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CSIR-CCMB

CENTRE FOR CELLULAR AND MOLECULAR BIOLOGY,
HYDERABAD

CONTENTS

DIRECTOR'S FOREWORD

VINAY KUMAR NANDICOORI
DIRECTOR, CCMB

वार्षिक प्रतिवेदन 2021-22 की प्रस्तावना लिखते हुए मुझे अत्यंत खुशी हो रही है। हमारे पहले प्रधान मंत्री, पंडित नेहरू ने कहा था, "विज्ञान केवल एक व्यक्ति की सत्य की खोज नहीं है; अगर यह समुदाय के लिए काम करता है तो यह उससे कहीं अधिक है। सीसीएमबी(CCMB) की स्थापना 1 अप्रैल, 1977 को हमारे संस्थापक निदेशक डॉ. पुष्पा मित्रा भार्गव द्वारा क्षेत्रीय अनुसंधान प्रयोगशाला, RRL, जिसे अब आईआईसीटी(IICT) कहा जाता है, की जैव रसायन के भीतर की गई थी। जिस भवन में हम काम कर रहे हैं, उसका उद्घाटन 26 नवंबर, 1987 को हुआ था। संस्थापक निदेशक, डॉ. पुष्पा भार्गव का दृष्टि बुनियादी आणविक जीव विज्ञान अनुसंधान में सबसे आगे एक संस्थान स्थापित करना है। इस तरह की महत्वाकांक्षी दृष्टि को पूरा करने के लिए अत्याधुनिक सही सुविधाओं की उपलब्धता की आवश्यकता होती है। इसके लिए स्ट्रक्चरल बायोलॉजी, प्लांट रिसर्च, सेल बायोलॉजी, डेवलपमेंटल बायोलॉजी, इकोलॉजी एंड कंजर्वेशन, और इंफेक्शियस डिज़ीज़ बायोलॉजी जैसी विविध विशेषज्ञता वाले वैज्ञानिक एक छत के नीचे हैं। इस वर्ष हमने अत्याधुनिक क्रायो-इलेक्ट्रॉन माइक्रोस्कोपी सुविधा की स्थापना की है, जिसका उद्घाटन सीएसआईआर-महानिदेशक डॉ. शेखर मांडे ने किया। अत्यधिक कुशल और समर्पित कर्मचारियों द्वारा अनुरक्षित केंद्रीकृत सुविधाओं वाले संस्थानों में सीसीएमबी अद्वितीय है।

हमने सदी में एक बार आने वाली महामारी के कारण संक्रमण की दूसरी और तीसरी लहर देखी है जिसने पिछले दो वर्षों से दुनिया को अपनी चपेट में ले रखा है। मैं डेल्टा वैरिएंट की वजह से दूसरी लहर के बीच में सीसीएमबी में शामिल हुआ, जिससे हमारे देश को भारी नुकसान हुआ। हममें से कई लोगों ने अपने कुछ सहयोगियों सहित अपने प्रियजनों को खो दिया। संभवतः दूसरी लहर के बाद हाइब्रिड प्रतिरक्षा और पूरे भारत में व्यापक टीकाकरण के कारण, SARS-nCOV2 के ओमिक्रॉन वैरिएंट के कारण होने वाली महामारी की तीसरी लहर दूसरी लहर की तुलना में बहुत हल्की थी। महामारी का सबसे बुरा समय हमारे पीछे है, और हम धीरे-धीरे सामान्य स्थिति की ओर बढ़ रहे हैं। महामारी के दौरान सीसीएमबी के योगदान पर गर्व करने के हमारे पास कारण हैं। हमने नया ड्राई स्वैब डायग्नोस्टिक तरीका विकसित किया , एक mRNA वैक्सीन प्लेटफॉर्म स्थापित किया है, और सीवेज, सीरो- और जीनोमिक सर्विलांस गतिविधियों में बड़े पैमाने पर शामिल हैं। हमने विभिन्न कंपनियों के लिए कई दवाओं का परीक्षण भी किया है, और सीसीएमबी द्वारा परीक्षण किए गए अणुओं में से एक, 2-डीऑक्सी-डी-ग्लूकोज (2-डीजी), अब व्यापक रूप से उपलब्ध है। सीसीएमबी SARS-nCOV2 के खिलाफ पहले थेरप्यूटिक एंटीबॉडी के विकास में भी शामिल था।

परीक्षण के समय के बावजूद, सीसीएमबी के वैज्ञानिकों ने जीव विज्ञान में सबसे उत्कृष्ट काम किया है, जो Science Advances, eLife, PNAS, EMBO J, और कई अन्य पत्रिकाओं में उत्कृष्ट प्रकाशनों में परिलक्षित है। डॉ. राजन शंकरनारायणन को ईएमबीओ के सहयोगी सदस्य के रूप में चुना गया। डॉ. चांडक के शोध को चिकित्सा विज्ञान में सन-फार्मा रिसर्च फाउंडेशन अवार्ड और प्रतिष्ठित जेसी बोस फेलोशिप से सम्मानित किया गया। डॉ अमित चट्टोपाध्याय और डॉ वसंत शिदे को भटनागर फैलोशिप से सम्मानित किया गया है। डॉ. दिव्या तेज सौपति सीएसआईआर-युवा वैज्ञानिक अवार्ड प्राप्तकर्ता है। इसके अलावा, सीसीएमबी के छात्रों ने विभिन्न भाषण पुरस्कार, सर्वश्रेष्ठ पोस्टर पुरस्कार और फेलोशिप जीते हैं। सभी सदस्य और छात्र पुरस्कार विजेताओं को बधाई। डॉ. सैकत चौधरी, जो क्रायो-ईएम का उपयोग करके सेल में साइटोस्केलेटल नेटवर्क के नियमन के आणविक आधार को समझने पर काम करते हैं, मई 2022 में सीसीएमबी में शामिल हुए। हम संगठित आउटरीच गतिविधियों के साथ भारत में बहुत कम संस्थानों में से हैं। इन गतिविधियों का विस्तार ओपेन डे से होता है, जो ऑनलाइन आयोजित किया गया इस साल और ऐसे कार्यक्रमों जिसमें स्कूली बच्चों द्वारा सीसीएमबी में एक सप्ताह या पंद्रह दिन बिताना शामिल है। हम उन कुछ सीएसआईआर संस्थानों में से हैं, जिनके पास इनक्यूबेशन सेंटर है - अटल इनक्यूबेशन सेंटर (एआईसी)। एआईसी-सीसीएमबी अपने पांचवें वर्ष में है, और 70 से अधिक स्टार्टअप सफलतापूर्वक केंद्र से गुजरे हैं।

संयुक्त राज्य अमेरिका में 4,651 की तुलना में भारत में प्रति 1,000,000 पर 140 शोधकर्ता हैं। देश के लिए विकास एक बड़ा अवसर है, और मुझे यकीन है कि आने वाले दशक में हम सभी इसका हिस्सा होंगे। हमारे मुख्य क्षेत्रों में आगे बढ़ते हुए उच्च गुणवत्ता वाले वैज्ञानिकों की भर्ती करके अनुसंधान को मजबूत करना आवश्यक है। कई क्षेत्रों में हमारी निपुणता को देखते हुए, व्यक्तिगत रूप से हमसे परे वैज्ञानिक समस्याओं को सहयोग करने और हल करने का एक सुनहरा अवसर है। हम आने वाले वर्षों में कई और उच्च-गुणवत्ता वाले प्रकाशनों, सम्मानों और पुरस्कारों की प्रतीक्षा कर रहे हैं।

It is my pleasure to write the foreword for the Annual Report 2021-22. Our first Prime Minister, Pandit Nehru, had stated, "Science was not merely an individual's search for truth; it was something infinitely more than that if it worked for the community." CCMB was established on Apr 1st, 1977, within the Biochemistry of Regional Research Laboratory, RRL, now called IICT, by our Founder Director Dr. Pushpa Mittra Bhargava. This building that we are working at was inaugurated on Nov 26th, 1987. The vision of the Dr. Pushpa Bhargava, was to establish an institute at the forefront of basic molecular biology research. Fulfilling such an ambitious vision requires the presence of state-of-the-art high-end facilities. Scientists with varied expertise such as Structural Biology, Plant Research, Cell Biology, Developmental Biology, Ecology and Conservation, and Infectious Disease Biology are under one roof. This year we have established a cutting-edge cryo-electron microscopy facility, which CSIR-Director General Dr. Shekhar Mande inaugurated. CCMB is unique among the institutions in having centralized facilities maintained by highly skilled and dedicated staff.

We have seen second and third waves of infection caused by a once-in-a-century pandemic that has engulfed the world for the past two years. I joined CCMB in the middle of the second wave caused by the Delta variant, which impacted our country hugely. Many of us lost our near and dear ones, including some of our colleagues. The third wave of the pandemic caused by the Omicron variant of SARS-nCOV2 was much milder than the second wave, likely due to the hybrid immunity after the second wave and extensive vaccination across India. The worst of the pandemic is likely behind us, and we are slowly limping toward normalcy. We have reasons to be proud of CCMB's contributions during the pandemic. We have developed a novel dry swab diagnostic method, established an mRNA vaccine platform, and were extensively involved in sewage, sero- and genomic surveillance activities. We have also tested many drugs for various companies, and one of the molecules, 2-deoxy-D-glucose (2-DG), tested by CCMB, is now widely available. CCMB was also involved in the development of the first therapeutic antibodies against SARS-nCOV2.

Despite testing times, CCMB scientists have worked at the forefront of biology, as reflected in excellent publications in journals such as Science Advances, eLife, PNAS, EMBO J, and many others. Dr. Rajan Sankaranarayanan was elected as an associate member of EMBO. Dr.Giriraj Chandak's research was recognized with the Sun-Pharma Research Foundation Award in Medical Science and the prestigious JC Bose fellowship. Dr. Amitabha Chattopadhyay and Dr. Vasant Shide are awarded Bhatnagar Fellowships. Dr. Divya Tej Sowpati was a recipient of the CSIR-Young Scientist Award. In addition, students of CCMB have won various oration awards, best poster awards, and fellowships. Congratulations are due to all the awardees among faculty members and students. Dr. Saikat Chowdhury, who works on deciphering the molecular basis of regulation of cytoskeletal networks in the cell using CryoEM, joined CCMB in May 2022. We are among very few institutes in India with organized outreach activities. These activities span from the open day, which was conducted online this year, to visits by school children, spending a week or fifteen days at CCMB. We are among the few CSIR institutes with an Incubation Centre – Atal Incubation Centre (AIC). AIC-CCMB is in its fifth year, and more than 70 starts up have gone successfully through the centre.

India has 140 researchers per 1,000,000, compared to 4,651 in the United States. There is a massive opportunity for growth, and I am sure we will all be part of it in the upcoming decade. Going forward, it is essential to strengthen research by recruiting high-quality scientists in our core areas. Given our core strength in many areas, there is a tremendous opportunity to collaborate and solve scientific problems beyond us individually. We look forward to many more high-quality publications, recognition, and awards in the upcoming years.

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: Megha SS, Medha Navodiyula, Ajay Gaur, Rashmi Agarwal

Research interests

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

Wild animal populations that once were large and widespread have become small and fragmented due to habitat loss, geographical fragmentation and other anthropogenic interferences. Small populations face greater demographic and genetic risks. Conservation genetics deals with genetic management of small populations, resolution of taxonomic uncertainties, use of molecular genetic analysis in wildlife forensics and understanding of species biology. The major efforts in our lab are towards the use of non-invasive sampling protocols and development of species-specific DNA markers to look into the genetic structure of existing populations in order to address issues of population and evolutionary genetics significance. Our group has successfully developed several polymorphic microsatellite and mitochondrial markers specific for big cats, ungulates, primates and other endangered Indian species. An important aspect of the phylogenetic approach adopted by our laboratory is generation of complete mitogenomes of several species important from the conservation point of view in India. In addition to the neutral markers spread over mitochondrial and nuclear genomes of animals, the diversity of the immunologically significant Major Histocompatibility Complex (MHC) is also being investigated.

We have initiated genetic studies in monitor lizards which are symbolic species within the reptiles existing in the old world. All the species of monitor lizards existing in India are Schedule I species under India's Wildlife Protection Act 1972 including *Varanus bengalensis* (Indian monitor lizard, Fig. 1 A), the most species targeted in the illegal trade. Monitor lizards are frequently taken into captive for meat and body parts that are often sold to suppress superstitious beliefs. Apart from Hatha Jodi (Fig. 1 B), the major number of monitor lizard specimens in illegal trade includes skin and leather products. People in remote villages also consume meat and eggs of monitor lizards believing them to possess therapeutic properties. There is a vast information gap with limited details about their ecology and no available genetic data. With increasing threat of illegal poaching, loss of habitat, climate change and highly unresolved phylogenetic relationship within related species, there is an ardent need to generate more genetic information and unfold their unique biology. Our preliminary data showed clear distinction between different species in India on the basis of partial sequence of four mitochondrial genes. Efforts are underway to generate complete mitochondrial sequence Indian monitor lizard. Apart from an enhanced understanding of relationships in monitor lizards, phylogenetic studies will also assist in designing their future conservation programs.

Fig 1 A. Indian monitor lizard, B. Hatha Jodi (precisely meaning "clasped hands" symbolizing two hands joined in prayer) is a plant root of Martynia annua that is rarely found in some remote regions of Nepal and India. There have been many cases wherein, dried monitor lizard genitals (Hemi-penis) are being traded as Hatha Jodi due to its resemblance to the plant root. Our lab for the first time identified the animal origin of Hatha Jodi using 'Universal Primer Technology developed at CCMB. (Photo courtesy: A. Internet, B. Ajay Gaur)

AMITABHA CHATTOPADHYAY

Membrane and Receptor Biology

From left to right: Muskan Gupta (Jointly with Raghunand Tirumalai), Akrati Bhat, Ashwani Sharma, Abhishek Kumar, Parijat Sarkar, Amitabha Chattopdahyay, Priyanka Bisht, Subhashree Shubhrasmita Sahu, Sandeep Shrivastava, K. Venkatlaxmi

Research Interests

- Interaction of membrane lipids and actin cytoskeletal with G protein-coupled receptors (GPCRs) and their 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

- Sarkar, P and Chattopadhyay, A (2021) Insights into Cellular Signaling from Membrane Dynamics. ***Archives of Biochemistry and Biophysics*** 701: 108794.
- Kharche S, Joshi M, Chattopadhyay A, Sengupta D (2021) Conformational Plasticity and Dynamic Interactions of the N-terminal Domain of Chemokine Receptor CXCR1. ***PLoS Computational Biology*** 17: e1008593.
- Sarkar P, Harikumar KG, Rawat SS, Das S, Chakraborty TK, Chattopadhyay A (2021) Environment-sensitive Fluorescence of 7-Nitrobenz-2-oxa-1,3-diazol-4-yl (NBD)-labeled Ligands for Serotonin Receptors. ***Molecules*** 26: 3848.
- Chattopadhyay A, Biswas SC, Rukmini R, Saha S, Samanta A (2021) Lack of Environmental Sensitivity of a Naturally Occurring Fluorescent Analog of Cholesterol. ***Journal of Fluorescence*** 31: 1401-1407.
- Kumar GA, Sarkar P, Stepniewski TM, Jafurulla M, Singh SP, Selent J, Chattopadhyay A (2021) Molecular Sensor for Cholesterol in the Human Serotonin1A Receptor. ***Science Advances*** 7: eabh2922.
- Pal S, Chakraborty H, Chattopadhyay A (2021) Lipid Headgroup Charge Controls Melittin Oligomerization in Membranes: Implication in Membrane Lysis. ***The Journal of Physical Chemistry B*** 125: 8450-8459.
- Sharma A, Kumar G, Chattopadhyay A (2021) Late endosomal/lysosomal accumulation of a neurotransmitter receptor in a cellular model of Smith-Lemli-Opitz syndrome. ***Traffic*** 22: 332.
- Sarkar P and Chattopadhyay A (2021) Cholesterol Footprint in High-Resolution Structures of Serotonin Receptors: Where are We Now and What Does It mean. ***Chemistry and Physics of Lipids*** 239: 105120.
- Pal S and Chattopadhyay A (2021) Hydration Dynamics in Biological Membranes: Emerging Applications of Terahertz Spectroscopy. ***The Journal of Physical Chemistry Letters*** 12: 9697–9709.

- Kumar GA and Chattopadhyay A (2021) Cholesterol-dependent Endocytosis of GPCRs: Implications in Pathophysiology and Therapeutics. ***Biophysical Reviews*** 13: 1007-1017.

- Sarkar P and Chattopadhyay A (2022) Cholesterol in GPCR Structures: Prevalence and Relevance. ***The Journal of Membrane Biology*** 255: 99-106.

- Pal S, Bose D, Chakrabarti A, Chattopadhyay A (2022) Comparative Analysis of Tryptophan Dynamics in Spectrin and its Constituent Domains: Insights from Fluorescence. The Journal of Physical Chemistry B 126: 1045-1053.

- Rao BD, Sarkar P, Chattopadhyay A (2022) Metabolic Depletion of Sphingolipids Does not Alter Cell Cycle Progression in Chinese Hamster Ovary Cells. ***Journal of Membrane Biology*** 255: 1-12.

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

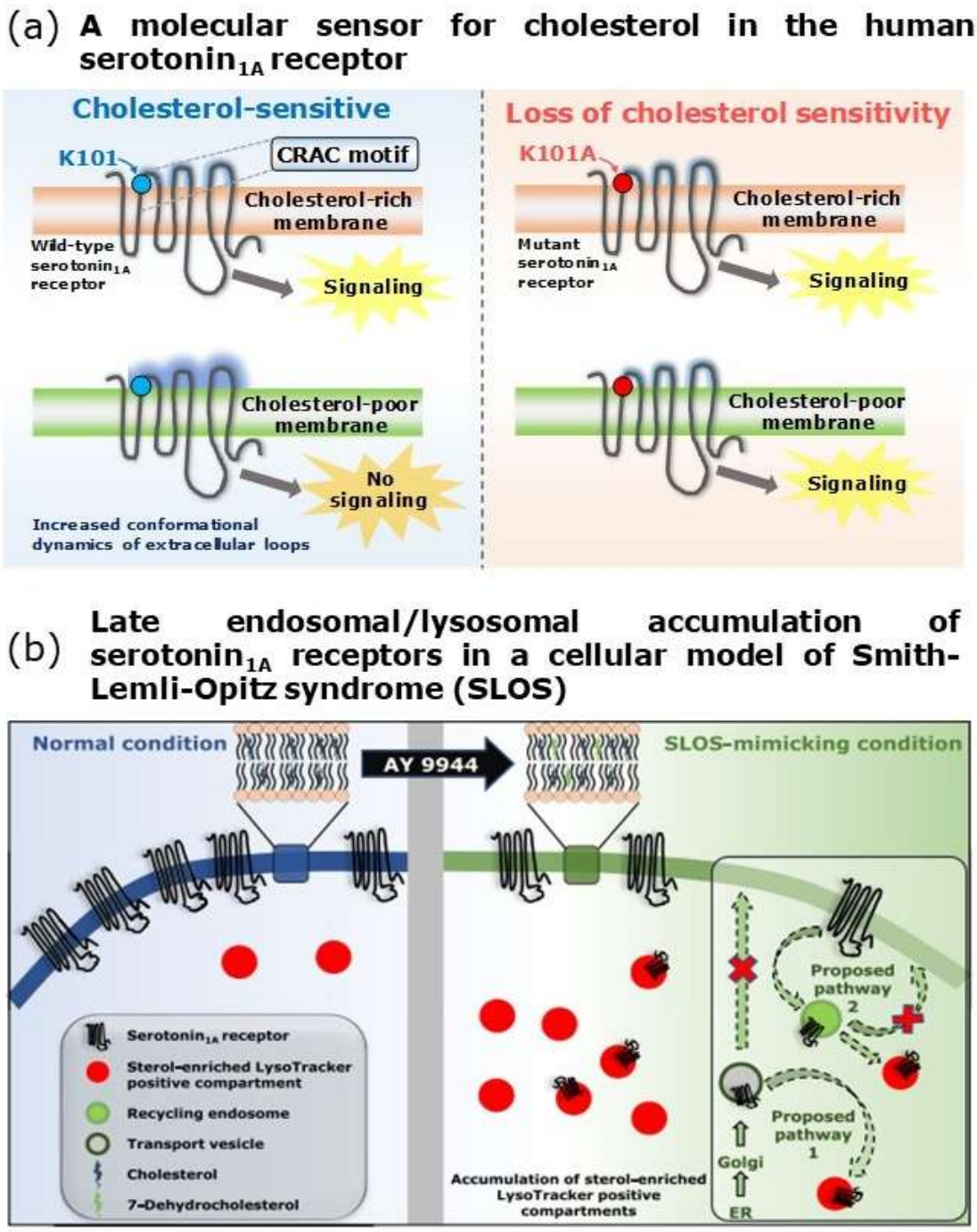


Fig: (a) Cholesterol sensitivity of GPCRs could be attributed to specific sequence and structural features, such as the cholesterol recognition/ interaction amino acid consensus (CRAC) motif, that facilitate their cholesterol-receptor interaction. We explored the molecular basis of cholesterol sensitivity exhibited by the serotonin-1A receptor by generating mutants of key residues in CRAC motifs in transmembrane helix 2 (TM2) and TM5 of the receptor. Our results show that a lysine residue (K101) in one of the CRAC motifs is crucial for sensing altered membrane cholesterol levels. Adapted from Kumar et al. (2021) Sci. Adv. 7: eabh2922.

(b) Smith-Lemli-Opitz Syndrome (SLOS) is characterized by accumulation of 7-dehydrocholesterol (the immediate biosynthetic precursor of cholesterol in the Kandutsch-Russell pathway) and an altered cholesterol to total sterol ratio. We generated a cellular model of SLOS in HEK-293 cells stably expressing the human serotonin-1A receptor using AY 9944 using an inhibitor for the enzyme 3β-hydroxy-steroid-Δ7-reductase (7-DHCR). Utilizing quantitative flow cytometry based assay, we showed that the plasma membrane population of serotonin-1A receptors was considerably reduced without any change in total cellular expression of the receptor. Notably, the receptors were trafficked to sterol-enriched LysoTracker positive compartments, which accumulated under these conditions. Adapted from Sharma et al. (2021) Traffic 22: 332-344.

ANANT B PATEL

Brain Energy Metabolism in Neurological and Psychiatric Disorders

From left to right (front row): Bedaballi, Prajakta
Second row: Chaynita, Akila, Anant, Vimala, Naveleen, Varadarajan, Ajay, Bhagidhar

Research interests

- Development of multinuclear NMR spectroscopy and stable 13C isotope (glucose and acetate) techniques to study neurometabolism
- Understanding energetics of excitatory and inhibitory neurotransmission in neurodegenerative and psychiatric disorders

Selected recent publications

- Ajay Sarawagi, Narayan Datt Soni, Anant Bahadur Patel (2021) Glutamate and GABA Homeostasis and Neurometabolism in Major Depressive Disorder. ***Front Psychiatry-Molecular Psychiatry*** 12: 637863.
- Conde R, Laires R, Goncalves LG, Rizvi A, Barroso C, Villar M, Macedo R, Simoes MJ, Gaddam S, Lamosa P, Puchades-Carrasco L, Pineda-Lucena A, Patel AB, Mande SC, Barnejee S, Matzapetakis M, Coelho AV (2021) Discovery of serum biomarkers for diagnosis of tuberculosis by NMR metabolomics including cross-validation with a second cohort. ***Biomedical Journal*** 45: 654-664.
- Adusmilli M, Sarath Babu N, Varadarajan KS, Idris MM, Patel AB (2021) 1H-[13C]-NMR investigation of brain energy metabolism in zebrafish: Impact of acute ethanol. ***Journal of Magnetic Resonance Open*** 10-11: 100030.
- Roy D, Puvvada M, Kapanaiah STK, Patel AB (2022) Enhanced Cortical Metabolic Activity in Females and Males of a Slow Progressing Mouse Model of Amyotrophic Lateral Sclerosis. ***Neurochemical Research*** 47: 1765-1777.

Amyotrophic lateral sclerosis (ALS) is the most common adult-onset progressive motor neuron degeneration disorder, characterized by skeletal muscle atrophy. The pathophysiology of ALS is not well-understood. Moreover, there are no reliable clinical markers for the diagnosis or prognosis of ALS. We have used transgenic SOD1G37R mice that exhibit a late-onset and slow progression of motor neuron degeneration starting from the age of 10 months to understand the neuropathology of ALS. The neuronal and astroglial metabolic activity in the central nervous system was investigated by ^{1}H-[^{13}C]-NMR spectroscopy together with an intravenous administration of [1,6 - ^{13}C2] glucose and [2-^{13}C] acetate in SOD1G37R mice. The metabolism of [1,6-^{13}C2] glucose in neurons labels glutamate-C4 and GABA-C2, and glutamine-C4 by the trafficking of these neurotransmitters into astrocytes. The kinetics of ^{13}C labeling of these amino acids provides a quantitative estimate of neuronal and astroglial metabolic activity, and neurotransmitter cycling in the brain. The motor function was assessed by measuring forepaw grip strength and coordination on a rotating rod. The SOD1G37R mice exhibit reduced grip strength, poor motor performance, and higher neurological scores with the progress of age. Moreover, there was a reduction in N-acetylaspartate (NAA) level in the spinal cord suggesting neurodegeneration in SOD1G37R. In contrast, the elevated level of myo-inositol along with increased acetate oxidation indicates heightened neuroinflammation in the SOD1G37R brain. The glutamatergic TCA cycle flux and neurotransmitter cycling were increased in the cerebral cortex of SOD1G37R. In contrast, there was a reduction in the neurometabolic activity in the spinal cord of these mice. Our findings suggest differential changes in neurometabolic activity across the central nervous system in SOD1G37R mice.

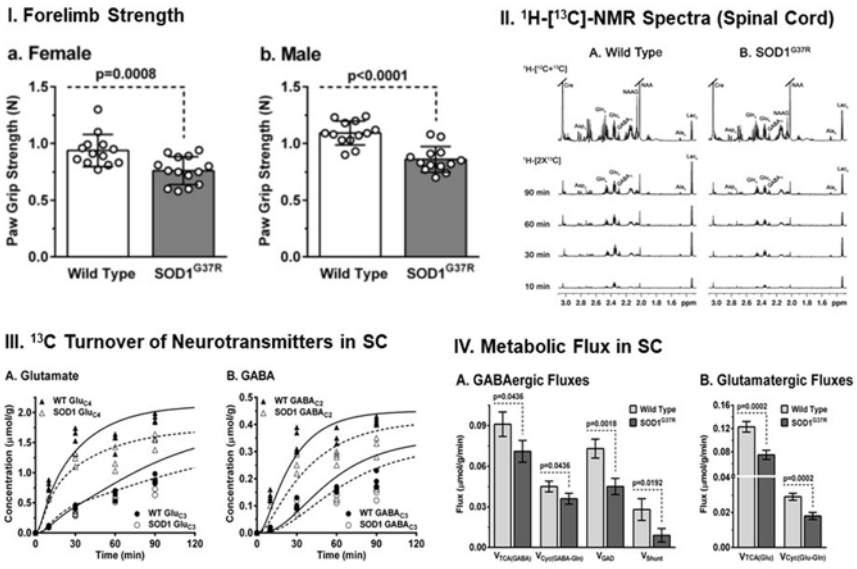


Fig: I. Forelimb strength in SOD1 G37R mice. The paw grip strength of mice was measured by lowering the animal over the top of the grid, and pulling it back horizontally across the length of the grid. II. 1H-[13C]-NMR spectra of spinal cord showing 13C labeling of amino acids from [1,6-13C2]glucose. The spectra in the uppermost panel in each group represent total signal {1H-[12C + 13C]} from metabolites, whereas edited spectra presented in the lower panel depict 13C-labeled metabolites {1H-[2x13C]} from 13C-labeled glucose at different time. Mice were infused with [1,6-13C2]glucose at different time points, and the brain metabolism was arrested by freezing the mice in liq. N2. Metabolites were extracted using ethanol extraction protocol, and 1H-[13C]-NMR spectra were recorded using a 600 MHz NMR spectrometer. III. 13C Turnover of glutamate and GABA in the spinal cord of SOD1 G37R mice. The 13C turnover of glutamate and GABA were generated by plotting the 13C label amino acids with time. The symbols indicate measurement from individual mice while the lines represent the best fit of a metabolic model to the measured data. IV. Metabolic flux associated with glutamatergic and GABAergic neurotransmission. The cerebral metabolic rates were obtained by fitting a three-compartment metabolic model to the 13C turnover of amino acids. Abbreviation used are: AlaC3, alanine-C3; AspC3, aspartate-C3; Cre, creatine; GABAC2, gamma-aminobutyric acid-C2; GABAC3, gamma-aminobutyric acid-C3; GABAC4, gamma-aminobutyric acid-C4; GluC3, glutamate-C3; GluC4, glutamate-C4; GlnC4, glutamine-C4; LacC3, Lactate-C3; NAA, N-acetyl aspartate.

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

- Uncovering the molecular mechanisms in etiology of neuropsychiatric disorders using animal models
- Discovery of markers and biomarkers for depressive and cognitive disorders
- Pre-clinical studies for CNS drug discovery

Selected recent publications

- Shams Ul Haq, Bhat UA, Kumar A (2021) Prenatal stress effects on offspring brain and behavior: Mediators, alterations and dysregulated epigenetic mechanisms. ***Journal of Bioscience*** 46: 34.
- Raghunath Reddy B, Sarath Babu N, Das T, Bhattacharya D, Lakshmi Ch, Murthy N, Kumar A, Idris MM, Chakravarty S (2021) Proteome profile of telencephalon associates attenuated neurogenesis with chronic stress induced mood disorder phenotypes in zebrafish model. ***Pharmacology Biochemistry & Behaviour*** 204: 173170.
- Asik RA, Suganthy N, Aarifa MA, Kumar A, Szigeti K, Mathe D, Gulyás B, Archunan G, Padmanabhan P (2021) Alzheimer`s Disease: A Molecular View of β-Amyloid Induced Morbific Events. ***Biomedicines*** 9: 1126.
- Das T, Kamle A, Kumar A, Chakravarty S (2021) Hypoxia induced sex-difference in zebrafish brain proteome profile reveals the crucial role of H3K9me3 in recovery from acute hypoxia. ***Frontiers in Genetics*** 12: 635904.

JARID1 or KDM5 family lysine demethylases mediate prenatal stress induced altered neurogenesis, circuitry and behavior in offspring mice

Early life stress has been recognized as a risk factor for several neuropsychiatric diseases. Using gestational stress or in utero stress model, also known as Prenatal Stress (PNS) model, some labs have induced psychopathologies such as anxiety, depression, schizophrenia, cognitive and autism spectrum disorders later in life of animals. PNS appears to cause long lasting changes in neural circuitries of offspring, which are mediated by various mechanisms including some epigenetic mechanisms. DNA methylation and DNA methyltransferase 1 (DNMT1) are dysregulated in certain brain regions of prenatally stressed rodents and this have implications for the expression of critical genes like BDNF (brain derived neurotrophic factor). However, the involvement of histone methylation and the epigenetic regulators such as histone lysine methyltransferases (KMTs) and demethylases (KMDs) has not been investigated in PNS models.

Using restraint stress model where a mouse dam was subjected to 4 days of stress twice daily from gestation day 15 to 18, we investigated the offspring behavior in adolescent, adult and old stage employing a battery of behavioural tests. Both male and female offspring developed cognitive as well as mood disorders in later phase of life. Since JARID1c demethylase and its target H3K4me2 & me3, the transcriptionally activating histone methyl marks is known to be involved in neurodevelopmental and intellectual disability disorder, we first mapped the expression levels of demethylases of JARID1 or KDM5 family. JARID1C or KDM5C, in addition to a few other members, was highly dysregulated in the hippocampus of PNS group.

Further, to uncover the underlying epigenetic and transcription regulatory network, high throughput transcriptomic & proteomic tools were used on the hippocampi of PNS and Control offspring brain. This led us to uncover the dysregulation in the expression of hundreds of genes/proteins, including of many more epigenetic regulators of various classes/families, in sex-specific manner. Furthermore, the magnetic resonance study revealed that PNS reduced the rate of neuronal glucose oxidation in male PNS offspring while increased it in female PNS offspring, as compared to respective controls. Most interestingly, the Environment Enrichment from weaning till 45 days could restore the altered neurometabolism and mood disorder phenotype in both sexes.

A S SREEDHAR

Stress Biology and Molecular Medicine

From left to right: Khanderao Paithankar, Amere Subbarao Sreedhar, Priyadarshini Singh, Amash Vijayalakshmi, R.S.Sreelakshmi, Shrikant P. Dharsakar

Research interests

- Molecular basis of conserved stress response mechanisms across species
- Unconventional roles of cancer chaperone Hsp90
- Regulation of Metabolic plasticity in cancer cells
- Canalization and epigenetic regulation of cancer mediated by Hsp90
- Cancer EMT and role of Hsp90 in phenotypic evolution

Selected recent publications

- AS Sreedhar (2021) Cancer vs. SARS-CoV-2 induced inflammation, overlapping functions, and pharmacological targeting. ***Inflammaopharmacology*** 29: 343-366.
- Pant A, Keerthi CK, Navyamol CD, Meghana Y, Narayanan MA, Paithankar K, Vijayalakshmi A, Sreedhar AS (2021) Hsp90 and its mitochondrial homologue TRAP-1 independently regulate hypoxia adaptations in *Caenorhabditis elegans*. ***Mitochondrion*** 60 : 101-111.

Cancer is an adaptive disease that exhibits adaptation over many intra- and extra-cellular factors, including microenvironment, therapeutic drugs, altered epigenetic landscape, metabolism, phenotypic transition, etc. Among a large family of heat shock proteins (Hsps), Hsp90 has been identified as a cancer chaperone since it contributes to conformational maturation and functional stabilization of mutated gene products. Our laboratory explores the unconventional and adaptive role of Hsp90 in cancer cells to understand its contribution to disease progression and develop novel antitumor strategies to combat cancer irreversibly. Earlier, we reported that Hsp90 facilitates tumor cell proliferation and metastasis, while its mitochondrial homolog TRAP-1 contributes to altered cellular energy metabolism. We subsequently demonstrated that Hsp90 contributes to tumor aggression by enhancing oncogene-mediated cell proliferation, acquired drug resistance, and tumor metastasis. At the same time, TRAP-1 promotes the synthesis of ATP through glycolysis. We demonstrated that TRAP-1 facilitates glutamine metabolism in response to compromised glycolysis or glucose depletion. Increased glutamine utilization occurred through activating the HIF2α-SLC1A5-GLS axis, indicating tumor-specific functions for TRAP-1. Similar to Hsp90 inhibitors in clinical trials against cancer, we propose using TRAP-1 inhibitors to interfere with tumor metabolism. Using tumor cells and *C. elegans* as model systems, we demonstrated that TRAP-1 maintains mitochondrial integrity despite negatively regulating oxidative phosphorylation in the presence of glucose. We extended our studies to bacteria and yeast systems to understand the conserved functions of Hsp90. We found that Hsp90 homolog HtpG is required to maintain cellular integrity and metabolic alterations in bacterial cells. Research is underway to understand HtpG and yeast homologs Hsc82/Hsp82 roles in regulating cellular energy metabolism.

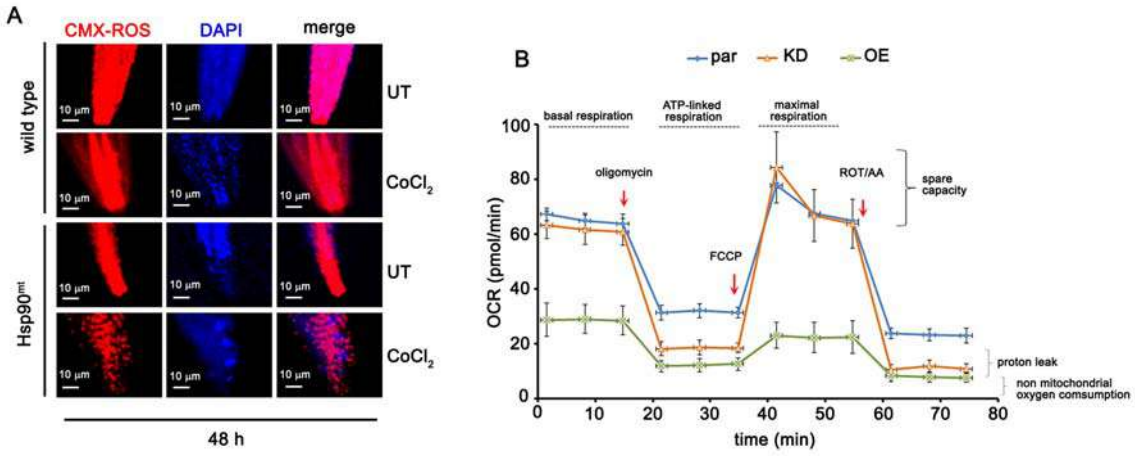


Fig 1A: Wild type and Hsp90 mutant (Hsp90mt) *C. elegans* showing a decreased number of mitochondria. The number of mitochondria is reduced in response to chemical hypoxia-induced by cobalt chloride (CoCl2). Blue: nuclear staining with DAPI; Red: mitochondria staining using CMX-Ros.
Fig 1B: Overexpression (OE) and knockdown (KD) of TRAP-1 in human neuroblastoma cells showing a decreased oxygen consumption rate measured using Agilent Seahorse Flux Analyzer.

