scientists. CPHMS conducts regular meetings with representatives from CPCSEA, IPC, CDSCO, OPSA, DBT, BIRAC, CSIR, DST, ICMR, HiMedia, Dr Reddy's Laboratories, NBIL, and eminent scientists from Indian academic institutes.

Project Team | cphms.aic@ccmb.res.in
Dr. Surat Parvatam, Chief Manager
Dr. Kasturi Mahadik, Sr. RA-Science Communication
Anushka Banerjee, RA – Science Communication
Kadambari Patil, Jr. RA – Science Communication

Making it happen: The Team AT AIC-CCMB

- Dr. N. Madhusudhana Rao, CEO
- Dr. Ramjee Pallela, COO
- Ritika Marampalli, Head – Corporate Relations
- Seshu V. Prasad, Manager – Instrumentation
- A.K. Nagamani, Secretary to CEO
- Dr. Surat Parvatam, Chief Manager, CPHMS
- Mir Ali, Acceleration Program Coordinator
- Anuj Kokate, Investment Manager
- Kadambari Patil, Jr. Research Associate – Science Communication, CPHMS
- Anushka Banerjee, Research Associate – Science Communication, CPHMS
- Meghna Girish, Program Coordinator, SPARSH
- Anil Kumar Konda, Manager-Accounts & Finance
- Dr. Kasturi Mahadik, Sr. Research Associate – Science Communication, CPHMS
- Aniket Kumar, Program Coordinator – TIDE



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:

Prof P. Balaram **Chairman**
Molecular Biophysics Unit
Indian Institute of Science
Bengaluru – 560012

Prof Roop Mallik
Member
Professor
Department of Biosciences &
Bioengineering, IIT Bombay
Powai, Mumbai – 400076

Dr Rajesh S. Gokhale **Member**
Head, Department of Plant
Molecular Biology
Delhi University, South Campus
New Delhi

Prof Anand Kumar Bachhawat
Member
Professor (Biology)
Indian Institute of Science Education
and Research (IISER)
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P.O. Manauli – 140 306

Prof Sandhya Visweswaraiah **Member**
Professor
Department of Molecular Reproduction,
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Ms Deepanwita Chattopadhyay
Member
Chairman and CEO
IKP Knowledge Park
Genome Valley,
Hyderabad-500101

Dr Subeer S. Majumdar **Member**
National Institute of Animal Biotechnology
Gachibowli, Hyderabad – 500032

Dr Arvind Sahu **Member**
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NCCS Complex,
S.P. Pune University Campus
Ganeshkhind, Pune – 411 007

Dr Sanjeev Khosla **Member**
Director
CSIR-Institute of Microbial Technology
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Dr Lalita Goyal **Member**
Senior Principal Scientist
Technology Management Directorate
Council of Scientific & Industrial Research
Rafi Marg, New Delhi - 110001

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

Dr Anant B. Patel **Secretary**
Senior Principal Scientist
CSIR-Centre for Cellular and Molecular Biology
Hyderabad

Management Council

Following is the composition of the Management Council of CCMB for the period 01.01.2019 to 31.12.2021 as approved under Rule-65 of the CSIR Rules 7 Regulations:

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

Dr N. Nagesh **Member**
Chief Scientist
CSIR-Centre for Cellular and Molecular Biology
Hyderabad

Dr A. Vijaya Lakshmi **Member**
Senior Principal Scientist
CSIR-Centre for Cellular and Molecular Biology
Hyderabad

Dr B. Kiran Kumar **Member**
Senior Scientist
CSIR-Centre for Cellular and Molecular Biology
Hyderabad

Dr C.B. Tripura Sundari **Member**
Senior Scientist
CSIR-Centre for Cellular and Molecular Biology
Hyderabad

Dr Seema Bhaskar **Member**
Principal Technical Officer
CSIR-Centre for Cellular and Molecular Biology
Hyderabad

Dr V.M. Tiwari **Member**
Director
CSIR-National Geophysical Research Institute
Hyderabad

Dr Archana B. Siva **Member**
Senior Principal Scientist & Head-BDG
CSIR-Centre for Cellular and Molecular Biology
Hyderabad

Finance & Accounts Officer **Member**
CSIR-Centre for Cellular and Molecular Biology
Hyderabad

Controller of Administration **Member-Secretary**
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.

Finance & Accounts

All financial matters pertaining to CSIR-CCMB, including budget planning, allocation and expenditure are taken care of by the Finance and Accounts section.

Planning Monitoring and Evaluation Group

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.

From left to right : Gulzar, Charan, Dr. Vishnupriya, Sujatha, B.V. Ramakrishna

Administration

The overall administration of the Centre and the supervision of ancillary services such as transport and telecommunications are under the purview of the administration. In addition, secretarial assistance is provided to the staff for the preparation of the reports, manuscripts and correspondence.

Stores & Purchase

CCMB has a modern stores building with a cold storage facility and separate rooms for the storage of solvents and acids. The Stores and Purchase section maintains an exhaustive inventory of inorganic chemicals, stationery, glassware, plastic ware and other items. The staff of this section carries out the processing of orders and the procurement of materials for the Centre.

Business Development Group

Business Development Group of 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 CCMB for patenting. The group also facilitates CCMBs connect with industry for contract & collaborative research projects, technical services, tech transfers, trainings, etc.

Dr. Archana Bharadwaj Siva (Head BDG & SDP Coordinator) and her group

Security

- Implementation of security related policies from time to time.
- Planning for preventive mechanisms to thwart any security threats.
- Liaison with local authorities.
- Event management.

Medical Services

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.

CSIR-CCMB Dispensary Services

CSIR-CCMB Dispensary Staff

Canteen Services

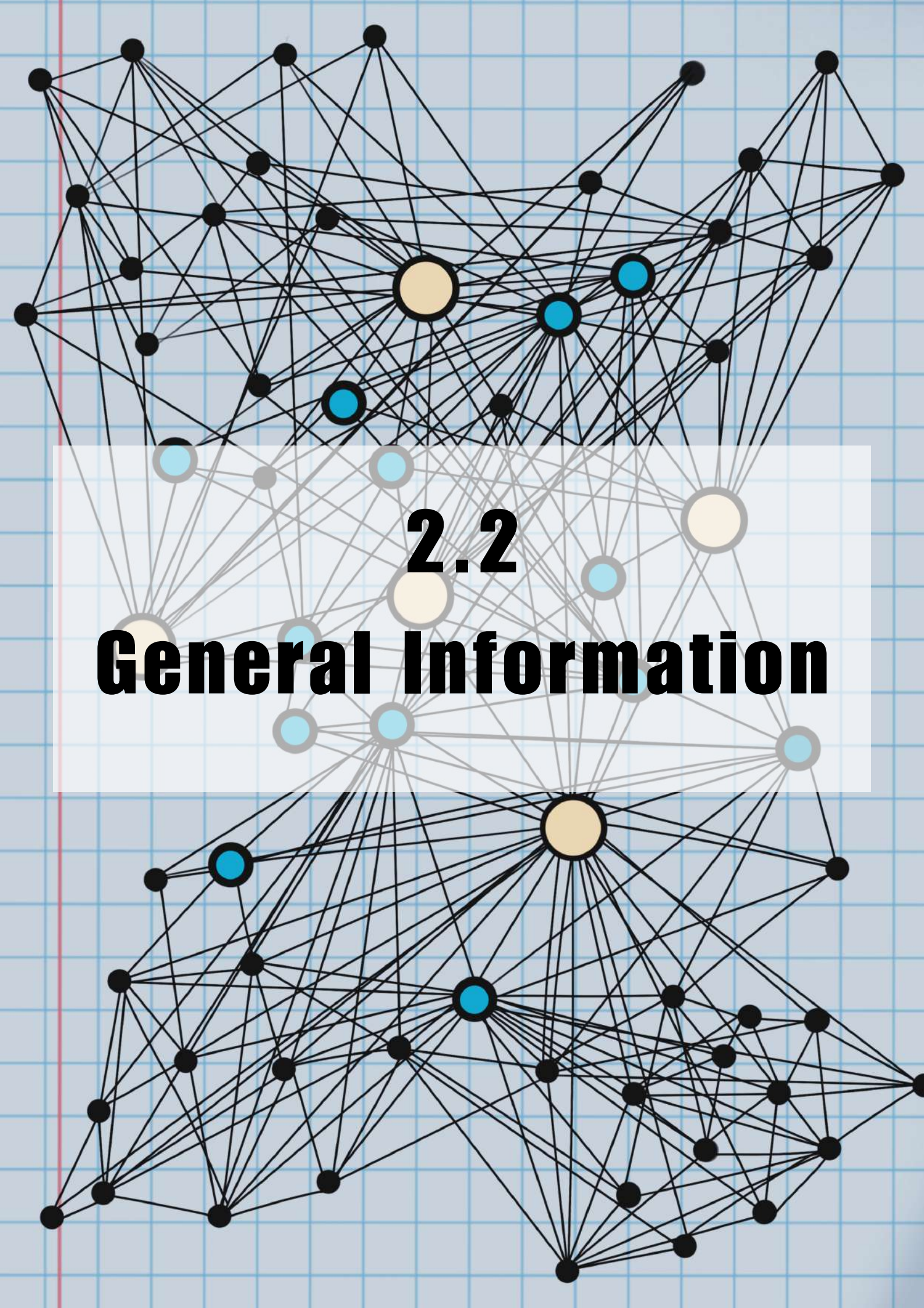
The CCMB Canteen provides food for CCMB staff, students, contract staff and visitors. We serve breakfast, lunch, dinner and high tea. We have Canteens at three different campuses- CCMB, LaCONES, CCMB Annexe-I and iHUB, CCMB Annexe-II. All canteens are operated with Canteen Smart Card System making it 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 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 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.

Guest House

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 CCMB.



2.2
General Information

2.2 A List of Publications

- Dutta A, Sarkar P, Shrivastava S, Chattopadhyay A(2022).Effect of Hypoxia on the Function of the Human Serotonin1A ReceptorACS Chem. Neurosci.10.1021/acschemneuro.2c00181
- Vishnu VV, Shah HS, Kumari S, Shekar PC(2022).CRISPR engineered mouse embryonic stem cells with Sox2-tdTomato and Gata6-GFP knock-in for endoderm differentiationStem Cell Res.10.1016/j.scr.2022.102900
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- Kumar S(2023).KIR signaling is regulated by electrostatic interaction of its cytosolic tail with the plasma membrane despite being neutral polyampholyteBiophys. J.
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- Rajan S(2022).Chiral proofreading during protein biosynthesis and its evolutionary implicationsFEBS Open Bio
- Srivastava R(2023).Role of smartphone devices in precision oncologyJ. Cancer Res. Clin. Oncol.10.1007/s00432-022-04413-3
- Nallamala MR(2022).Bacterial cell wall synthesis and its regulationFEBS Open Bio
- Vinayachandran V, Bhargava P(2022).Structural Features of the Nucleosomal DNA Modulate the Functional Binding of a Transcription Factor and Productive TranscriptionFront. Genet.10.3389/fgene.2022.870700
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associated with human heightNature10.1038/s41586-022-05275-y

2.2 B List of Patents

- Production of metal nanoparticles in aqueous solution. Sankalp Vinod Agarwal, Shyam Sunder Reddy, Marshal. NFNO:0230NF2013/IN; Filing Date: 31-10-2014; Application No.:3245DEL2013; Grant Date: 14-06-2022; Patent No.: IN399182

- Protein nanostructures for the delivery of therapeutic agents to the anterior segment of the eye. Saad Mohammad Ahsan, Chintalagiri Mohan Rao. NFNO:0153NF2015/IN; Filing Date: 17-11-2015; Application No.:3745DEL2015; Grant Date: 09-02-2023; Patent No.: IN421094

- A kit for detection of mutations associated with genetic disorders. Chandak Giriraj Ratan, Paliwal Sumit, Bayyana Swati, Donipadi VInay. NFNO:0087NF2019/ZA; Filing Date: 22-04-2022; Application No.:2022/04548

- A kit for detection of mutations associated with genetic disorders. Chandak Giriraj Ratan, Paliwal Sumit, Bayyana Swati, Donipadi VInay. NFNO:0087NF2019/EP; Filing Date: 25-04-2022; Application No.:20868556

- An RNAi-nanoparticle conjugate, composition and method of synthesis thereof. Rathna Venkata Naga Gundloori, Lekha Dinesh Kumar, Amarnath Ram Singam. NFNO:0168NF2022/IN; Filing Date: 15-12-2022; Application No.:202211072533

2.2 C Awards & Honors

Research Staff

Amitabha Chattopadhyay

- Elected President, Society for Neurochemistry India (SNCI)
- Delivered Foundation Day Lecture at CSIR-IIIM

G.R. Chandak

- 5th Venus International Healthcare Awards – VIHA 2022
- Adjunct faculty in Public Health Foundation of India for 3 years
- NASI-Council Prof. V. P. Sharma Memorial Lecture Award – 2022

Santosh Chauhan

- NASI-SCOPUS Young Scientist Award-2022
- Elected Fellow of Indian Academy of Sciences (IASc)-2023

Saikat Chowdhury

- Excellence in Microscopy award from the Electron Microscope Society of India (EMSI) at University of Delhi

G. Umapathy

- Prof. Pera Govindarajulu Gold Medal Oration award 2021

Sachin Singh

- 2nd prize in Oral presentation at the 10th International conference of LASA

R. Sankaranarayanan

- Associate Member of EMBO

Vinod Kumar

- Best Poster Award-SRBCE 2022

Students & Post-Docs

Raj Bahadur

- Best Poster Award in 44th All India Cell Biology conference

Abhishek Bharadwaj

- 1st prize in oral presentation under Basic research at the advances in cardiovascular medicine and research 2023 at PGIMER, Chandigarh

C.G. Gokulan

- Awarded with travel grant to attend the Copenhagen Bioscience Cluster Conference on Plant-Microbe Interactions held between 13-17th Nov 2022 at Copenhagen, Denmark
- Best Poster Award in the Second Indian Rice Congress held between 11th and 14th February 2023 at ICAR-National Rice Research Institute, Cuttack, Odisha
- Received Best Poster Award in the Current Trends and Future Prospects of Plant Biology held between 23rd and 25th February 2023 at the University of Hyderabad

Ananga Ghosh

- DST-SERB grant for ISEV 2022 in Lyon, France (May 2022)

Anusha Gudimella

- Best Poster Presentation-SRBCE 2022

Debabrata Jana

- Prof V C Sah award for Best Oral presentation in 44th All India Cell Biology conference.

Hanuman Kale

- SRBCE 2022 Young Investigator Award

Pradeep Kumar

- Best Poster Award-HySci 2022

Kamal Malukani

- 2nd poster at International conference on current trends and future prospects of plant biology at University of Hyderabad

Shemin Mansuri

- 2nd prize in oral presentation HySci 2023 March 17, 2023
- DBT Travel grant for Jacques Monod conference "Protein phase transitions in ageing related diseases: from atomic resolution to cellular solutions" (October 2022)

Annapoorna P.K.

- Best Poster Award- HySci 2022
- 2nd prize in Talk your Thesis in India Science Festival 2023

Priyanka Pant

- 1st prize in oral presentation HySci 2023 March 17, 2023 2023 March 17, 2023
- 3rd prize in oral presentation under Basic research at the Advances in Cardiovascular Medicine and Research 2023 at PGIMER, Chandigarh

Sneha Paturi

- Best oral presentation in NMRS, IISER Behrampur

Jaydeep Paul

- EMBO travel support and NMRS support for EMBO practical course: Structure, dynamics and function of biomacromolecules by NMR in Basel, Switzerland (August 2022)

Sivakumar Prakash

- 3rd Place in INYAS-SARANSH Three Minute Thesis Competition

Alka Sahu

- ReThink3R 2.0 Summer school in Berlin, Germany (August 2022)

Zeba Rizvi

- DST-SERB travel grant for EMBO Workshop on "Ubiquitin and ubiquitin like proteins in health and disease" in Cavtat, Croatia (September 2022)

Yogesh Sahu

- Best poster award at the Indian Academy of Neuroscience 2022

Priyadarshini Sanyal

- Best poster award at BTMO conference at IISc, Bengaluru

Shaik Shafiulla

- 3rd prize in poster presentation HySci 2023 March 17, 2023

Sakshi Shambhavi

- 3rd prize in poster presentation HY-SCI 2023 MARCH 17, 2023
- Best Poster Award in 48th National Seminars on Crystallography

Gayathri Sreedharan

- DST AWSAR Award 2021

Harshit Vaish

- Best sci-fiction writing HySci 2023 March 17, 2023

Vasundhra

- Presented at the UIAF World Anthropology Congress on January 12, 2023, University of Delhi

Amareshwar Vodapalli

- Best Poster Presentation at the International conference on Corona viruses- past, present & future

2.2 D Conferences & Symposia

International conference on Reproductive biology, comparative endocrinology and development

Spread over 3 days, from September 14-16, 2022, the conference had 54 invited speakers, 400 participants, 31 short talks and 100 poster presentations. There were talks delivered by experts as well as young researchers, poster discussions on the topics of reproductive biology, endocrinology and developmental biology. In addition, the public lectures were live streamed. Experts were interviewed about the social implications of their work and hosted on CCMB's social media handles.

India | EMBO Lecture Series

The Centre for Predictive Human Model Systems, AIC-CCMB organized an India | EMBO Lecture Series in association with CSIR-CCMB from October 31st – November 4th, 2022. This conference focused on microphysiological systems, their advances and applications in human-relevant research. The conference saw an impressive turnout with more than 100 participants and 26 speakers from all over India and abroad, where more than 50% of speakers and participants were women, and almost 20% were early career researchers. For many participants, it was their first physical conference after COVID-19, made all the more valuable by the waivers they received thanks to sponsorships from EMBO, India Alliance, The Company of Biologists, DBT, SERB, InSDB and CSIR.

EMBO Workshop

As part of EMBO India Research partnership programme, EMBO workshop was held on March 03, 2023. This was a forum EMBO fellows to network with life scientists in the city and the EMBO leadership and editorial staff to meet the CCMB community.

RF-India Consortium Meet

RF-India Consortium meet was hosted by CSIR-CCMB in Hyderabad on March 04, 2023, to discuss phase 2 of the project that focuses on surveillance of other pathogens of public health concern in India. This project is funded by Rockefeller foundation (RF). Partners from NCBS, TIGS, Ashoka University, IGIB and IISER-Pune attended this meeting. The objective of the meeting was to expand activities by forming an Alliance for Environmental Surveillance that will establish monitoring procedures and detection systems for other potential viral and bacterial pathogens including antimicrobial resistance (AMR) following the One Health framework.