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

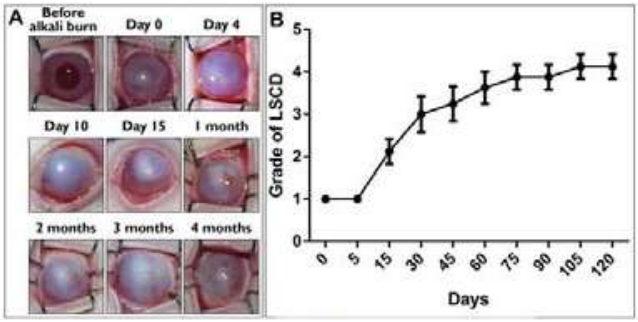
- To understand the repair, replacement or regeneration of dysfunctional cells and impaired or damaged tissues both, *in vitro* and *in vivo*
- Develop cellular models for disease modelling and drug testing

Selected recent publications

- Atish G, Dhwani D, Sadasivam K, Lipsa P, Ritu R, Bijay RP, Vaibhav J, Yash P, Ghalib ME, Kiran Kumar B, Venkatesan S, Mitali M, Anurag A, Bhavana P (2021) Adhatoda Vasica attenuates inflammatory and hypoxic responses in preclinical mouse models: potential for repurposing in COVID-19-like conditions. ***Journal of Respiratory Research*** 22: 99.
- Aditya K, Kalpita N, Yash P, Ghalib ME, Kiran Kumar Bokara⁎, Apruba S (2021) Antimicrobial silver nanoparticle-photodeposited fabrics for SARS-CoV-2 destruction. ***Colloid and Interface Science Communications*** 45: 100542.
- Madiha H, Vivek A, Ghalib ME, Yash P, Sushma R, Surekha K, Anmol, Gayatri P, Manjari S, Dhwani D, Arjun R, Sudipta B, Upendra S, Kiran Kumar B, Bhavana P, Mitali M (2022) Anti-SARS-CoV-2 potential of Cissampelos pareira L. identified by connectivity map-based analysis and *in vitro* studies. ***BMC Complimentary Medicine and Therapies*** 22: 114.
- Ghalib ME, Yash P, Sarena B, Sushma R, Ramakrishnan N, Kiran Kumar B⁎, Idris MM (2022) Gramicidin S and melittin: potential anti-viral therapeutic peptides to treat SARS-CoV-2 infection. ***Scientific Reports*** 12: 3446.

Limbal Stem Cell Deficiency (LSCD): LSCD, caused due to corneal injury, primarily by chemical/alkali burns, leads to compromised vision. Recently, several animal models of corneal alkali burn injury have become available. The majority of the studies with these animal models start interventions soon after the injury. However, in the clinical setting, there is a considerable delay before the intervention is initiated. Detailed knowledge of the molecular, histopathological, and clinical parameters associated with the progression of the injury leading to LSCD is highly desirable. In this context, we set out to investigate clinical, histopathological parameters of ocular surface alkali burn over a long period of time, post-injury. Limbal stem cell-deficient animal models of rabbits were created by alkali burn using sodium hydroxide, which was then assessed for their progression towards LSCD by grading the alkali burn, corneal haze, and vascularization. Additionally, cells present on the corneal surface after the burn was investigated by histology and immunophenotyping. (Experimental Eye Research, 2021)

COVID-19 treatment strategies: The COVID-19 pandemic has led to multipronged approaches for treatment of the disease. Since *de novo* discovery of drugs is time consuming, repurposing of molecules is now considered as one of the alternative strategies to treat COVID-19. Antibacterial peptides are being recognized as attractive candidates for repurposing to treat viral infections. In this study, we describe the anti-SARS-CoV-2 activity of the well-studied antibacterial peptides gramicidin S and melittin obtained from *Bacillus brevis* and bee venom respectively. (Scientific Reports 2022).



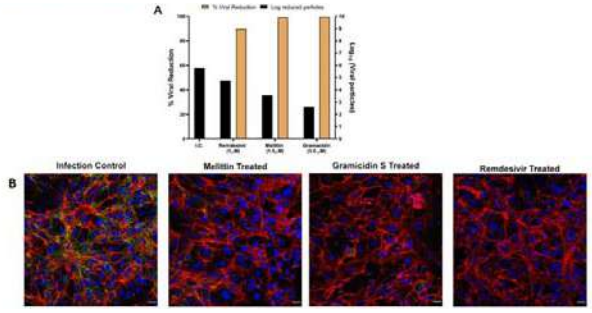


Fig 1: Progression of limbal stem cell deficiency (LSCD) after ocular surface alkali burn.
(A) Image panel showing the typical clinical presentation of LSCD in rabbits. Corneal edema, along with limbal ischemia, was noted immediately after the burn indicating damage to the limbus. Corneal neovascularization had begun on the fourth day after the burn that was prominently visible after two weeks. Conjunctivalization and vascularization had developed further in three months leading to total vision loss.
(B) Graph showing the mean grade of LSCD based on the limbal clock hours affected and conjunctival involvement (n=12). Grade of LSCD had increased after about a week of alkali burn and had stabilized at three months. T-test was used for statistical analysis with significance set to $p<0.05$

Fig 2: Melittin and gramicidin treatment reduced the SARS-CoV-2 viral load
(A) Melittin (1.5µM), Gramicidin (3.0 µM) were tested along with Remedesivir (1.0 µM) (X Axis) against SARS-CoV-2 *in vitro.* The graphs represent the % of viral reduction (Y axis) and log10 viral particles (Y' Axis). The Ct values of N gene were obtained using RT-qPCR in the supernatants at 24 hrs.
(B) Immunofluorescence staining images against RBD protein expression specific to SARS-CoV-2 in Vero cells. (RBD protein expression green) of SARS-CoV-2 virus at 24 hrs. (V) DAPI staining representing nucleus (blue) along with RBD protein expression of SARS-CoV-2 (green) at 24 hrs. (VI) Merged image of f-Actin (Phalloidin staining red), nucleus (DAPI, blue) and RBD protein of SARS-CoV-2 (green) at 24 hrs

DIVYA TEJ SOWPATI

Bioinformatics, Big Data, Algorithms in Biology

From left to right, front row: Krishna, Srividya, Malini, Payel, Pratheusa, Priya, Reuben, Sreelekshmi, Archana, Sofia
Back row: Nitesh, Tej, Onkar, Victor, Manish, Abhijeet, Wasim, Kiran, Saketh, Akshay

Research interests

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

Selected recent publications

- Vishnu VV, Muralikrishna Bh, Verma A, Nayak SC, Sowpati DT, Radha V, Chandra Shekar P (2021) C3G Regulates STAT3, ERK, Adhesion Signaling, and Is Essential for Differentiation of Embryonic Stem Cells. ***Stem Cell Reviews and Reports*** 17: 1465–1477.
- Kumar JV, Banu S, Sasikala M, Parsa KVL, Sowpati DT, Yadav R, Bharadwaj KT, Siva AB, Vishnubhotla R, Rao GV, Reddy DN (2021) Effectiveness of REGEN-COV antibody cocktail against the B.1.617.2 (delta) variant of SARS-CoV-2: A cohort study. ***Journal of Internal Medicine*** 291: 380-383.
- Singh NK, Srivastava S, Zaveri L, Bingi TC, Mesipogu R, Kumar SV, Gaur N, Hajirnis N, Machha P, Shambhavi S, Khan S, Soujanya M, Nagabandi T, Mishra RK, Tallapaka KB, Sowpati DT (2021) Host transcriptional response to SARS-CoV-2 infection in COVID-19 patients. ***Clinical and Translational Medicine*** 11: e534.
- Kulkarni O, Narreddy S, Zaveri L, Kalal IG, Tallapaka KB, Sowpati DT (2021) Evidence of Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) Reinfection Without Mutations in the Spike Protein. ***Clinical Infectious Diseases*** 73: e1239–e1241.
- Mlcochova P, et al. (2021) SARS-CoV-2 B.1.617.2 Delta variant replication and immune evasion. ***Nature*** 599: 114-119.
- Dhar MS, et al. (2021) Genomic characterization and epidemiology of an emerging SARS-CoV-2 variant in Delhi, India. ***Science*** 374: 995-999.

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

Ghanshyam Swarup

Research interests

- To explore 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

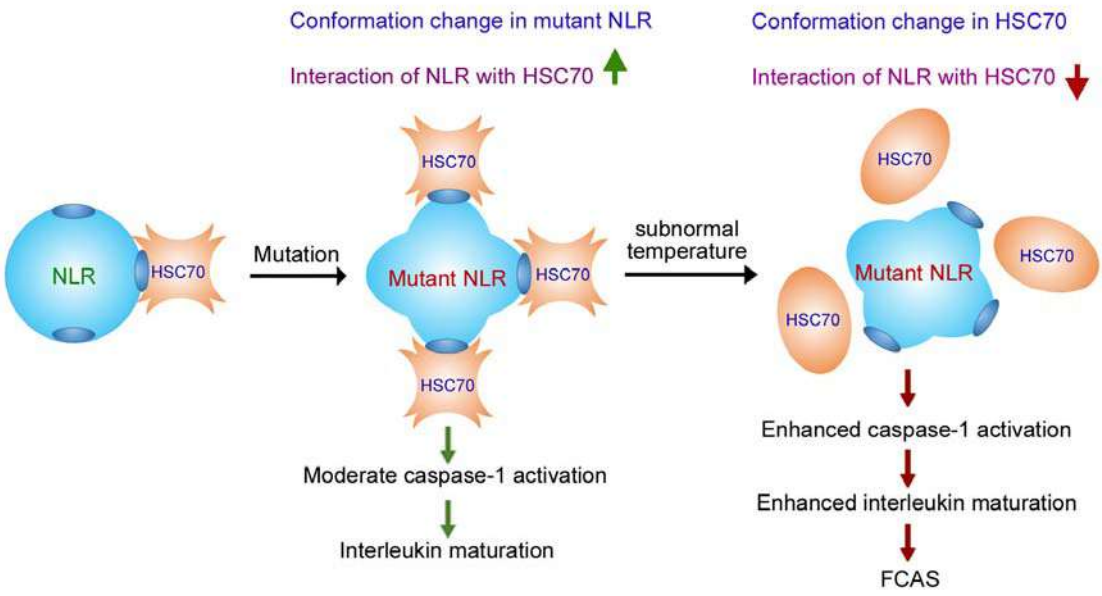
Selected recent publications

- Medchalmi S, Tare P, Sayyad Z, Swarup G (2021) A glaucoma- and ALS-associated mutant of OPTN induces neuronal cell death dependent on Tbk1 activity, autophagy and ER stress. ***FEBS Journal*** 288: 4576-4595.
- Sayyad Z, Vishwakarma S, Dave TV, Naik MN, Radha V, Kaur I, Swarup G (2021) Human primary retinal cells as an in-vitro model for investigating defective signalling caused by OPTN mutants associated with glaucoma. ***Neurochemistry International*** 148: 105075.

An important feature of several neurodegenerative diseases is the formation of pathological structures containing aggregated proteins. The autophagy receptor optineurin/OPTN is frequently observed in these structures. The role played by optineurin in these aggregates is not clear. We explored whether optineurin has a cytoprotective role in the cells having mutant protein aggregates. Our results show that in the absence of optineurin, mutant protein aggregates are highly toxic, revealing an autophagy-independent cytoprotective function of optineurin, which is mediated by its C-terminal domain.

Studies carried out on the pathogenesis of glaucoma using murine cell lines and animal models require to be validated in human cells. For this purpose, we explored the possibility of using human primary retinal cells (hPRCs) in culture. Our results suggest that hPRCs under appropriate culture condition show retinal ganglion cell-like properties. These cells can be used to explore the molecular mechanisms of cell death relevant for glaucoma pathogenesis and for testing of cytoprotective compounds.

Familial cold auto-inflammatory syndrome (FCAS) is a subset of heritable auto-inflammatory disorders wherein inflammatory symptoms aggravate upon exposure of the individual to subnormal temperature. Several mutations in various genes like NLRP3, NLRP12, PLCG2 and NLRC4 have been identified that cause cold-triggered inflammation. However, our understanding about the mechanisms by which cells perceive subnormal temperature, and what keeps the inflammation under check until exposure to low-temperature, is very limited. We hypothesize that chaperone protein HSC70 is a low temperature sensor, which can modulate the outcome of disease-causing mutations in auto-inflammatory disorders (Fig 1).



Proposed mechanism for low temperature-dependent regulation of NLRs by HSC70. In their inactive conformation, NLRs show weak binding to HSC70. A FCAS-causing gain-of-function mutation induces a conformational change in NLRs, which results in exposure of HSC70-binding sites enabling enhanced interaction with its negative regulator, HSC70. Interaction with HSC70 causes reduced inflammasome assembly, moderate caspase-1 activation and cytokine maturation, and moderate inflammation. Upon exposure to subnormal temperature, HSC70 undergoes conformational changes resulting in its inability to engage with its client proteins. Mutant NLRs relieved from HSC70-inhibition show enhanced inflammasome assembly and caspase-1 activation leading to enhanced cytokine maturation and their release. This leads to aggravated symptoms of FCAS disorders.

GIRIRAJ RATAN CHANDAK

Genomic Research on Complex Diseases

From left to right, front row: Inderdeo Mali, PSKDB Punyasri, Shagufta Tasneem, Bernadette Mathew, Sara Sajjadi
Middle row: Sulgae Sripal, Riya Dogra, Shoma Naskar, Giriraj Ratan Chandak, Seema Bhaskar, Mounika Challapalli, Manisha Arumalla, Anushri U, Palav Ashwini Dhaku
Last row: Ajay Deepak Verma, Sohail Rafik Mansuri, Alagu Sankareswaran, Swati Bayyana
On the top: Suraj Singh Nongmaithem, Prachand Issarapu, Ashutosh Singh Tomar, Varsha Kolaria

Research interests

- Genetic and epigenetic basis of non-communicable disorders like cardiometabolic, neurocognitive and related intermediate traits using gene-gene and gene-nutrient interaction and pre-/peri-conceptional nutritional intervention to understand causality

Selected recent publications

- Naushin S, et. al. (2021) Insights from a Pan India Sero-Epidemiological survey (Phenome-India Cohort) for SARS-CoV2. ***eLife*** 10: e66537.
- Azhar M, Phutela R, Kumar M, Ansari AH, Rauthan R, Gulati S, Sharma N, Sinha D, Sharma S, Singh S, Acharya S, Sarkar S, Paul D, Kathpalia P, Aich M, Sehgal P, Ranjan G, Bhoyar RC; Indian CoV2 Genomics & Genetic Epidemiology (IndiCovGEN) Consortium, et. al. (2021) Rapid and accurate nucleobase detection using FnCas9 and its application in COVID-19 diagnosis. ***Biosensors and Bioelectronics*** 183: 113207.
- Murali Krishna, Krishnaveni GV, Veena SR, Kalyanaraman Kumaran, Mohan Kumar, Kiran Nagaraj, Patsy Coakley, Samuel Christaprasad Karat, Giriraj R Chandak, Mathew Varghese, Martin Prince, Clive Osmond, Caroline HD Fall (2021) Size at birth, lifecourse factors and cognitive function in late life: Findings from the MYsore study of Natal effects on Ageing and Health (MYNAH) cohort in South India. ***International Psychogeriatrics*** 1-14.

- Graham SE, et. al. The power of genetic diversity in genome-wide association studies of lipids. ***Nature*** 600: 675-679.

- Suraj S Nongmaithem, Robin N Beaumont, Akshay Dedaniya, Andrew R Wood, Babatunji-William Ogunkolade, Zahid Hassan, Krishnaveni GV, Kalyanaraman Kumaran, Ramesh D Potdar, Sirazul A Sahariah, Murali Krishna, Chiara Di Gravio, Inder D Mali, Alagu Sankareswaran, Akhtar Hussain, Biswajit W Bhowmik, Abdul Kalam A Khan, Bridget A Knight, Timothy M Frayling, Sarah Finer, Caroline HD Fall, Chittaranjan S Yajnik, Rachel M Freathy, Graham A Hitman, Giriraj R Chandak (2022) Babies of South Asian and European ancestry show similar associations with genetic risk score for birth weight despite the smaller size of South Asian newborns. ***Diabetes*** 71: 821-836.

- Elie Antoun, Prachand Issarapu, Chiara di Gravi, Smeeta Shrestha, Modupeh Betts, Ayden Saffari, Sirazul A Sahariah, Alagu Sankareswaran, Manisha Arumalla, Andrew M Prentice, Caroline H D Fall, Matt J Silver, Giriraj R Chandak, Karen A Lillycrop, EMPHASIS Study Group (2022) DNA methylation signatures associated with cardiometabolic risk factors in children from India and The Gambia: results from the EMPHASIS study. ***Clinical Epigenetics*** 14: 6.

- Matt J Silver, Ayden Saffari, Noah J Kessler, Gririraj R Chandak, Caroline HD Fall, Prachand Issarapu, Akshay Dedaniya, Modupeh Betts, Sophie E Moore, Michael N Routledge, Zdenko Herceg, Cyrille Cuenin, Maria Derakhshan, Philip T James, David Monk (2022) Environmentally sensitive hotspots in the methylome of the early human embryo. ***eLife*** 11: e72031.

SOCS3 gene methylation is associated with height in children from Low and Middle Income Countries (LMIC): Implications for future risk of cardiometabolic risk

Human height is strongly associated with future risk of cardiometabolic disorders. It is strongly determined by genetic factors, but they account for only ~40% of phenotypic variance. Environmental factors including nutrition can also drive height differences, and DNA methylation (DNAm) might mediate this effect. We investigated epigenome-wide DNAm signatures associated with height in children from two LMIC populations by conducting a discovery epigenome-wide association study in children (5-7 yrs) from the Mumbai Maternal Nutrition Project (MMNP, India) using the Illumina EPIC array (850k CpGs) with FDR<0.05. We identified three height-associated CpGs; cg11047325, cg13343932 and cg18181703 (p=2.45x10-04-2.41x10-05), annotated to the second exon of the Suppressor of Cytokine Signalling 3 gene (SOCS3) which were replicated with similar effect sizes in three independent cohorts: Mysore Parthenon Cohort (5yr,India), Periconceptional Multiple Micronutrient Supplementation Trial (7-9yr,Gambia), and Early Nutrition and Immune Development Trial (2yr; 5yr, Gambia). No significant cis-mQTLs were identified and additional adjustment for height polygenic risk score (~3200 height-associated loci) confirmed association of SOCS3 methylation with child height independent of genetic influence. Maternal folate during pregnancy and socio-economic status were associated with SOCS3methylation (p=2.2x10-4) and (6.6x10-6), suggesting possible early environmental programming atSOCS3. However, Mendelian randomisation analysis showed no causal relationship between maternal folate and child SOCS3methylation. Functional characterization of this region showed enhancer activity, with methylation attenuating luciferase expression in HepG2 cells. Thus, we have identified a novel epigenetic regulator of height at SOCS3inLMIC children where environmental influences on height are greater.

Cohort	CpGs	Estimate (95% CI)	Estimate (in cm)	P value	Ethnicity
MMNP (n=685)	cg18181703	6.38 (4.87-8.62)	0.30	3.0E-11	Indian
	cg11047325	4.40 (3.47-5.80)	0.21	5.8E-11	
	cg13343932	5.23 (3.66-6.21)	0.25	3.0E-10	
MPC (n=553)	cg18181703	6.75 (4.87-8.62)	0.29	5.3E-12	
	cg11047325	4.64 (3.47-5.80)	0.20	2.8E-14	
	cg13343932	4.94 (3.66-6.21)	0.21	1.5E-13	
PMMST (n=284)	cg18181703	3.89 (0.34-7.43)	0.21	3.2E-02	
	cg11047325	2.31 (0.04-4.58)	0.12	4.7E-02	
	cg13343932	2.58 (0.08-5.08)	0.14	4.4E-02	
ENID (at 5y) (n=142)	cg18181703	2.80 (1.55-4.05)	0.11	2.3E-05	Gambian
	cg11047325	1.63 (0.82-2.45)	0.06	1.4E-04	
	cg13343932	1.97 (1.02-2.92)	0.08	8.1E-05	
ENID (at 2y) (n=238)	cg18181703	4.73 (1.94-7.52)	0.14	1.0E-03	

Table 1: Discovery and replication analysis of association of SOCS3 methylation with child height in Indian and The Gambian cohorts. Shaded area showing EWAS results from MMNP is the Discovery cohort, remaining are replication cohorts

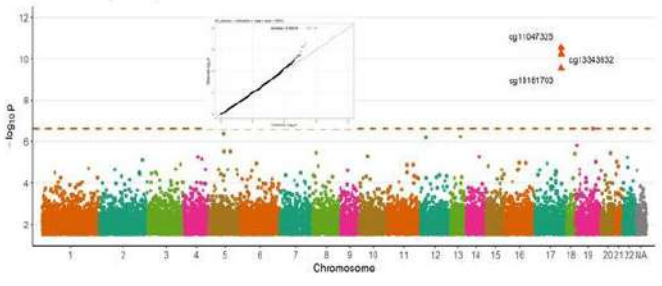


Figure 1: Manhattan plot of Epigenome-wide Association Study of child height showing three CpGs in *SOCS3* gene (red arrowheads) passing the genome-wide significance of 5x10-8. The genomic inflation factor is 0.98 suggesting no genomic inflation (Inset).

Cohort	CpG/PRS	Cor. Coef (95% CI)	P value	Variance (%)
MMNP (n=683)	cg18181703	0.23 (0.16-0.30)	1.59E-09	5.20
	cg11047325	0.23 (0.16-0.30)	7.77E-10	5.39
	cg13343932	0.18 (0.11-0.25)	2.69E-06	3.18
MPC (n=546)	cg18181703	0.28 (0.20-0.36)	1.88E-11	7.93
	cg11047325	0.31 (0.24-0.39)	5.72E-14	9.83
	cg13343932	0.30 (0.23-0.38)	3.41E-13	9.25
ENID (5y) (n=140)	cg18181703	0.29 (0.13-0.44)	4.61E-04	8.48
	cg11047325	0.26 (0.10-0.41)	1.61E-03	6.89
	cg13343932	0.27 (0.11-0.42)	1.21E-03	7.29
ENID (2yr) (n=236)	Cg18181703	0.21 (0.09-0.33)	1.03E-03	4.47

Table 2: Correlation between SOCS3 methylation and the height-PRS (using 3,290 height-associated SNPs) and the variance in height explained by CpG methylation in Indian and The Gambian cohorts

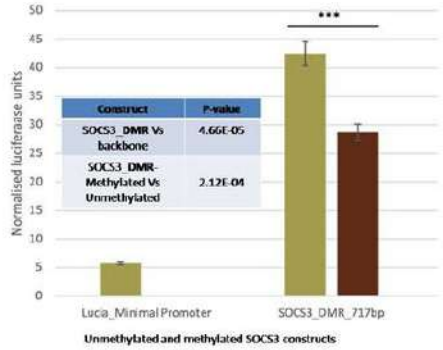


Figure 2: In vitro functional analysis of the differentially methylated region in *SOCS3* gene and effect of DNA methylation on the functional activity.

G UMAPATHY

Understanding Species Extinction and Conservation Physiology

From left to right: S. Manu, Manisha Ray, Mihir Trivedi, Gopi Krishnan, S. Sukanya, G. Umapathy, Vinod Kumar, Vinay Teja, Christina Grace, Anusha Kiran

Research interests

- Understanding species extinction in the human-dominated landscapes
- Conservation breeding and physiology
- eDNA and genomics in biodiversity conservation

Selected recent publications

- Jepsen EM, Scheun J, Dehnhard M, Kumar V, Umapathy G, Ganswindt A (2021) Non-invasive monitoring of glucocorticoid metabolite concentrations in native Indian, as well as captive and re-wilded tigers in South Africa. ***General and Comparative Endocrinology*** 308: 113783.
- Srivastava T, Kumar A, Kumar V, Umapathy G (2021) Diet drives differences in reproductive synchrony in two sympatric mountain ungulates in the Himalaya. ***Frontiers in Ecology and Evolution*** 9: 647465.
- Rodriguez-Ezpeleta N, Morissette O, Bean CW, Manu S, Banerjee P, Lacoursière-Roussel A, Beng KC, Elizabeth Alter S, Roger F, Holman LE, Stewart KA, Monaghan MT, Mauvisseau Q, Mirimin L, Wangensteen OS, Antognazza CM, Helyar SJ, Hugo de Boer, Marie-Eve Monchamp , Nijland R, Abbott CL, Doi H, Barnes MA, Leray M, Hablützel PI , Deiner K (2021) Trade-offs between reducing complex terminology and producing accurate interpretations from environmental DNA: Comment on "Environmental DNA: What's behind the term?" by Pawlowski et al., (2020). ***Molecular Ecology*** 30: 4601-4605.
- Purohit D, Manu S, Ram MS, Sharma S, Patnaik HC, Deka PJ, Narayan G, Umapathy G (2021) Genetic effects of long-term captive breeding on the endangered pygmy hog. ***PeerJ*** 9: e12212.
- Kumar V, Sood,S, Vasudevan, K, Umapathy G (2021) A practical method for storage, preservation and transportation of anuran urine samples using filter paper for hormone analysis. ***MethodsX*** 8: 101578.

Genetic effects of long-term captive breeding on the endangered pygmy hog

Long-term captive populations often accumulate genetic changes that are detrimental to their survival in the wild. Pygmy hog (*Porcula salvania*) is an endangered species with a small population inhabiting the tall sub-Himalayan grasslands of Assam, India. A conservation breeding program of pygmy hog from six founders has produced a multi-generational captive population destined for reintroduction into the wild. However, the impact of conservation breeding on its genetic diversity remained undocumented. Here, we evaluate temporal genetic changes in 39 pygmy hogs from eight consecutive generations of a captive population using genome-wide SNPs, mitochondrial genomes, and MHC sequences, and explore the relationship between genetic diversity and reproductive success. We find that pygmy hog harbors a very low genome-wide heterozygosity (H) compared to other members of the *Suidae* family. However, within the captive population we find excess heterozygosity and a significant increase in H from the wild-caught founders to the individuals in subsequent generations due to the selective pairing strategy. The MHC and mitochondrial nucleotide diversities were lower in captive generations compared to the founders with a high prevalence of low-frequency MHC haplotypes and more unique mitochondrial genomes. Further, even though no signs of genetic inbreeding were observed from the estimates of individual inbreeding coefficient F and between individuals (FIS) in each generation, the kinship coefficient showed a slightly increasing trend in the recent generations, due to a relatively smaller non-random sample size compared to the entire captive population. Surprisingly, male pygmy hogs that had higher heterozygosity also showed lower breeding success. We recommended steps to minimize the genetic effects of long-term captive breeding.

Pygmy hog at conservation breeding centre at Guwahati, Assam

HITENDRA K PATEL

Plant-Pathogen Interactions and Plant Breeding

From left to right, first row: Hitendra K. Patel, Raju Madnala, Kranthi Brahma, Vinoth Kumar K, Md. Jamaloddin, Bipin Kumar
Second row: Donald James, Kamal Kumar Malukani, Rajkanwar Nathawat, Sohini Deb, Vishnu NM, Komal Awalellu
Third row: Gokulan CG, Namami Gaur, Palash Ghosh, Rennya PR, Deepak Niranjan, Gattu Niranjan, Anjana Sharma

Research interests

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

Selected recent publications

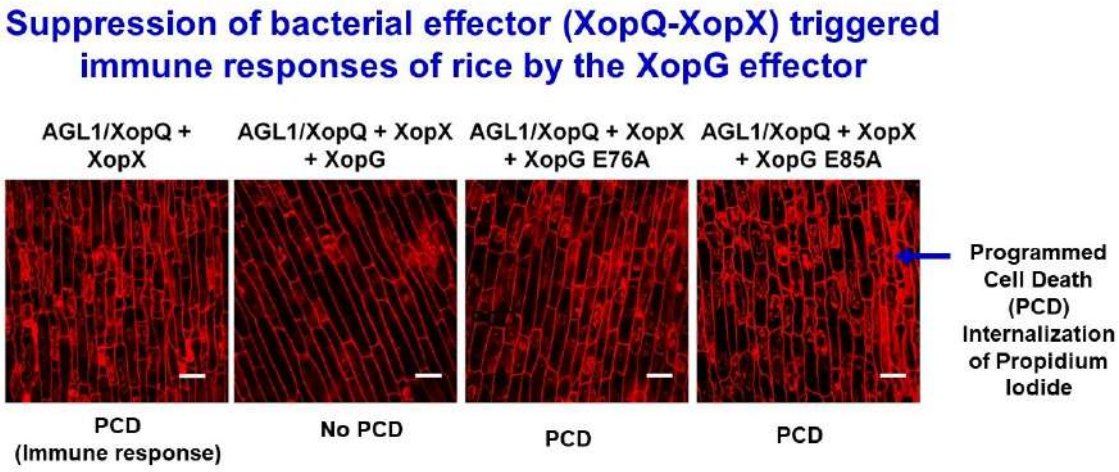
- Sharmila Roy, Pragya Mittal, Lavanya Tayi, Sahitya Bondada, Malay K Ray, Patel HK, Sonti RV(2021) *Xanthomonas oryzae* pv. *oryzae* exoribonuclease R is required for complete virulence in rice, optimal motility, and growth under stress. ***Phytopathology*** 112: 501-510.

- Potupureddi G, Vishalakshi Balija, Suneel B, Gokulan CG, Awalellu K, Swathi L, Karteek J, Gayathri MG, Mohammad E, Milton M, Srikanth A, Rajender B, Gouri Shankar L, Padmakumari AP, SubbaRao LV, Sundaram RM, Viraktamath BC, Ravindra Babu V, Kranthi B, Raju M, Patel HK, Sonti RV, Sheshu Madhav M (2021) Mutation resource of Samba Mahsuri revealed the presence of high extent of variations among key traits for rice improvement. ***PLoS One*** 16: e0258816.

- Sohini D, Vishnu Narayanan M, Gokulan CG, Hitendra K Patel HK, Sonti RV (2021) Arms and ammunitions: effectors at the interface of rice and it's pathogens and pests. ***Rice (N Y)*** 14: 94.

Rice crop is susceptible to many biotic and abiotic stresses. The biotic stresses that currently we are trying to address include bacterial blight [caused by a bacterial pathogen *Xanthomonas oryzae pv. oryzae* (Xoo)], sheath blight (caused by a fungal pathogen *Rhizoctonia solani*), and yellow stem borer (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 enhanced tolerance against the above-mentioned biotic stresses. Using functional genomics approach and transcriptome analyses we have identified candidate genomic loci that might be responsible for enhanced tolerance phenotype to these biotic stresses. We are further validating the association of these markers/candidate regions with enhanced tolerance to biotic stresses.

In parallel, we are also characterizing the role of type III secretion system (T3SS) secreted effector proteins of Xoo in induction and suppression of rice immune responses. Xoo employs multiple T3SS secreted effectors such as XopU, XopV, XopP, XopG, and AvrBs2 to suppress rice immune responses that are induced by the interaction of two other effectors, XopQ and XopX. We have further characterized that the XopG interaction with XopQ and XopX is important for suppression of effector (XopQ-XopX) induced immune responses. The XopG E76A and XopG E85A mutations affect the ability of XopG to interact with XopQ-XopX and to suppress effector (XopQ-XopX) triggered immunity. Studies on mechanism of plant defense responses are ongoing in the lab.



When transiently expressed via Agrobacterium (AGL1), the XopG E76A and XopG E85A mutations affect the ability of XopG to interact with XopQ-XopX and to suppress effector triggered immunity.

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

- Understanding the control of meiosis and germ cell formation in plants using *Arabidopsis* as a model
- 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.

Selected recent publications

- Mahesh S, Bethoju K, Nalli A, Frank K, Siddiqi I (2021) Functional analysis of a conserved domain in SWITCH 1 reveals a role in commitment to female meiocyte differentiation in Arabidopsis. ***Biochemical Biophysical Research Communications*** 551: 121-126.

We have further explored the role of a novel gene *SHUKR* (*SKR*) that is required for pollen development and male fertility in *Arabidopsis*. *SKR* is a late emerging gene found only in the eudicots and is absent in the monocots as well as basal angiosperm lineages (collaboration with L Aravind, NIH, USA). We have characterized expression and function of *SKR*. The results supported by the genetic data suggest that *SKR* has a function in meiosis that is required for post-meiotic development of spores into the gametophyte. This is an unexpected finding as the sporophyte and gametophyte form distinct generations in land plants and previous studies indicate gametophyte development to be controlled by genes that act postmeiotically. We find that *SKR* acts through control of protein turnover and loss of *SKR* leads to misregulation of a large number of pollen-enriched genes, many of which are part of the ubiquitin proteasome system (UPS). The results reveal a new regulatory interface between the sporophyte and gametophyte in eudicots.

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 pre-meiotic 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.

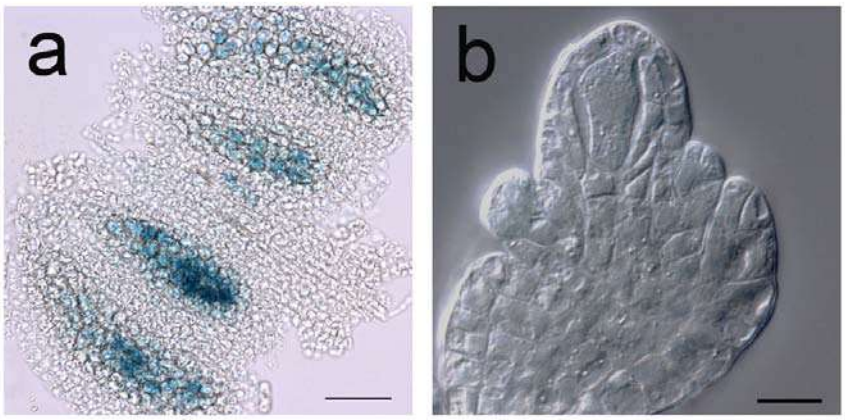


Figure 1: Male-meiosis-specific expression of *proSKR:GUS*.
(a) Meiotic stage anthers. (b) Meiotic stage ovule

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

- Molecular phylogenetics and systematics
- Macroecology & macroevolution
- Soil arthropods
- Tropical forests

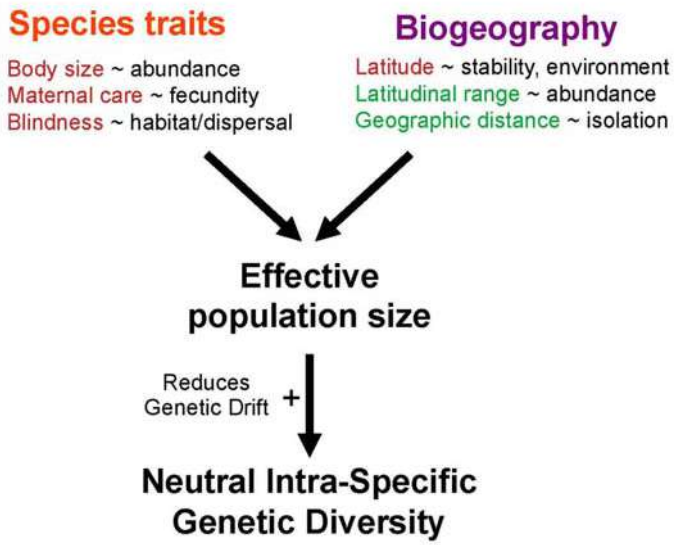
Selected recent publications

- Krishnadas M, Sankaran M, Page N, Joshi J, Machado S, Nataraj N, Chengappa SK, Kumar V, Kumar A, Krishnamani R (2021) Seasonal drought regulates species distributions and assembly of tree communities across a tropical wet forest region. ***Global Ecology and Biogeography*** 30: 1847-1862.
- Joshi J and Agarwal I (2021) Integrative Taxonomy in the Indian Subcontinent: Current Progress and Prospects. ***Journal of the Indian Institute of Science*** 101: 125-149.
- Bharti DK, Edgecombe GD, Karanth KP, Joshi J (2021) Spatial patterns of phylogenetic diversity and endemism in the Western Ghats, India: A case study using ancient predatory arthropods. ***Ecology and Evolution*** 11: 16499-16513.

Tropical forests are storehouses of biodiversity, and identifying the drivers of high biodiversity continues to interest biologists. Below are the major updates on two ongoing projects.

1. Intraspecific genetic diversity is an essential component of biodiversity, as it informs the ecological and evolutionary processes shaping populations. We investigated its drivers in centipedes, an ancient group of soil arthropods with low dispersal ability, showing variation in species traits and biogeography. We found a wide variation in genetic diversity across 120 species representing all centipede orders in COI sequences. Over a fifth of this variation was explained by species traits and biogeography. Genetic diversity was higher in centipedes which were smaller in body size, show maternal care, were distributed at lower latitudes and were separated by greater distances (Bharti et al. 2022; in review)

2. The disproportionately high diversity of orgamisms in tropical rainforests is posited to be due to its age and climatic stability, which allows for persistence and slow accumulation of lineages, "museum", or conversely due to increased speciation rates, "cradles". To test this hypothesis, we modelled the distribution of 473 woody plant species in conjunction with a comprehensive species-level phylogeny. We dissected the spatial patterns of evolutionary diversity using different phylogenetic diversity and endemism measures. We found that Western Ghats followed the museum and the southern Western Ghats is both a museum and cradle model for evolutionary diversity. Our results highlight the global value of the southern Western Ghats – an engine of plant diversification and persistence (Gopal et al. 2022, in prep).