2.2 E MoUs & Agreements

- CHELLARAM DIABETES RESEARCH CENTRE PUNE - A Collaboration to understand the "Generation of a genetic risk score to discriminate between type1and type 2 diabetes" in Indians. 2nd May 2022, 3 years

- TAPADIA DIAGNOSTICS RESEARCH - A research in understanding the genetic basis of type 1 diabetes (T1D) and type 2 diabetes (T2D) in collaboration withfunding organization i.e. Chellaram Diabetes Research Centre (CDRC), Chellaram Diabetes Institute. 1st June 2022, 3 years

- MADRAS CROCODILE BANK TRUST – A Collaboration towards expanding and revitalizing the field of Genomic studies of India's Chelonians. 16th June 2022, 1 year

- INSTITUE OF NUCLEAR MEDICINE & ALLIED SCIENCES (INMAS) DEFENCE RESEARCH & DEVELOPMENT ORGANISATION (DRDO) - A collaboration for the proposal of "C13 NMR Spectroscopy based Neurotransmitter metabolism in Brain Post Blast Exposure". 27th June 2022, 18 months

- NAGPUR MUNICIPAL CORPORATION HOSPITAL (NMCH) - A collaboration to extend the benefits of biochemical screening, genetic screening, carrier detection, prenatal diagnosis, clinical and genetic counseling for Sickle Cell Anaemia. 15th July 2022, 3 years

- LV PRASAD EYE INSTITUTE (LVPEI) - A collaboration project on Optimizing the processes for Isolation ,preservation, Transportation, Delivery of Human Limbus - derived Stromal/Mesenchymal Stem cells for Clinical use in a cGMP facility, 20th July 2022, 1 year

- IMMORTALIGHT (OPC) PRIVATE LIMITED, HYDERABAD - A collaboration for "Exploring the SARS-CoV2 inhibitory and/or anti-Covid19 efficacy activities of selected Natural/Ayurvedic/Herbal products/formulations prepared by IMMORTALIGHT LTD." 28th July 2022, 1 year

- JSS ACADEMY OF HIGHER EDUCATION & RESEARCH, MYSURU - A research project to understand the genetic basis of T1D and T2D and for facilitating robust diagnosis of the two common subtypes of diabetes and enabling informed treatment options.19th September 2022, 3 years

- INDIAN INSTITUTE OF TECHNOLOGY, HYDERABAD(IITH) AND HYDERABAD EYE RESEARCH FOUNDATION (HERF)(LVPEI) AND CSIR-CCMB - A research project on Therapeutic potential of decellularized cornea matrix (DCM) hydrogel for corneal scars and stromal replacement in trauma conditions- 26th September 2022, 3 years

- NATIONAL CHEMICAL LABORATORY (NCL)- PUNE & ZEROHARM SCIENCES PVT. LIMITED, HYDERABAD - Licensing the Technology/Know-how for the feasibility evaluation for anti-Cancer drug applications. 17th October 2022, 14 years

- ASHOKA UNIVERSITY, HARYANA - A Collaboration to convenience 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". 25th October 2022, 1 year 7 months

- NATIONAL CENTRE FOR BIOLOGICAL SCIENCES, BENGALURU (NCBS) - A phase -II research project of the Rockefeller foundation grant awarded to CSIR-CCMB-An addendum to the existing MoU dated 21st Sep 2021, 18th November 2022

- THE OFFICE OF THE PROJECT MANAGER, GANGA POLLUTION CONTROL UNIT - UTTAR PRADESH - A Collaboration to conduct environmental surveillance of sewage and waste water by sampling across various locations in prayagraj identified by UPJN and CSIR-CCMB.22nd November 2022, 2 years

- CSIR- INSTITUTE OF GENOMICS & INTEGRATIVE BIOLOGY (IGIB) DELHI - A Collaboration to Undertake a project in the Genomics surveillance program for SARS-CoV2: Consortium of India and Sri Lanka which is being funded by wellcome trust. 25th November 2022

- PASTEUR INSTITUTE, SHILLONG, MEGHALAYA - A Collaboration for conducting studies to understand microbial genomics and their contributions in human infectious diseases under the broader umbrella of financial support to CSIR-CCMB from the Rockefeller Foundation for the project “Setting up pathogen surveillance systems beyond SARS-CoV-2.”16th December 2022, 1 and a half year

- HYDERABAD EYE RESEARCH FOUNDATION (LVPEI) HYDERABAD - A Collaboration for conducting studies to understand microbial genomics and their contributions to ocular diseases and jointly conduct outreach activities under the broader umbrella of financial support to CSIR-CCMB from the Rockefeller Foundation for the project “Setting up pathogen surveillance systems beyond SARS-CoV-2.” 20th December 2022, 1 and half year

- AIIMS BIBINAGAR - A Collaboration related to Environmental surveillance for prevalence of various microbes and AMR grnrs in addition to SARSCoV2 – 2nd December 2022,1 and half year

- VAIDYARATNAM P S VARIER’S ARYA VAIDYA SALA,KOTTAKKAL - A research project related to“Exploring the SARS-CoV-19 inhibitory, and/ or anti-Covid19 efficacy activities of selected Ayurvedic products/ formulations prepared by AVS”, 29th December 2022, 3 years

- PUNE KNOWLEDGE CLUSTER FOUNDATION, PUNE (PKCF) - A Collaboration related toconvenience a consortium of R&D research and clinical institutions to advance pathogen genomics surveillance to track various SARS-CoV-2 variants and accelerate bio informatics and global data sharing as a part pf philanthropic financial support from the rockefeller foundation for the project initially titled as COVID-19. 2nd January 2023, 1 year 5 months

- OSMANIA MEDICAL COLLEGE, HYDERABAD - A Collaboration to follow the objectives as per National Medical Commission(NMC) in order to train the Undergraduate students to attend at least two procedures being performed in the departments & ensure that the objectives are fulfilled and completed during the period. 9th January 2023

- THE WEST BENGAL ZOO AUTHORITY - A Collaboration related to strategies and protocols towards studying wildlife conservation, the major immediate focus being behaviour and landscape ecology of the Himalayan black bear. 12th January 2023, 3 years

- SREE RAGHAVENDRA HOSPITALS PVT.LTD/FERTILITY CENTER, HYDERABAD (SRFC) - A Collaboration related to research work in human fertility sciences. Presently the focus would be towards establishing a blastoid and endometrial organoid based robust cell culture model mimicking embryo implantation events in human development. 23nd January 2023, 3 years

- TELANGANA STATE FOREST DEPARTMENT & WILDLIE RESEARCH AND CONSERVATION - A Collaboration related to all charges related to Wildlife Diagnostic services as specified and carried out by CCMB for cases involving up to 100 samples in a calendar year, that are received from TSFD through a designated authority (DFO/FDOs of TSFD and curator for Nehru zoological park Hyderabad) will not be charged by the CCMB. 27th January 2023, 5 years

- CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD - A Collaboration related toDevelop new genetic diagnostic tests of relevance to India, to promote the NGS based Diagnosis & to develop Knowledge-based mining of the NGS data for genetic correlates of diseases. 30th January 2023, 3 years

- CHELLARAM DIABETES INSTITUTE, PUNE MAHARASHRTA - A Collaboration to understand the genetic basis of T1D and T2D and facilitating robust diagnosis of the two common sub-types of diabetes and enabling informed treatment options.15th February 2023, 2 years

2.2 F Invited Talks

Prof. Satyajit Mayor
NCBS, Bangalore
7th Founder`s day Lecture
The edge of a cell, a living fabric: When Physics meet Biology at the surface of living cells

Dr. Neha Bhatia
Max Planck Institute for Plant Breeding Research, Cologne, Germany
Developmental patterning and morphogenesis in plants

Ms. Uma Magal
Film maker
Documentary movie screening on a story of `Other Kohinoors, The Rocks of Hyderabad` by Rajani Mani followed by discussion with the filmmaker

Dr. Lakshman Sundaram
Deep learning & Artificial Intelligence Research at Illumina, & visiting scholar, Stanford University, USA.
Integrative single-cell analysis of cardiogenesis identifies developmental trajectories and non-coding mutations in congenital heart disease

Dr. Purusharth I Rajyaguru
Associate Professor, Department of Biochemistry, Indian Institute of Science, Bengaluru
How do RNP condensates disassemble?

Prof. T.V. Kattimani
Vice-Chancellor, Central Tribal University of Andhra Pradesh (CTUAP),Vizianagaram
National Education Policy 2020- Equity and Inclusion in Science Education

Dr. Anasuya Chakrabarty
DST-INSPIRE Faculty Fellow, National Institute of Biomedical Genomics (NIBMG), Kalyani, WB
Widespread sex-differences in the multivariate genetic architecture of human complex traits

Dr. J. Mahita
La Jolla Institute for Immunology, California, USA
Investigating biomolecular recognition through an interdisciplinary lens: Lessons from proteins of the immune system

Dr. D. Srinivasa Reddy
Director, CSIR-IICT, Hyderabad
Efforts in Drug Discovery through Natural Products and Silicon-Incorporation Approach

Dr. Ashish A. Malik
University of Aberdeen, UK
From genes to ecosystems: trait-based scaling to link soil microbiomes to carbon cycling under anthropogenic change

Dr. Yamuna Kalyani Mahthiharan
Stanford University School of Medicine, CA, USA
Lipid-dependent gating of G protein coupled inwardly rectifying potassium (GIRK) channels

Dr. Sagar Koduri
Dana Faber Cancer Institute, Harvard Medical School, USA
Positive Selection Screens for Oncoprotein Degraders

Dr. Tanvi Deora
University of Washington, USA
Mechanics and neural control of movement in natural contexts

Prof. Gagandeep Kang
Christian Medical College, Vellore
Typhoid-overlooked and underestimated

Dr. Kundan Sengupta
IISER, Pune
The diverse roles of lamins in the maintenance of chromosomal stability in cancer cells

Dr. Satyanarayan Rao
University of Colorado Denver, Colorado, USA
Transcription Factors and DNA: From Binding to Biomarker

Dr. Priyamvada Acharya
Duke University School of Medicine, USA
The Rise and Spread of OMICRON

Dr. K V Abhinav
University of College of London and Birkbeck, UK
Structural studies on conjugative type IV secretion system

Dr. Shashank Shekhar
Emory University, Atlanta, USA
Depolymerization - the forgotten child of actin dynamics

Dr. K. Thangaraj
Director, CDFD
Ancient DNA - a genetic thread that connects our past and present

Dr. Sandeep Ameta
National Centre for Biological Sciences, Bengaluru
Evolvable synthetic chemical systems

Dr. Shraddha Karve
Ashoka University, Haryana
Evolutionary novelties

Prof. Philip Rosenthal
CCMB Biologue
Antimalarial drug resistance in Africa

Dr. Sourav Kumar Dey
Weill Cornell Medical College, New York, USA
Repurposing riboswitch aptamers for RNA imaging and biosensor applications

Dr. Yuli Xing
Mission Support Specialist, Abcam, USA
Optimisation techniques for ICC & Immunohistochemistry

Prof. Manu Prakash
Stanford University, USA
CCMB Biologue: Topological puzzles in cell biology: How geometry shapes cellular form

Dr. Siva Chavadi (In association with Zelle Biotechnology Pvt Ltd)
New England Biolabs, USA
NEBNext Single Cell/Low Input RNA sequencing

Dr. Sunil K. Sukumaran
Assistant Professor, Nutrition & Health Sciences University of Nebraska–Lincoln, USA
Mucosal immunity at the taste papillae

Dr. Varsha S. Pathare
School of Biological Sciences, Washington State University, USA
Understanding and predicting plant responses to changing climate

Ms. Rajani Mani
A documentary movie screening on a story of `Colonies in Conflict` by Ms Rajani Mani focuses on the state of bees in urban societies followed by discussion on how films can be used for science communication.

Dr. Shirsendu Ghosh
Research Associates, Cornell University, USA
Visualizing the Molecular Process of Life using Super/High-resolution Fluorescence Microscopy and Single Molecule Spectroscopy

Dr. Kaushik Pal
Department of Physics, Iowa State University, USA
Studying single-molecule integrin-tension and DNase activity in invadosome using DNA-based fluorogenic probes

Dr. Paulomi Sanghavi
Wellcome Trust Early Career Fellow @ IIT Bombay
Intracellular Motors and Membranes During Pathogen Infection

Dr. Imtiyaz Yaseen
EMBO Long Term Fellow, University of Edinburgh
Understanding the Role of Epigenetic Mechanisms in Microbial Pathogenesis

Mr. Amit Goswamy
Wildlife biologist and a film-maker
A documentary movie screening on a story of `Environmental Crisis` by Amit Goswamy followed by screening of documentary movie - The Last Tribe.

Dr. Pragya Rashmi
Mental Health Counsellor, CCMB
Orientation session - Mental Health Services at CCMB

Dr. Pravat Kumar Parida
UT Southwestern Medical Center, Dallas, TX, USA
Deciphering the Targetable Metabolic Vulnerabilities in Breast Cancer Brain Metastases

Dr. Shashi Thutupalli
NCBS, Bangalore
CCMB Biologue : Towards a synthetic biology from a physical perspective

Dr. Sravanti Uppaluri
Azim Premji University, Bengaluru
Using a capacities based approach to teach and learn biology in India

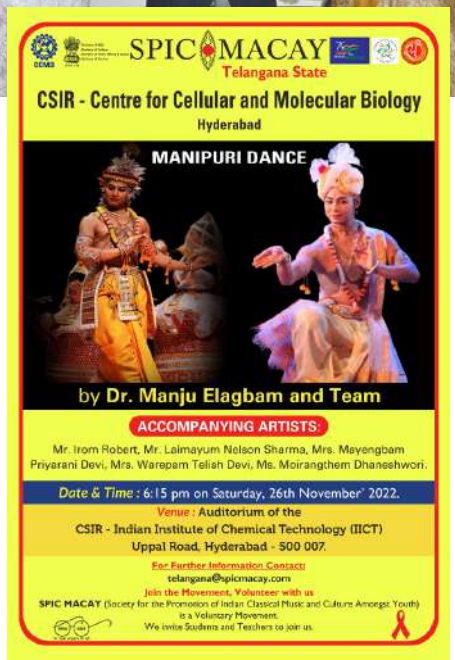
2.2 G Events

Independence Day (August 2022)

CCMB celebrated 76th Independence day on August 15, 2022. Dr. Vinay Nandicoori, Director, CCMB, hoisted the flag and distributed prizes and certificates to staff and students who won in various competitions conducted by CCMB staff club on the occasion of Independence day.

35th CCMB Foundation Day

CSIR-CCMB laboratory complex in the campus at Habsiguda was officially dedicated to the nation and cause of science in the year 1987 on November 26. CSIR-CCMB continues to celebrate this day every year as its Foundation Day. The day is marked by students' symposia in the forenoon and a popular lecture by a distinguished scientist of international repute in the afternoon followed by a cultural program and dinner with all the staff and their families. On November 26, 2022, Prof. Ajay Kumar Sood, Principal Scientific Advisor to Government of India, delivered the 35th Foundation day lecture on *"Nature Inspired Science: Our journey"*. In the cultural program, Manipuri dance was performed by Manju Elangbam and troupe.



Visit of Lt. Governor of Ladakh

Lt. Governor of Ladakh Shri Radha Krishna Mathur visited CCMB on December 14, 2022. The distinguished visitor was taken on a tour to various centralized facilities in CCMB including the NGS facility.

Visit of IAS officers

The 2022 batch of IAS officers visited CCMB on Jan 25, 2023 to understand the capacities and capabilities of research institutes.

CCMB Alumni Meet

CCMB hosted its first alumni meet on February 21, 2023, to build a connect between the current batch of PhD students and its illustrious alumni.There were panel discussions on *non-academic career track* and *academic career track* with alumni as panelists and fresh graduates as moderators.

7th Founder's Day

In remembrance of its Founder-Director Dr. Pushpa M. Bhargava, CSIR-CCMB staff and students celebrate his birthday February 22nd as CCMB-Founder's Day. The proceedings include popular talk by an eminent scientist or a distinguished personality and CCMB student's programme called Sci-Setu where CCMB alumnus are invited to share their journey of success with the PhD students of CCMB. The event is closed with a cultural program followed by contributory dinner for the staff, students and their family members. On February 22, 2023, CCMB invited Prof. Satyajit Mayor, Director, NCBS, to deliver 7th Founder's Day talk. As part of Sci-Setu, Dr Kasturi Mitra, Associate Professor, Ashoka University and Dr G Aneeshkumar Arimbasseri, NII delivered the alumni talks. There was also a panel discussion on Workforce management in Academia.

Visit of Telangana State judges

35 newly appointed judges to the Telangana State visited CCMB via the Telangana State Judicial Academy, to understand how DNA Fingerprinting and wildlife forensics help us in solving conflicts.

2.2 H Science Outreach & Popularization Programs

SciTales by CCMB

It is CCMB's dedicated popular science website that allows our scientists, mostly PhD students as well as those from other research institutes and universities to write about their work or the broader research questions CCMB scientists are working on for general public. In addition, it also hosts interactive science content in form of zines, videos, podcasts, posters, and games/hands-on activities (for classroom settings).

Zines: We made short, crisp and easy to print as well as easy to share digital zines that talk of the research questions underway in the labs of CCMB.

Videos: We have made animation videos to explain the molecular biology research from CCMB labs. In addition, we also made a series of videos in collaboration with Telangana Social Welfare Residential Degree College teachers. The teachers offered us topics for videos of experiments that the undergraduate curriculum prescribes and their students would benefit from knowing but the lack of lab facilities in their colleges restricts them from actually carrying them out. The videos help them get a glimpse of how such experiments are done in reality. In addition, we added a real-life question to each of those videos to make them educational and relatable.

Podcasts: CCMB scientist, Megha Kumar is the advisor for the podcast initiative – India Asks Why, funded by the IndiaBioscience outreach grant. The second season of the series with six episodes was published this year.

Games and hands-on activities: We have developed a module of games and activities that can be used in classroom settings to explain DNA, and processes such as transcription and translation. We have designed a board game, Fastest Protein First to gamify the protein making process in a cell. We have designed activity sheets on building a paper origami model of DNA as well as isolation of DNA using household items.

Teacher Training Workshop

We trained 30 teachers from Telangana state government schools on using our different interactive modules on genes and genetics in their classrooms. In addition, they interacted with CCMB geneticists to understand how the understanding of genes helps us in diagnosing diseases better.

Public Lecture on Human Evolution

To celebrate the 2022 Nobel Prize in Physiology for the discoveries concerning genomes of extinct hominins and human evolution to Svante Pääbo, we organized a public lecture by K Thangaraj to understand the research better.

Study Tours

We welcome schools and colleges across the year to visit our institute's facilities. In 2022-23, around 1100 students visited the campus through the study tours.

Open Day

We celebrated the CCMB Open Day on Sept 26 on the occasion of CSIR Foundation Day celebrations. On this first physical Open Day since the COVID-19 pandemic, the CCMB main campus had 6000 visitors, mostly school students and educators across Telangana and the neighbouring states. The visitors had a chance to interact with CCMB scientists and PhD students to understand and discuss their work. the COVID-19 pandemic, the CCMB main campus had 6000 visitors, mostly school students and educators across Telangana and the neighbouring states. The visitors had a chance to interact with CCMB scientists and PhD students to understand and discuss their work.

CCMB Science Festival

We started the CCMB Science Festival as a dedicated program for engaging the city's college students of science. The festival was attended by 600 students from the city's colleges. The festival not only offered the visiting students a detailed discussion on the research underway in CCMB labs and the tools used but also an opportunity to present their own research in a poster competition.

Participation in Science Festivals

We participated in the India International Science Festival 2022 organized at Bhopal as well as in the India Science Festival 2023, organized at Hyderabad.

Young Innovators Program

More than 200 students registered for the Young Innovators Program. They attended the inaugural session, with a talk by Ullas Kolthur on <> and participated in a selection test. Based on their performance in the test, 30 of them, representing schools of diverse communities, were selected for an intensive week-long program at CCMB. During this week, they visited CCMB labs, performed hands-on experiments and had in-depth discussions on life in science.

Milo CCMB

This is a special program conducted for the Telangana state schools. In 2021-22, the program started for the Telangana Social Welfare Residential Educational Institutes Society (TSWREIS) schools. They are a network of more than 200 schools spread across the state. During that year, we made seven videos covering much of the breadth of the work at CCMB, especially those with established and potential societal impact and circulated those to the schools via their teachers. The students sent us the questions on each topic of the videos, which were shared with the concerned scientists. This was followed by an online session with the scientist where they addressed the questions shared with them previously.