Schematic figure representing the theoretical drivers of intra-specific genetic diversity. Life history traits and biogeography associated with species can influence their effective population size, which has a positive relationship with neutral genetic diversity. Variables with a negative influence on effective population size are highlighted in red and those with a positive influence in green

JYOTSNA DHAWAN

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

From left to right, first row: Jyotsna Dhawan, Lamuk Zaveri, Puja Singh
Second row: Debarya Saha, Swetha Sunder, AS Priti, Ananga Ghosh
Third row: Saher Chawla, Akshita Jukanti, Kartik Jatwani, Tulisa Ray

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

Selected recent publications

- Zaveri L and Dhawan J (2021) Inducible expression of Oct-3/4 reveals synergy with Klf4 in targeting Cyclin A2 to enhance proliferation during early reprogramming. ***Bioscience Biotechnology Research Communications*** 587: 29-35.
- Gala HP⁎, Saha D⁎, Venugopal N, Aloysius A, Purohit G, Dhawan J (2022) A transcriptionally repressed quiescence program is associated with paused RNA polymerase II and is poised for cell cycle re-entry. ***Journal of Cell Science*** 135: jcs259789.
- Yao G, Dhawan J, Barr AR (2022) Editorial: Cellular dormancy-State determination and plasticity. ***Frontiers in Cell and Developmental Biology*** 10: 984347.

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 cell cycle and cell fate in other stem cells. Two recent studies are summarized below:

Non-canonical regulation of RNA polymerase promoter proximal pausing in muscle cell quiescence and activation

Quiescence is well-known to be associated with low transcription, but the mechanisms responsible are still emerging. In cultured myoblasts and muscle stem cells, we found that repression of both total RNA content and active synthesis correlate with decreased RNA Polymerase II (RNAPII) expression and activation. Integrating RNAPII occupancy and transcriptome profiling, we identified repressed networks and a role for promoter-proximal RNAPII pausing in G0. Strikingly, enhanced pausing in G0 was seen on genes networks encoding regulators of RNA biogenesis and release of pausing was associated with increased expression in G1. A targeted screen of RNAPII regulators revealed that knockdown of Aff4 (a positive regulator of elongation) unexpectedly enhances expression of G0-stalled genes and hastens the G0-G1 transition and S phase, while NELFb, a canonical regulator of pausing appears to be dispensable. We propose that Aff4 plays a non-canonical role in RNAPII pausing specifically on G0-repressed genes in muscle cells, contributing to transcriptional control of quiescence and the timing of the G0-G1 transition. (See Fig 1)

An inducible reprogramming system reveals Cyclin A2 as an early target of Oct-3/4 and Klf4

During reprogramming of somatic cells, heightened proliferation is one of the earliest changes observed. While other early events such as mesenchymal-to-epithelial transition have been well-studied, the mechanisms by which the cell cycle switches from a slow cycling state to a faster cycling state are still incompletely understood. We created a 4-Hydroxytamoxifen (OHT) dependent Oct-3/4 Estrogen Receptor fusion (OctER) which could reprogram MEFs to pluripotency. During early reprograming, OctER and Klf4 in combination hastened the cell cycle in an OHT dose-dependent manner, suggesting that OctER is the driver of this transition. We identified Cyclin A2 as a likely target of Oct-3/4 + Klf4, via a dose-dependent induction of Cyclin A2 promoter-reporter activity. Our results suggest that Cyclin A2 is a key early target during reprogramming, and support the view that a rapid cell cycle assists the transition to pluripotency. (See Fig 2)

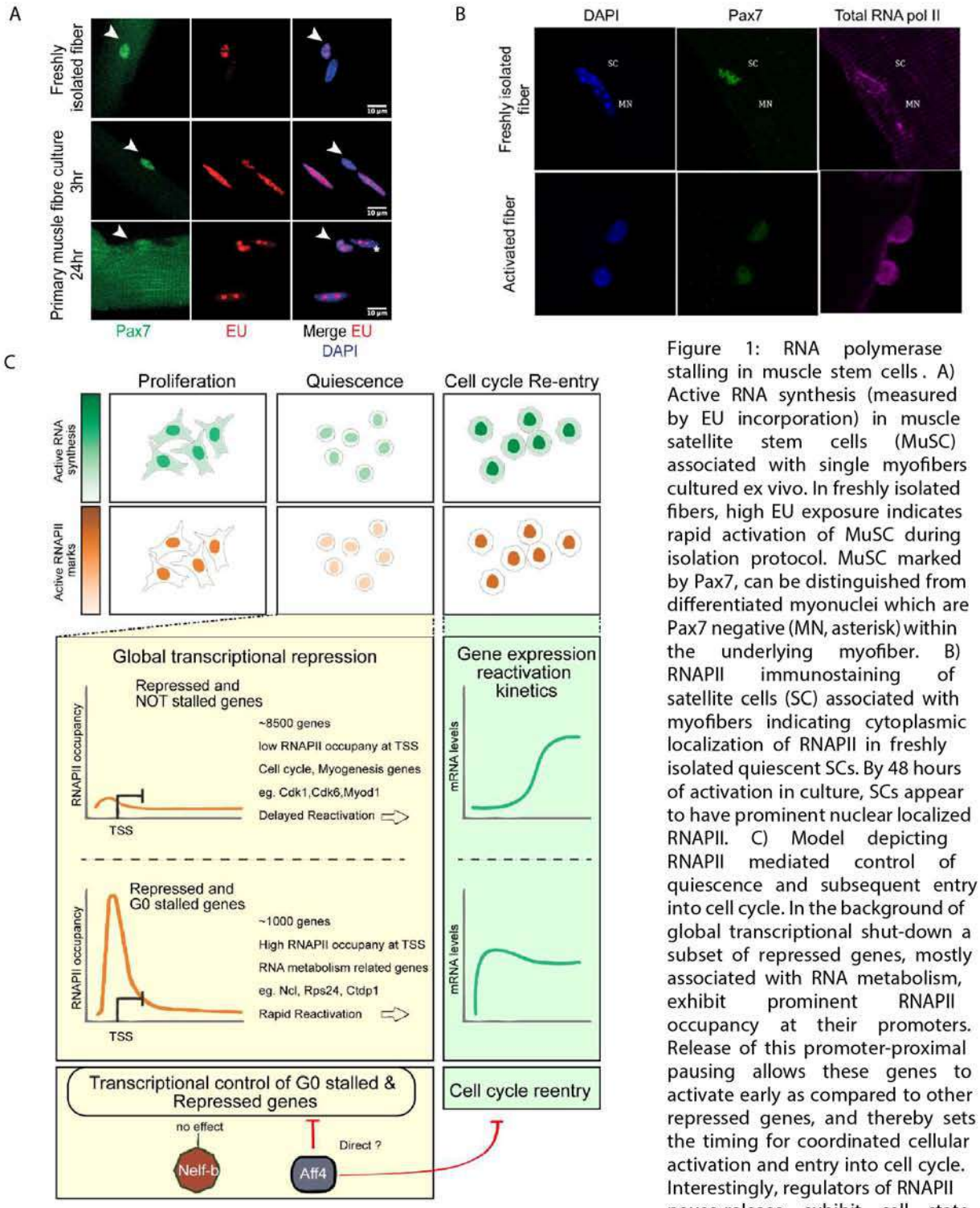


Figure 1: RNA polymerase stalling in muscle stem cells. A) Active RNA synthesis (measured by EU incorporation) in muscle satellite stem cells (MuSC) associated with single myofibers cultured ex vivo. In freshly isolated fibers, high EU exposure indicates rapid activation of MuSC during isolation protocol. MuSC marked by Pax7, can be distinguished from differentiated myonuclei which are Pax7 negative (MN, asterisk) within the underlying myofiber. B) RNAPII immunostaining of satellite cells (SC) associated with myofibers indicating cytoplasmic localization of RNAPII in freshly isolated quiescent SCs. By 48 hours of activation in culture, SCs appear to have prominent nuclear localized RNAPII. C) Model depicting RNAPII mediated control of quiescence and subsequent entry into cell cycle. In the background of global transcriptional shut-down a subset of repressed genes, mostly associated with RNA metabolism, exhibit prominent RNAPII occupancy at their promoters. Release of this promoter-proximal pausing allows these genes to activate early as compared to other repressed genes, and thereby sets the timing for coordinated cellular activation and entry into cell cycle. Interestingly, regulators of RNAPII pause-release exhibit cell state specific functions: Nelfb does not appear to affect quiescence maintenance and activation, whereas Aff4 plays a significant role in restraining expression of G0-stalled genes and premature cell-cycle entry.

KARTHIKEYAN VASUDEVAN

Ecology and Conservation of Endangered Species

From left to right (Front row): Afsar Soghra, K. Rajyalakshmi, Sripuram Srinivas, Siddharth Bhatia, Avni Blotra, Gayathri Sreedharan, Harika Katakam
(Back row): Alka Sahu, Karthikeyan Vasudevan, Yashwant Singh, Ravi Singh, Javaid Hameed

Research Interests

- Disease ecology - understanding dynamics of chytridiomycosis in amphibian populations
- Conservation biology - studying reproductive ecology of a long-lived riverine specialist crocodile - gharial (*Gavialis gangeticus*)
- Toxinology of venoms - understanding envenomation in humans by snakes and address human-snake conflict

Selected recent publications

- Srivastava T and Vasudevan K (2021) Conservation of hangul, Cervus hangulu – Paving the way ahead. ***Current Science*** 121: 485-489.
- Jha A, Seneviratne S, Prayag HS, Vasudevan K (2021) Phylogeny identifies multiple colonisation events and Miocene aridification as drivers of South Asian bulbul (Passeriformes: Pycnonotidae) diversification. ***Organisms Diversity & Evolution*** 21: 783-794.
- Bhatia S, Blotra A, Vasudevan K (2021) Immunorecognition capacity of Indian polyvalent antivenom against venom toxins from two populations of *Echis carinatus*. ***Toxicon*** 201: 148-154.
- Engel MS, et. al. (2021) The taxonomic impediment: a shortage of taxonomists, not the lack of technical approaches. ***Zoological Journal of the Linnean Society*** 193: 381-387.

Our work on amphibians in Tillari Conservation Reserve (TCR), northern Western Ghats has revealed promising abundance and composition of forest dwelling frogs in cashew plantations in the tropical semi-evergreen forest landscape. Plantation crops in tropical human-modified landscapes provide important alternative habitat for biodiversity outside protected areas. Cashew is an important plantation crop and it provides economic and societal benefits. However, its role as a supplementary habitat for frogs is not well understood. We assessed composition and abundance of frog communities in cashew plantations, forest edges, and forest interiors in TCR. Species composition of cashew plantations differed significantly from forests, and was positively influenced by understorey and canopy cover. Cashew plantations had near equal abundance of anurans as that of forest edges and interiors. Reduced understorey and low canopy cover represent habitat modifications that occur in cashew plantations. Cashew plantations in TCR served as important supplementary habitat for anurans.

In TCR, hill streams are seasonal and they support diverse taxa. Among them, frogs use the fluctuating hydrologic regime to reproduce and recruit young into the population. Hydroperiod of seasonal streams is dictated by monsoons. We hypothesised that the monsoon causes a pulse perturbation in streams. Thereby, selection pressure that operates on frogs that prompt adaptations to cope with the fluctuating hydroperiod. We tested this hypothesis on skittering frog (*Euphlyctis cyanophlyctis*) populations between 2018 and 2020 using Capture-Mark-Recapture technique. We estimated capture, recapture, survival probabilities and average displacement of skittering frogs during the monsoon pulse (precipitation with heavy flows) and recovery (no precipitation and receding flows) periods from five seasonal streams. Fitness of frogs influenced tenancy during the hydroperiod and relative humidity influenced frog's displacements in the recovery period. Population was stable over the years when the hydroperiods and intensity of precipitation fluctuated. It implies that strategies that promote resilience to fluctuating hydrologic regimes are present in the frog population. Long-term monitoring data might help in defining thresholds of such resilience in seasonal streams.

Amboli bush frog, Pseudophilautus amboli, a prominent species found in the cashew plantations in Tillari Conservation Reserve, Maharashtra. This frog has direct development and no tadpole stages are involved.

KRISHNAN H HARSHAN

Host-Virus Interactions: Molecular Perspectives

From left to right: Anayat Raffi Sheikh, Amit Kumar, Vishal Sah, Dixit Tandel, Abdul Hamid Siddiqui, Prangya Parmita Sahoo, Poojitha Sai Potharaju, Malabika Bhowmik, Haripriya Parthasarathy, Divya Gupta, Sanjana Bhattacharya, Krishnan H Harshan, Pooja Ravicanti, and Mohan Singh Moodu

Research interests

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

Selected recent publications

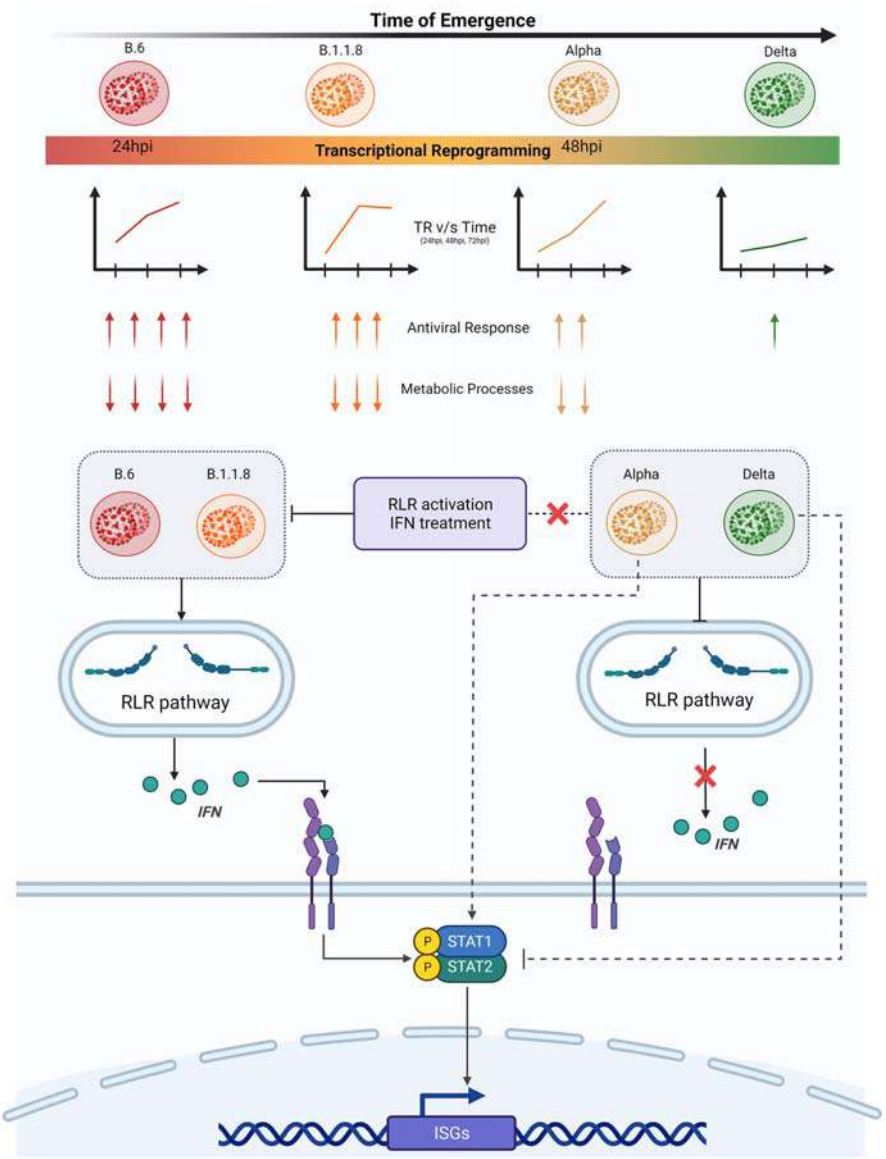
- Gupta D, Parthasarathy H, Tandel D, Sah V, Vedagiri D, Harshan KH (2021) Inactivation of SARS-CoV-2 by β-propiolactone Causes Aggregation of Viral Particles and Loss of Antigenic Potential. ***Virus Research*** 305: 198555.

- Vedagiri D, Gupta D, Mishra A, Krishna G, Bhaskar M, Basu A, Nayak D, Kalia M, Veettil MV, Harshan KH (2021) Retinoic acid Inducible Gene-I like Receptors Activate Snail and Slug to Limit RNA Viral Infections. ***Journal of Virology*** 95: e0121621.

- Gupta D, Ahmed F, Tandel D, Parthasarathy H, Vedagiri D, Sah V, Krishna Mohan B, Khan RA, Kondiparthi C, Savari P, Jain S, Reddy S, Kumar MJ, Khan N, Harshan KH (2022) Equine immunoglobulin fragment F(ab')2 displays high neutralizing capability against multiple SARS-CoV-2 variants. ***Clinical Immunology*** 237: 108981.

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 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 disease outcomes would be keenly studied in understanding the process of viral evolution.

Additionally, through our collaboration with Industry partner VINS Bioproducts Pvt Ltd, we have developed an equine based antibody against SARS-CoV-2 and its has been 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

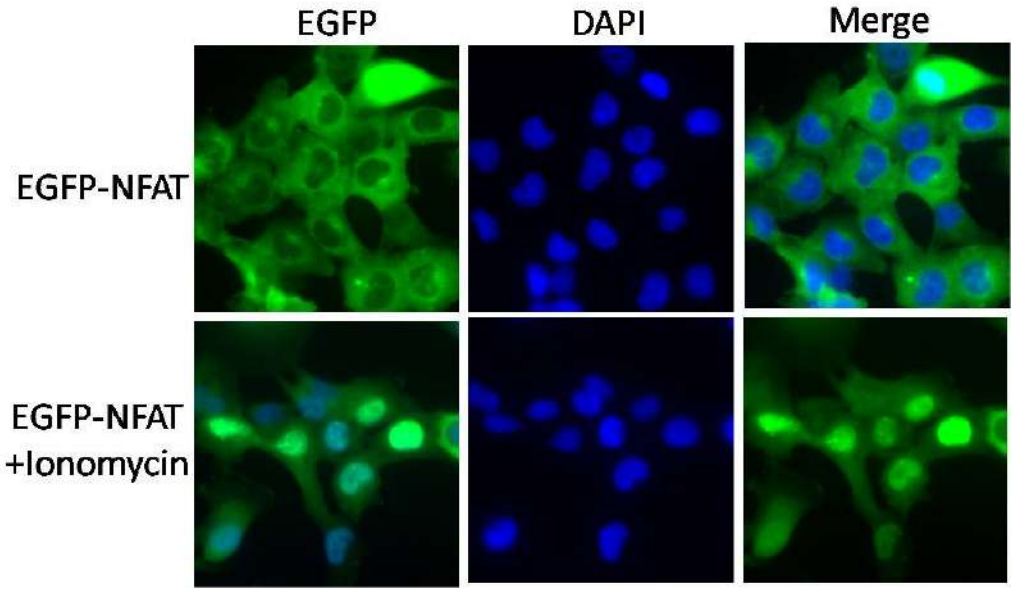
Cardiovascular Biology

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

Research interests

- Cardiovascular diseases, RNA biology, Gene regulation

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.



Ionomycin treatment causes translocation of NFAT from cytosol to nucleus

K THANGARAJ

Evolutionary and Medical Genetics

From left to right: Lomous Kumar, Purushotham V, Narmadha, G. Mala, Nipa Basak, Pratheusa Machha, S. Deepa Selvi Rani, K. Thangaraj, Rajan Kumar Jha, Jaydeep AB, Sagnik Dhar, Sudhakar, Sunil Kumar Tripathi, Haneef
Inset images (top to bottom): Sunitha Kundur, Nitin Tupperwar, Agyaya Pratap, Jagamohan Chhatai, Deepak Kumar Kashyap

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 (2022) Exome sequencing and functional analyses revealed CETN1 variants leads to impaired cell division and male fertility. ***Human Molecular Genetics*** 0: ddac216.

- 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 (2022) The matrilineal ancestry of Nepali populations. ***Human Genetics*** doi: 10.1007/s00439-022-02488-z

- 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.

- Alpaslan-Roodenberg S, et al. (2021) Ethics of DNA research on human remains: five globally applicable guidelines. ***Nature*** 599: 41-46.

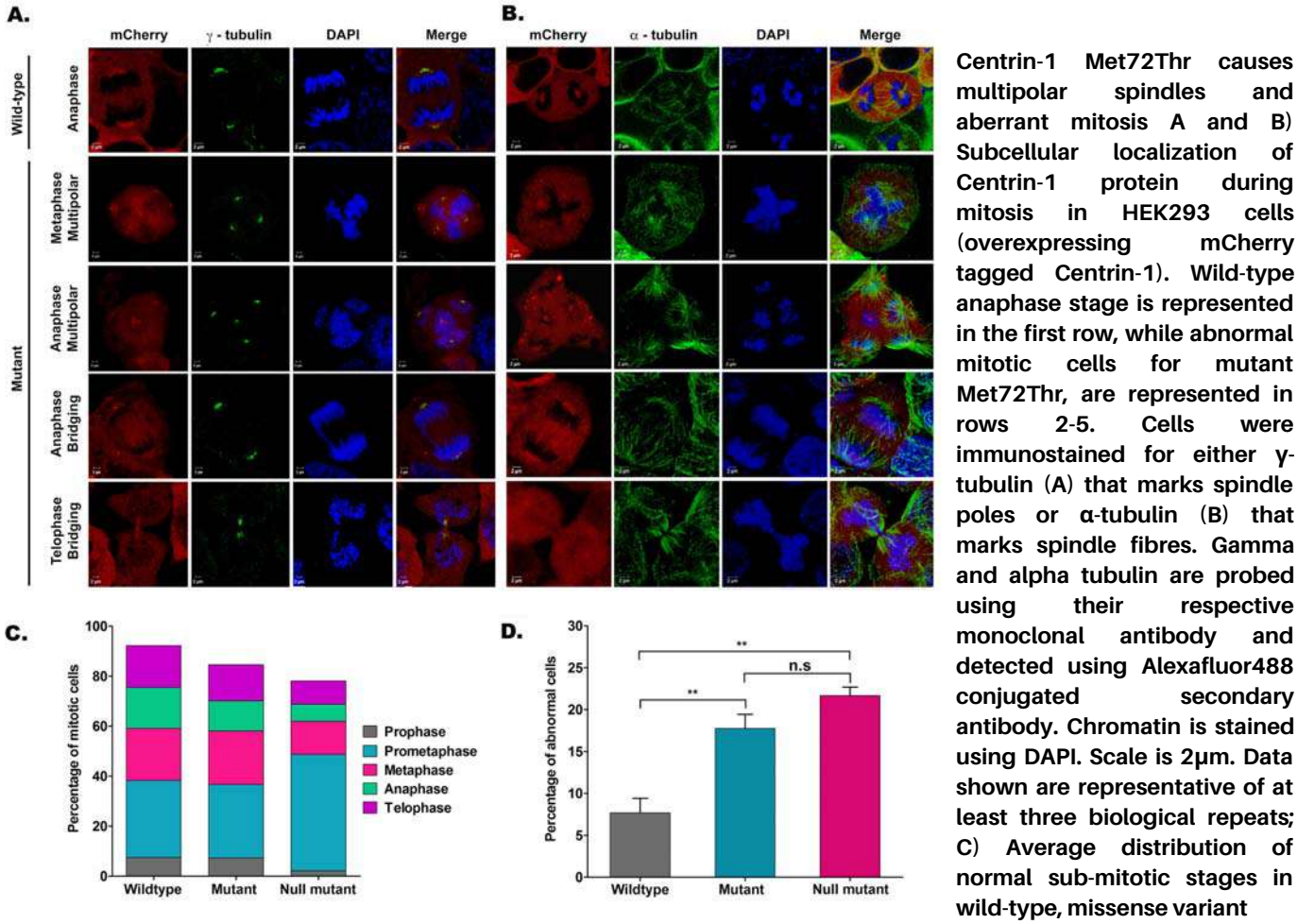
- Kuthethur R, Prasad K, Chakrabarty S, Kabekkodu SP, Singh KK, Thangaraj K, Satyamoorthy K (2021) Advances in mitochondrial medicine and translational research. ***Mitochondrion*** 61: 62-68.

- Badarukhiya JA, Tupperwar N, Nizamuddin S, Mulpur AK, Thangaraj K (2021) Novel FCN2 Variants and Haplotypes are Associated with Rheumatic Heart Disease. ***DNA and Cell Biology*** 40: 1338-1348.

Selected research highlights of my group are as follow: The Tibetan plateau and high mountain ranges of Nepal are one of the challenging geographical regions inhabited by modern humans. To understand the genetic history of these populations, we have analyzed mtDNA sequences of 999 Nepalese and compared with 38,622 published mtDNA sequences from rest of the world. Our analysis revealed that the prehistoric Himalayan settlers of Nepal were similar to that of the low-altitude extant Nepalese (LAN), but differ from contemporary high-altitude Sherpas (*Hum. Genet. 2022*).

In 2014, 157 years after the Sepoy Mutiny of 1857, several unidentified human skeletons were discovered in an abandoned well at Ajnala, Punjab. The most prevailing hypothesis suggested them as Indian soldiers who mutinied during the Indian uprising of 1857. The mtDNA haplogroup distribution and clustering pattern of these skeletons rejected the local ancestry and indicated their genetic link closest possible geographical affinity toward the eastern part of India, largely covering the Gangetic plain region (*Front. Genet. 2021*).

Human spermatogenesis requires an orchestrated expression of numerous genes in various germ cell subtypes. Our previous studies found that about 25% of genetic causes for male infertility, however, about 75% cause for male infertility is not known. Therefore, we performed exome sequencing in 47 idiopathic infertile men, followed by replication study (844 infertile men and 709 controls). We found 17 variants in twelve genes that includes 8 novel genes (*BRDT, CETN1, CATSPERD, GMCL1, SPATA6, TSSK4, TSKS and ZNF318*). One candidate gene *CETN1* variants were functionally characterized and found that p.Met72Thr leads to multipolar cells, fragmented nuclei during mitosis leading to cell death and impaired spermatogenesis (*Hum. Mol. Genet. 2022*).



Centrin-1 Met72Thr causes multipolar spindles and aberrant mitosis A and B) Subcellular localization of Centrin-1 protein during mitosis in HEK293 cells (overexpressing mCherry tagged Centrin-1). Wild-type anaphase stage is represented in the first row, while abnormal mitotic cells for mutant Met72Thr, are represented in rows 2-5. Cells were immunostained for either γ-tubulin (A) that marks spindle poles or α-tubulin (B) that marks spindle fibres. Gamma and alpha tubulin are probed using their respective monoclonal antibody and detected using Alexafluor488 conjugated secondary antibody. Chromatin is stained using DAPI. Scale is 2µm. Data shown are representative of at least three biological repeats; C) Average distribution of normal sub-mitotic stages in wild-type, missense variant Met72Thr and null mutant; D) Quantification of abnormal mitotic cells expressing wild-type, missense mutant and hypomorphic (null) mutant. N > 300 cells per experiment. Error bar represents the SEM. (One-way ANOVA test, ** p<0.05, n.s - nonsignificant).

LEKHA DINESH KUMAR

Wnt Signalling, Cancer, and Biomarker Discovery

From left to right: Rohitesh Gupta, Indresh KG, Mohana Priya, Lekha Dinesh Kumar, Eshani Ganjoo, Ankit Singh, Nilesh Patil

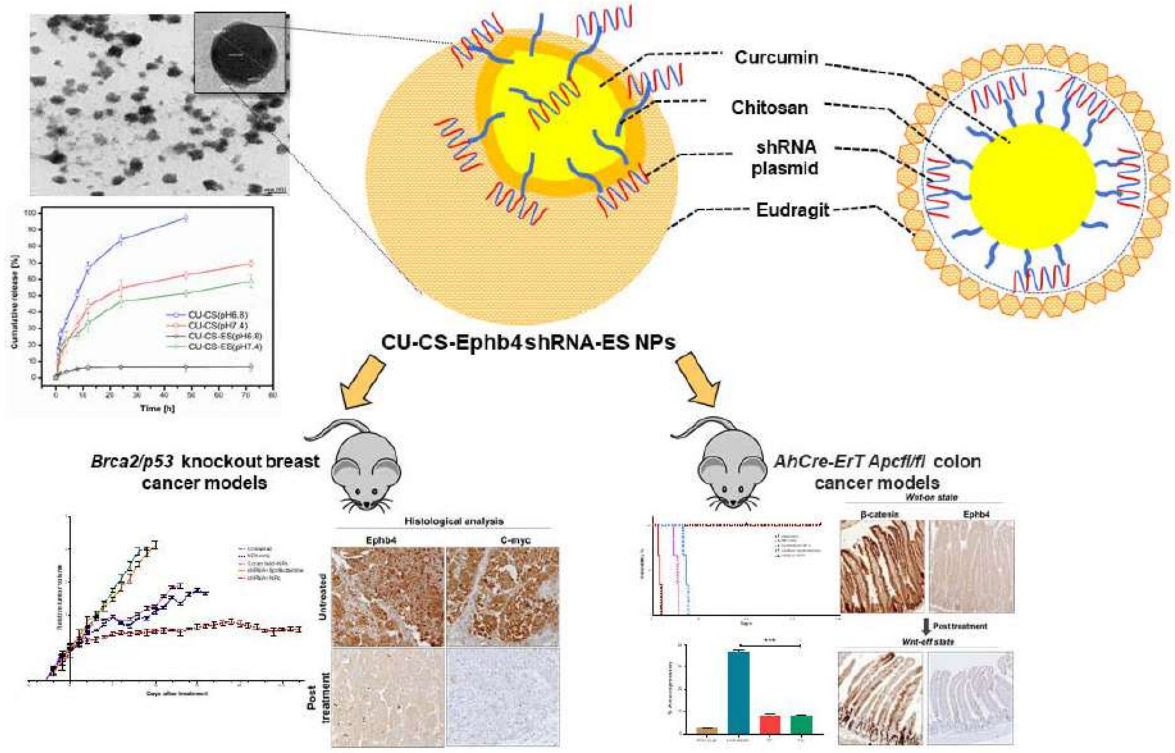
Research interests

- 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 and leukemias
- Mechanisms of drug resistance

Selected recent publications

- Swaminathan G, Shigna A, Kumar A, Byroju VV, Durgempudi VR, Dinesh Kumar L (2021) RNA Interference and Nanotechnology: A Promising Alliance for Next Generation Cancer Therapeutics. ***Frontiers in Nanotechnology*** 3: 694838.
- 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*** 40: 102504.

Cancer is a debilitating disease and one of the leading causes of death in the world. Surgery, chemotherapy and radiotherapy have been the main stream modalities in the management of the disease. Due to their various draw backs, there is an imminent need for novel and targeted therapies with least side effects. RNA interference (RNAi) based gene therapies has gained attention due to its precise potential for targeting multiple genes, thus ushering promises for the development of biological drugs. However, the delivery to primary site of tumors remains a challenge for RNAi based therapies. Nanoparticles, with their enhanced permeability and retention (EPR) effect, have been found to overcome the limitations of RNAi-based therapies. With their high transportation capacity, nanocarriers could target RNAi molecules to tumor tissues and protect them from enzymatic degradation. Accumulating evidence has shown that tyrosine kinase Ephb4 is over-expressed in various cancers. Therefore, we report here the development and pre-clinical validation of curcumin-chitosan-loaded: eudragit-coated nanocomposites conjugated with Ephb4 shRNA as a feasible bio-drug to suppress colon and breast cancer. The proposed bio-drug is non-toxic and compatible with a higher uptake efficiency and we have demonstrated the effective site-specific delivery of this bio-drug and the successful silencing of their respective target genes *in vivo* in autochthonous knockout models of breast and colon cancer. While mammary tumors showed a considerable decrease in size, oral administration of the bio-drug conjugate to Apc knockout colon models exhibited prolonged animal survival period by six months. Hence, this study has provided empirical proof that the combinatorial approach involving RNA interference and nanotechnology is a promising alliance for next-generation cancer therapeutics.



Graphical abstract showing drug delivery to mice cancer models using RNA interference and nanotechnology and further validation for prolonged survival

MANDAR V DESHMUKH

Molecular Basis of Evolutionary Divergence in RNAi Initiation

From left to right, top row: Upasana Rai, Sneha Paturi, Ramdas Aute, and Jaydeep Paul
Central row: Mandar V Deshmukh and Debadutta Patra
Bottom row: Priti Chanda Behera
Background: 600 MHz NMR Spectrometer

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. We show that the subtle differences in structure and dynamics in highly homologous proteins incite the evolutionary divergence in the RNAi pathway. These studies extend our understanding of one of the fundamental biological processes that are vital in infection, cancer, and development.

Selected recent publications

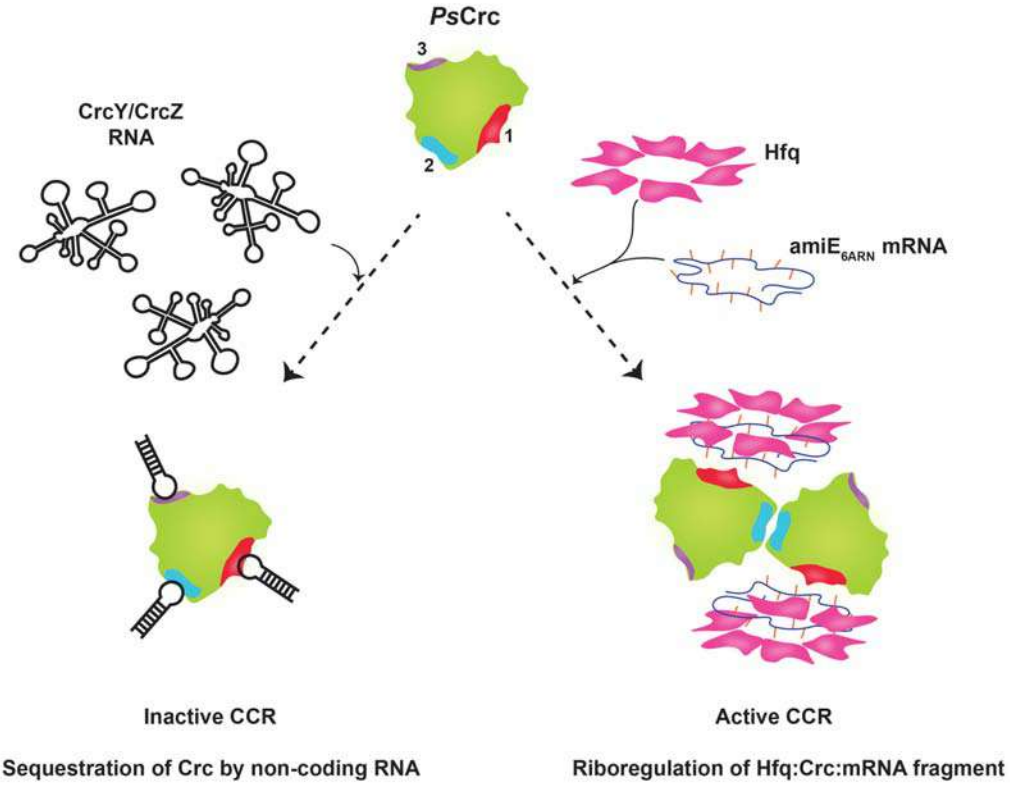
- Paturi S and Deshmukh MV (2021) A glimpse of "Dicer Biology" through the structural and functional perspective. ***Frontiers in Molecular Biosciences*** 8: 643657.

- Sharma R, Paul J, Paturi S, Ray MK, Deshmukh MV (2022) Crc of *Pseudomonas syringae* Lz4W utilizes the dominant RNA binding site for mutually exclusive interactions with Hfq:mRNA and CrcY/Z RNA. ***Journal of Magnetic Resonance*** 10-11: 100047.

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 the RNAi initiation is a convoluted dynamic process tailored for evolutionary advantages to organisms.

Towards this aim, we have defined the functional roles of RDE-4 in *C. elegans*, DRB2, DRB3, DRB4, and DRB7.2 in *A. thaliana* and R2D2 in *D. melanogaster*. During this year, we showed that the assembly of the DRB4:DRB7.2 complex is a critical step in regulating the endo-IR precursor RNA processing in plants. The structural divergence in DRB4D3 from its homologues in humans and flies (TRBPD3/R2D2D3/LoqsPD-D3) is a significant event that allows plants to tailor the components of their RNAi machinery for diverse gene regulatory pathways.

Our results imply a delicate balance in a highly homologous pathway that is tuned to alter the fate of gene regulation. Surprising heterogeneity in the structure and function of dsRBPs suggests that the RNAi initiation is unique for each organism and depends on the step-wise assembly of the Dicer, dsRBP, and the initiator dsRNA. Evolutionary differences in the key RNAi components imply that higher eukaryotes have tailored their RNAi pathway uniquely to adapt to environmental stress and to improve immune response.



A proposed model for the function of PsCrc in two distinct pathways. PsCrc utilizes its three distinct binding sites to associate with regulatory non-coding RNA (CrcY/CrcZ RNA) during the inactive CCR (left panel). The engagement of all three RNA interaction sites of PsCrc to stabilize Hfq:Crc:mRNA complex in the CCR active ribo-regulation (right panel).

MANJULA REDDY

Bacterial Cell Wall Synthesis and its Regulation

From left to right (First row): Balaji Venkataraman, Pavan Kumar Chodisetti (Second row): Suraj Meher, Nilanjan Som, Shambhavi Garde, Manjula Reddy, Vaidehi Rajguru, Bhargavi Krishna Sree, Raj Bahadur (Third row): GSN Reddy, Krishna Leela, Moneca Kaul, Krishna Chaitanya; Fourth row: Hanumantha Rao, Shravan Balasubramaniam

Research interests

- Understanding cell wall synthesis and its regulation

Selected recent publications

- Bahadur R, Chodisetti PK, Reddy M (2021) Cleavage of Braun's lipoprotein Lpp from the bacterial peptidoglycan by a paralog of l,d-transpeptidases, LdtF. ***Proceedings of the National Academy of Sciences of the United States of America*** 118: e2101989118.