After this priming, based on the performance in a selection test, 30 students were selected to spend a week in CCMB labs in Apr 2022, following a program similar to the Young Innovators Program.

In 2022-23, the program has continued not only with the TSWREIS schools but also the Telengana Tribal Welfare Residential Educational Institutes Society schools.

Praramb

To further improve upon our outreach to rural students of Telangana, we collaborated with Pratham Digital. We shared our DNA-based resources to Pratham, which they circulated with their centres across the state. The middle-school students associated with their centres participated in the activities, and based on their investment in the activities, Pratham selected 50 of them for a 2-day workshop at the centre by CCMB PhD students. Following up on that, Pratham selected 25 students to spend 3 days at CCMB.

Royal Society of Chemistry and CSIR

As a part of CSIR's collaboration with the Royal Society of Chemistry (RSC), we have supported their activities. We hosted RSC's Global Battery Challenge with 50 high school students. We, along with CSIR-IICT and CSIR-NGRI, supported the RSC-Yusuf Hamied Educational Initiative and hosted a residential workshop for high school students. The three institutes brought in the novelty of discussing problems of biology and geophysics in an otherwise chemistry camp, emphasizing on how chemistry is a part of these problems too, and the inter-disciplinarity of scientific pursuits today.

Science Khel Khel Mein

As a part of CSIR's collaboration with the Atal Tinkering Labs, we have worked with one of the ATL schools, the Telangana State Model School, Imampet and hosted a workshop on using Arduino to build devices, as requested by the school. The school has also actively participated in the other outreach programs at CCMB.

World AMR Awareness Week

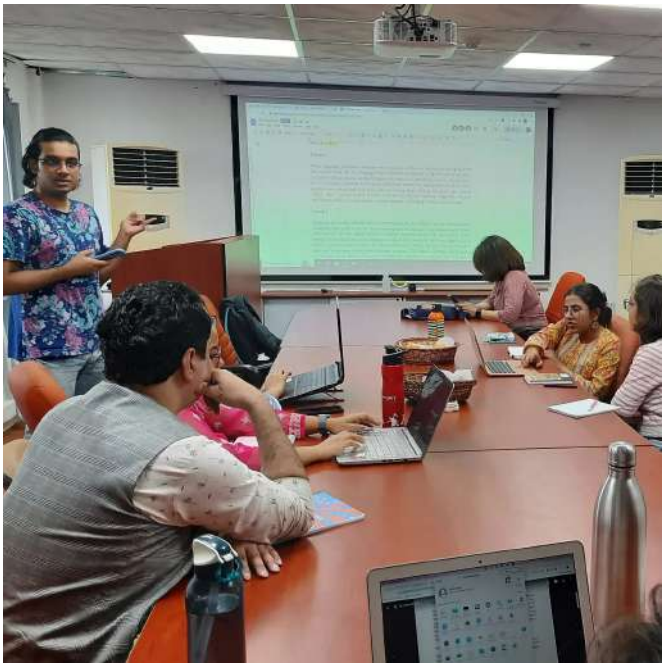
We organized a 3-day workshop for school students on explaining microbes, microbial infections, ways of preventing them and the rise of antimicrobial resistance on the occasion of World Antimicrobial Awareness Week celebrations.

Wildlife Week Celebrations

We celebrated the Wildlife Week with school students by organizing a drawing competition for middle- and high-schoolers, and fancy dress competition for primary school children.

Science Journalism Workshop

We organized an intensive 2-day workshop for our students to introduce them to science journalism. Sayantan Datta from the Krea University and Sandhya Ramesh from The Print were the resource persons for the workshop.



2.2 I Media coverage

16 press notes were sent out in 2022-23 in English, Hindi and Telugu. CCMB is active on social media via Facebook, Twitter, Instagram, LinkedIn and YouTube. It maintains an active connect with journalists, helping a wide coverage of science research at CCMB and discussions inspired from it.

2.2 J Staff, Research Students, Project Staff

(As on 31.03.2023)

SCIENTIFIC RESEARCH GROUPS

A S Sreedhar Group

A S Sreedhar	Senior Principal Scientist
K R Paithankar	Principal Technical Officer
Shrikant Dharaskar	Ph.D. student
Priyadarshini Singh	Ph.D. student
Prateekshya Das	Ph.D. student

Karthik Bharadwaj Group

Karthik Bharadwaj	Scientist
Wasimuddin	Project Scientist-III
Lamuk Zaveri	Project Scientist-II
M. Shivalaxmi	Project Scientist-II
Chandreswara Raju K	Senior Project Associate
Deepak Kumar Kashyap	Senior Project Associate
Surya Narayan Mishra	Senior Project Associate
Priyanka Garg	Senior Project Associate
Sneha N	Project Associate-II
Bishwadeep Singha	Project Associate-II
Payel Mukherjee	Project Associate-II
Jandhyala Sai Krishna	Project Associate-II
Renuga Devi	Project Associate-I
Kottapalli Srividya	Project Associate-I
N Uma Venkata Sai Malini	Project Associate-I
Sreelekshmi M S	Project Associate-I
Gulafsha Khan	Project Associate-I
Himasri B	Project Associate-I
Vodapalli Amareshwar	Project Associate-I
Neha Singh	Project Associate-I
Banda Lavanya	Project Associate-I
Aman Kumar Suryan	Project Associate-I
Rachiraju Hema Sindhuja	Project Associate-I
Victor Banerjee	Project Associate-I
Faisal Irshad	Project Associate-I
R.Ramnivas Bhagat	Project Associate-I
Shalini Kumari	Laboratory Assistant
Priya Pandey	Laboratory Assistant
Gudla Sateesh Kumar	Scientific Admin. Assist.

Venkata R Aditya Chalamcharla Group

Venkata R Aditya C	Senior Scientist
Anubhav Bhardwaj	Sr. Technical Officer (1)
Harsh Kapoor	Ph.D. student
Annapoorna K P	Ph.D. student
Sauvik Dasnaskar	Ph.D. student
Alluri Vaishnav Varma	Ph.D. student

G R Chandak Group

G R Chandak	Chief Scientist
P Ashok	Lab Assistant
Sara Sajjadi	Ph.D. student
Swati Bayyana	Ph.D. student
Sohail Rafik Mansuri	Ph.D. student
Alagu Sankareswaran	Ph.D. student
Seema Bhaskar	Project Manager
Sumit Paliwal	Project Scientist-II
Suraj Singh Nongmaithem	Project Scientist-II
Harsha Lad	Project Scientist-II
Rajnish Kumar Singh	Project Scientist-I
Arumalla Manisha	Project Associate-II
Dimple Lavanuru	Project Associate-I
Korra Bhanu Teja	Project Associate-I
Anushri U	Project Associate-I
Jandhyala Vyshnavi	Project Associate-I
Archana D	Project Associate-I
Jukanti Akshitha	Project Associate-I
Shagufta Tasneem	Project Assistant
Sulgae Sripal	Project Assistant
Punya Sri PSKDB	Project Assistant

Amitabha Chattopadhyay Group

Amitabha Chattopadhyay	CSIR Bhatnagar Fellow
Ashwani Sharma	Ph.D. student
S. Shubhrasmita Sahu	Ph.D. student
Abhishek Kumar	Project Associate-I
Akrati Bhat	Project Associate-I

Ch Mohan Rao Group

Ch Mohan Rao	CSIR-Distinguished Scientist

Saikat Chowdhury Group

Saikat Chowdhury	Senior Scientist
Justus Francis	Ph.D. student
Pathri Achyutha Krishna	Ph.D. student
Palash Kumar Seal	Ph.D. student
Rishav Mitra	Project Associate-I

Mandar V Deshmukh Group

Mandar V Deshmukh	Sr. Principal Scientist
Sneha Paturi	Ph.D. student
Jaydeep Paul	Ph.D. student
Aute Ramdas Annasaheb	Ph.D. student
Debadutta Patra	Ph.D. student
Priti Chanda Behera	Ph.D. student
Supriti Das	Ph.D. student
Nilam Waghela	Ph.D. student

Jyotsna Dhawan Group

Jyotsna Dhawan	Emeritus Scientist
Swetha S	Ph.D. student
Ananga Ghosh	Ph.D. student
Priti A S	Ph.D. student

G Umapathy Group

G Umapathy	Sr. Principal Scientist
Vinod Kumar	Technical Officer
Gopikrishnan P	Ph.D. student
Manisha Ray	Ph.D. student
Manu S	Ph.D. student
Krupa Vinay Teja P	Ph.D. student
G Anusha	Ph.D. student
Neeldeep Ganguly	Project Associate-I
Abhijeet Mondal	Project Associate-I
Reuben Jacob Mathew	Project Associate-I

Ajay Gaur Group

Ajay Gaur	Sr. Principal Scientist
Akshar	Project Associate-I

H H Krishnan Group

H H Krishnan	Sr. Principal Scientist
M Mohan Singh	Technical Officer
Vishal Sah	Ph.D. student
Dixitkumar Nanubhai Tandel	Ph.D. student
P. Sai Poojitha	Ph.D. student
Prangya Paramita Sahoo	Ph.D. student
Ravicanti Abhiram Pooja	Project Associate-I
Aswathi Chandran K V	Project Associate-I
Pragada Rajesh	Project Associate-I

K Thangaraj Group

K Thangaraj	Chief Scientist (on lien)
G Mala	Prl. Technical Officer
S Deepa Selvi Rani	Sr. Technical Officer (3)

Nitin C Tupperwar Group

Nitin C. Tupperwar	Principal Scientist

Arvind Kumar Group

Arvind Kumar	Sr. Principal Scientist
Sachin Singh	Senior Scientist
Annapoorna P Karthyayani	Ph.D. student
Aditya Undru	Ph.D. student
Bhanu Pranav N S	Ph.D. student
Arpan Mukhoti	Ph.D. student
Devika Dnyanraj Mahimkar	Ph.D. student