- Lee MS, Hsieh KY, Kuo CI, Garde S, Reddy M, Chang CI (2022) Structural basis for the peptidoglycan editing activity of YfiH. ***mBio*** 13: e0364621.

- Mallikarjun J, SaiSree L, Hima Bindu P, Anupama K, Reddy M, Gowrishankar J (2022) Modulation of RecFORQ- and RecA-mediated homologous recombination in Escherichia coli by isoforms of translation initiation factor IF2. ***Journal of Bacteriology*** 204: e0056921.

Peptidoglycan (PG) is an essential shape-defining constituent of most bacterial cell walls. It is a large, covalently cross-linked macromolecule made up of several linear glycan polymers cross-bridged to each other by short peptide chains forming a mesh-like sacculus. Because PG forms a continuous network around the bacterial cytoplasmic membrane, opening the mesh by cleavage of the cross-bridges is critical for insertion of new PG material during its expansion. We have earlier shown a set of redundant cross-link specific endopeptidases, MepS and MepM are crucial for PG expansion and hence for cell viability in *Escherichia coli.* In an attempt to find additional factors required for PG enlargement, we discovered that overexpression of MltD, a membrane-bound lytic transglycosylase that cleaves the glycan strands of the PG sacculi compensates the absence of MepS and MepM. Further genetic and biochemical analyses established a role for MltD in PG enlargement along with the endopeptidases, MepS and MepM. Interestingly, MltD exhibits a complex multi-layered regulation at the step of post-translational stability. It is degraded by a periplasmic proteolytic machinery comprised of an adaptor-protease duo, NlpI-Prc and in addition, undergoes RpoS-dependent stationary-phase specific degradation. Overall, our results show that coordinated cleavage of both the glycans and the peptide cross-links facilitates the opening of the PG mesh for successful expansion of the cell wall during growth of a bacterium.

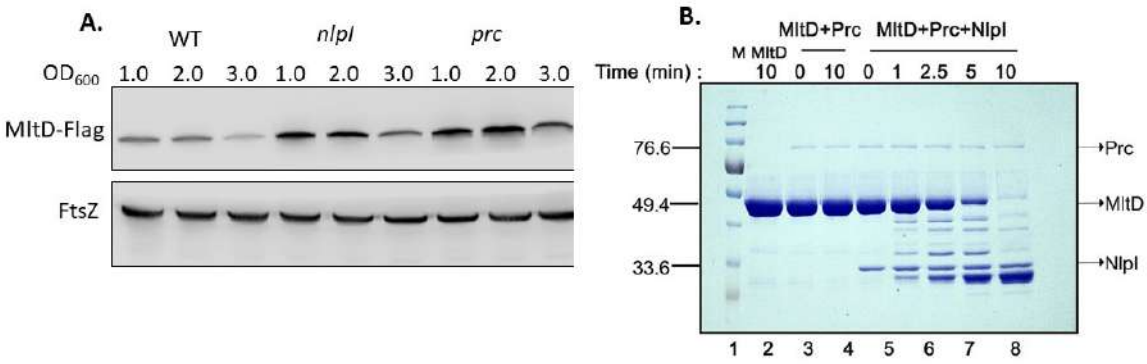


Fig. 1. MltD is a substrate of NlpI-Prc proteolytic system. A. Western blot showing MltD-Flag levels in wild type (WT), and its mutant derivatives lacking NlpI or Prc. Cells were collected at regular intervals, and cell lysates were separated by SDS-PAGE and processed. FtsZ is used as a loading control. B. In vitro degradation assay showing the degradation of MltD by addition of NlpI, Prc or both. M is mol wt marker.

MEGHA KUMAR

Cell and Developmental Biology

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

Research interests

- Developmental biology
- Cell biology
- Developmental genetics
- Neurodevelopment
- Mitosis

Selected recent publications

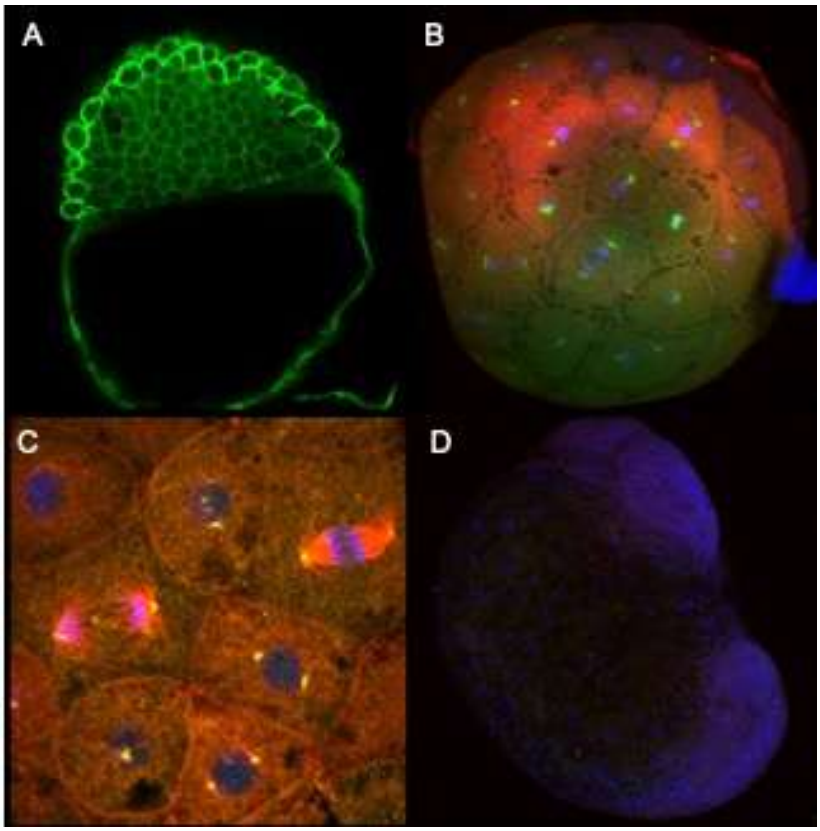
- Matharu NK, Yadav S, Kumar M, Mishra RK (2021) Role of vertebrate GAGA associated factor (vGAF) in early development of zebrafish. ***Cells and Development*** 166: 203682.

- Iyer S, Mukherjee S, Kumar M (2021) Watching the embryo: Evolution of the microscope for the study of embryogenesis. ***BioEssays*** 43: e2000238.

- Mukherjee S, Iyer S, Prasad T, Kumar M (2021) Epigenetic Regulation of Chromatin during Mitosis in Embryos. ***Journal of Embryology & Stem Cell Research*** 5: 1-6.

- Kumari A, Kumar C, Pergu R, Kumar M, Mahale SP, Wasnik N, Mylavarapu SVS (2021) Phosphorylation and Pin1 binding to the LIC1 subunit selectively regulate mitotic dynein functions. ***Journal of Cell Biology*** 220: e202005184

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. We use zebrafish as the model system to study cell division dynamics during embryonic development. The zebrafish embryos are amenable to live cell imaging, genetic manipulation and high throughput genetic screens. My group is also interested in ecotoxicology and embryo toxicology. In one of our projects, we aim to assess the impact of common industrial byproducts on embryonic development. Our long-term goal is to elucidate the molecular mechanisms which form the basis of developmental defects upon exposure to these industrial byproducts.



A: Fluorescence image of zebrafish blastula, with phalloidin at cell membranes. B: Zebrafish blastula with DNA (blue), spindle pole (green) and tubulin cytoskeleton (red). C: High resolution confocal image of mitotic cells of zebrafish blastula. D: High resolution confocal sum projection reconstruction of 1 day old zebrafish embryo.

MEGHNA KRISHNADAS

Community and Functional Ecology

From left to right: Ashish Nambiar, Leela Prasad, Vikhyath Premugh, Lavanya Vanga, Meghna Krishnadas, Rishiddh Jhaveri, Vinayak Saini, Rajaditya Das, Sharath, Malvika Kamath

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.

Selected recent publications

- Krishnan A, Osuri AM, Krishnadas M (2022) Small mammals reduce distance dependence and increase seed predation risk in tropical rainforest fragments. ***Biotropica*** Early view. https://doi.org/10.1111/btp.13137.

- Krishnadas M, et al. (2021) Seasonal drought regulates species distributions and assembly of tree communities across a tropical wet forest region. ***Global Ecology and Biogeography*** 30: 1847–1862.

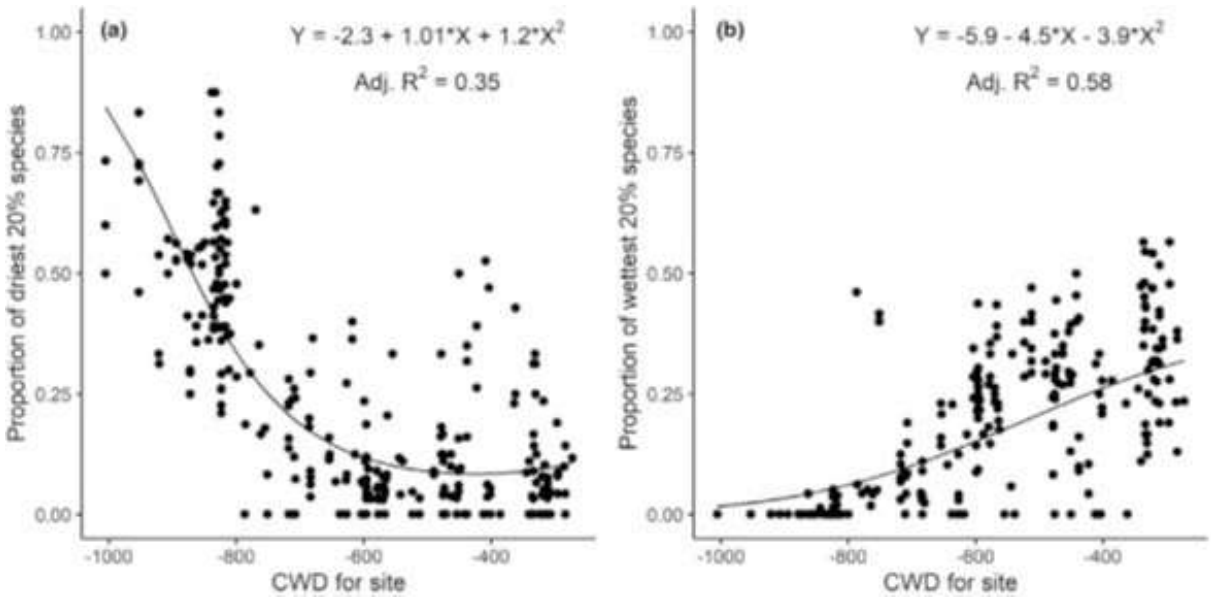
- Krishnadas M, Stump SM (2021) Dispersal limitation and weaker stabilizing processes decrease the ability of forest fragments to maintain diversity. ***Journal of Ecology*** 109: 2137-2151.

- Shahabuddin G, Goswami R, Krishnadas M, Menon T (2021) Decline in forest bird species and guilds due to land use change in the Western Himalaya. ***Global Ecology and Conservation*** 25: e01447.

This past year, our lab focused on the following objectives:

- The role of large-scale climate gradients in shaping species distributions
- The role of intra- and interspecific trait variation in mediating species distributions
- Changes to biotic interactions in human-modified forest

Towards the first objective, I analyzed how seasonal drought influences tree species distributions across the Western Ghats. The second objective was explored via three projects, two of which were MSc thesis and the third being led by a JRF funded by SERB Startup Research Grant. In his MSc thesis, Ashish Nambiar from Wildlife Institute of India explored the relative extent of trait variation within and across six tree species across an elevation gradient (200-2000 m ASL). Rajaditya Das from IISER-Pune focused on environmental gradients at smaller spatial scales of light and water availability across a fragmented forest. The third project in this objective, funded by SERB project, looks at intraspecific trait variation in the distribution of tree species in dry forests of the Eastern Ghats of peninsular India. Finally, the third objective is being explored by my PhD students Rishiddh and Vinayak, aided by dissertation students and interns in the lab. Rishiddh and MSc student Tejaswini conducted a field study to assess whether species' leaf mass per area (LMA), indicative of defensive capacity, explain spatial patterns in the herbivory they experience as seedlings. Vinayak is exploring how plant traits correlate with the soil microbiome that plants cultivate around them in a tropical wet forest.



CWD = climatic water deficit

M M IDRIS

Bio-mechanisms of Regeneration

From left to right: Sarena Banu, V. Naga Sowmya, P.V. Anusha. Mohammed Idris

Research interests

- Understanding the biomechanism of regeneration in alternate model animals
- Understanding the biomechanism of wound healing in zebrafish model system
- Development of primary reference standard and impurities for Biologics
- Understanding the SARS-CoV-2 infection in host human.

Selected recent publications

- Banu S, Gaur M, Nair S, Ravikrishnan T, Khan S, Mani S, Bharathi S, Mandal K, Anusha Kuram N, Vuppaladadium S, Ravi R, Murhty Ch. LN, Quoseena M, Sarath Babu N, Idris MM (2022) Understanding the complexity of epimorphic regeneration in zebrafish: A Transcriptomic and Proteomic approach. ***Genomics*** 114: 110300.

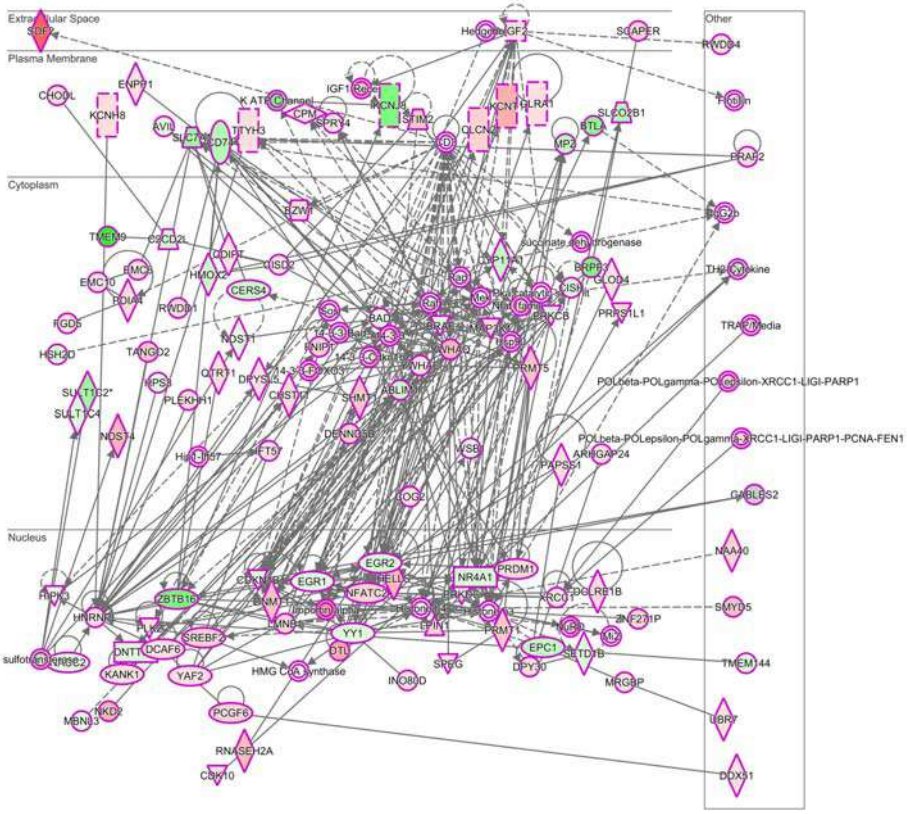
- Enayathullah MG, Parkeh y, Banu S, Ram S, Nagara R, Kumar BK, Idris MM (2022) Gramicidin S and Melittin - Potential anti-viral therapeutic peptides to treat SARS-CoV-2 infection. ***Scientific Reports*** 12: 3446.

- Singh N, Dev I, Pal S, Yadav SK, Idris MM, Ansari KM (2022) Transcriptomic and Proteomic insights into patulin mycotoxin-induced cancer-like phenotypes in normal intestinal epithelial cells. ***Molecular and Cellular Biochemistry*** 477: 1405-1416.

Our group works on understanding the molecular and genetic aspects involved in tissue and organ regeneration in alternate model animals like zebrafish, geckos, ascidians and echinoderms. Understanding the bio-mechanisms of regeneration and the association of various genes (or proteins) in the regenerating environment is of high significance, as it might help us engineer non-regenerating systems into regenerating systems for therapy and healing. Our group also works on in understanding the biomechanism of wound healing in zebrafish model system involving genomics and proteomics approaches.

Epimorphic regeneration of zebrafish caudal fin tissue is complex and complete. A total of 1408 genes and 661 proteins were found differentially regulated during regeneration of zebrafish caudal fin tissue based on high throughput transcriptomics and iTRAQ based quantitative proteomics analyses. PRMT, SLC, interleukin, HOX, neurotransmitter and several novel genes were found to be associated with regeneration for its differential regulation during the mechanism. Based on the network and pathway analysis it was found that the differentially regulated genes and proteins were found allied with cell cycle control of chromosomal replication, Nervous system development and cellular development, growth and proliferation pathway. This study has mapped a detailed insight of the gene/protein changes in regenerating tissue more effectively.

Our group is also involved in understanding the role of innate immunity in human during SARS-CoV-2 infection. We have studied the antimicrobial properties of Gramicidin S, melittin and defensin during SARS-CoV-2 infection. It was found that many defensin genes were downregulated in SARS-CoV-2 infection, suggesting that innate immunity is compromised in SARS-CoV-2 infection. Antimicrobial activity of Gramicidin S and melittin, demonstrated that it is a promising candidate for repurposing to treat viral infections. Our group also works on the development of primary reference standards for biopharmaceuticals, monograph development and DNA barcode development for medicinal plants as per the requirement of Indian Pharmacopeia commission.



Cellular development, growth and proliferation pathway associated with zebrafish caudal fin regeneration based on network pathway analysis of differentially expressed genes/proteins

MUKESH LODHA

Mechanism of Epigenetic Inheritance in Plants

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

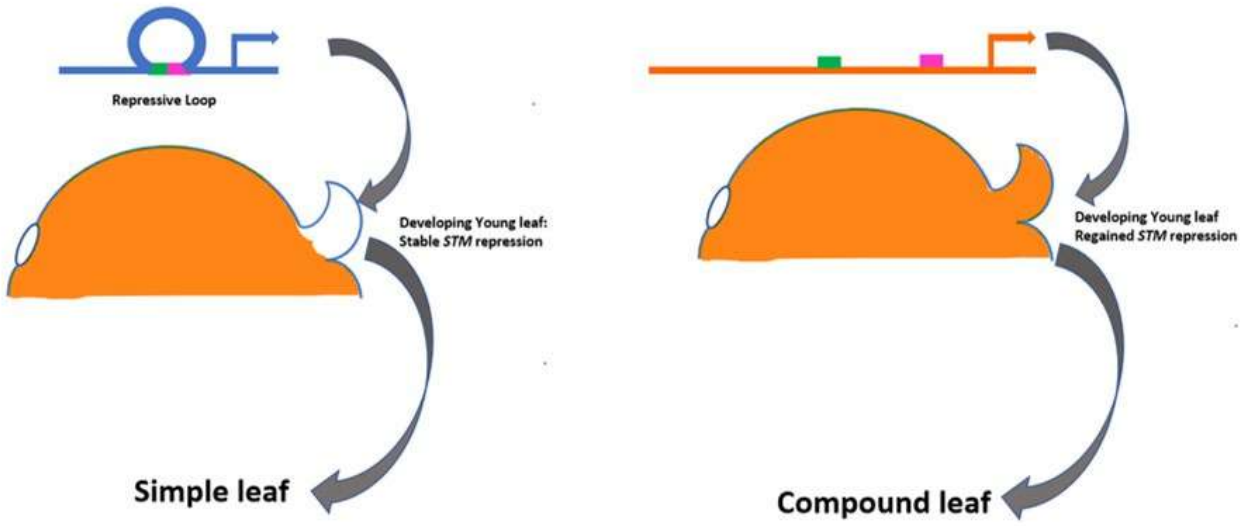
Research interests

- Plant epigenetic
- Developmental biology

Selected recent publications

- Jampala P, Garhewal A, Lodha M (2021) Functions of long non-coding RNA in *Arabidopsis thaliana* (Review). ***Plant Signaling and Behavior*** 16: 1925440.

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. A large share of our understanding of epigenetics is achieved through developmental genes. Our group is using one of the important developmental regulators, SHOOT MERISTEMLESS (STM) as a tool to understand epigenetic regulation in plants. It is a homeodomain transcription factor. It plays important role in shoot meristem stem cell regulator and determining factors in leaf complexity. In simple and compound leaf species STM is expressed in the shoot apical meristem and is down regulated in leaf primordia. In simple leaf species 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 inleaf primordial but is not maintained. STM reactivation in developing leaves is necessary for compound leaf formation. 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 which recruits it to the locus. 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 not formed. As a result of this STM regains expression and transforms developing leaf into a compound one. Very likely, loop formation is determined by the distance between the Polycomb and Trithorax recruiting elements.



Model depicting development of simple and compound leaves. Orange color represents zone of STM expression

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

- Biochemical and biophysical studies characterizing macromolecular interactions. Main focus on the interaction of different forms of DNA (double, triple and quadruplex forms) with natural and synthetic small molecules and metals.
- Studies to understand the mode of interaction of synthetic anti cancer molecules in enhancing anti-cancer/pro-apoptotic activity among cancer cells and reduce cancer cell proliferation both under *in vitro* and *in vivo* conditions
- Research on the aspects that bring industry and academics together

Selected recent publications

- Singu PS, Chilakamarthi U, Mahadik NS, Keerti B, Valipenta N, Mokale SN, Nagesh N, Kumbhare RM (2021) Benzimidazole-1,2,3-triazole hybrid molecules: synthesis and study of their interaction with G-quadruplex DNA. ***RSC Medicinal Chemistry*** 12: 416-429.
- Tokala R, Mahajan S, Kiranmai G, Sigalapalli DK, Sana S, John SE, Nagesh N, Shankaraiah N (2021) Development of β-carboline-benzothiazole hybrids via carboxamide formation as cytotoxic agents: DNA intercalative topoisomerase IIα inhibition and apoptosis induction. ***Bioorganic Chemisry*** 106:104481.

- Sigalapalli DK, Kiranmai G, Devi GP, Tokala R, Sana S, Tripura C, Jadhav GS, Kadagathur M, Shankaraiah N, Nagesh N, Babu BN, Tangellamudi ND (2021) Synthesis and biological evaluation of novel imidazo[1,2-a]pyridine-oxadiazole hybrids as anti-proliferative agents: Study of microtubule polymerization inhibition and DNA binding. ***Bioorganic and Medicinal Chemisry*** 43: 116277.

- Sigalapalli Dk, Kiranmai G, Tokala R, Tripura C, Ambatwar R, Nunewar SN, Kadagathur M, Shankaraiah N*, Nagesh*, Babu BN*, Tangellamudi ND (2021) Targeting Tubulin Polymerization and DNA Binding of 4-Thiazolidinone -umbelliferone Hybrids: Synthesis and Cytotoxicity Evaluation. ***New Journal of Chemistry*** 45: 18908-18923.

- Swain B, Abhay, Singh P, Angeli A, Aashritha K, Nagesh N, Supuran CT, Arifuddin M (2021) 3-Functionalised benzenesulphonamide based 1,3,4-oxadiazoles as selective carbonic anhydrase XIII inhibitors: Design, synthesis and biological evaluation. ***Bioorganic Medicinal Chemistry Letters*** 37: 127856.

A series of copper(II) compounds 1–4 were synthesized and developed as fluorogenic probes to measure the cardiac marker homocysteine (Hcy) without any interference from other bioanalytes prevalent in human blood plasma including, cysteine and glutathione. Water solubility, remarkable fluorescence enhancement (55–111 fold), and low detection ability (nearly 2.5 μM) make the probe suitable for clinical testing of cardiac samples. Results from clinical examination of cardiac samples showed reliability in the results obtained. Testing the samples with out synthetic molecular probe and comparison with a clinically approved commercial immunoassay kit, validates the prospect of the molecular probe for direct measurement of Hcy in human plasma.

Continuous monitoring of stress through detecting specific biochemical markers such as cortisol plays a crucial role in the early detection of various diseases. Electrochemical aptamer sensor involving binding induced conformational change allows the continuous measurement of biomarkers. A reagent-less aptamer-based biosensing platform that allows a continuous and real-time cortisol measurement is developed in this context. The aptamer is conjugated with methylene blue, which acts as a redox reporter to probe the cortisol binding quantitatively on the sensor surface. The cortisol specific aptamers were chemically modified with amine and thiol functional groups to facilitate redox reporter conjugation and attachment of aptamer to a gold electrode, respectively. The sensor achieves a clinically meaningful cortisol concentration ranging from 0.05 ng/mL to 100 ng/mL and provides good selectivity when challenged with structurally similar targets. The reagent-less measurement capability was also demonstrated using an undiluted human serum. The newly developed cortisol sensor can enable the systemic cortisol measurement for providing insights into cortisol related clinical conditions and medical treatments.

Besides this, several studies involving synthetic molecules interaction with macromolecules were also carried out. Among them, the 4-thiazolidinone-based indolo-pyrroloazepinone and indolo/pyrroloazepinone-oxindoles conjugates have shown excellent anticancer activity along with Topoisomerase I inhibition. These sets of molecules are candidates for the preparation of anti-cancer molecules.

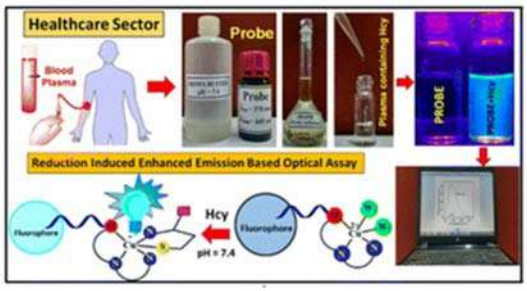


Figure-1

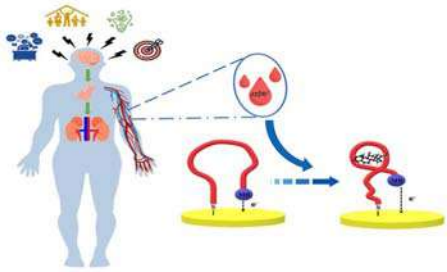


Figure-2

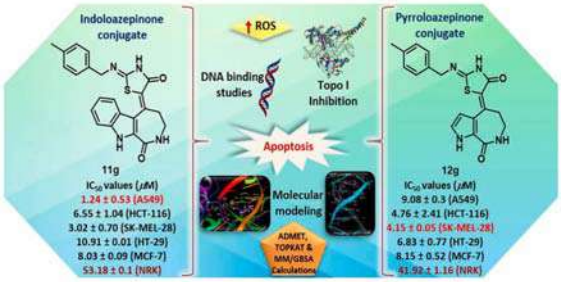


Figure-3

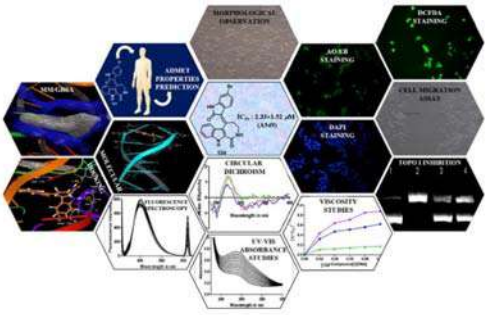


Figure-4

Fig 1: Copper(II) compounds interaction specifically with Homocysteine with enhanced fluorescence. This unique molecule is used specifically to develop a synthetic probe for the detection of homocysteine in human plasma.
Fig 2: Development of reagent-free and reusable electrochemical aptamer-based cortisol sensor. This electrochemical sensor can be used to measure cortisol in undiluted human serum.
Fig 3: Design, synthesis of DNA-interactive 4-thiazolidinone-based indolo-pyrroloazepinone conjugates as potential cytotoxic and topoisomerase I inhibitors. These synthetic conjugates were shown to exhibit anticancer and Topo I inhibition activity.
Fig 4: The indolo-pyrroloazepinone-oxindoles derivatives were also exhibited potential cytotoxicity among cancer cells, has DNA-intercalating ability and inhibitors of Topo I. These sets of molecules were also shown to exhibit potential anti-cancer acitivity.

PAVITHRA L CHAVALI

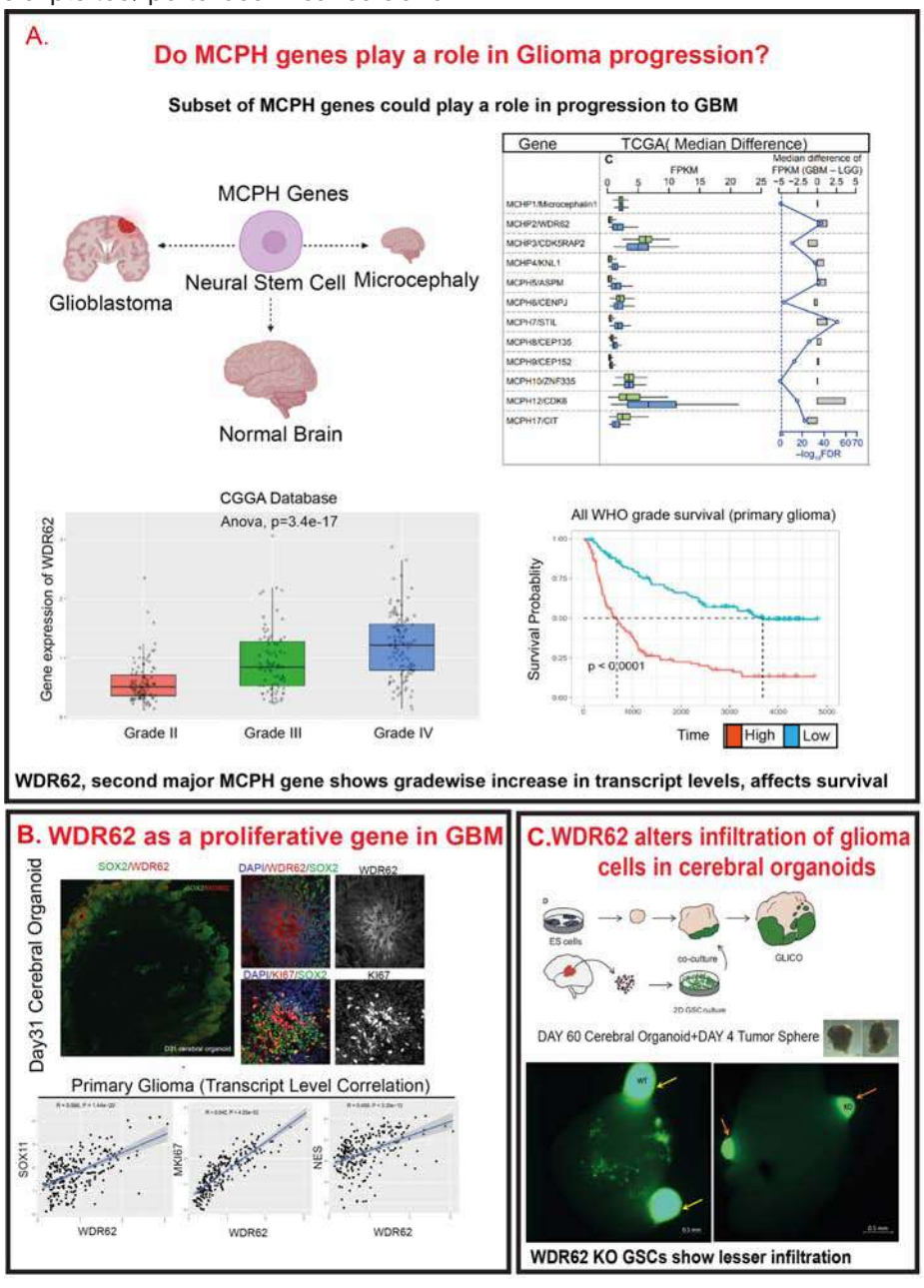
Cellular and Developmental Biology

From left to right: Rajashree Ramaswami, Tejas, Deena David, Dhruv Kumar Shakyawar, Pavithra Chavali, Sourav Ganguli, Mallesh, Shwetha, Aswathy krishnan

Research interests

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

Genes regulating early embryonic development are increasingly shown to play roles in diseases such as cancer and are also utilised by pathogens for their sustenance. In this context, our lab studies the roles of certain neurodevelopmentally important genes, called Microcephaly genes (MCPH genes), the loss of which leads to small brain phenotype in humans. Interestingly, these genes are key players in cancers and infections, although the molecular mechanisms remain unclear. Research in our lab focuses on elucidating the roles of such major MCPH genes in neural development and identify if the same pathways are exploited/ perturbed in cancers and other diseases.In the past year, we categorised our work into role of developmental proteins in cancers and infections, especially in the context of SARS-CoV-2. In the last year we carried out research on two MCPH genes namely, WD40 repeat containing protein 62 in neural cancers and Musashi1 in SARS-CoV-2 infections. We have deciphered how the developmental protein WDR62 is altered in higher grade cancers and its implications in disease progression. Similarly, we have identified a role of stem cell RBP Msi1 in SARS CoV2 biology, where in the stem cells remain less permissive for infection.



Computational analysis of TCGA and CGGA datasets for median difference between Lower Grade Glioma and Glioblastoma for MCPH genes shows that multiple MCPH genes, including WDR62 is overexpressed in higher grade gliomas. B. Immunostaining of human cerebral organoid showing staining of WDR62, SOX2 and KI67. Bottom panel shows correlation of WDR62 with proliferative marker KI67 and with stem cell marker SOX11 and NESTIN in patient samples. C. GliCOR model of invasion using wild type brain organoids and tumor spheres from wild type and WDR62 Knock-out Glioma cells depicts invasion by WDR62 KO is defective.

P CHANDRA SHEKAR

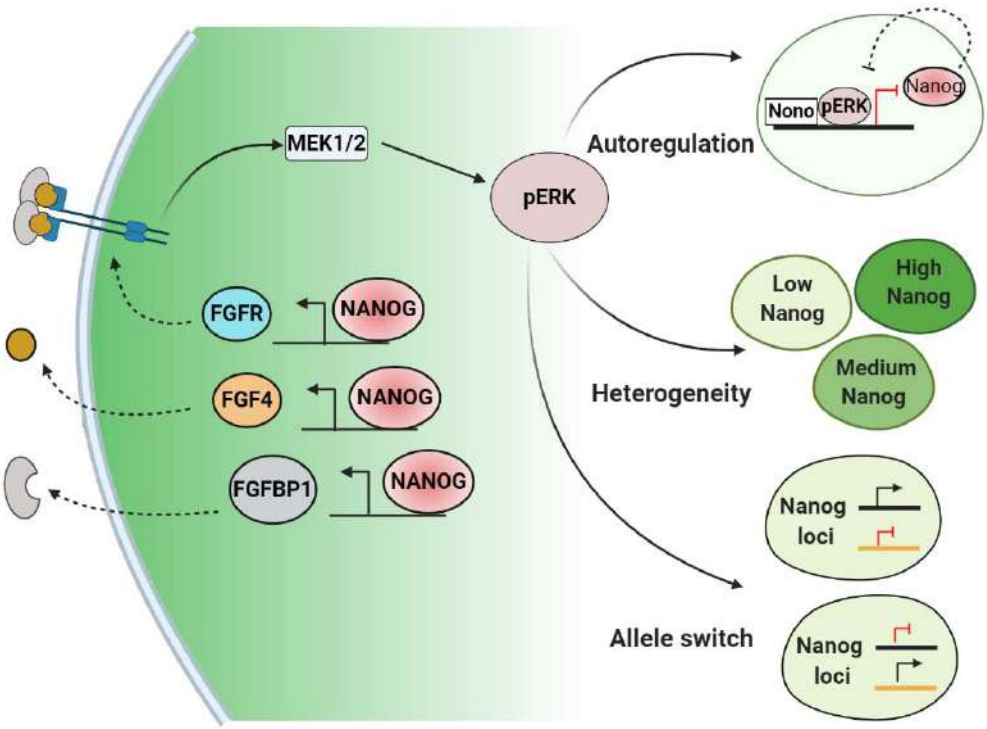
Early Embryonic Development in Mouse

From left to right: Satish, Vishnu V Vijay, P Chandra Shekar, Hanuman T Kale, Mansi Srivastava, Purnima Sailasree, Ankita Mishra, Diava Kumari. Sitting from left to right: Niharika Tiwary, Debabrata Jana, Karthik M, Elarani Majhee

Research interests

- Understanding transcriptional, chromatin, and metabolic regulation of stem cell state transitions.
- Deciphering the mechanisms governing the development of mammalian blastocysts, with specific emphasis on lineage segregation into the pluripotent and the extraembryonic layers.
- Utilising the principles of embryonic development and embryo-derived stem cells to construct synthetic embryos

The self-renewal and differentiation potential of Embryonic stem cells is maintained by the regulated expression of core pluripotency factors. Among the core factors – Oct4, Sox2 and Nanog, Nanog shows heterogeneous expression. However, it is unclear how the heterogeneous expression of Nanog is induced and maintained. The ectopic overexpression of Nanog in pluripotent cells resist their differentiation, thereby embryos fail to undergone normal embryogenesis. Hence, maintaining the expression of Nanog in ES cells within threshold limits is essential for retention of differentiation potential along with self-renewal. This level is maintained in ES cell by an auto feedback repression loop. However, it remains unclear how the pluripotent stem cells perceive the NANOG levels and execute autorepression. Here, we show that a dose-dependent induction of Fgfbp1 and Fgfr2 by NANOG activates an autocrine mediated ERK signaling in high-Nanog cells to trigger autorepression. pERK recruits NONO to the Nanog locus to repress transcription by preventing POL2 loading. The Nanog autorepression process establishes a self-perpetuating NANOG-pERK reciprocal regulatory circuit. We further demonstrate that the reciprocal regulatory circuit induces the pERK heterogeneity and ERK signaling dynamics in pluripotent stem cells. Collectively our data suggests that NANOG induces Fgfr2 and Fgfbp1 to activate ERK signaling in Nanog-high cells to establish a NANOG-pERK reciprocal regulatory circuit. This circuit regulates ERK signaling dynamics and Nanog autoregulation in pluripotent cells. We also show that MEK1/2 is essential for monoallelic expression of Nanog. We suggest that MEK1/2 acts as pivot to integrate different aspects of Nanog expression in pluripotent stem cells.