Dhananjay Chaturvedi Group

Dhananjay Chaturvedi	Senior Scientist
Sarasij Pal	Ph.D. student
Megha Menon	Project Associate-I

Janesh Kumar Group

Janesh Kumar	Sr. Principal Scientist
Sanjay Kumar Suman	Technical Officer
Swathi P	Ph.D. student
Aswini Kumar Gupta	Ph.D. student
Ithayaraja	Prl. Project Associate
Somanath Baral	Project Associate-II

Lekha Dinesh Kumar Group

Lekha Dinesh Kumar	Sr. Principal Scientist
Rohitesh Gupta	Sr. Research Associate

Megha Kumar Group

Megha Kumar	Senior Scientist
Sharda Ravi Iyer	Ph.D. student
Tuhina Prasad	Ph.D. student

Santosh Kumar Group

Santosh Kumar	Senior Scientist
Sitanshu Kumar Sarangi	Ph.D. student
Ketaki Bhagwat	Ph.D. student
Etikala Apoorva	Ph.D. student
Niladri Koner	Project Associate-I
Blessie Rajakumar	Project Associate-I

Mukesh Lodha Group

Mukesh Lodha	Principal Scientist

M Mohammed Idris Group

M Mohammed Idris	Sr. Principal Scientist

Rakesh Kumar Mishra Group

Rakesh Kumar Mishra	AcSIR Distinguished Emeritus Professor
Rashmi Upadhyay Pathak	Sr. Principal Scientist
Phanindhar K	Ph.D. student
Soujanya M S	Ph.D. student
Avvaru Akshay Kumar	Ph.D. student
Saketh Murthy	Ph.D. student
Ravina Saini	Ph.D. student
Sonu Yadav	Ph.D. student
Ashish Bihani	Project Associate-I
Anil Kumar K	Field worker
Runa Hamid	Job contract

N Nagesh Group

N Nagesh	Chief Scientist
Ira Bhatnagar	Principal Scientist
C B Tripura Sundari	Senior Scientist

Vinay K Nandicoori Group

Vinay K Nandicoori	Director
V Purushottam	Technical Officer
Yogita Kapoor	Ph.D. student
Priyadarshini Sanyal	Ph.D. student
Abhishek Saha	Ph.D. student
Amit Chakraborty	Ph.D. student
Sutashree Nath	Ph.D. student
Aruna Panda	Project Manager
Aparna Shenvi	Technical Associate
Asis Kumar Khuntia	Project Associate-II
Sidra Khan	Project Associate-II

P Chandra Shekar Group

P Chandra Shekar	Principal Scientist
Niharika Tiwary	Ph.D. student
M Karthik	Ph.D. student
Elarani Majhee	Ph.D. student
Hanuman Kale	Senior Project Associate
Debabrata Jana	Project Associate-II
Ankita Mishra	Project Associate-I

Anant B Patel Group

Anant B Patel	Chief Scientist
K S Varadarajan	Sr. Technical Officer (1)
Dipak Roy	Ph.D. student
Kamal Saba	Ph.D. student
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
Navleen Kour Anand	Project Associate-I

Hitendra Kumar Patel Group

Hitendra Kumar Patel	Sr. Principal Scientist
Raju Madanala	Sr. Technical Officer (3)
Vinoth Kumar	Technician
Gokulan C G	Ph.D. student
Komal Ashok Awalellu	Ph.D. student
Anjana Sharma	Ph.D. student
Praveen Kumar Nayak	Ph.D. student
Nazia Khatoon	Sr. Project Associate
Maliha A	Sr. Project Associate
Jamaloddin	Sr. Project Associate
Vishnu Narayanan M	Project Associate-II
Rajkanwar Nathawat	Project Associate-I
Jagati Rajasri Anjali	Project Associate-I
Gattu Niranjan	Project Associate-I
Rennya P R	Project Associate-I
Apoorva Masade	Project Associate-I
Devika Talwar	Project Associate-I
Nisha Sao	Project Associate-I
Manchineella Shiva Kumar	Field Assistant
Hemsagar Patel	Field Assistant
Rupdhar Yadav	Field Assistant
Vutukuri Rani	Field Assistant

R Nagaraj Group

R Nagaraj	INSA Senior Scientist

Swasti Raychaudhuri Group

Swasti Raychaudhuri	Principal Scientist
Shemin Mansuri	Ph.D. student
Harshit Vaish	Ph.D. student
Pooja Ramesh Gupta	Ph.D. student
Aanchal	Ph.D. student
Suparna Ghosh	Ph.D. student
Pallavi Rao T	Ph.D. student
Sristi Chakraborty	Project Associate-I

Manjula Reddy Group

Manjula Reddy	Chief Scientist
G S N Reddy	Prl. Technical Officer
Shambhavi Garde	Ph.D. student
Moneca Kaul	Ph.D. student
G Bhargavi Krishnasree	Ph.D. student
Suraj Kumar Meher	Ph.D. student
Vaidehi Mihir Rajguru	Ph.D. student
Nallamotu Krishna Chaitanya	Ph.D. student
Stuti Chatterjee	Ph.D. student
Debnita Mongal	Ph.D. student
Loka Ram Prasad	Ph.D. student**
Pradyumna Swanand Paranjape	Ph.D. student**
Balaji Venkataraman	Prl. Proj. Associate
Nilanjan Som	Prl. Proj. Associate
Raj Bahadur	Sr. Project Associate
Khatal Anil Gyndyaba	Project Associate-I
Syeda Meher Fatima	Laboratory Assistant

**co-guide

Kumaraswamy Regalla Group

Kumaraswamy Regalla	Senior Scientist
R Abishek Bharadwaj	Ph.D. student
Priyanka Pant	Ph.D. student
Disha Nanda	Ph.D. student
Jyothi K C	Project Associate-I

Rajan Sankaranarayanan Group

Rajan Sankaranarayanan	Outstanding Scientist
P Shobha Krupa Rani	Sr. Principal Scientist

Biswajit Pal	Principal Scientist
P Sambhavi	Sr. Technical Officer (1)
Jotin Gogoi	Project SRF
Sudipta Mondal	Ph.D. student
Pradeep Kumar	Ph.D. student
Sakshi Shambhavi	Ph.D. student
Koushick S	Ph.D. student
Mukul J S	Ph.D. student
Santhosh K	Ph.D. student
Suhail Madhar Hanif S	Ph.D. student
Nisha Gupta	Ph.D. student
Sai Uday Kiran P	Ph.D. student**
Bapin Kumar Panda	Project Associate-I
R R Viola Valamathi	Project Associate-I
Nikita Shukla	Project Associate-I
Pujaita Banerjee	Project Associate-I

**co-guide

Imran Siddiqi Group

Imran Siddiqi	CCMB Emeritus Scientist
Sivakumar P	Ph.D. student
Ginkuntla Saikiran Goud	Ph.D. student
Kaladhar Bethoju	Job Contract

Puran Singh Sijwali Group

Puran Singh Sijwali	Senior Principal Scientist
Deepak Kumar	Ph.D. student
Srinivas Reddy G	Ph.D. student
Somesh Machhindra G	Ph.D. student
Kanika Saxena	Ph.D. student
Manash Kumar Behera	Ph.D. student
Pritam Das	Ph.D. student
Pragati Patra	Ph.D. student
Zeba Rizvi	Project Associate-II
Kajal Pandey	Project Associate-I

Divya Tej Sowpati Group

Divya Tej Sowpati	Scientist
Nitesh Kumar Singh	Sr. Technical Officer (1)
Partheusa Machha	Ph.D. student**
Sofia Banu	Ph.D. student
Arvind Kumar	Ph.D. student
Avvaru Akshay Kumar	Project Associate-II
Onkar Vasantrao Kulkarni	Project Associate-II
Priya Singh	Project Associate-I
Thota Kiran	Project Associate-I
Sangepu Jyothi	Laboratory Assistant

** Joint student with Dr K Thangaraj

Ghanshyam Swarup Group

Ghanshyam Swarup	INSA Senior Scientist
Swetha Medchalmi	Project Scientist-I

Raghunand R Tirumalai Group

Raghunand R Tirumalai	Principal Scientist
Ravi Prasad Mukku	Ph.D. student
Korak Chakraborty	Ph.D. student
Simran Sharma	Ph.D. student
Muskan Gupta	Project Associate-I
Jennifer Albert	Project Associate-I

Shrish Tiwari Group

ShrishTiwari	Senior Principal Scientist
Prachi Singh	Senior Scientist
P Ramesh	Prl. Technical Officer
Deepti Rao	Ph.D. student
Tummala Nikhila Sai	Project Associate-I

Karthikeyan Vasudevan Group

Karthikeyan Vasudevan	Chief Scientist
B Sambasiva Rao	Principal Scientist
S Harika	Sr. Technical Officer (1)
K Rajya Lakshmi	Sr. Technical Officer (1)
Afsar Sogra	Lab Assistant
Ravi Kumar Singh	Ph.D. student
Gayathri Sreedharan	Ph.D. student
Avni Blotra	Ph.D. student
Alka Sahu	Ph.D. student
Yashwant Singh Panwar	Ph.D. student
Snehalatha Vadigi	DST Inspire Faculty
Ranjit Kumar Sahoo	DST Inspire Faculty
Biswajita Swain	Proj. Technical Assistant
Swapnil Kiran	Project Associate-I
Naveen Kumar C	Project Associate-I
Mubashir Majid Dar	Project Associate-I
Neha Sharma	Project Associate-I
Siripuram Srinivas	Field Assistant

P Anuradha Reddy Group

P Anuradha Reddy	Principal Scientist
Simran Singh	Project Associate-I

V Radha Group

V Radha	Emeritus Scientist

Vasant Shinde Group

Vasant Shinde	CSIR Bhatnagar fellow
Nagarjuna Pasupuleti	Senior Project Associate
Ganesh Bhongale	Project Associate-II
Garima Singh	Project Associate-I
E R Divya Jyothi	Scientific Admin. Assist.

Pavithra Chavali Group

Pavithra Chavali	Senior Scientist
Sourav Ganguli	Ph.D. student

Deena T David	Ph.D. student
Dhruv Kumar Shakyawar	Prl. Proj. Associate
Aswathy G Krishnan	Project Associate-II

Ishwariya Venkatesh Group

Ishwariya Venkatesh	Senior Scientist
Yogesh Sahu	Ph.D. student
Anisha S Menon	Ph.D. student
Manojkumar K	Senior Project Associate

Sonal N Jaiswal Group

Sonal N Jaiswal	Senior Scientist
Nandan J	Ph.D. student
K Aishwarya Arun	Ph.D. student
Priyanka Pandey	Ph.D. student
Sachin Gupta	Ph.D. student
Reshmi Varghese	Senior Project Associate

B Kiran Kumar Group

B Kiran Kumar	Senior Scientist
Hariharan K	Project Associate-I
Khyathi Ratna P	Project Associate-I
Jessie Thomas	Project Associate-I
Nehal Goyal	Project Associate-I
Yogesh Sardana	Project Associate-I

Meghna Krishnadas Group

Meghna Krishnadas	Senior Scientist
Vinayak Prakash Saini	Ph.D. student
Rishiddh Jhaveri	Ph.D. student
Shubham	Ph.D. student
Mustaqeem Ahmad	SERB National PDF
Souparna Chakrabarty	Sr. Project Associate
Devi Tejaswini	Project Associate-I
Bandaru Peddiraju	Project Associate-I
Athulya A	Field worker
Rashmi Rai	Field worker

Jahnavi Joshi Group

Jahnavi Joshi	Senior Scientist
Aditi	Ph.D. student
Abhishek Gopal	Ph.D. student
Pragyadeep Roy	Ph.D. student
Nehal Gurung	Ph.D. student
Maya Manivannan	Project Associate-I
Payal Dash	Proj. Technical Assistant

Sriram Varahan Group

Sriram Varahan	Senior Scientist
Dhrumi Miteshkumar Shah	Ph.D. student
Nivedhitha R	Project Associate-I
Avanti	Project Associate-I

Santosh Chauhan Group

Santosh Chauhan	Sr. Principal Scientist
Jagamohan Chhatai	Sr. Technical Officer (1)
Vennela Ambadas Nampalli	Ph.D. student
Soumya Kundu	Project Associate-II

S&T Resource Group

P Kavin Kennady	Sr. Principal Scientist
V Vijaya Bhaskar	Sr. Principal Scientist
Suman Siddharth Thakur	Principal Scientist
Manoj Kumar Balyan	Senior Scientist
S Thanumalayan	Sr. Technical Officer (3)

Innovation Cell

A Vijaya Lakshmi	Sr. Principal Scientist
Y V Subbalakshmi	Sr. Technical Officer (3)
Hemalatha	Senior Steno
Y Raghavendra Babu	Technician (1)
K Srinath	Lab Attendant (2)

CCMB-Atal Incubation Centre

N Madhusudhana Rao	Chief Executive Officer
Ramjee Pallela	Chief Operating Officer
Ritika Marrampalli	Comm. Manager
Ashish Kumar Perukari	Manager – Technology & Innovations

TECHNICAL GROUPS

RESEARCH FACILITIES

Animal House

M Jerald Mahesh Kumar	Sr. Principal Scientist
N Sairam	Technical Officer
S Prashanth	Technician (2)
M Nageswara Rao	Lab Assistant
K Raju	Lab Assistant
M Rajeshwari	Multitask Staff
Lalaiah B	Job contract
Pacha Ravi	Job contract

BSL 2/3 facility

Amit Kumar	Technical Officer

Diagnostics Facility

M K Kanakavalli	Sr. Technical Officer (1)

Drosophila Facility

V Bharathi	Sr. Technical Officer (3)
K Ramachandra Rao	Sr. Technical Officer (2)

Imaging Facility

Nandini Rangaraj	Chief Scientist
Nitla Venkata Mahesh	Scientist
C Subbalakshmi	Prl. Technical Officer
G Srinivas	Sr. Technical Officer (2)
T Avinash Raj	Sr. Technical Officer (1)
Suman Bhandari	Technical Officer

Integrated Structural Biology Facility

Shiv Pratap Singh Yadav	Scientist
Ravikumar Reddi	Scientist
R Rukmini	Prl. Technical Officer
A Harikrishna	Sr. Technical Officer (2)
Sandeep Shrivastava	Sr. Technical Officer (1)
R Phanindranath	Sr. Technical Officer (1)
K Mallesham	Technical Officer

Next Generation Sequencing Facility

Mohammad Jafurulla	Sr. Technical Officer (2)
A Sreenivas	Sr. Technical Officer (2)
Tulasi Nagabandi	Sr. Technical Officer (2)

Proteomics Facility

V Krishna Kumari	Prl. Technical Officer
B Raman	Prl. Technical Officer
Y Kameshwari	Prl. Technical Officer
K Ranjith Kumar	Technical Assistant

Tissue Culture Facility

Zareena Begum	Prl. Technical Officer
V R Sundareswaran	Prl. Technical Officer
B V V Pardhasaradhi	Prl. Technical Officer
D Parthasarathi	Sr. Technical Officer (2)
M Sanjeev Chavan Naik	Technical Officer
S Easra	Senior Technician (2)
T Dayakar	Lab Assistant

Transgenic Knockout Facility

B Jyothi Lakshmi	Sr. Technical Officer (2)
S Purnima Sailasree	Sr. Technical Officer (2)
Asha Kumari	Sr. Technical Officer (1)

Wildlife Forensics Facility

O V Padmalatha	Sr. Technical Officer (2)
B Kranthi	Sr. Technical Officer (1)

Zebrafish Facility

M L Arvinda Swamy	Sr. Technical Officer (1)

SUPPORT FACILITIES

Academic Cell

Manjula Reddy	Dean, Academic Affairs
H H Krishnan	AcSIR coordinator
S Madhuri	I/c Academic Cell
V Anitha	Project Assistant
S Ramya	AcSIR Executive Assistant

Business Development, Human Resources & Documentation Group

Archana B Siva	Sr. Principal Scientist
R Leela Kumari	Prl. Technical Officer
Divya Singh	Sr. Technical Officer (2)
K Anitha	Technician (1)
Viswajit Mulpuru Senior	Project Associate
Arti Manoharbhai Patel	Project Associate-I
Nahid Anjum	Project Associate-I
Yogesh Lakshmirajama B	Project Associate-I
Sushmitha Raj Nitta	Project Associate-I
Varnali Acharya	Project Associate-I

Engineering Services

G C Thanu	Senior Suptd. Engineer
Ch Bikshamaiah	Senior Suptd. Engineer
G Rajendra Prasad	Senior Suptd. Engineer
Devidas M Nikhar	Suptd. Engineer
B Vijaya Kumar	Executive Engineer
K Nagendrababu	Executive Engineer
A Varaprasada Rao	Executive Engineer
V Prabhakar	Senior Technician (2)
Ch Ravindra Babu	Senior Technician (2)
M Tirumala Rao	Senior Technician (2)
Ananda S Pahurkar	Senior Technician (2)
A J Narsing Rao	Senior Technician (2)
K Shankar	Senior Technician (1)
D Vinod Kumar	Technician (1)
L Kumar	Technician (1)
Anirban Adhikari	Technician (1)
Mallikanti Srinu	Technician (1)
Suresh Babu Mareedu	Technician (1)
S Venkata Sastry	Lab Assistant
T Venkateswara Rao	Lab Assistant
M Mazhar Ali	Lab Assistant
K Nagabhushanam	Lab Assistant
Syed Khundmier	Lab Assistant
C Rosaiah	Lab Assistant
V Shankar Rao	Lab Assistant
B Satyanarayana	Lab Assistant
T Sambasiva Rao	Lab Attendant (2)
G Ramesh	Job contract

Fine Biochemicals
Kishore Joshi Prl. Technical Officer
Syed Sayeed Abdul Lab Attendant

Information Technology (IT) Group
Geetha Thanu Sr. Principal Scientist
Sublari Balaraju Principal Scientist
Aparna Kumari Senior Scientist
Biswajit Roy Scientist
P Nagalinga Chary Prl. Technical Officer
P Radhakrishna Murthy Prl. Technical Officer
K Sambasiva Rao Sr. Technical Officer (3)
N Siva Rama Prasad Sr. Technical Officer (3)
A Padmavathi Devi Sr. Technical Officer (3)
S Mahalingam Sr. Technical Officer (3)
K Ramachary Sr. Technical Officer (2)
Sreekanth Mamidala Sr. Technical Officer (1)
M Srinivasa Rao Lab Assistant

Instrumentation Group

N Ravindra Chakravarthi	Sr. Technical Officer (3)
U S T R B Bapi Raju	Prl. Technical Officer
Dattatrya N Gurkhel	Sr. Technical Officer (3)
K Sanjeev Kumar	Sr. Technical Officer (2)
A Syam Kumar	Sr. Technical Officer (2)
A Bala Murugan	Sr. Technical Officer (1)
Sudatt T Tambe	Sr. Technical Officer (2)
Devender Sundi	Sr. Technical Officer (1)
Chetan R Khapekar	Technical Officer
Amol Mandlik	Technical Assistant
Angothu Ramesh	Technical Assistant

Laboratory Technical Services & Horticulture

K Lakshmi Rao	Chief Scientist
Mani Ramana Rao	Senior Stenographer
P Gyaneshwar	Lab Assistant
L Laxman Dora	Lab Assistant
M A Jaleel	Lab Assistant
B Sanjeeva Rao	Lab Assistant
M M Rajendran	Job contract

Planning, Monitoring and Evaluation (PME)

M R Vishnu Priya	Chief Scientist
B V Ramakrishna	Prl. Technical Officer
Y Sujatha	Prl. Private Secretary
Gulzar Khan	Lab Attendant (2)
Venkata Charan Kumar B	Job contract

Research Grants Office

Sravanti Vaidya	Project Scientist –III
M B Madhavi	Sr. Technical Officer (2)
Chivukula Pavani	Scientific Admin. Assist.
R Srinivasachary	Scientific Admin. Assist.