The illustration depicts that FGF/ERK autocrine signaling components are induced by NANOG in pluripotent cells with high Nanog expression to trigger autoregulation. pERK recruits NONO to repress Nanog transcription to execute autoregulation, which is the underlying mechanism for the induction of Nanog heterogeneity and biallelic expression in pluripotent stem cells.

PURAN SINGH SIJWALI

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

From left to right: (A) Udit, Renu, Amisha, Nivya, Gayathri, Kanika, Manas
(B) Somesh, Zeba, Priyanka, Pritam
(C) Lavanya, Manish, Srinivas, Puran

Research interests

Ubiquitin proteasome system, autophagy, antimalarial targets, neddylation, cullin-RING ubiquitin E3 ligases, proteases, malaria vaccine, DNA-protein crosslinks

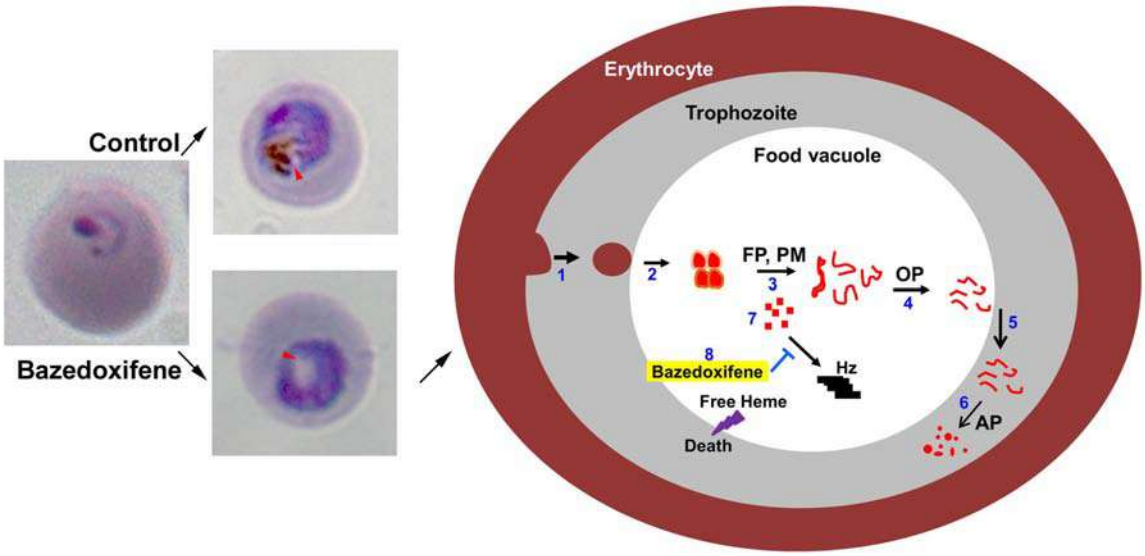
Selected recent publications

- Sudhakar R, Das D, Thanumalayan S, Gorde S, Sijwali PS (2021) Plasmodium falciparum Atg18 localizes to the food vacuole via interaction with the multi-drug resistance protein 1 and phosphatidylinositol 3-phosphate. ***Biochemical Journal*** 478: 1705-1732.

- Rex DAB, Patil AH, Modi PK, Kandiyil MK, Kasaragod S, Pinto SM, Tanneru N, Sijwali PS, Keshava Prasad TS (2022) Dissecting *Plasmodium yoelii* Pathobiology: Proteomic Approaches for Decoding Novel Translational and Post-Translational Modifications. ***ACS Omega*** 7: 8246-8257.

Despite a remarkable improvement in healthcare and continued drug discovery efforts, malaria control efforts are continuously challenged by the emergence of drug resistant parasite strains. Given a long and risky development path of new drugs, repurposing existing drugs for the treatment of malaria is an attractive and shorter path. Tamoxifen, a selective estrogen receptor modulator (SERM) for the treatment and prevention of estrogen receptor positive breast cancer, possesses antibacterial, antifungal and anti-parasitic activities. Hence, we assessed tamoxifen, raloxifene and bazedoxifene, which represent the first, second and third generation SERMs, respectively, for antimalarial activity. Raloxifene and bazedoxifene inhibited the erythrocytic development of Plasmodium falciparum with sub micromolar IC50 concentrations. Among the three, bazedoxifene was the most potent and also decreased *P. berghei* infection in female mice, but not in male mice.

However, bazedoxifene similarly inhibited *P. falciparum* growth in erythrocytes of male and female origin, which highlights the importance of sex-specific host physiology in drug efficacy. Bazedoxifene was most potent on early ring stage parasites, and about 35% of the treated parasites did not contain hemozoin in the food vacuole. Bazedoxifene-treated parasites had almost 34% less hemozoin content than the control parasites. However, both control and bazedoxifene-treated parasites had similar haemoglobin levels, suggesting that bazedoxifene inhibits hemozoin formation and toxicity due to accumulation of free heme could be a mechanism of its antimalarial activity. Since bazedoxifene is in clinical use and bazedoxifene-chloroquine combination showed additive anti-parasitic effect, bazedoxifene could be an adjunctive partner of currently used antimalarial regimens.



Model of bazedoxifene action. Treatment of *P. falciparum* at the ring stage with bazedoxifene results in trophozoites without hemozoin formation, whereas trophozoites developed from control parasites contain hemozoin in the food vacuole (marked with arrowhead). The model summarizes haemoglobin catabolism and inhibition of hemozoin formation. The *Plasmodium* trophozoite stage developing within the erythrocyte takes up haemoglobin through a cytostome-like organelle (1) and deliver it in vesicles to the food vacuole (2). Multiple classes of proteases, including the cysteine proteases falcipains (FP) and aspartic proteases plasmepsins (PM) degrade haemoglobin (3) into oligopeptides. Oligopeptidases (OP) hydrolyze oligopeptides into smaller peptides (4), which have been proposed to be transported into the parasite cytosol (5). In the cytosol, aminopeptidases (AP) hydrolyze oligopeptides into free amino acids (6), which are used by the parasite for protein synthesis. A by-product of haemoglobin degradation is free heme (7), which is polymerized into a nontoxic polymer, known as the hemozoin (Hz). Bazedoxifene inhibits hemozoin formation (8), resulting in the accumulation of free heme, which could cause parasite death.

RAGHUNAND R TIRUMALAI

Physiology and Pathogenic Mechanisms of *Mycobacterium tuberculosis*

From left to right: Raghunand Tirumalai, Shiela Chetri, Muskan Gupta, Korak Chakraborty, Tanya Bhandari, Ravi Prasad Mukku, Jennifer Albert, Kokavalla Poornima

Research interests

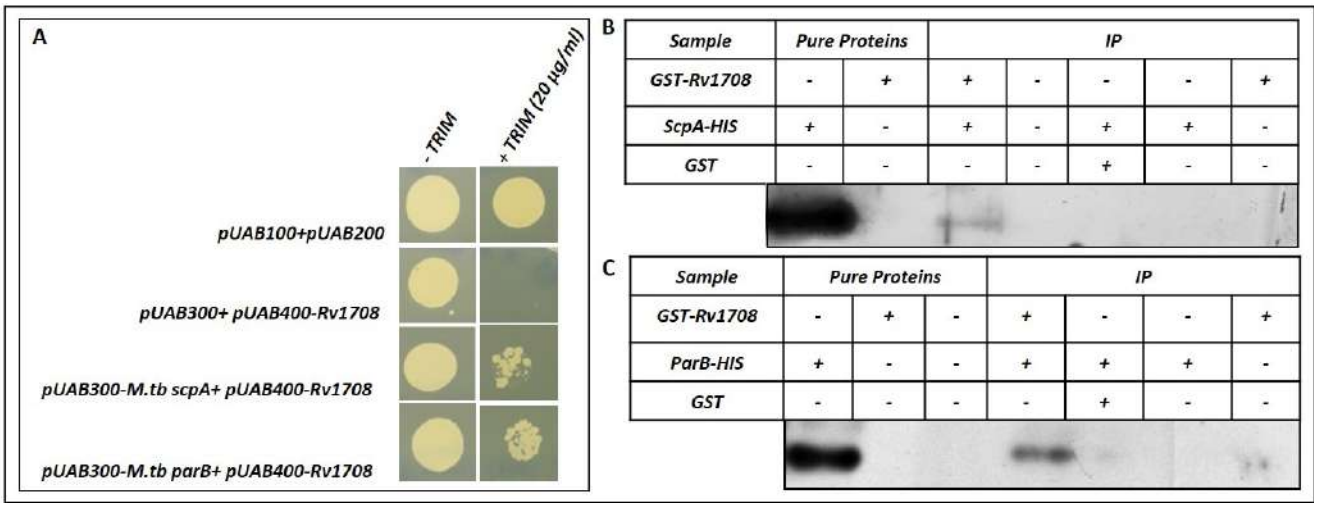
Our group studies the physiology and pathogenic mechanisms of *Mycobacterium tuberculosis* (*M.tb*), the causative agent of human tuberculosis. Research in our laboratory is focussed towards:

- Characterising the events at the host-pathogen interface
- Identification of bacillary virulence factors
- Discovering novel antibiotic resistance mechanisms

Selected recent publications

- Dutta A, Mukku RP, Aditya Kumar G, Jafurulla Md, Raghunand RT, Chattopadhyay A (2022) Integrity of the Actin Cytoskeleton of Host Macrophages is Necessary for Mycobacterial Entry. ***The Journal of Membrane Biology*** 255: 623-632.

Characterization of Mycobacterial homologues of *Escherichia coli* MinD: A major virulence trait of *M.tb* is its ability to enter a latent state within the human host in the face of an acquired immune response. Since cell division is intimately linked to metabolic shut down, understanding the mechanism of septum formation and its integration with other events in the division pathway is likely to offer clues to the molecular basis of latency. The aim of this study was to identify and functionally characterize mycobacterial homologs of the *E. coli* septum site specification protein MinD (Ec MinD). Sequence homology based analyses suggested that the genomes of both *M.tb* and the saprophyte *Mycobacterium smegmatis* (*M.smegmatis*) encode two putative homologues of Ec MinD - Rv1708/MSMEG_3743 and Rv3660c/MSMEG_6171 respectively. Both Rv1708 and MSMEG_3743 were observed to fully complement the mini-cell phenotype of the *E. coli* ΔminDE mutant HL1 but the other set of homologues only partially complemented the mutant phenotype. Over-expression of MSMEG_3743 but not MSMEG_6171 in *M.smegmatis* led to cell elongation and a drastic decrease in CFU counts vs controls, indicating the essentiality of MSMEG_3743 in the process of cell-division. Sequence analysis of MSMEG_3743 showed the presence of a conserved Walker A motif, the functional role of which was confirmed by a radiolabelled ATPase activity assay. In a mycobacterial protein fragment complementation (MPFC) assay, Rv1708 was observed to interact with the cell-division associated proteins ScpA and ParB, pointing to a link between septum formation and mycobacterial chromosome segregation. In summary we have demonstrated that Rv1708 and MSMEG_3743 are true mycobacterial homologues of Ec MinD, adding one more missing piece to the mycobacterial cell division puzzle.



Identification of Interacting partners for Rv1708 (A) MPFC assay showing interaction of Rv1708 with *M.tb* ScpA and M.tb ParB. (B, C) Biochemical validation of Rv1708-M.tb ScpA and Rv1708-M.tb ParB interactions respectively. TRIM - Trimethoprim

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 proofreading mechanisms in cells that maintain high fidelity during translation of the genetic code
- Insights into lipid metabolite-producing enzymes that can form complex lipids or bioactive lipopeptides

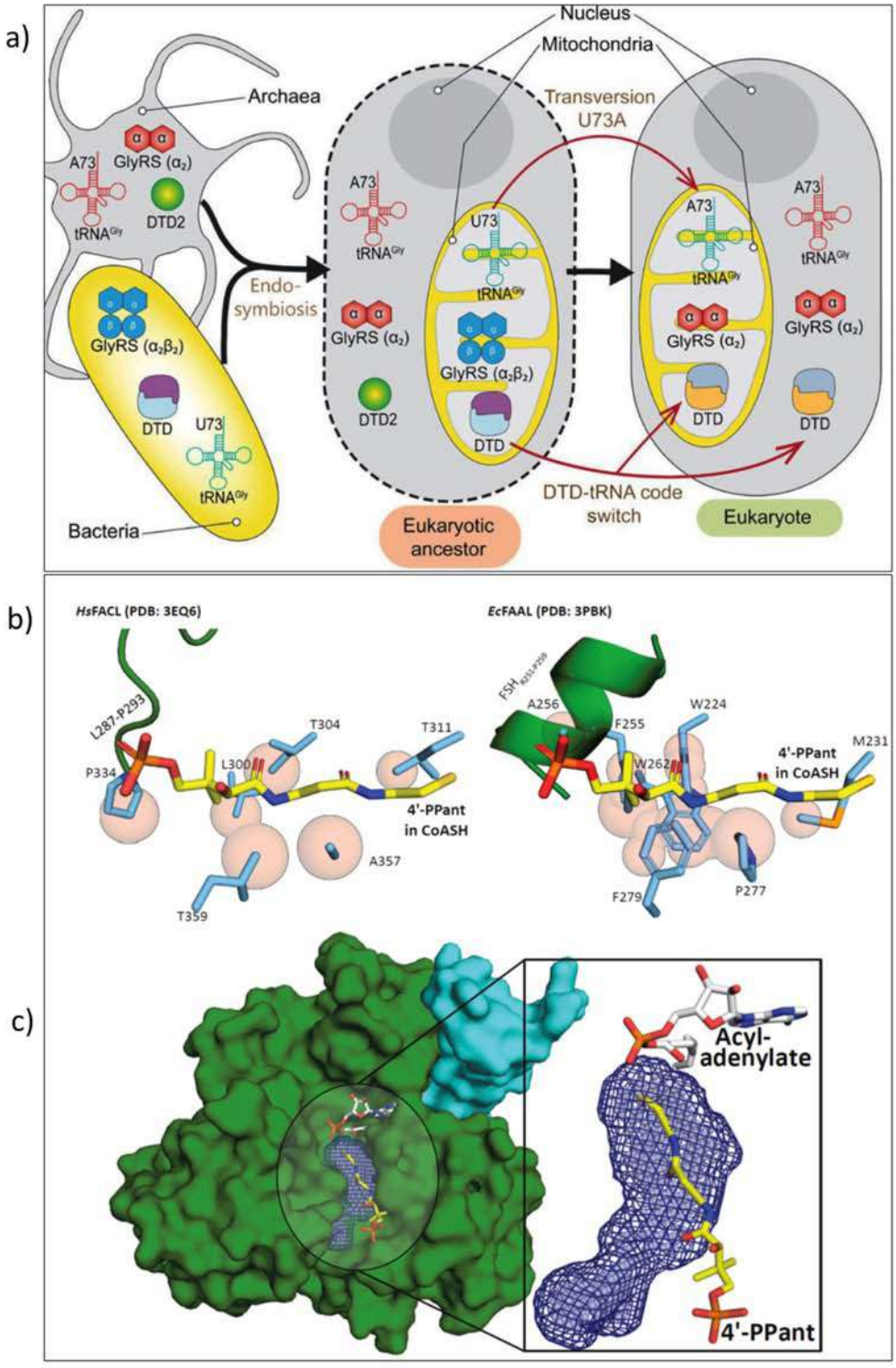
Selected recent publications

- Gogoi, J., Bhatnagar, A., Ann, K.J., Pottabathini, S., Singh, R., Mazeed, M., Kuncha, S.K., Kruparani, S.P. and Sankaranarayanan, R. (2022) Switching a conflicted bacterial DTD-tRNA code is essential for the emergence of mitochondria. ***Science Advances.*** 8: eabj7307, 1-9. DOI: 10.1126/sciadv.abj7307.

- Patil, G.S., Kinatukara, P., Mondal, S., Shambhavi, S., Patel, K.D., Pramanik, S., Dubey, N., Narasimhan, S., Madduri, M. K., Pal, B., Gokhale, R. S. and Sankaranarayanan, R. (2021) A universal pocket in fatty acyl-AMP ligases ensures redirection of fatty acid pool away from coenzyme A-based activation. ***eLife.*** 10:E70067 DOI: 10.7554/eLife.70067.

D-aminoacyl-tRNA deacylase (DTD) removes D-amino acids mischarged on tRNAs via an L-chirality rejection mechanism. The L-chirality rejection based operation of DTD allows its activity on Gly-tRNAs. We reported that N73rd base of tRNAs regulate DTD's activity—dubbed as discriminator-code—that determines whether the Gly-tRNA will be deacylated by DTD or not. We showed that the discriminator code of eukaryotic DTD has switched compared to bacterial DTDs in order to avoid misediting of the archaeal derived cytoplasmic Gly-tRNA Gly in eukaryotes. We also show that the mitochondrial tRNA Gly has undergone a U73A transversion in order to be compatible with eukaryotic DTD. We have proposed that the switch in discriminator code of eukaryotic DTDs and U73A transversion of mito-tRNA Gly are a part of multiple other optimizations important for emergence of mitochondria from a bacterial endosymbiont inside an archaeal host.

Fatty acyl-AMP ligases (FAALs) transfer fatty acids to 4'-phosphopantetheine arm of acyl-carrier protein (ACP) instead of Coenzyme-A (CoA) towards biosynthesis of virulent lipids in mycobacteria and pharmaceutically important polyketides and lipopeptides in microbes. We are trying to delineate how FAALs reject chemically identical CoA. Our study showed that FAALs block the canonical CoA-binding pockets and utilize alternative binding sites which distinguish adenosine 3′,5′-bisphosphate-containing CoA from holo-ACP. These features helped to identify the presence of FAAL-like proteins and their emergence in plants, fungi, and animals. The universal distribution of FAALs suggests that they share a parallel evolutionary history with fatty acyl-CoA ligases (FACLs) for ensuring a CoA-independent activation and redirection of fatty acids towards lipidic metabolites. Currently, we are investigating the structural and functional aspects of FAAL-like domains in eukaryotic model systems such as yeast, flies and mice.



a) A model depicting optimizations: Mitochondrial-tRNA Gly U73A transversion and eukaryotic DTD's discriminator-code switch, important for the emergence of mitochondria in eukaryotes from a proteobacterial endosymbiont engulfed by an archaeal host
b) Smaller residues lining CoA pocket in FACL (left), compared with bulkier residues and FAAL-specific helix at the entry blocking the canonical pocket in FAALs (right)
c) Alternative pocket identified(blue mesh) in FAALs (green surface representation) is evolved for accepting ACP and rejecting CoA

RAKESH K MISHRA

Genome Organization and Epigenetic Regulation

From left to right, top row: Ravina Saini, Soujanya M. S., Sonu Yadav, Rakesh Kumar Mishra, K. Phanindhar, Avvaru Akshay Kumar
Bottom row: Saketh Murthy, Ashish Bihani, Nikhil Hajirnis, Runa Hamid, Rashmi Upadhyay Pathak, Shubhanshu Pandey

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 aging

Selected recent publications

- Pathak RU, Soujanya M, Mishra RK (2021) Deterioration of nuclear morphology and architecture: A hallmark of senescence and aging. ***Ageing Research Reviews*** 67: 101264.
- Hemalatha M, Kiran U, Kuncha SK, Kopperi H, Gokulan CG, Mohan SV, Mishra RK (2021) Surveillance of SARS-CoV-2 spread using wastewater-based epidemiology: Comprehensive study. ***Science of The Total Environment*** 768: 144704.
- Matharu NK, Yadav S, Kumar M, Mishra RK (2021) Role of vertebrate GAGA associated factor (vGAF) in early development of zebrafish. ***Cells & Development*** 166: 203682.
- Hamid R and Mishra RK (2021) Book Review: Experiments with Drosophila for Biology Courses (Edited by S. C. Lakhotia and H. A. Ranganath; Published by Indian Academy of Sciences, Bengaluru). ***Proceedings of Indian National Science Academy*** 87: 423–426.
- Hajirnis N, Mishra RK (2021) Homeotic Genes: Clustering, Modularity, and Diversity. ***Frontiers in Cell and Developmental Biology*** 9: 718308.
- Kopperi H, Tharak A, Hemalatha M, Kiran U, Gokulan CG, Mishra RK, Mohan SV (2021) Defining the methodological approach for wastewater-based epidemiological studies-Surveillance of SARS-CoV-2. ***Environmental Technology & Innovation*** 23: 101696.
- Iyer V, Tushir S, Verma S, Majumdar S, Gayen S, Mishra RK, Tatu U (2021) The role of nuclear organization in trans-splicing based expression of heat shock protein 90 in Giardia lamblia. ***PLoS Neglected Tropical Diseases*** 15: e0009810.

- Gokulan CG, Kiran U, Kuncha SK, Mishra RK (2021) Temporal stability and detection sensitivity of the dry swab-based diagnosis of SARS-CoV-2. ***Journal of Biosciences*** 46: 95.

- Verma S, Pathak RU, Mishra RK (2021) Genomic organization of the autonomous regulatory domain of eyeless locus in *Drosophila melanogaster*. ***G3 (Bethesda)*** 11: jkab338.

- Pradhan SJ, Reddy PC, Smutny M, Sharma A, Sako K, Oak MS, Shah R, Pal M, Deshpande O, Dsilva G, Tang Y, Mishra RK, Deshpande G, Giraldez AJ, Sonawane M, Carl-Philipp Heisenberg, Galande S (2021) Satb2 acts as a gatekeeper for major developmental transitions during early vertebrate embryogenesis. ***Nature Communications*** 12: 6094.

- Tharak A, Kopperi H, Manupati H Kiran U, Gokulan CG, Moharir SC, Mishra RK, Mohan VS (2022) Longitudinal and Long-term Wastewater Surveillance for COVID-19: Infection dynamics and Zoning of Urban Community. ***International Journal of Environmental Research and Public Health*** 19: 2697.

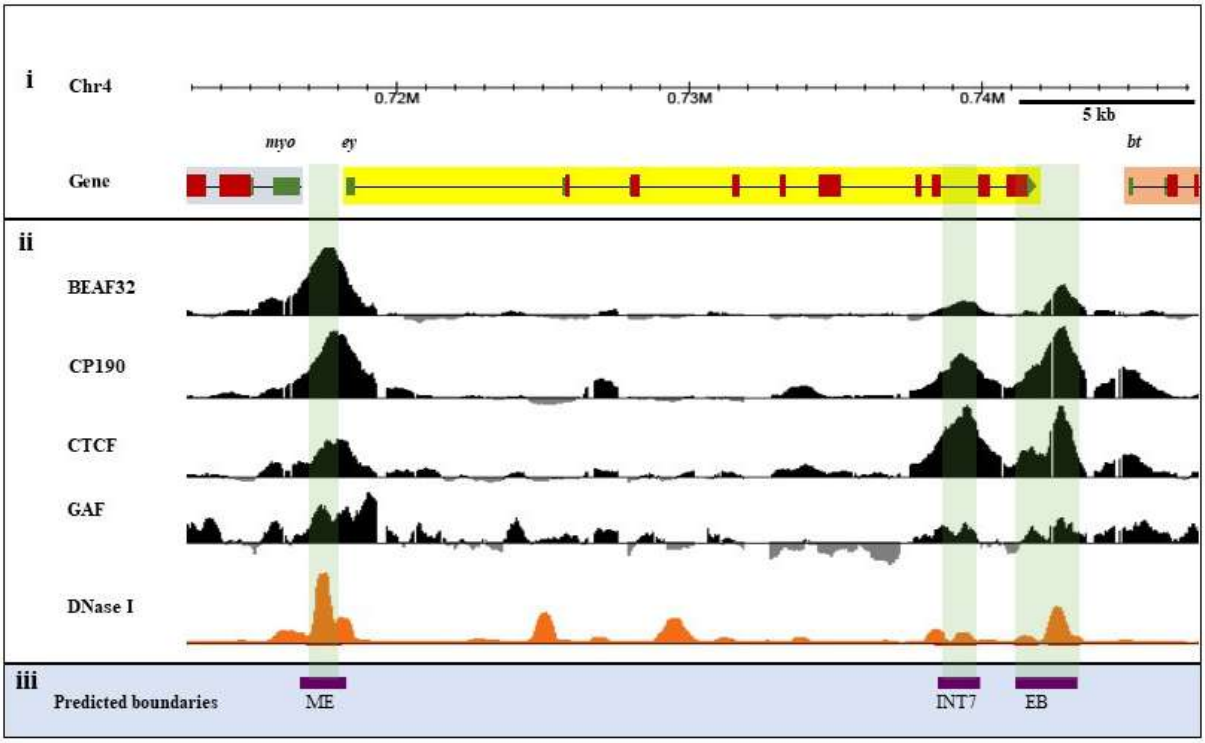
- Pathak RU, Bihani A, Sureka R, Varma R, Mishra RK (2022) *In situ* nuclear matrix preparation in *Drosophila melanogaster* embryos/tissues and its use in studying the components of nuclear architecture. ***Nucleus*** 13: 116-128.

Packaging of genomic DNA has regulatory consequences on expression of genes during development. This regulation is based on chromatin structure in which coding and non-coding elements of the genome play an important role. Chromatin domain boundary elements, the topologically independent structural units of higher order chromatin organization, and cellular memory elements, that maintain the expression state of genes by means of chromatin structure, regulate the expression of genes. Such epigenetic regulatory mechanisms control genes at many loci in the eukaryotic genome and are conserved during evolution.

Our group is interested in understanding how genetic information in the form of genomic sequence is interpreted by the developmental mechanisms, and how cell type-specific packaging of the genome in the context of nuclear architecture is achieved and maintained throughout the lifespan. Some of our findings during the period of this report are:

In Drosophila, expression of *eyeless* (*ey*) gene is restricted to the developing eyes and central nervous system. However, the flanking genes, *myoglianin* (*myo*) and *bent* (*bt*) show a different spatial and temporal expression pattern. Earlier, we had identified a boundary element intervening *myo* and *ey* genes (ME boundary) that prevents a crosstalk between the cis-elements of these genes. Our search further to identify cis-elements that define the domain of *ey* gene and maintain its expression pattern, has uncovered another boundary element between *ey* and *bt*, the EB boundary. The two boundaries interact in long-range to impart functional autonomy to the *ey* locus and insulate it from differentially regulated flanking regions. Our study proposes a general regulatory mechanism by which a gene can be maintained in a functionally independent domain in gene-rich euchromatin.

The architecture of interphase nucleus is fairly complex and dynamic. Studying features of nuclear architecture, including compartmentalization and spatial distribution of multiprotein complexes, helps us to understand various nuclear processes. Nuclear Matrix (NuMat) is a biochemically defined entity that provides us with a snapshot of the features of the nuclear architecture. We have developed a protocol to isolate and visualize NuMat *in situ* in the intact embryo or tissues of *Drosophila melanogaster.* This protocol couples the power of *Drosophila* genetics with cell biological observation of the nuclear architecture.



***Ey* locus on the fourth chromosome showing *ey, myo* and *bt* genes. ChIP-chip data showing binding of boundary proteins (BEAF-32, CP190, CTCF, GAF). The two boundaries ME and EB in the region have been identified and characterized by us and have been shown to play an important role in defining expression status of the genes at the locus.**

R NAGARAJ

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

R. Nagaraj

Research interests

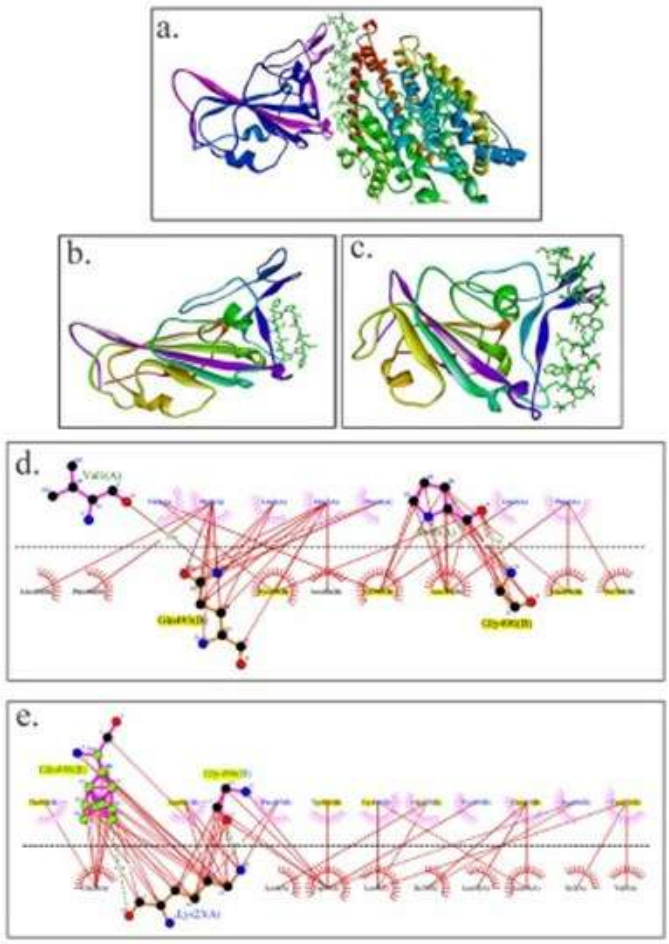
- Biology of host-defensin peptides
- Theoretical analysis of protein structures

Selected recent publications

- Enayathullah MG, Parekh Y, Banu S, Ram S, R, Kiran Kumar B, Idris MM (2022) Gramicidin S and melittin: potential anti-viral therapeutic peptides to treat SARS-CoV-2 infection. ***Scientific Reports.*** 12: 3446, doi.org/10.1038/s41598-022-07341-x.

- 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. doi:10.4103/ijmr.ijmr_2798_21

The ability of peptides such as melittin, Gramicidin S and defensins to inhibit the antiviral activity of SARS-CoV-2 against cultured Vero cells, was investigated in collaboration with the groups of Mohammad Idris and Kiran Kumar. Melittin and Gramicidin S could effectively inhibit the ability of SARS-CoV-2 to infect cells. Human defensins and their variants were less effective. Human beta defensin 3 showed moderate activity. Proteomics analysis indicated that more than 250 proteins were differentially regulated in the Gramicidin S and melittin treated SARS-CoV-2 infected Vero cells against control SARS-CoV-2 infected Vero cells. Proteomics studies indicated that metabolic change caused by SARS-CoV-2 pathogenesis result in long-term metabolic disorders in COVID-19 patients, and this varies according to pathogen severity. Carbon sources, specifically glycolysis and glutamine lysis pathways, have been found to play critical roles in SARS-CoV-2 viral replication and production. Non-oxidative pentose phosphate pathways (PPP) are also involved in viral replication. Our findings showed that several proteins are strongly associated with carbon metabolism and non-oxidative PPP. Gramicidin and melittin may function as viral inhibitors by suppressing intercellular metabolic regulators. Molecular docking studies suggest that both the peptides have structural features that would favor binding to RBD of the spike protein. Gramicidin S and melittin bind to the ACE2 binding domain of spike. The amino acid residues of spike involved in binding to ACE 2 interact with the amino acids of melittin and Gramicidin S. Our investigations indicate that both these peptides could be attractive candidates for repurposing to treat SARS-CoV-2 infection.



Structures of RBD of spike proteins and peptides and RBD binding region of ACE2. (a) RBD and ACE, (b) RBD and Gramicidin S, (c) RBD and melittin. The ACE2 binding region in RBD is colored violet. In ACE2, Gramicidin S and melittin, the peptide regions binding to RBD are represented as sticks. LigPlots of interaction between ACE2 binding domain of the spike protein and (d) Gramicidin S and (e) melittin. The residues of the RBD involved in binding to ACE2 are in yellow. The structures in panel (a-c) were generated using Discovery Studio v19.1.0.18287. The figures in panel (d, e) were generated using LigPlot.

SAIKAT CHOWDHURY

Structural biology of macromolecular machinery and cryo-electron microscopy

From left to right: Harikrishna Adicherla, Justus Francis, Rishav Mitra, Pathri Achyutha Krishna, Rajesh Palle, Saikat Chowdhury

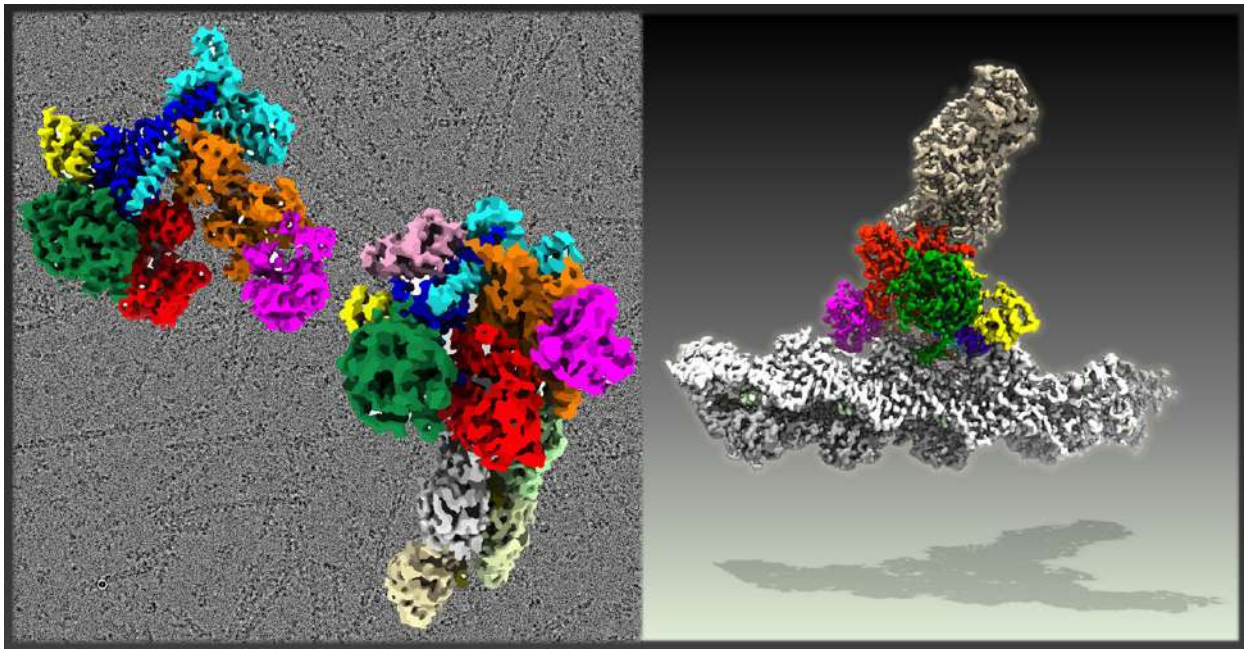
Research interests

- 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

Selected recent publications

- Anzelon TA, Chowdhury S, Hughes SM, Xiao Y, Lander GC, Ian J MacRae (2021) Structural basis for piRNA targeting. ***Nature*** 597: 285-289.

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. Arp2/3 complex is an important actin filament nucleator that nucleates both linear and branched actin networks for efficient generation and distribution of forces. While efforts over two decades have identified different classes of activating molecules, also called the nucleation promoting factors (NPFs), however, the precise mechanism by which they transform Arp2/3 complex to nucleation-competent state is still unclear. 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.



Structures of inactive Arp2/3 (top left), active Arp2/3 complex with nucleated linear actin filament (middle) and branched actin (right), determined by high resolution cryogenic electron-microscopy. The left side image has a micrograph containing actin filaments nucleated by Arp2/3 complex in the background.

SANTOSH KUMAR

Receptor Signalling and Immune Response

From left to right: Fatima, Kashmiri, Blessie, Sitanshu, Neladri, Ketaki, Apoorva, Santosh

Research interests

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

Effector cells of our immune system, such as T cells and natural killer cells, protect us from infection and cell transformation. They detect abnormal changes at the surface of other cells using receptors that induce signaling upon phosphorylation of tyrosine-based motifs in their cytosolic tail. Inhibitory receptors that restrain cytotoxicity of natural killer cells by binding to class I human leukocyte antigens (HLA-I) on healthy cells also signal through phosphorylation of tyrosine motifs in their cytosolic tail. A major focus of the lab at this moment is to understand how HLA-I-specific inhibitory receptor controls responses of human natural killer cells.

We are also putting efforts to initiate a research program to understand responses of cytotoxic lymphocytes, such as natural killer cells and T cells, in human infections.

Regulation of tyrosine phosphorylation of inhibitory receptor (Sitanshu Kumar Sarangi)

We show that tyrosine phosphorylation in inhibitory receptor tail is regulated by electrostatic interaction, despite the tail being overall neutral, with the plasma membrane. Segregated clusters of oppositely-charged residues in the disordered tail confer intrinsic abilities of both binding and unbinding. Our results, on how this unusual electrostatic interaction regulates signaling, advance understanding of the regulation of tyrosine phosphorylation and the biology of intrinsically-disordered regions in proteins.

Regulation of the activities of human natural killer cells by Zn^{+2} (Ketaki Bhagwat)

The functions of the inhibitory receptor, KIR, requires Zn^{+2}. Our results show that the cytotoxicity of human natural killer cells is also dependent on Zn^{+2}, suggesting multifaceted roles of Zn^{+2}in controlling natural killer cell responses. We are working to gain insight into the underlying mechanism.

Cytotoxic lymphocyte responses in *Helicobacter pylori* infection (Etikala Apoorva)

While considered as an extracellular bacterium, *H. pylori* modulates the activities of gastric epithelial cells by injecting proteins into them. Interactions of infected epithelial cells with cytotoxic lymphocytes are not well explored. We show that the infected epithelial cells, in culture, upregulate the surface expression of HLA-C. It is possible that the infected cells escape the attack by natural killer cells by upregulating HLA-C, a ligand of inhibitory receptor, on their surface. We will work on samples from *H. pylori* infected individuals to test this hypothesis.

SHRISH TIWARI

Sequence Analysis of Biomolecules

From left to right: Prachi Singh, Nikhila Sai Tummala, Shrish Tiwari, Ramesh Palaparthi, 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

Selected recent publications

- Reddy HM, Bhattacharya R, Tiwari S, Mishra K, Annapurna P, Jehan Z, Praveena NM, Alex JL, Dhople VM, Singh L, Sivaramakrishnan M, Chaturvedi A, Rangaraj N, Shiju TM, Sreedevi B, Kumar S, Dereddi RR, Rayabandla SM, Jesudasan RA (2021) Y chromosomal noncoding RNAs regulate autosomal gene expression via piRNAs in mouse testis. ***BMC Biology*** 19: 198.

We have built a chromosomal level assembly for Samba Mahsuri (SM), using short read- and long read-sequences, as well as optical mapping of the genome. We are now using this assembly as the reference genome against which we can align reads from mutant genomes to identify variations. Earlier we used the Nipponbare genome as proxy, by aligning reads from wild type SM and mutant SM to Nipponbare genome and the filtering out SNPs that were unique to the mutant. We re-analysed the mutant genome SM93, which has the desired characteristics of high yield and early maturation, with the SM reference genome and found the all the loci associated with early flowering that had come up in the previous analysis. In addition, we found a new locus associated with the phenotype of interest.

Aligning our reference SM genome to Nipponbare genome revealed a 6MB inversion near the centromere of chromosome 6. This inversion was missing when we aligned SM to the Indica genome. Since there are several rice genomes available, we confirmed this inversion by aligning SM to all available rice genomes. We are now looking at the evolutionary implications of this discovery.

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

Early maturation phenotype of SM93: after 103 days (A) SM plants in the flowering stage, (B) SM93 plants in the grain filling stage

SONAL NAGARKAR JAISWAL

Developmental Biology

From left to right, starting from top: Sonal Nagarkar Jaiswal, Priyanka Pandey, Aishwarya K, Reshmi Varghese, Nandan J, Brinda Palliyana

Research interests

- Regulation of neural stem cell self-renewal, differentiation and quiescence during development
- Neurodevelopmental diseases

The presence of an intact and fully developed nervous system is essential for the survival and proper functioning of animals. Central to the development of such a complex and highly organized system are multipotent stem cells known as Neural Stem Cells (NSCs). By contrast, in adults, the vast majority of adult NSCs are relatively quiescent, and only a fraction of them divide rarely to ensure replacement of damaged cells. NSC self-renewal, quiescence and differentiation are highly regulated processes, any defects in these processes lead to neurodevelopmental disorders such as microcephaly, autism, epilepsy and brain tumor. Therefore, to develop therapeutic approaches to these inherited or acquired disorders, it is important to understand the cellular processes underlying NSC biology.

In past, we performed genetic screens and isolated several genes that are enriched in NB, and whose loss leads to defects in brain development.These genes are evolutionarily conserved and have been implicated in several neurological diseases such as Down syndrome, Alzheimer's and Parkinson's diseases, but their function in brain development is unclear. Currently, we are focusing on three genes that were isolated from the screen: (1) CSN7, a subunit of COP9 Signalosome, (2) CG32069, a homologue of human Immediate Early Response 3 Interacting Protein 1(IER3IP1) and (3) CG12050, a homologue of human WDR75. Knockdown of all three leads to a small brain phenotype indicating that these are crucial for brain development. We aim to uncover the roles of these genes in Drosophila NB and hNSC maintenance using a series of targeted genetic manipulations.

SRIRAM VARAHAN

Cellular Metabolism, Microbial Genetics and Microbial Pathogenesis

From left to right: Narasimhulu, Vinit Sahu, Sasi Bhushan, Sriram Varahan, Dhrumi Shah, Lakshmi Sai Sree, Nivedhitha R

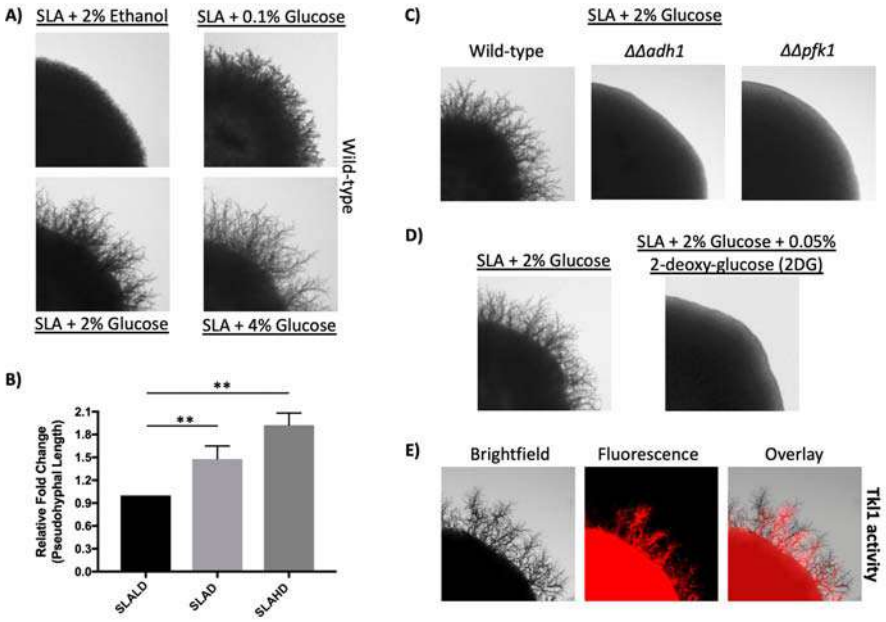
Research interests

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

Selected recent publications

- Varahan S, Laxman S (2021) Bend or break: how biochemically versatile molecules enable metabolic division of labor in clonal microbial communities. ***Genetics*** 219: iyab109.

Fluctuations in nutrient availability is one of the most common challenges encountered by unicellular organisms. 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 would serve as excellent model systems to address this as they exhibit a remarkable degree of cell state transitions in response to nutrient fluctuations. Our group will employ simple fungal models (*Saccharomyces cerevisiae*), as well as pathogenic fungi (primarily *Cryptococcus neoformans*), to understand how conserved metabolic events regulate cell state transitions in response to nutrient fluctuations, and how this influences fungal pathogenesis.



Breakdown of glucose is essential for pseudohyphal differentiation (a type of cell state transition that occurs in response to nitrogen limitation) in *S. cerevisiae* A) Wild-type *S. cerevisiae* cells were spotted onto synthetic low ammonium (SLA) medium with varying concentrations of glucose as follows: SLA+ 2% ethanol, SLA+ 0.1% glucose, SLA+ 2% glucose and SLA+ 4% glucose. In SLA with 2% ethanol, no glucose was added. Colonies were allowed to develop for 10 days and were imaged using a high resolution bright-field microscope. B) Length of pseudohyphae was measured in each of these different mediums using ImageJ software. Statistical significance was calculated using unpaired t test ** represent P<0.01 and error bars represent standard error of mean. A total of 9 colonies were used for each different media condition. C) Wild-type *S. cerevisiae* along with the *adh1* and *pfk1* deletion strains 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 bright-field microscope. D) Wild-type *S. cerevisiae* was spotted onto synthetic low ammonium (SLA) medium with 2% glucose and synthetic low ammonium (SLA) medium with 2% glucose and 0.05% of the glycolysis inhibitor, 2-deoxy-glucose (2DG). Colonies were allowed to develop for 10 days and were imaged using a high resolution bright-field microscope. E) Spatial distribution of mCherry fluorescence across a pseudohyphal colony, indicating the expression of glycolytic activity dependent reporter (*tkl1* reporter). Colonies containing the *tkl1* 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.

SWASTI RAYCHAUDHURI

Proteotoxicity in Age-related Diseases

From left to right: Richa, Harshit, Sristi, Suparna, Pallavi, Swasti, Aanchal, Pooja, Alivelu, Rajlekha, Shemin

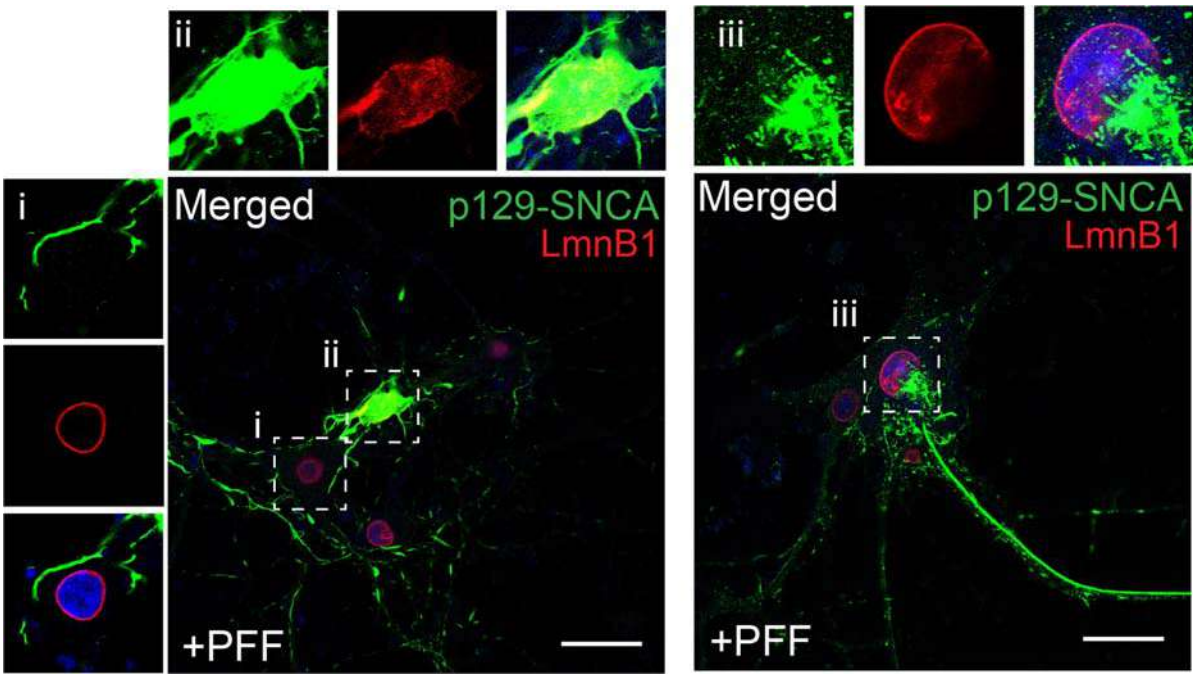
Research interests

- Quality control of respiratory complex biogenesis
- Cause and consequences of spatiotemporal organization of protein inclusion bodies

Respiratory complexes are multi-subunit protein complexes with a central function in aerobic energy metabolism. Earlier, we found that the protein subunits of respiratory complexes are aggregation-prone. We also observed that these complexes associate with each other and are engaged in higher-order supercomplex formation to protect cellular respiration during stress. Now, we figured out that the subunits of respiratory complexes display a mosaic pattern of amino acid sequence evolution. Sequences of the mitochondrial matrix exposed subunits are conserved across eukaryotes. Subunits embedded into the mitochondrial inner membrane display sequence diversity between fungi, plants, and metazoans. Correlations of sequence evolution with the aggregation propensity of the subunits and supercomplex formation are now being investigated.

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 is obscure, 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. We figured out that

1. LBs are a dump-yard of amyloidogenic α-Synuclein for eventual degradation
2. The degradation rate is slower than the accumulation of α-Synuclein filaments into LBs
3. Overgrown LBs deregulate cytoskeleton-nucleoskeleton connections and damage the nuclear envelope
4. Remodelling of cytoskeleton activity by pharmacological or genetic manipulation rescues the nuclear envelope and nuclear activity
5. Follow-up work on identifying the detailed mechanisms of LB-cytoskeleton and LB-nucleoskeleton interactions are ongoing.



Damaged nuclei in mouse neurons containing Lewy Body like α-Synuclein inclusion bodies. (i) neuron with smaller α-Synuclein filaments. (ii-iii) neurons with large Lewy Body like α-Synuclein filaments. p129-SNCA - phosphorylated α-Synuclein, LmnB1 - Lamin B1 marking inner nuclear envelope, DAPI - nucleus, PFF - prefromed fibrils of recombinant α-Synuclein

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

- Human disease genetics with a focus on rare genetic disorders

Selected recent publications

- Naushin S, et. al. (2021) Insights from a Pan India Sero-Epidemiological survey (Phenome-India Cohort) for SARS-CoV2. ***eLife*** 10: e66537.
- Singh NK, Srivastava S, Zaveri L, Bingi TC, Mesipogu R, Santosh Kumar V, Gaur N, Hajirnis N, Machha P, Shambhavi S, Khan S, Soujanya M, Nagabandi T, Mishra RK, Bharadwaj KT, Sowpati DT (2021) Host transcriptional response to SARS-CoV-2 infection in COVID-19 patients. ***Clinical and translational medicine*** 11: e534.
- Mlcochova P, et al. (2021) SARS-CoV-2 B.1.617.2 Delta variant replication and immune evasion. ***Nature*** 599: 114-119.
- Dhar MS, et al. (2021) Genomic characterization and epidemiology of an emerging SARS-CoV-2 variant in Delhi, India. ***Science*** 374: 995-999.
- Kumar JV, Banu S, Sasikala M, Parsa KVL, Sowpati DT, Yadav R, Bharadwaj KT, Siva AB, Vishnubhotla R, Rao GV, Reddy DN (2021) Effectiveness of REGEN-COV antibody cocktail against the B.1.617.2 (delta) variant of SARS-CoV-2: A cohort study. ***Journal of Internal Medicine*** 291: 380-383.
- Laxmaiah A, et. al. (2021) SARS-CoV-2 seroprevalence in the city of Hyderabad, India in early 2021. ***IJID Regions*** 2: 1-7

With rapid advancement of sequencing technologies, it is becoming more and more possible to discern the impact of genetics on human health and disease. Our lab intends to capitalize on this progress in understanding the etiopathogenesis of ultra rare genetic disorders/ syndromes. In this context we are currently working on a novel intellectual disability syndrome caused by mutations in DPH2 gene.

In addition, our lab is currently handling diverse projects like Genome India, Indian Breast Cancer Genome Atlas and various SARS-CoV2 genomics based surveillance activities. As a crucial member of the INSACOG consortium, the team is involved in tracking the evolution and surveillance of the SARS-CoV2 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. The lab is also an integral part of ongoing COVID-19 vaccination studies/trials at CSIR-CCMB. Our work on clinical outcomes in vaccinated and unvaccinated individuals during the second wave led to the identification of lower antibody levels as a poor prognostic marker in vaccinated individuals. During the last year, we have also successfully established satellite sequencing centres at Pasteur Institute, Meghalaya and Siddartha Medical College, Andhra Pradesh.

VEGESNA RADHA

Signaling and Regulation of Cell Fate

From left to right: Abhishek, Gowthaman, Lavanya, Tulasi, Radha

Research Interests

Identifying and characterzing molecules that serve as master regulators of cell and tissue differentiation in vertebrates. Our attempt is to understand how these fundamental processes are controlled, and how deregulation results in pathological situations.

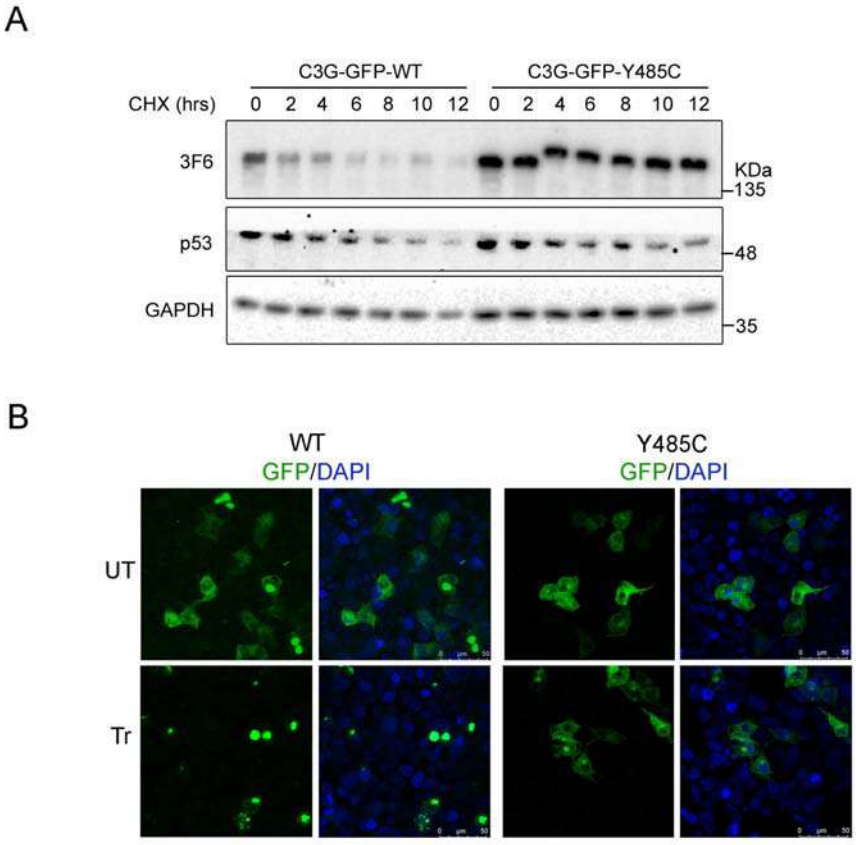
Selected recent publications

- Vishnu VV, Muralikrishna B, Verma A, Nayak SC, Sowpati DT, Radha V, Chandra Shekar P (2021) C3G Regulates STAT3, ERK, Adhesion Signaling, and Is Essential for Differentiation of Embryonic Stem Cells. ***Stem Cell Reviews and Reports*** 17: 1465-1477.

- Raghawan AK, Radha V, Swarup G (2021) HSC70 as a sensor of low temperature: role incold-triggered autoinflammatory disorders. ***FEBS Journal*** doi: 10.1111/febs.16203.

Understanding the regulation and function of RAP GEF1 during development, and how developmental defect associated mutants of human RAP GEF1 are defective in signaling to various cellular functions, was the focus of work during the year. Four mutations in human RAP GEF1 are associated with overlapping phenotypes and developmental defects (courtesy, Dr. Alexandre Raymond, Switzerland). One of the mutants, Y485C, shows enhanced stability due to reduced proteasomal degradation, and is likely to dominantly inhibit RAP GEF1 mediated signaling. Our results showed that the Y485C mutant is compromised in its ability to activate Akt and phosphorylate GSK3 beta, kinases essential for regulating cell metabolism, survival, and differentiation. A child with L557P mutation, showed severe abnormalities in brain development. We, therefore, wished to examine how this mutant is defective by modelling brain organoids using iPSCs. Fibroblasts from the patient were transformed into iPSCs using episomal vectors expressing Yamanaka factors. Mutant iPSCs, were characterized using phenotypic features, alkaline phosphatase assay, and marker expression. They will be compared with normal iPSCs during brain organoid growth.

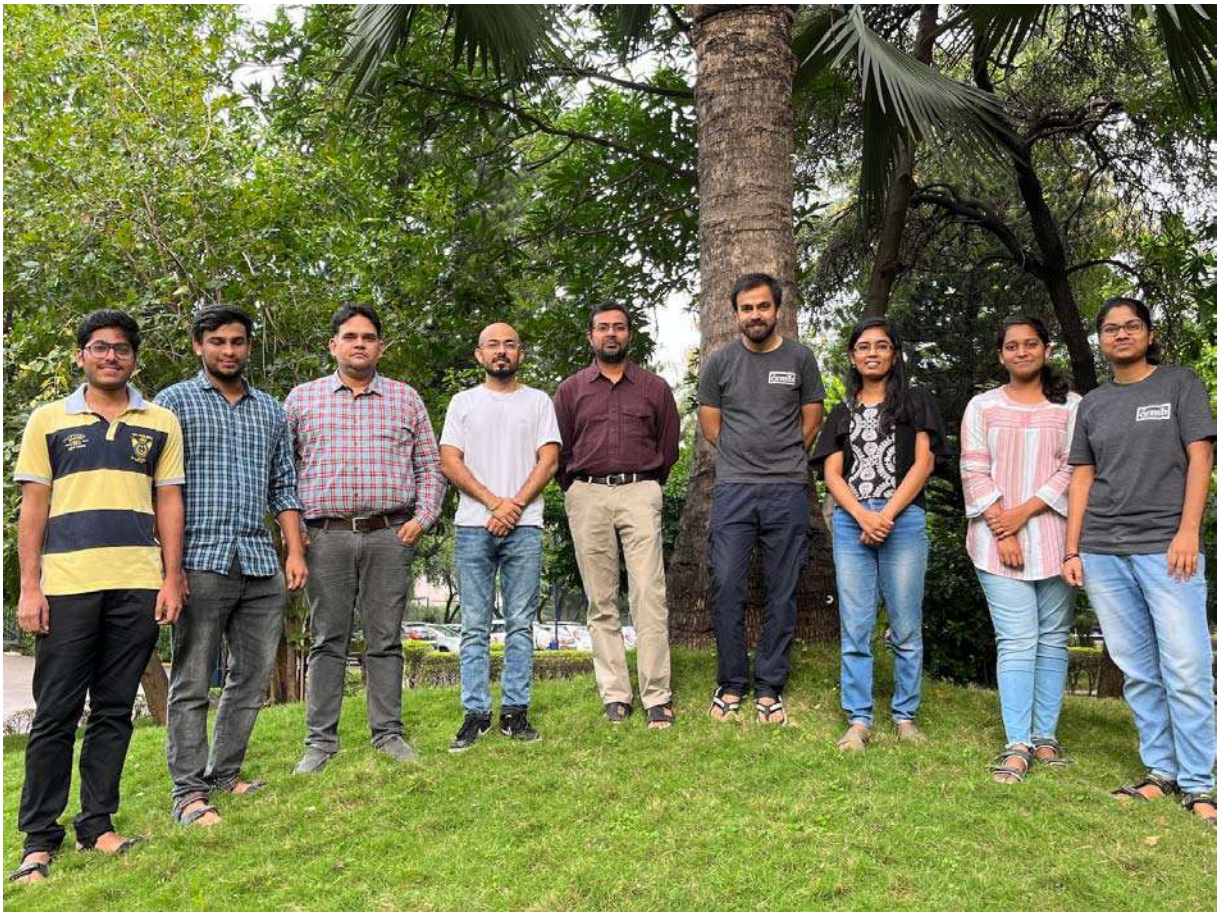
Studies using mouse and zebrafish tissues showed the presence of a splicing hotspot in RAP GEF1 where casette exons are included or excluded in a tissue specific manner. Unique properties that these exons confer are being examined. Unlike in all other vertebrates, Zf-RAP GEF1 is expressed from 2 loci on chromosomes 8 and 21. Altered expression of splice variants is seen from these loci during development, and in adult tissues. Knockdown experiments identified RAP GEF1 as an essential for normal embryonic development in zebrafish.



A. Y485C mutant of RAP GEF1 is more stable than the wild type protein. Protein levels of the WT and mutant proteins were monitored over time after inhibition of protein synthesis with cycloheximide, by Western blotting. Levels of endogenous p53, an unstable protein was examined as a treatment control, and GAPDH as a loading control. B. Proteasome inhibition potentiates aggregate formation by the WT protein, but not the mutant. HEK293 cells expressing WT-GFP and Y485C mutant were left untreated (UT) or treated (Tr) with 25mM MG132 for 24 hrs.

VENKAT CHALAMCHARLA

Transcription and Chromatin Regulation

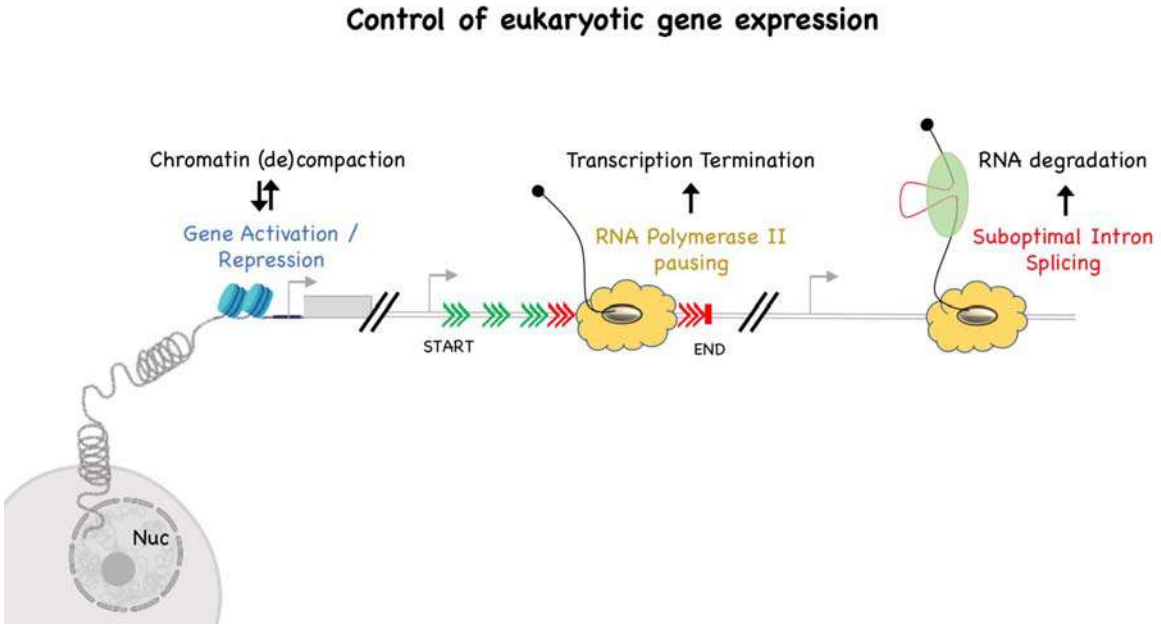


From left to right: Vaishnav, Diwakar, Anubhav, Harsh, Venkat, Sauvik, Annapoorna, Aarthi, Monika

Research interests

- Control of transcription elongation and termination by RNA Polymerase II
- Pre-mRNA processing
- Chromatin dynamics
- Gene regulation
- Genome instability
- Cellular quiescence
- Yeast genetics
- *Schizosaccharomyces pombe*

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*. Active maintenance of the quiescence gene-expression program, and transcriptional reprogramming to prioritize cell growth in response to a wide range of mitogenic signals, governs the remarkable longevity of quiescent G0 cells. Advances in the fundamental understanding of cellular quiescence will benefit several fields relevant to human health, such as stem cell biology and cancer biology. 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: Abhishek Saha, Yogita Kapoor, Asis Kumar Khuntia, Priyadarshini Sanyal, Vinay K. Nandicoori, Sutashree Nath, V. Purushotham, Amit Chakraborty, Sanskrita, Babu Ram Nepali

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)

Selected recent publications

- Khan MZ, Singha B, Ali MF, Taunk K, Rapole S, Gourinath S, Nandicoori VK (2021) Redox homeostasis in *Mycobacterium tuberculosis* is modulated by a novel actinomycete-specific transcription factor. ***EMBO J*** 40: e106111.
- 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.

- Gupta S, Mishra DK, Khan MZ, Saini V, Mehta D, Kumar S, Yadav A, Mitra M, Rani P, Singh M, Nandi CK, Das P, Ahuja V, Nandicoori VK, Bajaj A (2022) Development of a Highly Specific, Selective, and Sensitive Fluorescent Probe for Detection of Mycobacteria in Human Tissues. ***Advanced Healthcare Materials*** 11: e2102640.

- Mlcochova P, et al. (2021) SARS-CoV-2 B.1.617.2 Delta variant replication and immune evasion. ***Nature*** 599: 114-119.

- Dhar MS, et al. (2021) Genomic characterization and epidemiology of an emerging SARS-CoV-2 variant in Delhi, India. ***Science*** 374: 995-999.

- Pal S ,Soni V , Kumar S , Jha SK , Medatwal N , Rana K , Yadav P , Mehta D , Jain D , Sharma P , Kar R , Srivastava A , Patil VS , Dasgupta U , Nandicoori VK , Bajaj A(2021) A hydrogel-based implantable multidrug antitubercular formulation outperforms oral delivery. ***Nanoscale*** 13: 13225-13230.

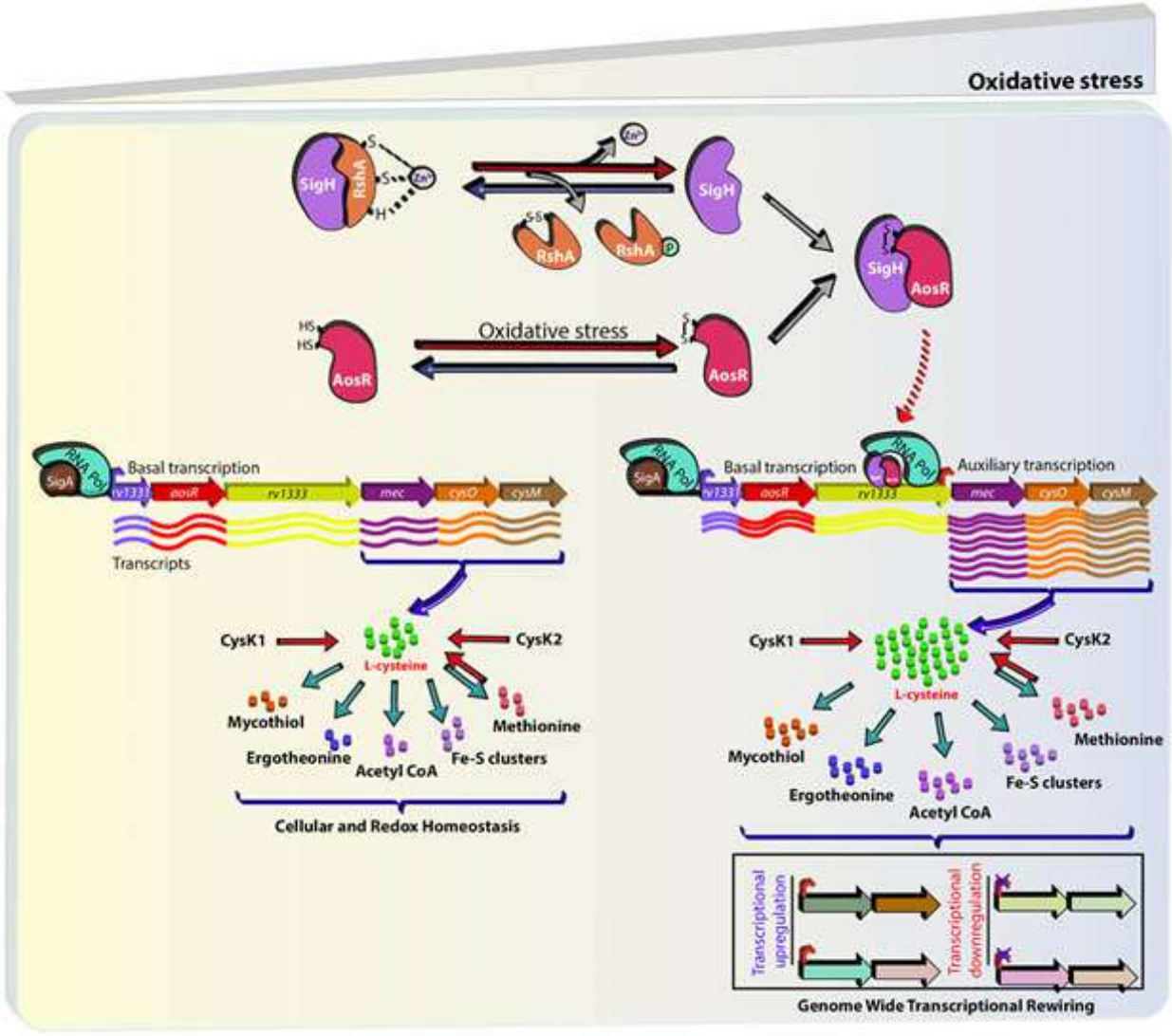
- Agarwal M, Soni V, Kumar S, Singha B, Nandicoori VK (2021) Unique C-terminal extension and interactome of Mycobacterium tuberculosis GlmU impacts its in vivo function and survival of pathogen. ***Biochem J*** 11: 2081.

Deciphering the role of cell signaling in *Mycobacterium tuberculosis* biology

Mycobacterium tuberculosis (*Mtb*) is an airborne pathogen that has co-evolved with its human host to establish the continual loop of inhalation, active to chronic infection, latency, dissemination to virtually any organ, and transmission to other individuals. In order to effectively treat tuberculosis, it is imperative to find newer targets, which are important for the *in-vivo* bacterial survival and persistence. We work on delineating the signaling mechanisms in *Mtb*. We also investigate the role of phosphorylation in modulating cell division, cell wall synthesis, transcription and secretion of proteins. In addition, we investigate the role of pathogen mediated double stranded DNA damage in the host macrophages and their role in the intracellular survival of *Mtb*.

We explored available TnSeq datasets to identify transcription factors (TFs) that are essential for *Mtb* survival inside the host. The analysis identified a single TF, Rv1332 (AosR), conserved across actinomycetes with a so-far uncharacterized function. AosR mitigates phagocyte-derived oxidative and nitrosative stress, thus promoting mycobacterial growth in the murine lungs and spleen. Oxidative stress induces formation of a single intrasubunit disulphide bond in AosR, which in turn facilitates AosR interaction with an extracytoplasmic-function sigma factor, SigH. This leads to the specific upregulation of the CysM-dependent non-canonical cysteine biosynthesis pathway through an auxiliary intragenic stress-responsive promoter, an axis critical in detoxifying host-derived oxidative and nitrosative radicals.

Our study shows that the AosR-SigH pathway is critical for detoxifying host-derived oxidative and nitrosative radicals to enhance *Mtb* survival in the hostile intracellular environment.



Model depicting the proposed role of AosR during oxidative stress:
In response to oxidative stress, SigH is liberated from its cognate anti-sigma factor (RshA) and an intramolecular disulfide bond is formed in the AosR. This subsequently results in oxidative stress-dependent interaction between AosR and SigH that together binds to an auxiliary promoter upstream of mec. Increased transcription of mec-cysO-cysM results in enhanced production of cysteine-derived antioxidant molecules. Increased production of cysteine through non-canonical cysteine biosynthesis protects mycobacteria cells from phagocyte-derived oxidative and nitrosative stress. Inhibition of this redox-regulatory circuit results in genome-wide transcription changes.

1.1B Research Facilities

Advanced Microscopy and Imaging Facility (AMIF)

Atomic Force Microscope (AFM)

Nanonics Imaging Ltd (Multiview 1000) Atomic force microscope (AFM) is a high-resolution scanning probe microscope which measures forces between the tip of a probe and the sample surface with piconewton sensitivity, and, thus, a topographic image of the sample surface is obtained.

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

Left to right : Angothu Ramesh, Suman Bandari, Nandini Rangaraj, Chivukula Subbalakshmi, N Ravindra Chakravarthi, Adicharla Harikrishna

Raman Spectroscopy and Raman Rapid Imaging Model: RENISHAW InVia Raman Microscope

In Raman spectroscopy, the sample is illuminated with a monochromatic laser beam (532 nm, 633 nm or 780 nm) and the Raman spectrum is obtained from the resultant inelastic scattered light intensity, as a function of frequency shifts. 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 include biofluids, fixed and live cells, thick tissue specimens, bacteria, plant materials, drugs, semiconductors, nanomaterials, polymers, proteins, organic and inorganic compounds.

Scanning Electron Microscope

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 include nanomaterials, bacteria, normal and tumor cells, organic and inorganic materials, dental and bone implants among others.

It is also equipped with confocal, live-cell confocal, high resolution, super resolution and regular microscopes

Confocal Microscopes

Models: Leica TCS SP8, Zeiss LSM 880, Olympus FV 3000

Confocal microscope scans specimens in the XY-plane along with the Z-plane thus allowing data collection in 3D. The users are provided with additional computers and suitable software for data analysis while the main systems are being used for data acquisition. This facility uses inverted microscopes with various objectives and receives illumination from various laser lines (405, 458, 477, 488, 514, 532, 543, 561, 594 and 633 nm).

The systems are provided with facilities for scanning and analysis of single and multi- labeled samples combined with DIC, 3D reconstruction, kinetic analysis, ratio analysis, spectral analysis, Fluorescence Recovery after Photo bleaching (FRAP) and Fluorescence Resonance Energy Transfer (FRET).

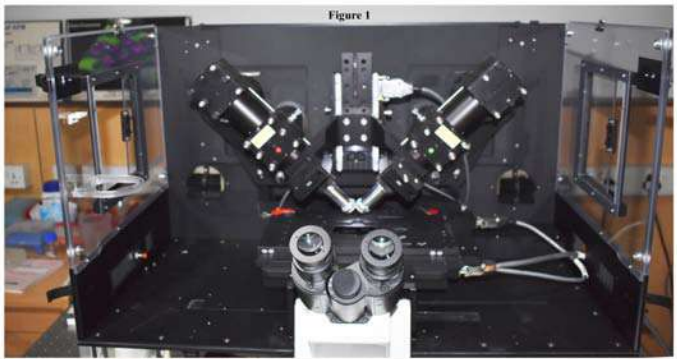
The Leica TCS SP8 is a classical confocal microscope. It has three PMT detectors and additional two highly sensitive hybrid detectors.