Science Communication & PR

B V Ramakrishna	Public Relations Officer
Somdatta Karak	Science communication & Outreach Officer
Bharath Kumar Atthe	Senior Project Associate

ADMINISTRATION & MANAGEMENT

Director's Office

Vinay K Nandicoori	Director
D Lavanya	Sr. Technical Officer (3)
B V N Naveen Kumar	Sr. Technical Officer (1)
K Lakshmi Rao	Chief Scientist
S Madhuri	Staff Officer & I/c. Academic Cell
Somdatta Karak	Science Communications & Public Outreach Officer

Administration

Sailaja Maddaly	Controller of Administration
Chandan Kumar	Administrative Officer
J Venu	I/c Transport
Noopur Rani Prasad	Hindi Officer
M Vanisree	Principal Private Secretary
S Kanchanamala	Section Officer (G)
N C Vamshi Krishna	Section Officer (G)
KKVSS Sreedevi	Section Officer (G)
K Madhavi	Receptionist
Ram Gopal	Asst. Section Officer (G)
Manju Singh	Asst. Section Officer (G)
Maqsood Ali	Asst. Section Officer (G)
T Rajani	Asst. Section Officer (G)
Ch Sridevi	Asst. Section Officer (G)
N K Naveen Kumar	Private Secretary
Abdul Raheem Qureshi	Sr. Secretariat Assistant (G)
Ashok Kumar Swasani	Sr. Secretariat Assistant (G)
Savita Kumari	Junior Hindi Translator
Ambe Naveen Kumar	Jr. Secretariat Assistant (G)
Mohd Pasha	Senior Technician (2)
M Devendra Nath	Senior Technician (2)
D Ramesh	Senior Technician (2)
Mahender Vynala	Technician (1)
Mohd Gazanfar Ali	Lab Assistant
K Krishnamacharyulu	Lab Assistant
Ch Chandrashekar	Lab Assistant
S Yadaiah	Lab Assistant
Savitri Luhura	Lab Assistant
M Sharada	Bearer (Adm)
K Satyanarayana	Job contract
Ambepu Kavitha	Project Assistant

Finance & Accounts

Kolla Ramesh	Controller of Finance & Accounts
K Sudhakar	Section Officer (F&A)
M V Subba Rao	Senior Stenographer
V V L Prasanna	Asst. Section Officer (G)
Vimala Prakash	Asst. Section Officer (F&A)
P L Janaky	Asst. Section Officer (F&A)
G Anuradha	Sr. Secretariat Assistant
W Sudhakar	Senior Technician (2)
M Vishnu Yadav	Technician (1)
K Venkateshwarulu	Lab Assistant

Stores & Purchase

S Gnanaprakasam	Sr. Controller of Stores & Purchase
G Sainadh	Private Secretary
K L Kavitha	Private Secretary
S Aruna	Asst. Section Officer (S&P)
S S Lakshmi	Sr. Secretariat Assistant (S&P)
N S Sandeep Kumar	Sr. Secretariat Assistant (S&P)
D Balaji Prasad	Senior Technician (2)
S Riyasat Ali	Senior Technician (2)
Preethi Arjunan	Jr. Secretariat Assistant (S&P)
Mohd Yakub Akheel	Lab Attendant (2)

Medical Services

V Venugopal Rao	Medical Officer
Madhurakavi Sahithi	Medical Officer
T Nagalakshmi	Sr. Technical Officer (1)
A Mahesh	Technical Officer
U V Sitaramamma	Senior Technician (2)
G Sujatha	Job contract
Nusrath Banu	Job contract

Security

C V Tirumala Rao	Senior Security Officer
Raveendra Kumar KVVS	Senior Security Officer*

* On deputation

Guest House

Anil Kumar Sahu	Principal Technical Officer
G Christy Wilson	Senior Technician (3)
Benedict	Senior Technician (2)
K Ramesh Babu	Senior Technician (2)
Mohd Jaffar	Lab Assistant

Canteen

Vikram Kumar	Sr. Technical Officer (1)
M Venkatesan	Senior Technician (2)
N Aruna	Lab Assistant
R Suresh Kumar	Lab Assistant

2.3 JONAKI-BRIT/DAE ^{32}P Labelled Biomolecules Laboratory

The Labelled Biomolecules Laboratory, Regional Centre (RC), Jonaki, Board of Radiation & Isotope Technology (BRIT), Department of Atomic Energy, situated in the Centre for Cellular & Molecular Biology (CCMB) campus is serving the various national laboratories, universities, industrial research centres, and hospitals involved in biotechnology, agriculture, life sciences & medical research by providing ^{32}P labelled nucleotides since 1988.

We supply ^{35}S labelled amino acids and a range of 99m Tc-radiopharmaceutical cold kits produced at Radiopharmaceutical laboratory of BRIT in Mumbai. Cold kits are for use in conjunction with 99m Tc-Pertechnatate, in imaging of human organs for diagnosis and treatment, to the nuclear medicine centres of the hospitals and diagnostic centres in and around Andhra Pradesh. In order to expand the service we will soon begin supply of 99m Tc sodium pertechnetate from radio-pharmacy laboratory at RC, JONAKI.

JONAKI, BRIT has a patented FRET based qPCR chemistry which has been validated. Real time M.tb detection kit based on the above FRET technology have been developed and clinically evaluated in collaboration with Nizam's Institute of Medical Sciences (NIMS), Hyderabad. Proto type kits are under evaluation before they are introduced as regular products. We supply Taq DNA polymerase, PCR master mix, and DNA Isolation kits across the country on a regular basis.

LIST OF PRODUCTS

RADIOACTIVE BIOCHEMICALS

1. ^{32}P Nucleotides:

CODE	PRODUCT
101	[γ ^{32}P] ATP
102	[α ^{32}P] dCTP
103	[α ^{32}P] dATP
104	[α ^{32}P] dGTP
106	[α ^{32}P] ATP
107	[α ^{32}P] GTP
108	[α ^{32}P] UTP
109	[α ^{32}P] CTP
1010	[3'5'- α ^{32}P] pCP
1011	[γ ^{32}P] GTP
LCP 32	[32P]-Orthophosphoric acid

The above products are available in two formulations (dry ice and ambient temperature shipments) fortnightly.

2. ^{35}S Amino acids:

CODE	PRODUCT
LCS 1/LCS 2	^{35}S Methionine
LCS 3	^{35}S Cysteine
LCS 7	^{35}S Methionine-Cysteine mix Eleg mix
LCS 6	^{35}S Glutathione
LCS 8	Protein *in vivo* twin label mix

NON-RADIOACTIVE BIOCHEMICALS

CODE	PRODUCT
LCK-1	Nick Translation Kit
LCK-2	Random Primer Kit
LCK-1601	dNTP mix for PCR (1 set of 4 dNTPs in 4 x 25 µl)
LCK-1602	dNTP mix for PCR (3 set of 4 dNTPs in 4 x 25 µl)
LCK-1603	dNTP mix for PCR (5 set of 4 dNTPs in 4 x 25 µl)
LCK-1604	dNTP mix for PCR (10 set of 4 dNTPs in 4 x 25 µl)
LCE-101	Taq DNA Polymerase Enzyme (100 Units)
LCE-102	Taq DNA Polymerase Enzyme (250 & 500 Units)
LCE-103	Taq DNA Polymerase Enzyme (1000-4000 Units)
LCE 104	Taq DNA Polymerase Enzyme (5000-50000 Units)
LCE 105	Taq DNA Polymerase Enzyme (60000 up to 90000 Units)
LCE 1000	Bulk packs more than 100000 units on enquiry

PMX 01	PCR Master Mix [100 Rxn (2 x 50)]
PMX 02	PCR Master Mix [250 Rxn (5 x 50)]
PMX 05	PCR Master Mix [500 Rxn (5 x 100)]
PMX 10	PCR Master Mix [1000 Rxn (5 x 200)]
PMX 1000	PCR Master Mix (On enquiry)
LCK1701	*M.tuberculosis* PCR detection kit (25 reaction kit)
LCK 1702	*M.tuberculosis* PCR detection kit (50 reaction kit)
LCK 20	Genomic DNA Isolation kit (50 reaction kit)
LCK 21	Genomic DNA Isolation kit (100 reaction kit)
LCK 22	DNA Isolation kit (Plasmid) (50 reaction kit)
LCK 23	DNA Isolation kit (Plasmid) (100 reaction kit)
LCK 24	DNA Gel Purification kit (50 reaction kit)
LCK 25	DNA Gel Purification kit (100 reaction kit)
LCK 26	PCR Product Purification kit (50 reaction kit)
LCK 27	PCR Product Purification kit (100 reaction kit)

Staff of JONAKI (as on 31-03-2020)

1. Ms Papia Hazra, OIC, RC HYDERABAD
2. Dr B.R. Varma, Manager
3. DR. T.K. Sankaranarayan, Manager
4. Mr N. Ambedkar
5. Mr M. Srineevasulu
6. Mr S. Srikanth
7. Mr T.K. Sudhir
8. Ms T. Raja Rajeswari
9. Mr M.B. Kumbhar10. Mr P.B. Morey
11. Mr Jagdish Chandra
12. Mr S. Venkatesh
13. Mr Yakub Ali

Order for all products can be directly placed with:
OFFICER-IN-CHARGE,
REGIONAL CENTRE, JONAKI,
BRIT, CCMB CAMPUS, UPPAL ROAD,
HYDERABAD-500 007

E mail: rcrhyderabad@britatom.gov.in