The Zeiss LSM 880 is a high resolution confocal microscope. In a classical confocal microscope, the pinhole is set at 1 AU which improves resolution by a factor of 1.06. The resolution can be further increased by making the pinhole smaller but the signal to noise ratio drops significantly. The Zeiss LSM 880 has a hexagonal microlens array that connects to a linear GaAsP detector which collects all light of an airy disk simultaneously. Each detector element functions as a single very small pinhole of 0.2 AU. This enables efficient imaging by making use of all the photons collected by the objective. This gives a resolution of 140 nm laterally and 400 nm axially.

The Olympus FV 3000 is a live cell Laser Scanning Confocal microscope for real-time imaging with solid state lasers and GaAsP detectors. It also has an additional chamber for maintaining samples at temperatures ranging from ambient to 40°C with continuous supply of CO_2 for imaging live samples over long time periods.

The facility also has a Leica TCS SP8 X 3D STED super resolution microscope and a Marianas 3i light sheet microscope system.

Leica TCS SP8 X 3D STED Super Resolution Microscope



Marianas 3i Light Sheet Microscope

Leica TCS SP8 X 3D STED Super Resolution Microscope overcomes the diffraction limit of light and allows investigators to study sub-cellular structures in greater detail than achieved with a standard confocal microscope. The Leica STED system uses a picosecond longer wavelength laser to deplete the fluorescence emitted from a shorter wavelength dye creating a doughnut shaped excitation. The emission thus given by the sample is detected using standard detection systems creating a X-Y resolution of 40nm.

Marianas 3i Light Sheet Microscope is a dual inverted selective plane illumination imaging system. It consists of two symmetrical optical paths for light sheet imaging. Two objectives are placed at right angles above a sample mounted horizontally. A light sheet is projected onto the sample from one objective and imaged through the other objective using high speed high resolution sCMOS cameras. This way a stack is collected by moving the light sheet through the sample. The role of the objective is exchanged to collect another stack in the perpendicular direction and the data sets are computationally merged to yield a 3D data set with isotropic resolution. The scanned sheet method reduces phototoxicity, allows 3D imaging and long term time lapse imaging at high spatial and temporal resolution.

Apart from above advanced microscopes, the facility also has the following fluorescence microscopes.

Advanced Fluorescence Zeiss AxioZoom V16 Stereo Microscope with Apotome

This is a high resolution stereo microscope with optical sectioning using the structured illumination principle having a color camera and a monochrome camera for fluorescent samples. The system can be used for fluorescence, bright field and DIC imaging with a zoom ratio of 16. It can be used to scan *Drosophila*, zebrafish, plant samples and 96-well plates. Tile scans can also be done on the system. 3D reconstruction is a part of the Zen analysis software.

Universal Research Microscope Model Axioplan 2 Imaging with Film and Digital Cameras

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

Axioimager Z2 Fluorescence Imaging System with Fully Motorized Microscope

This is an advanced system with fully motorized microscope for imaging both, black and white and color images and also acquire Z-sections. A color 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.

Apotome Fluorescence Imaging system with Fully Motorized Axioimager. Z1 Microscope and Monochrome Digital Camera

This is a highly sophisticated and motorized fluorescence microscope with DIC attachment. The system is used to observe the biological specimens with fluorescence technique and acquire Z-sections at good resolution. The system works on structured illumination principle to get high quality images and is capable of acquiring images on both DIC and fluorescence. The optical tomography technique uses optical grid for structured illumination. The images are analysed using Zen software.

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 1999. The registration number is 20/GO/RBi/S/99/CPCSEA for the purpose of Research and breeding of mice, rats, rabbits, hamsters, and Guinea pigs for in-house purposes and commercial trading purposes.

The main objective of the 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 PI can raise the online animal request as per IAEC approved project for supply of animals and inventory platform to regulate animal census, mortality, animal production, and supply details and monitoring platform to generate the data of microbial, genetic monitoring with microenvironmental parameters of animal rooms such as temperature and relative humidity. CCMB Animal House also provides orientation and training programs to authorized animal house users [students & project staff] to maintain high standards of humane, ethical, and responsible use of animals in their research.

The 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 the individually ventilated caging systems (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 12 hr light and dark cycles. The Animal House team comprises of one veterinarian and 7 trained staff members who are involved in the breeding, management of various lab animals, and providing technical support to various ongoing research projects. The total number of projects approved for animal experimentation under the Institutional Animal Ethical Committee this year is 123.

Principal Technical Officer, Mr. Rajasekar retired on July 31, 2021 and Senior Technical Officer, Mr. Jedy Jose has been transferred to CSIR-NIIST, Thiruvananthapuram. Also, lab assistants, Mr. R. Ellesh and Mr. P. Ravi retired from service in June, 2021.

During this year the below transgenic/ knockout mice received from Jackson laboratory, USA:

Strain Name	Animal Model	Sources
B6.Neat 1 Ko mice [Neat 1 lac Z mice] https://knowledge.brc.riken.jp/resource/animal/card?__lang__=en&brc_no=RBRC06302	Neat1 ncRNA knock-out mice. A lacZ was inserted immediately downstream of the transcription start site of Neat1. TT2 ES cells were used to generate the knockout mice. An FRT-flanked neo cassette was removed by crossing with FLP mice. The mutant mice were backcrossed to C57BL/6N.	**RIKEN, Japan**
B6.Cg-Tg(SOD*G93A)1Gur/J mice ; Strain#:**004435** https://www.jax.org/strain/004435	Model for ALS. Hemizygotes exhibit a phenotype similar to amyotrophic lateral sclerosis (ALS) in humans; becoming paralyzed in one or more limbs with paralysis due to loss of motor neurons from the spinal cord. Motor neuron degeneration has been associated with function and/or degeneration of astrocytes, the major glial cell type of the nervous system	**Jackson Laboratory, USA**

B6C3 female Tg (APPswe,PSEN1dE9) 8SDbo/Mmjax Strain#:**004462** https://www.jax.org/strain/004462	Mouse model for Alzheimer's disease. APP/PS1 are double transgenic mice expressing a chimeric mouse/human amyloid precursor protein (Mo/HuAPP695swe) and a mutant human presenilin 1 (PS1-dE9), both directed to CNS neurons. Both mutations are associated with early-onset Alzheimer's disease. These mice may be useful in studying neurological disorders of the brain, specifically Alzheimer's disease, amyloid plaque formation and aging.	**Jackson Laboratory, USA**
Pitx3 <aka/2 J mice https://www.jax.org/strain/000942	Mouse model for Parkinson's disease. Mice homozygous for the *Pitx3^{ak}* mutation exhibit microphthalmia (small eyes) and aphakia (no lens) related to arrested lens development. The mesencephalic dopamine system is malformed and as a result, homozygotes fail to develop dopaminergic neurons of the substantia nigra. Homozygotes display sensorimotor deficits specific to the nigrostriatal pathway such as the challenge beam and pole test and the test for spontaneous exploratory activity in a cylinder. These deficits can be reversed by L-DOPA administration. This mutant mouse strain may be useful in studies of Parkinson's disease	**Jackson Laboratory, USA**

Number of animals supplied during this year are as follows:

Mice: 7845 Rats: 22 Rabbits: 52

Retirement day function of Mr. Rajasekar, Principal Technical Officer and Mr. Ellesh , lab assistant along with animal house staff

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.

Cell Culture & Histology Facility

Cell culture is important in cellular and molecular biology because it allows researchers to examine the biology, biochemistry, physiology (e.g., ageing), and metabolism of both healthy and diseased cells. Animal Tissue Culture (TC) facility is the most frequently utilized facilities at CCMB, Hyderabad. Cultured cells are used to study the differentiation and proliferation of normal and diseased cells in cancer, diabetic, musculoskeletal, and cardiovascular disorders, and in developmental stages from human and mouse stem cells to terminally differentiated cells from a wide range of tissues. Cell culture facility lab is equipped with sophisticated instruments and equipment includes biosafety cabinets, CO incubators, inverted and upright microscopes, an electroporator, a dedicated cold room, deep freezers, and cryopreservation containers. In addition to helping with the production of monoclonal antibodies, primary cell derivation, and the development of over-expression and knockdown cell lines, dedicated professionals also provide training to CCMB staff members.

2

The cell culture facility offers the CCMB research staff with a centralized facility for the growth of animal cells in culture and provide cell lines to researchers.

The TC facility laboratory also provides training/education on the proper handling of aseptic cell culture techniques to CCMB personnel and researchers from other institutions/academia, allowing them to become self-reliant, thereby releasing additional staffing resources and contributing to the fight against fatal diseases.

The central cell culture facility recruits participants through a countrywide advertisement and provides cell culture training so that they may perform their experiments independently and successfully execute their scientific operation.

Short tandem repeat (STR) analysis is a useful tool for identifying mismatched cell lines genetically. Upon request, TC facility provides these services to both CCMB and non-CCMB clients. We identify cell lines and screen for cross-contamination using STR profiling (genotype). Moreover, the TC facility provides services to CCMB users whose cells are contaminated with mycoplasma.

The TC facility aids researchers from within or outside of CCMB so that they may address the answers to their scientific questions.

Immunofluorescence, flow cytometry, and protein purification are all potential applications for monoclonal antibodies that TC facility is involved in the production of *via* the hybridoma technology. This results in saving costs in CCMB's antibody procurement process and enables improved resource use. In addition to this, it will provide an endless supply of antibodies and may open the door to commercialization in compliance with the Atmanirbhar Bharat Abhiyaan.

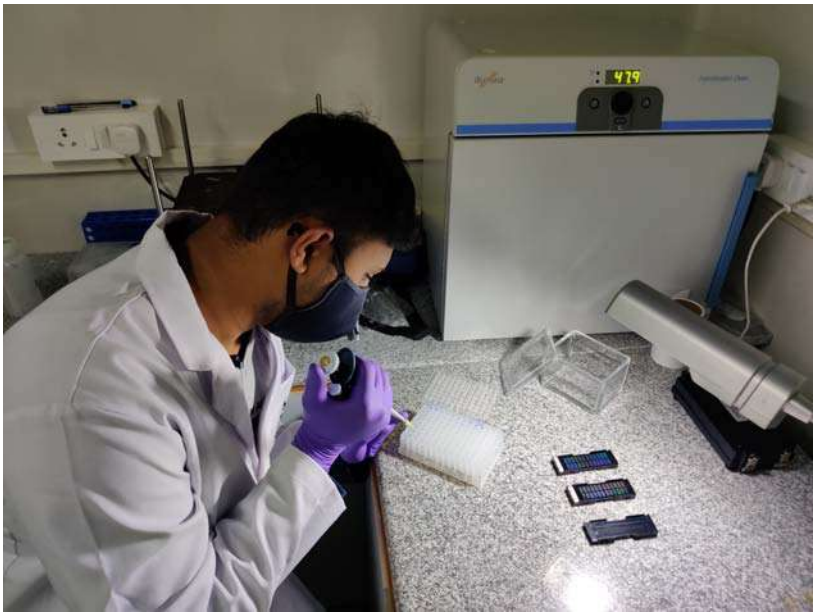
The ability to produce 3D cell populations from stem cells has enabled the production of organoid cultures that recapitulate the characteristics of human organs. Using organoids, scientists may investigate how cells interact with their environment, diseases, and treatments. These organoids may be exploited for both fundamental and translational research. The TC facility aids in the production of organoids obtained from iPSCs, particularly intestine organoids, in order to explore basic science and discover treatments for debilitating diseases.

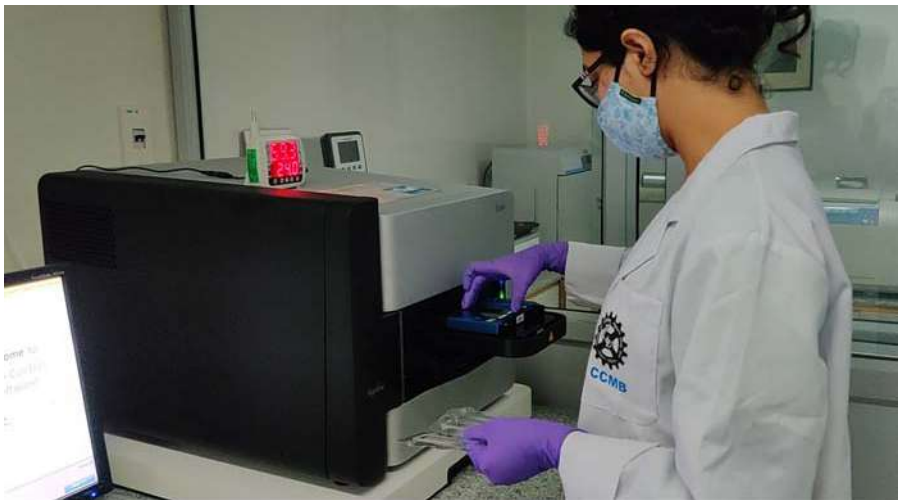
From left to right: Phulamma, Robert, S Easra, V R Sundereswaran, D Partha Sarathi, Dayakar, B V V Pardhasaradhi, Avtar Singh, Ch Varalakshmi and Zareena Begum

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 Centre at CSIR-Centre for Cellular and Molecular Biology (CSIR-CCMB) is a newly established pan-CSIR facility. It was inaugurated by Dr. Shekhar Mande, then Director-General of CSIR on 25th. March 2022. This is the third such state-of-the-art Electron Microscopy (EM) Centre to be established in the country. The centre houses a 120kV Talos L120C cryogenic electron microscope with a fast readout Ceta camera that is used for imaging and screening of cryogenic biological specimen and for high-resolution imaging of room temperature samples and thin sections of biological specimen. For near-atomic resolution or ultra-high-resolution structure determination the centre also has a 200kV Talos Arctica cryogenic electron microscope, equipped with a Falcon IV direct electron detector and a Ceta-D camera. For high-throughput automated imaging the EPU software suite is used. Both the microscopes and cameras are from Thermo Fisher Scientific.

Ultrastructure of macromolecular complexes persevered at near-native conditions are imaged at cryogenic temperatures (-179 °C) using these microscopes. Understanding the molecular architecture of macromolecular complexes at such resolutions helps us to understand how they function and how defects in them cause diseases.

This facility is also equipped with sample vitrification robot, Vitrobot Mark IV, Glow Cube glow discharge unit for making hydrophilic support films, Carbon Evaporator, and a Zeiss cryogenic ultra-microtome for preparation of ultra-thin sections of biological specimen.

Along with other structural biology facilities (X-ray and NMR) and imaging facilities at CSIR-CCMB this facility will help researchers to understand the molecular underpinnings of life at unprecedented details. This will help in delineating the underlying cause of diseases and development of new therapeutics and drugs for cure. This facility is not only being used by CSIR-CCMB scientists, but also by users from other institutes in India and pharmaceutical industries.

The operations of the centre is overseen by Mr. Harikrishna Adicherla, Mr.Sandeep Shrivastava, 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.

Top: 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, Amol Mandlik, Harikrishna Adicherla and Sandeep Shrivastava

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

The Drosophila fly facility has a state-of-the-art set up for maintenance and generation of transgenic flies and a dedicated fly food production unit (Nectar). Apart from constant use by research groups, the facility offers training. The key activities of this facility include use of genetically modified flies to reveal gene function in development, as well as the use of flies to study the function of genes from other organisms, including humans. The function and interaction of disease genes involved in cancer, and neurodegenerative disorders are modeled here, and studies include drug screening for molecules that counteract the effects of specific disease mutations. They also investigate functional relevance of non-coding sequences of complex genomes, in particular the repetitive part, in nuclear architecture, chromatin organization and gene regulation.

Publications:

1. Drosophila Hox genes induce melanized pseudo-tumors when misexpressed in hemocytes
Titus Ponrathnam, Ravina Saini, Sofia Banu & Rakesh K Mishra
Scientific Reports volume 11, Article number: 1838 (2021)

2. Genomic Organization of the autonomous regulatory domains of eyeless locus in Drosophila melanagaster
Shreekant Verma, Rashmi U Pathak, Rakesh K Mishra
G3 Genes|Genomes|Genetics, Volume 11, Issue 12, December (2021)

3. Homeotic Genes: Clustering, Modularity, and Diversity
Nikhil Hajirnis and Rakesh K Mishra
Front. Cell Dev. Biol., 11 August (2021)

4. Choline Transporter regulates olfactory habituation via a neuronal triad of excitatory, inhibitory and mushroom body neurons
Runa Hamid , Hitesh Sonaram Sant, Mrunal Nagaraj Kulkarni.
PLoS Genetics, (2021)

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 4.5 TB 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. 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 2 PB. A further 2 PB is currently envisaged to meet the large genomic data storage requirements.

The HPCF 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 HPCF provides IT infrastructure to facilitate 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.

Next-Gen Sequencing (NGS) Facility

The Next Generation Sequencing (NGS) facility at CCMB hosts a gamut 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.

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.

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.

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.

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

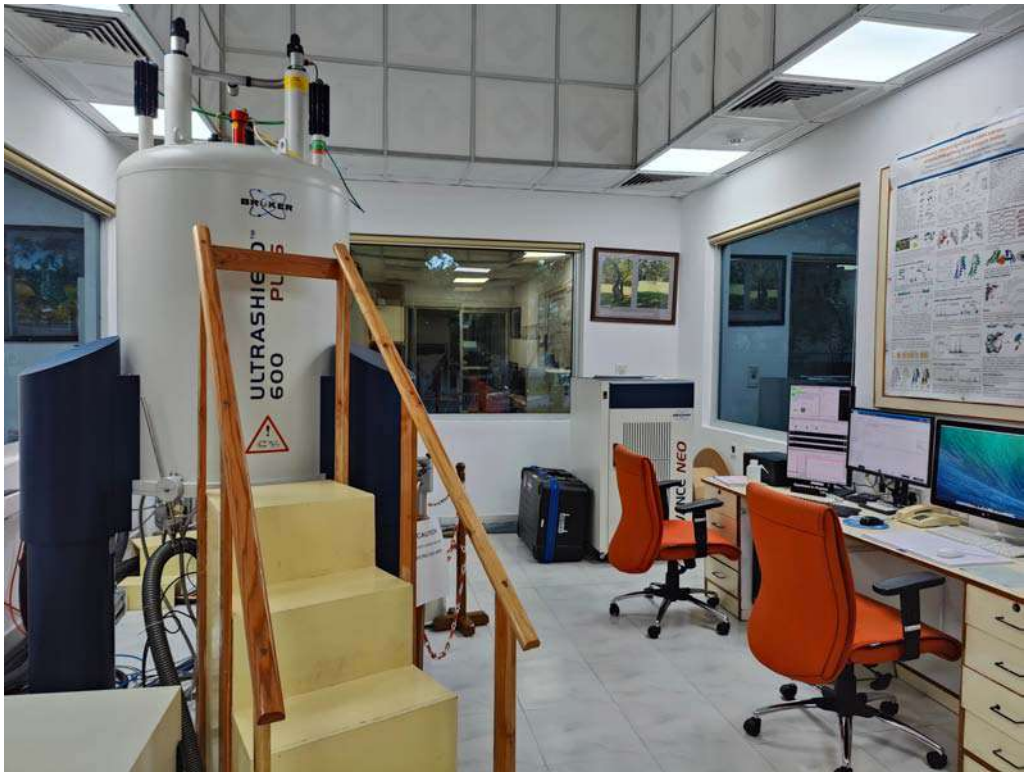
Right image: From left to right: Sreenivas, Valli, Jyothi, Tej, Karthik, Tulasi, Jafri, Balakrishna

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, K Ranjith Kumar, V Krishna kumari, Y Kameswari, 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.

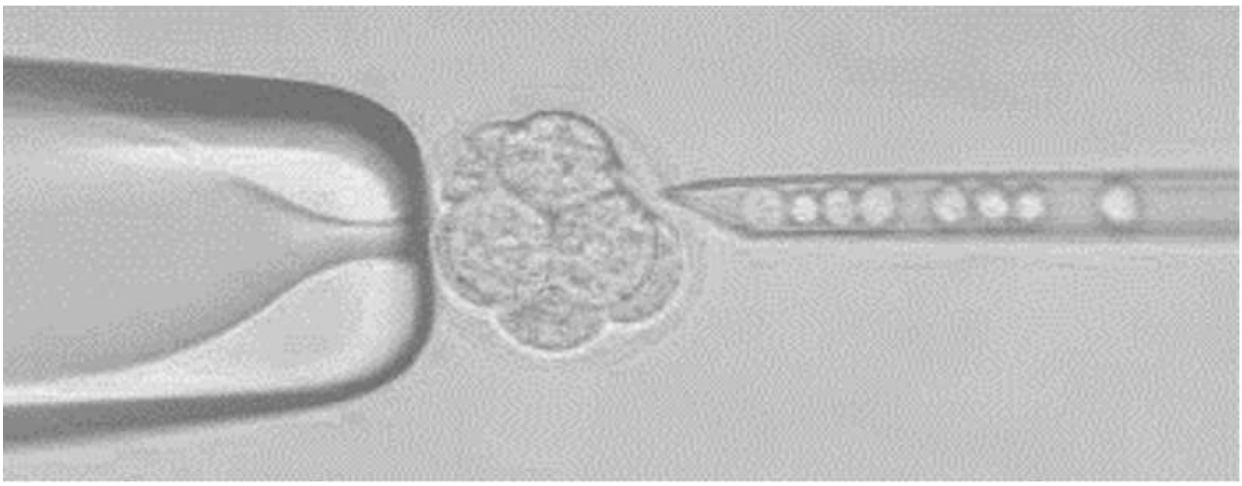
3) TLD service
As per the AERB and IARP mandate the occupational radioisotope workers should be periodically monitored for the radioactive exposure. CCMB radioisotope facility caters to nearly 30 radioisotope workers, and monitors their radiation exposure the exposure is monitored through TLD. The TLD 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

High Throughput (HT) Crystallization Facility

A state-of-the-art HT-Crystallization facility provides complete solution for crystallization of macromolecules. Three major operational 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. There are several microscopes, one of which has a polariser, for the inspection of plates for crystal growth. It is supported by dynamic light scattering (DLS), which is a useful tool to diagnose size distribution, stability, and aggregation state of macromolecules in solution prior to crystallization.

Facility In-charge: Biswajit Pal

X-ray Crystallography Facility

Structural Biology X-ray facility provides state-of-the-art resources to elucidate three dimensional structures of macromolecules and their complexes at atomic level. 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. Molecular modeling studies are performed using Intel Quad-Core windows and linux-based workstations.

Facility in-charge: R. Rukmini

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 solutions. 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.

Facility in-charge: R. Rukmini

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

Zebrafish facility caters to the needs of different research groups of CCMB and collaborative projects of various institutes (CDFD, LVPEI, IIT-Hyderabad). Apart from providing staged embryos, juveniles and adult fishes for research, we also help users with micromanipulation to generate and maintain desired transgenic fish lines.

The zebrafish Facility provides training and logical support to students from different universities of India and abroad. Facility also offers medium scale testing of various biological potential drug molecules / bioactive agents and developing transgenic fishes. The stock room contains all the stock transgenic lines and wild type strains of the facility. The other rooms are equipped with light dark and temperature controllers to house the ongoing experimental zebrafish for all the users.

Each of these housing rooms are equipped with aeration and pump systems. The zebrafish facility is equipped with

- large scale breeding & embryo collection
- live feed (Artemia) hatching facility
- Advanced automated standalone systems maintain lines for developmental biology, cell biology and behavioural biological studies
- high end microscopy and imaging system (Model M205 FA) that has motorized advanced stereo fluorescence for multichannel fluorescence and bright-field imaging
- micromanipulation systems and trained staff to help researchers generate transgenic fish
- A computer aided tracking system (Danio vision with behavior analysis software) for research on behavioural aspects

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

Ground floor - housing systems, microinjection room, behavioral assay set up

1.1C Research Resources

Instrumentation

New equipment installed during the year 2021-22:

- Model: EVOS M5000 Integrated Cell Imaging system with microscope and camera; make: M/s Thermo Fisher, USA
- Model: HELIOS CYTOF Mass Cytometer system; make: M/s Fluidigm Corporation, USA
- Model: TALOS L 120S Transmission Electron Microscope (TEM) system; make: M/s Thermo Fisher Scientific
- Model: TALOS ARTICA Cryo Transmission Electron Microscope (TEM system); make: M/s Thermo Fisher Scientific
- Model: Chemidoc and Gel Imaging system; make: M/s Bio-Rad
- Model: Chemidoc MP Imaging system; make: M/s Bio-Rad
- Model: FUSION-SOLO 6S EDGE V0.70 Auto IR/NIR Chemiluminescence and Fluorescence Imaging Systems; make: M/s Vilber Lourmat
- Model: Mosquito HV-5 Deck & DFD 6 Genomics Systems Dragonfly; make:M/s SPT Labtech
- Model: Bioflow 120 Fermentor system; make: M/s Eppendorf
- Model: EXPLORIS 240 Orbitrap Mass Spectrometer system; make: M/s Thermo Fisher Scientific
- Cryo attachment for Ultra Microtome
- Model: Quant Studio 5 Real Time PCR system; make: M/s Thermo Fisher Scientific

New equipments procured and installed during the year 2021-22

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 designing, implementing, and managing IT infrastructure and services in-house. The group facilitates scientific collaborations by providing secure and faster data transfers; assisting scientists in the creation of computing facilities required for R&D projects; and protecting the organization's network and research data from cyber-attacks

The IT group creates and manages the CSIR-CCMB website, intranet site, and other websites for various national and international conferences organised by the institute. The team also develops many online applications and tools to automate and manage R&D facilities and administrative work. The IT group has also developed applications for CSIR Head Quarters, for online acceptance, review, funding, and reporting of project proposals submitted by all CSIR scientists and also by researchers in academic, research, and industry.

CSIR-CCMB is connected by a 1 Gigabit dedicated leased line connection from NKN, a 100 Gbps dedicated leased line from BSNL, and a 10 Mbps dedicated leased line connection. The LAN is built with a high-speed 10 Gbps network backbone and switched 1 Gbps connections to systems. 40 Gbps links are provided for the new data centre, the Genome India Project and the NGS facility. Secured wireless connectivity is implemented in all the buildings on the campus. Annex campus-LaCONES and MBT are connected to the main campus through site-to-site VPN.

The IT group manages high-performance computing clusters, other computing facilities, storage systems, etc. to support the research facilities and other research activities smoothly. Other facilities like surveillance cameras, biometric systems, fire alarm systems, telephones, and closed-circuit TV are also managed by the group.
The IT group organised a lecture by Shri S Harinath, Assistant Commissioner of Police, Cyber Crimes, Telangana, in connection with the National Cyber Security Awareness Month, on October 8, 2021, to create awareness of cyber-crimes for CSIR-CCMB staff and students.

Sponsored Project:
The Information Technology group received a grant of 150,000 euros for the project "Network infrastructure upgrade" from Asi@Connect, funded by the TEIN*CC. According to the project goal, the existing network on all three campuses was successfully upgraded to be more efficient and adaptable to meet the organization's current and future needs for accelerating research activities.

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

Rajbhasha Unit

This unit helps the institute 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 for its employees at regular intervals. This unit helps scientists in preparing papers, articles, reports in Hindi. This unit also ensures issue of official documents in Hindi as per the OL Act Provisions. It also facilitates issuing of press releases/communiques in Hindi.

Rajbhasha Unit of CCMB conducts "HINDI FORTNIGHT" in the month of September every year. Various Hindi competitions and programmes are organized on the occasion. This year Hindi Fortnight has been conducted from 01 Sep 2021 concluding the valedictory function on 14th September, 2021 on virtual mode. 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 organisation. Every year, we invite an 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.

An inspection on the official work done in Hindi by CCMB was conducted by Regional Implementation Office, Bangalore, Ministry of Home Affairs, Govt of India in the month of November 2021.

06 staff of CCMB were nominated to attend Hindi training conducted by Hindi Teaching Scheme, Govt of India. Out of them, 03 attended and passed Pragya classes and 02 attended Parangath , and passed the exam. They were awarded with cash awards and advance increment as per the GoI rules and provisions.

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 the PRATIBHA programme is to provide a platform to the inherent talents of research students and staff of CCMB. The programme is held annually, usally in the month of June. 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, etc. CCMB staff have found them useful to gain basic knowledge in these areas.

The Rajbhasha Unit has a very rich library consisting 3046 Hindi Books on various subjects viz., classic works of Hindi literature, science, translations and books of general interest, Personality development, etc. This year 91 books have been added to this collection.

1.2
Academics

1.2 A Academic Cell & PhD Program

CSIR-CCMB imparts training to doctoral students in an academic program linked either to Jawaharlal Nehru University (JNU), New Delhi or Academy of Scientific and Innovative Research (AcSIR). The PhD program is run by an Academic Cell, which consists of two Academic Coordinators and an 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.

CCMB-PhD 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.

CSIR-CCMB selects candidates for the PhD program in August and January each 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-JNU, CCMB-ACSIR and CCMB-JGEEBILS streams. 7 students joined for August 2021 and 10 students joined for January 2022 PhD programs. 11 students gave their PhD colloquia and 4 students submitted PhD thesis during April 2021 to March 2022. 27 students have been awarded PhD degree from JNU/AcSIR during this academic year.

1.2 B PhDs Awarded

List of students awarded with PhD degrees during April 2021 to March 2022

Pavan Kumar Chodisetti

Studies on Bacterial Cell Wall Synthesis: Role of Peptidoglycan Hydolases (06-04-2021)
Guide: Dr Manjula Reddy

A Srinivasan

Computational analysis of chromatin domain boundaries and Polycomb Response Elements in Insects (13-04-2021)
Guide: Dr Rakesh K Mishra

Mohd Mazeed

Insights into D-aminoacyl-tRNA deacylase (DTD) function in land plants (15-04-2021)
Guide: Dr R Sankaranarayanan

Shams Ul Haq

Early life stress induced remodeling of mouse hippocampal circuitry causing adult neuropsychiatric disorders (18-06-2021)
Guide: Dr Arvind Kumar

Shagufta Khan

Paternal Transgenerational Epigenetic Inheritance in Drosophila melanogaster (22-06-2021)
Guide: Dr Rakesh K Mishra

Shivali Rawat

Study of aggregation-prone proteins in mammalian cells (23-06-2021)
Guide: Dr Swasti Raychaudhuri

Dhiviya Vedagiri

Investigating the Role of Epithelial Mesenchymal Transition (EMT) in Human Viral Infections (25-06-2021)

Guide: Dr H H Krishnan

Divya Sriram

Understanding molecular mechanisms involved in C3G-induced differentiation (14-07-2021)

Guide: Dr V Radha

Preethi Jampala

Roles of cis Regulatory Motifs and Chromatin Modifying Factors in Regulation of Homeobox Transcription Factor, SHOOT MERISTEMLESS (STM) in Plants (16-07-2021)

Guide: Dr Mukesh Lodha

Upasana Rai

Structural-functional insights of DRB2 during RNA recognition in *A. thaliana* (19-07-2021)

Guide: Dr Mandar V Deshmukh

Rajan Kumar Jha

Mitochondrial and nuclear factors in multi-systemic disorders (20-07-2021)

Guide: Dr K Thangaraj

Asmita D Pawar

Exploring Calcium-binding Properties of Novel Bacterial β-sheet Proteins (30-07-2021)

Guide: Dr Yogendra Sharma

Patil Gajanan Shrikant

Structural and functional characterisation of fatty acyl-AMP ligases from diverse organisms (03-08-2021)

Guide: Dr R Sankaranarayanan

Survi Mahesh

Understanding meiosis and its regulation in Arabidopsis thaliana (13-10-2021)

Guide: Dr Imran Siddiqi

V Rajesh Iyer

Understanding Genome-Environment Interactions at Molecular, Cellular and Organismal Level (03-11-2021)

Guide: Dr Satish Kumar & Dr K Thangaraj

Akhil Kotwal

Role of Hsp90 in the epigenetic and cell cycle regulation of cancer (05-11-2021)

Guide: Dr. A S Sreedhar

Venkata Pardha Saradhi A

Control of reproductive development in Arabidopsis thaliana: Cell cycle states of the gametes prior to and after fertilization (09-11-2021)

Guide: Dr Imran Siddiqi

Ashutosh Singh Tomar

Understanding Molecular Mechanism of Intergenerational Programmimg of Diabesity in Offspring of Women with Gestational Diabetes Mellitus (16-11-2021)

Guide: Dr G R Chandak

Nipa Basak

High altitude adaptation(s) in Tibetan population: Biochemical, Epigenetic and Genetic perspectives (07-12-2021)

Guide: Dr K Thangaraj

Prachand Issarapu

Understanding the Epigenetic Mechanisms Linking Maternal Nutrition and Offspring Health (08-12-2021)

Guide: Dr G R Chandak

Ashis Kumar Pradhan

Identification and characterisation of OAD genes involved in polyamine regulated OAZ1 and t-OAZ1 degradation (09-12-2021)

Guide: Dr Manjula Reddy

Narayan Datt Soni

Investigations of Brain Energy Metabolism in Mouse models of Alzheimer's Disease Using 13C NMR Spectroscopy (15-12-2021)

Guide: Dr Anant B Patel

Debabrata Jana

Regulation of Core Pluripotency Network in ES cells and Self-Organization (20-12-2021)

Guide: Dr P Chandra Shekar

V Devi Prasad

Analysis of Immune Memory in B Lymphocytes (13-01-2022)

Guide: Dr Tushar Vaidya

Chhavi Dawar

De novo transcriptome analysis of embryonic GAM and Brain tissues of Indian Mugger: search for candidate gene(s) having putative role in temperature-dependent sex determination (21-01-2022)

Guide: Dr Ramesh K Aggarwal

Satyajeet Sunil Salunkhe

Analysis of Generation of Immune Memory (01-02-2022)

Guide: Dr Tushar Vaidya

Manish Bhattacharjee

Study of protein neddylation in malaria parasites (21.03.2022)

Guide: Dr Puran S Sijwali

1.2 C Training Programs

Dissertation Research Training Program

CCMB offers Dissertation Research Training Program, an interdisciplinary research training program for students from M.Sc/M.Pharm/ M.Tech/ M.D/ B.Pharm/ B.D.S/ B.Tech to do either six months or a one-year research projects. The students must work under the supervision of a scientist at CCMB/ LaCONES (CCMB Annex-I)/ CRF (CCMB Annex-II) to complete a small research project toward partial fulfillment of their academic degrees. 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. As part of training, students are taken for laboratory visits to other campuses within CCMB, i.e., Medical Biotechnology Complex and LaCONES. On successful completion of their research work, students are encouraged to give a poster presentation to the CCMB scientific community. After submitting the dissertation report, they also receive a certificate. Since CCMB receives many applications, a stringent selection criterion is applied to select the students. In 2021 - 2022, 57 students enrolled and completed their dissertation research training at CCMB.

Project-based Research Training

The project-based student training program encourages students who have completed their studies in M.Sc/M.Pharm/M.Tech/MD/ B.Pharm/BDS/B.Tech and would like to spend time learning and improving their laboratory skills. Unlike the dissertation 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. The program also 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. As part of training, students are also taken for laboratory visits to other campuses within CCMB, i.e., Medical Biotechnology Complex and LaCONES. In 2021-22, 10 students benefitted from the program.

Summer Training Program

The program is open to students from all branches of life science studying at any Indian university / college / research institute. The program is offered to students still pursuing their studies, M.Sc. students who have completed their 1st year, B.Tech/ B.Pharm students who completed 3rd year, Integrated B.Tech-M.Tech, B.Sc-M.Sc or BVSc students who completed 4th year and MBBS/BDS in any year of their study. M.Tech/ M.Pharm students are not eligible for the summer training program at CCMB.

The program duration is 60 days (~eight weeks) between May-July every year. Online applications are invited through a notification in March of every year. Each selected student is assigned to a scientist who mentors them to execute a small project work. A lecture series on popular science topics, scientific ethics, good laboratory practices, and opportunities in life sciences are organized for the students. At the end of the program, students submit a 'Project Report' of the work done and also required to make a poster presentation. The program is mainly intended to give students real-time exposure/ hands-on experience to inculcate zeal for research.

Every year, CCMB accommodates 60 students. This year, CCMB called for the applications online.

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

Skill/Training Development Program

Under the CSIR Integrated Skill Initiative, CCMB has been conducting its Skilling/Training Programs from 2017. Various Skilling Programs were conducted this year, with a view to cater to both academia and industry needs.

About five different trainings spanning from one day to 4 weeks benefiting around 327 candidates were held during 2021-22 in various advanced areas of CCMB expertise namely, COVID-19 diagnostics, Wildlife Forensics, Cell Biology, Microbiology, Bacterial Genetics, Molecular Biology, and Animal Cell Culture. The ultimate aim of these programmes is to improve employability and career advancement (through reskilling/upskilling) in the area of life sciences.

Online and onsite Training Programs for scientists/ lab technicians/ doctors/ paramedical staff/students/ diagnostic labs were conducted on "The Dry Swab Based Direct method of COVID-19 testing", a rapid cost effective and safer method for testing SARS-COV-2 which was developed by CCMB. During this process CCMB successfully trained 289 personnel from various private and government institutes.

To address the constant need of faculty to upgrade their knowledge in the cutting edge areas of life sciences, a two week training program on "Basic Techniques in Genetics and Molecular Biology" was conducted for the faculty of Science degree colleges in Telangana benefiting 10 candidates.

A hands-on-training workshop on "Basic Techniques in Cell and Molecular Biology" for undergraduate students of Bhavan's Vivekananda college, Sainikpuri under DBT STAR College Scheme, was conducted and 18 students had participated in the program.

In a view of successful partnership with the line agencies involved in controlling and preventing wildlife crime, a hands-on training on DNA-based wild life forensics for Officers of Regional Forensic Science Laboratory (RFSL) Nagpur, was conducted. four RFSL officers participated in the program.

A short term course on "Basic Techniques in Animal Cell Culture" was held, and six participants participated.

Several entry-level skilling courses in Instrumentation, laboratory attendants, animal attendants, etc. are in the pipeline as well.

"Basic Techniques in Animal cell culture"- 21st - 25th March 2022

1.3
Innovation Hub (iHUB)

1.3 A Services

Consolidated Diagnostics Facility at iHUB

The molecular and chromosomal diagnostic activities run in a centralized facility at the CSIR-CCMB, Annexe-II. Last year witnessed addition of several new diagnostic tests in to our armamentarium. Next-Generation Sequencing (NGS) services are now being offered to various hospitals across the country. Utility of diagnostic exome sequencing has been expanded by the addition of Copy Number Variations (CNV) detection pipelines in analysis of raw data. Whole genome analysis is now being offered for diagnostic purposes as well. Genetic counseling services are being provided to more than 50 patients and families every month. 1848 patients from 1708 families have benefited our testing services.

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

Laboratory for Conservation of Endangered Species (LaCONES) of CSIR-CCMB provides DNA-based species, individual identification, sexing and rehabilitation services to the nation for the purpose of wildlife crime investigation. It is one of the major on-going activities in LaCONES. Biological specimens confiscated in wildlife related crimecases are forwarded by state forest, judiciary, police and custom departments to LaCONES.

During the period (April 2021 – March 2022) a total of 282 wildlife crime cases were received for different analyses. The forwarded biological samples comprised of 511 types such as cooked/raw meat, skin, venom, tusks, bones, claws, hair, feces, blood stains, saliva swabs and Hatha Jodi samples. During this period, a revenue of more than Rs. 23 lakhs was generated towards the DNA analysis fee charges.

Left image: Wildlife forensic lab
Right image: Wildlife forensics team. From left to right: Raghavendra Babu, Ajay Gaur, Anuradha Reddy, O V Padmalatha

1.3 B Atal Incubation Centre-CCMB

Overview

Atal Incubation Centre – Centre for Cellular and Molecular Biology (AIC-CCMB) is in its fifth year of enabling research to become tangible, value-based solutions for the nation's greater good. As an incubator focused on accelerating life science technologies, we have quickly become the go-to place for robust industry-academia collaborations and plug & play wet research facilities.

- Currently operating at 100% occupancy, we are now actively looking to expand beyond our 20,000 sq ft space in the CRF complex.
- We are considered one of the top 5 biotechnology incubation centre's in India, with one of the largest facilities for shared wet research, industry-standard equipment and operating facilities.
- Our ecosystem has expanded, with industry stalwarts joining our mentor pool for effective mentoring and training.
- Startups from all over India and the globe are seeking incubation at our centre.
- With three new funding programs, innovative startups now have access to seed funding right from ideation stage.

Programs under AIC-CCMB (past 12 months)

- Providing services to the startups in the incubator
- Executing supported programs from DST, DBT and MeitY
- Managing the seed fund support given by DST, SSF and under CSR from various corporates
- Promotion of a Center for Predictive Human Model Systems (CPHMS)
- Execution of projects for indigenous kit development, which were supported by BMGF and Rockefeller on COVID-19 testing kits
- Execution of mRNA project for COVID-19 vaccine

Incubation activities

We currently house 26 startups physically and over 10 startups virtually. The physically incubated startups have all taken space ranging from 100 sq ft to 900 sq ft to set up their own labs in the incubator. These startups are developing technologies in the areas of stem cell therapies, CarT cell therapies, monoclonal antibody production, milk proteins by fermentation, mRNA platforms, controlled drug release, and poultry vaccines, to name a few. In addition, we also physically incubate 5 SPARSH fellows as well as 8 startups virtually as part of MeitY TIDE 2.0 program.

As a part of the incubation programs, AIC-CCMB conducts numerous trainings and workshops for both startups and their staff. We enable constant interactions with the advisors and mentors, besides our own team to create an immersive hand-holding ecosystem for the founders. We are happy to report that our efforts have prompted three students of CCMB to find their own enterprises with us and have also raised external seed funding.

- Jobs created by incubator: 30+
- Jobs created by incubatees: 100+
- Women incubatees supported: 20
- Total IPs facilitated: 29, includes 22 patents, 2 copyrights, 3 trademarks filed by startups

Following agency-supported programs have been executed at the incubator:

Technology Incubation and Development of Entrepreneurship (TIDE 2.0)

TIDE 2.0 is a program supported under MeitY Startup Hub (MSH) by the Ministry of Electronics and Information Technology (MeitY), GoI.
8 startups were selected under this program under two categories - Grant-in-Aid and Entrepreneur-in-Residence.

- Grant–in–aid – INR 7 lakhs each to 4 companies per cohort
- Entrepreneur-in-Residence – INR 4 lakhs each to 4 innovators per cohort

Each cohort is supported for 1 year for a total period of 5 years.

SPARSH Social Innovation Immersion Program (SIIP)

SIIP is an 18-month duration fellowship program of BIRAC, Govt. of India. SPARSH aims at creating a pool of biotech "Social Innovators" who can identify needs and gaps within communities and then can help bridge the gaps either through innovative product development or service.

CYCLE 1: The first cohort of SPARSH fellows was recruited by August 2020 and graduated from the fellowship in March 2022. The extension in the fellowship was primarily due to pandemic related restrictions. We have successfully completed the first cycle in the thematic area "Aging and Health" with 4 out of 5 of our fellows forming their startups to take their innovations forward. All 4 fellows used the Rs. 5 lakhs kick start grant to develop their prototypes and have been able to raise funding from private & public funding with our support. The fellows presented their innovations at the BIRAC SPARSH Tech Showcase organized at FITT IIT-Delhi with knowledge partner Tata Institute of Social Sciences and received accolades for the same. The thematic area for SPARSH program Cycle 2 at AIC-CCMB is Mother & Child health. We are happy to report that the call was opened in October 2021 and has concluded with the selection of 5 fellows for this center.

National Science & Technology Entrepreneurship Development Board (NSTEDB) sanctioned a quantum of Rs, 5.25 crore grant to AIC-CCMB under the NIDHI SSS scheme. This flagship SEED fund program of NSTEDB has allowed us to provide the much need bridge funding for promising healthcare startups at our centre. Five start-ups were supported under the Seed Support Program of NSTEDB, DST.

Startup India Seed Fund Scheme (SISFS)

AIC-CCMB was awarded the Startup India Seed Fund Scheme (SISFS), a flagship funding program by Startup India, Govt. of India to provide capital at the seed and 'Proof of Concept' development stage. This grant enables AIC-CCMB to provide financial assistance to startups for proof of concept, prototype development, product trials, market entry, and commercialization for life sciences startups. So far, 2 startups have benefited from this scheme, namely XEEED IO Private Limited and Njyme Solutions Private Limited.

COVID-19 Technology Deployment (CoviTeD) Accelerator Program

AIC-CCMB launched the COVID-19 Technology Deployment (CoviTeD) Acceleration Program in 2021 with the intent to fact-track the deployment of innovations for the management of COVID-19 and related diseases in India. The project is supported by the Security Printing and Minting Corporation of India Limited (SPMCIL) CSR initiative. The program provided high-impact mentoring, and financial, regulatory, and marketing support to take these products and technologies to market.

Till date, we have supported 7 startups in 3 cycles so far.

Centre for Predictive Human Model Systems (CPHMS)

CPHMS is India's first think tank dedicated to enabling a shift from observational science to a paradigm where we can begin to predict biological consequences based on accumulated information in human-relevant contexts. CPHMS regularly conducts webinars & workshops to train and create awareness of research conducted in India's human-relevant technologies.

The team has conducted

- 9 monthly webinar talks
- A multi-stakeholder round table was conducted in September 2021 titled, "Enabling a shift towards human-relevant paradigms in biomedical research and drug discovery in India"

CPHMS proposed to conduct a lecture course on "Microphysiological systems: Advances and applications in human-relevant research" to the European Molecular Biology Organization (EMBO). The proposal was accepted, and EMBO with Wellcome DBT India Alliance has sanctioned a grant of €27,827 to conduct this lecture series. CCMB and AIC-CCMB will be jointly conducting the EMBO lecture series from Oct 31st to Nov 4th 2022 at IICT Auditorium.

mRNA Vaccine technology platform for India

CSIR-CCMB, in collaboration with other CSIR institutes, jointly worked on an "mRNA platform for Vaccines and Biotherapeutics" to initiate a program for an indigenously developed mRNA vaccine platform against SARS-CoV-2. The work on the project began in May 2021.

AIC-CCMB, under the leadership of CCMB, worked on an "mRNA platform for Vaccines and Biotherapeutics". The objective of this project is to indigenously developed mRNA vaccine platform against SARS-CoV2 in collaboration with other CSIR institutes. AIC-CCMB formed a team of researchers to explore the details of the technology from available public information and focused on developing an mRNA vaccine similar to Moderna and Pfizer with their intention to design a COVID pan vaccine and enhance 4o to 8o stability. The team successfully replicated the mRNA technology and established proof of concept at a lab scale. In mice, two doses of the developed mRNA vaccine candidate induced anti-Spike antibodies. These antibodies were more than 90% efficient in neutralizing the infection, causing interaction of SARS-CoV-2 with the cognate human ACE-2 receptor. To test the efficacy of the mRNA vaccine candidate, pre-clinical studies were conducted involving live challenge experiments in hamsters. The results showed that compared to controls, hamsters inoculated with two doses of the CCMB's mRNA vaccine candidate were substantially protected from live SARs-CoV-2 virus infection. All this was achieved in a record time of less than 1 year.

Student Innovators Program (SIP)

AIC-CCMB constantly engages with the next generation of entrepreneurs through various channels. The Atal Innovation Mission (AIM) Student Innovators Program (SIP) is one such avenue. The program aims to identify young talented individuals and nurture them to develop an interest in problem-solving and eventually take up entrepreneurship. Here, in-house mentors (program coordinators) work with student teams and the faculty in-charge of the team to refine their prototypes and improve their Technology Readiness Levels. The engagement usually lasts 8-11 weeks, with a week-long extensive boot camp as well. In the last 3 years, we supported 11 teams (29 students & 12 faculty members) across the country. Teams mentored by AIC-CCMB have been recognized as top teams (National top 20) every year. We have received this recognition for 2 projects every year since 2019.

Way Forward

AIC-CCMB is focusing on evolving from an incubation center to an innovation center and helping attract funding on focused programs, either as grants or investments, that reflect CCMB strength. We have completed five years with satisfactory deliverables. Our sustainability is partial and would require support from national grants. Also our expansion is limited given the physical constraints of the facility. Our future plans would include both an operational shift from being only an incubator and also to expand its space for wider interactions with stakeholders of life sciences in the state.

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)
Mohali, Knowledge City, SAS Nagar
P.O. Manauli – 140 306

Prof Sandhya Visweswaraiah **Member**
Professor
Department of Molecular Reproduction,
Indian Institute of Science
Bangalore 560012

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**
National Centre for Cell Science (NCCS)
NCCS Complex,
S.P. Pune University Campus
Ganeshkhind, Pune – 411 007

Dr Sanjeev Khosla **Member**
Director
CSIR-Institute of Microbial Technology
Sector 39-A, Chandigarh – 160014

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

The primary responsibility is to assist the Director, CCMB in project management activities and act as a liaison between the Director and other research groups, CSIR-HQ and other organizations. The PME takes care of various in-house, sponsor, collaborative, grant-in-aid and NMITLI projects and provides inputs related to projects. In addition, PME provides information to project audit agencies, parliamentary queries and RTI queries.

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

From left to right : Charan, Gulzar, Sujatha, Vishnupriya, 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 and Wildlife Forensics) 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 & commercialization and skill/training programmes.

Security

Teh security team handles all security related aspects of the institution, internal & external.

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.

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: Consultation, diagnostic services, Pharmacy and Physiotherapy. Earlier (till Jan 2021), there is combined medical facilities for IICT and CCMB. At present Dispensary is temporarily accommodated in CRF. Pressently only consultation services are availble. At present CCMB Health center ismanned by 3 doctors, 2 lab technitians, 1 Physiotherapist, 1 female nurse and 1 receptionist. Dispensary Soft ware developed by It Department CCMB and ready for use.

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

- Thakur SS (2021). Proteomics and its application in endocrine disorders. ***Biochimica Et Biophysica Acta-Proteins and Proteomics*** 10.1016/j.bbapap.2021.140701
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2.2 B List of Patents

- Kit for detecting melanoma. Srivastava Avinash, Mishra Rakesh Kumar. NFNO: 0186NF2018/CA; Filing Date: 23-07-2021; Application No.: 3127759

- Kit for detecting melanoma. Srivastava Avinash, Mishra Rakesh Kumar. NFNO: 0186NF2018/US; Filing Date: 23-07-2021; Application No.:17/425611

- Kit for detecting melanoma. Srivastava Avinash, Mishra Rakesh Kumar. NFNO: 0186NF2018/EP; Filing Date: 26-07-2021; Application No.:20744302.9

- Kit for detecting melanoma. Srivastava Avinash, Mishra Rakesh Kumar. NFNO: 0186NF2018/AU; Filing Date: 26-07-2021; Application No.: 2020211817

- Kit for detecting melanoma. Srivastava Avinash, Mishra Rakesh Kumar. NFNO: 0186NF2018/NZ; Filing Date: 04-08-2021; Application No.: 778757

- A novel facile aqueous based extraction of progesterone metabolites from faeces sample for non-invasive, simple, affordable and farmer friendly paper based kit for pregnancy detection in cattle and buffaloes. Govindhaswamy Umapathy, Amit Asthana, Chintalagiri Mohan Rao, Vinod Kumar, Suresh Gopi. NFNO: 0091NF2018/CA; Filing Date:03-09-2021; Application No.: 3132566

- A novel facile aqueous based extraction of progesterone metabolites from faeces sample for non-invasive, simple, affordable and farmer friendly paper based kit for pregnancy detection in cattle and buffaloes. Govindhaswamy Umapathy, Amit Asthana, Chintalagiri Mohan Rao, Vinod Kumar, Suresh Gopi. NFNO: 0091NF2018/US; Filing Date: 05-09-2021; Application No.17/436602

- A novel facile aqueous based extraction of progesterone metabolites from faeces sample for non-invasive, simple, affordable and farmer friendly paper based kit for pregnancy detection in cattle and buffaloes. Govindhaswamy Umapathy, Amit Asthana, Chintalagiri Mohan Rao, Vinod Kumar, Suresh Gopi. NFNO: 0091NF2018/RU; Filing Date: 06-09-2021; Application No.2021126211

- A novel facile aqueous based extraction of progesterone metabolites from faeces sample for non-invasive, simple, affordable and farmer friendly paper based kit for pregnancy detection in cattle and buffaloes. Govindhaswamy Umapathy, Amit Asthana, Chintalagiri Mohan Rao, Vinod Kumar, Suresh Gopi. NFNO: 0091NF2018/AU; Filing Date: 06-09-2021; Application No.: 2020233121

- A novel facile aqueous based extraction of progesterone metabolites from faeces sample for non-invasive, simple, affordable and farmer friendly paper based kit for pregnancy detection in cattle and buffaloes. Govindhaswamy Umapathy, Amit Asthana, Chintalagiri Mohan Rao, Vinod Kumar, Suresh Gopi. NFNO: 0091NF2018/EP; Filing Date: 13-09-2021; Application No.: 20766051.5

- Recombinant extracellular chitinase from Brevibacillus laterosporus for biological control and other industrial uses. Lakshmi Prasanna Gangavaramu, Madhusudana Rao Nalam, Veerabhadra Rao Arravapalli. NFNO: 0154NF2021/US; Filing Date: 17-09-2021; Application No.: 17/478390

- A kit for detection of mutations associated with genetic disorders. Chandak Giriraj Ratan, Paliwal Sumit, Bayyana Swati, Donipadi Vinay. NFNO: 0087NF2019/JP; Filing Date: 23-03-2022; Application No.: 2022-518652

- A kit for detection of mutations associated with genetic disorders. Chandak Giriraj Ratan, Paliwal Sumit, Bayyana Swati, Donipadi Vinay. NFNO: 0087NF2019/US; Filing Date: 24-03-2022; Application No.: 17/763340

- A kit for detection of mutations associated with genetic disorders. Chandak Giriraj Ratan, Paliwal Sumit, Bayyana Swati, Donipadi Vinay. NFNO: 0087NF2019/CN; Filing Date: 24-03-2022; Application No.: 202080066965.4

- 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: 14-06-2021; 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/CN; Filing Date: 15-05-2018; Application No.: 2016800668640; Grant Date: 01-06-2021; Patent No.: ZL2016800668640

- Production of metal nanoparticles in aqueous solution. Sankalp Vinod Agarwal, Shyam Sunder Reddy, Marshal. NFNO: 0230NF2013/AU; Filing Date: 06-12-2018; Application No.: 2018274973; Grant Date: 08-07-2021; Patent No.: AU2018274973

- Biomarkers useful for detection of grades of human breast cancer. Dinesh Kumar Lekha, Verma Vinod Kumar, Appukuttan Nair Rekha, Jem Prabhakar, Katoor Jayasree. NFNO: 0037NF2011/US; Filing Date: 13-12-2018; Application No.16/219572; Grant Date: 05-10-2021; Patent No.: US11136628

- Recombinant extracellular chitinase from Brevibacillus laterosporus for biological control and other industrial uses. Lakshmi Prasanna Gangavaramu, Madhusudana Rao Nalam, Veerabhadra Rao ArravapalliNFNO: 0154NF2021/US; Filing Date: 05-09-2018; Application No.16/122612; Grant Date: 09-11-2021; Patent No.: US11168314

- Production of metal nanoparticles in aqueous solution. Sankalp Vinod Agarwal, Shyam Sunder Reddy, Marshal. NFNO: 0230NF2013/CA; Filing Date: 02-05-2016; Application No.: 2929431, Grant Date: 14-12-2021; Patent No.: CA2929431

2.2 C Awards & Honors

Research Staff

G R Chandak

- Member of the Governing Board of National Institute of Biomedical Genomics (NIBMG), Kalyani.
- Technical Advisory Committeeof the Biological SciencesDivision, Indian Statistical Institute for the term of 2020-2022
- Member of Selection Committee, Biotechnology Research Innovation and Technology Excellence (BRITE) Awardees.
- Elected INSA Fellow
- Sun Pharma Science Foundation Research Award-2021
- JC Bose Fellow 2021

Divya Tej Sowpati

- CSIR Young Scientist Award in Life Sciences

Manjula Reddy

- Elected NASI fellow

G Umapathy

- Associate Editor, Frontiers in Conservation Science (Animal conservation)

Mandar Deshmukh

- Member, Scientific Advisory Board , CIPLA

Mandar Deshmukh

- 2020 NMRS Subramanian Award of National Magnetic Resonance Society, India

Suman Thakur

- Editorial Board member, Journal of Proteome Research

Amitabha Chattopadhyay

- CSIR Bhatnagar Award

Students & Postdocs

Sakshi Shambhavi

- Best Poster Award in 48th National Seminars on Crystallography

Bharti Dharapuram

- Third Place in Poster Presentation, Early Career Biogeography Conference

Prakash Sivakumar

- Third Place in INYAS-SARANSH Three Minute Thesis Competition

Suparna Ghosh

- Best lightning talk Award Annual Meeting of Proteomics Society

Kinatukara Priyadarshan

- Ben Barres Spotlight Award

Gayathri Sreedharan

- DST AWSAR Award 2021

Rohitesh Gupta

- DST AWSAR Award 2021

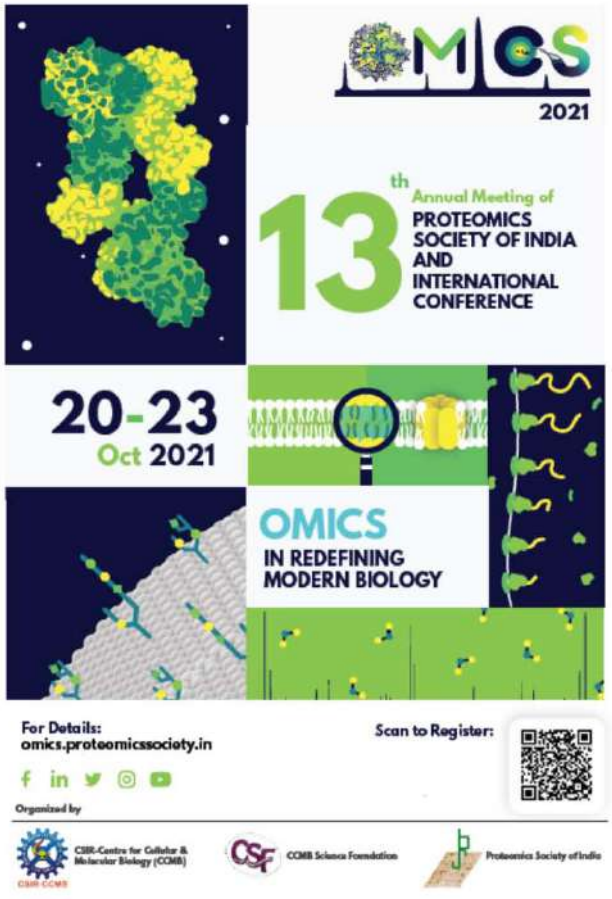
Nipa Basak

- Bruno Durrer Fellowship to attend XIII World Congress on Mountain Medicine, 2021

2.2 D Conferences & Symposia

OMICS-2021

The OMICS-2021 virtual conference on "Omics in Redefining Biology" was organized by Proteomics Society of India (PSI) in collaboration with CSIR-Centre for Cellular and Molecular Biology (CCMB) & CCMB Science Foundation from October 21 to 23, 2021. The conference was preceded by "A Preconference Education Day" on October 20, 2021. OMICS-2021 was successfully organized with Plenary sessions, lightning talks and a panel discussion on "Ethics in communicating science".



International e-conference on Recent Advances in Reproductive Technologies in Wildlife Conservation

Advetcon 2021 e-conference was held from November 11 to 13, 2021 in CCMB to highlight the current status of reproductive technologies in wildlife conservation and management. 710 registered participants from 24 countries included students, wildlife biologists, veterinarians, conservationists, scientists, forest and zoo managers. There were 10 sessions, 24 talks and 10 short presentations.

2.2 E MoUs & Agreements

- EUROFINS GENOMICS PRIVATE LIMITED - Outsourcing of DNA Seq facility to provide onsite sequencing services at CCMB. Hyderabad, 1st April 2021, 3 years

- AIC-CCMB - DIAGNOSTICS RELATED - Collaborating to facilitate forensic services and clinical diagnostic services to people at large, by engaging & Collaborating with AIC for increased access to affordable diagnostic and other R&D sevices to people at large through technology intervention. Hyderabad, 1st April 2021, 5 years

- NATIONAL INSTITUTE OF EDUCATION AND RESEARCH (NIPER) - To foster and promote academic and research collaborations, faculty and students exchange, teaching programmes in the areas of mutual interest, and to facilitate establishment of common research programs in the domain of testing of drug candidate molecules and drug delivery systems using cell and molecular biology tools. Hyderabad, 15th April 2021, 5 years

- TELANGANA MINORITIES RESIDENTIAL EDUCATIONAL INSTITUTION SOCIETY (TMREIS) - 1. Collaboration in Teaching , Research and Training in selected and advances thrust areas in S&T 2. To collaborate & write project proposals in areas of mutual interest and submit to various agencies for funding 3.Exchange of scientists, faculty & students in collaborative projects on areas of expertise. Hyderabad, 15th April 2021, 3 years

- Capital Health Services India Private Limited - Collaborating for technology/know-how transfer of the "Dry-Swab Technology" from CSIR-CCMB to Capital Health for commercialization of Covid RT PCR based test kits based on Dry-Swab Technology, developed and owned by CSIR-CCMB. 28th April 2021, 5 years

- AHF-ASIAN INSTITUTE OF GASTROENTEROLOGY (AIG) - The project will typically involve identification and recruitment of Covid-19 positive cases and their phenotypic characterization at AIG-AHF and subsequent genetic analysis at CSIR-CCMB. The final results will be collated, and the analysis will be conducted jointly. Hyderabad, 20th May 2021, 1 year

- BIOSMART BIOLOGICALS PRIVATE LIMITED - For technology/know-how transfer of the “Dry-Swab Technology” from CSIR-CCMB to Biosmart for commercialization of COVID RT-PCR-based test kits based on Dry-Swab Technology, developed and owned by CSIR-CCMB. Mumbai, 24th May 2021, 5 years

- ECOGEAR Energy Solutions Private Limited - ECOGEAR has expressed interest in collaborating with CSIR-CCMB to jointly bring in and validate the technology for “BIO Non-watering Circulating Flush toilet” in Indian markets. Hyderabad, 25th May 2021, 10 years

- NATIONAL INSTITUTE OF IMMUNOLOGY (NII) - Transfer of Mice. Delhi, 23rd June 2021, 5 years

- VINS BIOPRODUCTS LIMITED - Jointly conceived a project entitled “Development of inactivated COVID19 virus as antigen for the production of therapeutic immunoglobulin fragment for treatment of COVID-19 infection” in May 2020 and VINS had agreed to support & fund this PROJECT. 23rd June 2021, 1 year

- IMMORTALIGHT (OPC) PRIVATE LIMITED - For exploring the SARS-CoV2 inhibitory and/or anti-COVID-19 efficacy activities of selected natural/Ayurvedic/herbal products/formulations prepared by IMMORTALIGHT LTD. Hyderabad, 28th July 2021, 1 year

- ROCKEFELLER FOUNDATION, USA - Financial support to create a consortium to advance pathogen genomics to track SARS-CoV-2 variants and accelerate bioinformatics and global data sharing. New York, USA, 28th July 2021, 2 years & 10 months

- PUNE KNOWLEDGE CLUSTER (PKC) IUCAA - Consortium of R&D research and clinical institutions to advance pathogen genomics to track SARS-CoV-2 variants and accelerate bioinformatics and global data sharing as a part of philanthropic financial support from the Rockefeller foundation for the project "COVID-19". Pune, 28th July 2021, 2 years & 10 months

- NATIONAL CHEMICAL LABORATORY (NCL), PUNE - Consortium of R&D research and clinical institutions to advance pathogen genomics to track SARS-CoV-2 variants and accelerate bioinformatics and global data sharing as a part of philanthropic financial support from the Rockefeller foundation for the project "COVID-19". Pune, 28th July 2021, 2 years & 10 months

- SBI Foundation, Mumbai - CSR grant to establish the SBI Foundation Centre of Excellence (CoE) for Genomics Guided Pandemic Prevention. Mumbai, 12th August 2021, 1 year

- INDIAN INSTITUTE OF SCIENTIFIC EDUCATION & RESEARCH (IISER-PUNE) - Consortium of R&D research and clinical institutions to advance pathogen genomics to track SARS-CoV-2 variants and accelerate bioinformatics and global data sharing as a part of philanthropic financial support from the Rockefeller foundation for the project "COVID-19". Pune, 18th August 2021, 3 years

- OSMANIA MEDICAL COLLEGE & HOSPITAL - CCMB and OMC are desirous of collaborating for undertaking the research project on “Medical Genetic Research and Diagnostics with initial focus on COVID-19”. Hyderabad, 18th August 2021, 3 years

- ESIC HOSPITAL - CCMB and ESIMCH are desirous of collaborating for undertaking the research project on “Medical Genetic Research and Diagnostics with initial focus on COVID-19”. Hyderabad, 18th August 2021, 3 years

- TATA INSTITUTE FOR GENETICS & SOCIETY (TIGS) - TIGS will establish a virtual research centre at CCMB, which will focus on modern genetics & genomics for beneficial and ethical societal impact in the fields of health and agriculture, and this centre will be supported by both CSIR-CCMB & TIGS jointly. Bangalore, 19th August 2021, 5 years

- EMD MILLIPORE CORPORATION, USA - Technology License Agreement BURLINGTON, USA, 9th September 2021, Lifetime till shelf life of technology

- STATE OF ANDHRA PRADESH, THROUGH THE HEALTH, MEDICAL AND FAMILY WELFARE DEPARTMENT (SATELLITE) ANDHRA PRADESH - Collaborating to establish a Satellite Centre of SBI Foundation Centre of Excellence for genomics guided pandemic prevention in partnership with CSIR-CCMB in the state of Andhra Pradesh. Andhra Pradesh, 9th September 2021, 3 years

- THE DEPARTMENT OF HEALTH AND FAMILY WELFARE, GOVERNMENT OF MEGHALAYA (SATELLITE) SHILLONG - Collaborating to establishing a Satellite Centre of SBI Foundation Centre of Excellence for genomics guided pandemic prevention in partnership with CSIR-CCMB in the state of Meghalaya. Meghalaya, 14th September 2021, 3 years

- NATIONAL CENTRE FOR BIOLOGICAL SCIENCES (NCBS) - Consortium of R&D research and clinical institutions to advance pathogen genomics to track SARS-CoV-2 variants and accelerate bioinformatics and global data sharing as a part of philanthropic financial support from the Rockefeller foundation for the project "COVID-19". Mumbai, 21st September 2021, 2 years & 8 months

- APOLLO HOSPITALS ENTERPRISE LIMITED & INDRA CHEMICAL MANUFACTURING PRIVATE LIMITED - CSIR-CCMB and Apollo to develop and commercialize COVID test kits based on DArRT-PCR technology, developed and owned by CSIR-CCMB; and Indra Chemical Manufacturing Company to manufacture the DArRT-PCR test kits. Hyderabad, 29th September 2021, 3 years

- INSTITUTE OF GENOMICS & INTEGRATIVE BIOLOGY (IGIB) - Consortium of R&D research and clinical institutions to advance pathogen genomics to track SARS-CoV-2 variants and accelerate bioinformatics and global data sharing as a part of philanthropic financial support from the Rockefeller foundation for the project "COVID-19". New Delhi, 24th August 2021, 3 years

- Mahatme Eye Bank Eye Hospital - To extend benefits of genetic screening, carrier detection, clinical and genetic counseling for Sickle Cell Anaemia and also towards developing better genetic markers, predict clinical course and response to hydroxyurea therapy in patients. Nagpur, 18th October 2021, 3 years

- WILDLIFE SOS - To develop research strategies and protocols to monitor gut microbiome profile and metabolome profiles of captive animals in comparison to wild. New Delhi, 1st November 2021, 5 years

- L V Prasad Eye Institute (LVPEI) - Collaborative Research and Development (R&D) with a focus on frontier areas of mutual interest particularly medically oriented cell and molecular biology, biochemistry and biophysics, genetics and nano-biology. Hyderabad, 4th December 2021, 5 years

- Telangana State Council of Science and Technology (TSCOST) - Capacity building in the area of biotechnology teaching; decided to support a Skill Vigyan Program submitted by CSIR-CCMB. Hyderabad, 2nd December 2021, 3 years

- RABINDRANATH TAGORE UNIVERSITY, (RNTU) - For “Exploring the SARS-CoV2 inhibitory and/or anti-COVID-19 efficacy activities of selected natural/Ayurvedic/herbal products/formulations prepared by RNTU BHOPAL”. Bhopal, 7th December 2021, 1 year

- NEERI - To conduct environmental surveillance of sewage and waste water by sampling across various pan-India locations, mutually identified by CSIR-NEERI and CSIR-CCMB. Nagpur, 28th January 2022, 2 years

- SEMANTIC WEB INDIA PRIVATE LIMITED-AIC-CCMB-TRIPARTITE - For “Developing a software platform - Sandhi Gene Variant Analysis” extension of January 27, 2021 agreement. 27th January 2022, 1 year

- Mankind Pharma Limited - For technology/know-how transfer of “Early Detection of Pregnancy Technology” from CSIR-CCMB to MANKIND for commercialization of point-of-care device based on pregnancy detection technology, developed and owned by CSIR-CCMB. Arjun Juneja, Delhi, 4th March, 2022, 3% Royalty + GST on net sales, 5 years

- LVPEI-IIT HYDERABAD-TRIPARTITE - To conduct a research program entitled “Biomimetic hydrogel for the treatment of blinding corneal diseases”. The collaboration will further generate new knowledge and practices for the treatment of corneal diseases. 15th March 2022, 5 years

- National Council of Science Museums (NCSM) - represented by Visvesvaraya Industrial and Technological Museum (VITM), Bengaluru - For establishment of Mobile Science Exhibition (MSE) bus on the theme “In your Genes- decode and deter genetic disorders” for CCMB, CSIR, Hyderabad’. 28th March 2022, 7 months

2.2 F Invited Talks

Dr. Dhiraj Kumar
International Centre for Genetic Engineering and Biotechnology, New Delhi
"Tracing the trajectory of Mycobacterium tuberculosis in the host cells"

Prof. VijayRaghavan
Principal Scientific Adviser, Govt.of India
6th Founder`s day Lecture
Dr Rana Anjum and Dr Suresh Chintalapati (Alumni talks)

Dr. Ashish Jha
Research Associate in the Kerala Bird Atlas Project, Kerala Agricultural University, Thrissur
Kerala Bird Atlas: Citizens doing the science

Dr. Abhishek Subramanian
Laboratory of Angiogenesis and Vascular Metabolism,
VIB-KU Leuven Center for Cancer Biology, Leuven, Belgium
Making sense of the whole: Computational systems biology approaches to decipher biological mechanisms

Dr. Shekhar C. Mande
Secretary, DSIR and Director General, Council of Scientific & Industrial Research.
CCMB Foundation Day Lecture: Big Data Analytics: waiting to be tapped by Life Sciences

Dr. Sriram Sridharan
Computational Biologist, Department of Molecular Genetics, Erasmus University Medical Center, Netherlands
Genomic signatures underlying DNA replication stress and its clinical relevance

Prof. Ullas S. Kolthur
Professor, Department of biological sciences, TIFR, Mumbai
Plasticity & memory of molecular mechanisms: Linking metabolic inputs to cellular & organismal physiology, from development to aging

Prof. Shankar Srinivas
Oxford University, UK
Cardiac Cartography: delineating the emergence of cellular diversity in the mouse and human heart

Dr. Shanu Jain
Postdoctoral Fellow at NIDDK, NIH, USA
G Protein-Coupled Receptor Based Drug Discovery for Type 2 Diabetes and Liver Metabolic Disorders

Dr. Nikhil Gandasi
Researcher/Assistant Professor, Unit of Physiology, Gothenburg University, Sweden
Subcellular view of islets to understand type-2 diabetes

Dr. Mohan Prem Anand Marimuthu
Comai Lab, UC Davis
Centromere epigenetic conflict trigger uniparental genome loss in hybrids

Dr. Feroj Ahmed
Beatson Institute for Cancer Research, Glasgow, UK
Investigation and exploitation of the ubiquitin machinery to inhibit cancer

Dr. Sourish Ghosh
Postdoctoral Visiting Research Fellow, National Institutes of Health, Bethesda, USA
Tracking Footprints of Viruses: Revealing Alternative Modes of Viral Exit from Host Cell

Dr. Rahul Bhowmick
Assistant Professor, Center for Chromosome Stability, University of Copenhagen
Replication stress management in cancer cells

Dr. Laasya Samhita
DBT/Wellcome Trust India Alliance Early Career Fellow at NCBS, Bengaluru
Mistakes can be good: the evolutionary potential of translation errors

Dr. Prasad Krishnamurthy
Vice President, R&D at CuraTeq Biologics and Satyalakshmi Oruganty Lead Business Consulting at IDBS-Danaher
Career paths and Decisions for PhDs

Dr. Ishwariya Venkatesh
Research Asst. Professor, Marquette University, Milwaukee, USA
Molecular strategies to promote Spinal Cord repair: Barriers and Solutions

Dr. Krishna Suddala
Postdoctoral Visiting Fellow, NIH, USA
Unraveling riboswitch mechanisms by a combined investigation of RNA structure, dynamics and interactions

Dr. Mukesh Thakur
Zoological Survey of India, Kolkata
From molecules to monitoring: conservation genetics and genomics in applied wildlife conservation

Dr. Sriram Varahan
DBT-Wellcome Trust India Alliance Early Career Fellow, InStem, Bengaluru
Metabolic basis of cellular specialization in microbial systems

Dr. Subramanian Sankaranarayanan
Purdue University, Indiana, USA
Unravelling the Molecular Basis of Pollination

Dr. Ganesh Bagler
Associate Professor, Indraprastha Institute of Information Technology, Delhi
Computational Gastronomy: A Data Science Approach to Food

Dr. Amarjeet Temburni
Associate Professor at Delaware State University, USA
Astrocytes, the Conductors of Neuronal Symphony

Prof. Vasant Shinde
Professor of Archaeology, Deccan College Postgraduate and Research Institute, Pune
Archaeogenetic Research at Rakhigarhi: Recent Perspective and Future Directions

Dr. Tandrika Chattopadhyay
Visiting Fellow, Department of Biological Science, Tata Institute of Fundamental Research
Oscillatory control of Metabolic Homeostasis

Dr. Mayuri Rege
DST INSPIRE Faculty, Ramnarain Ruia College, L. Nappo Road, Matunga, Mumbai
On-demand genome folding using a novel optoepigenetic tool

CCMB Biologue

CCMB Biologue is a student-led initiative that invites varied experts in life sciences for online talks. These talks are open for all to attend.

Prof. Fiona Watt
Centre for Stem Cells and Regenerative Medicine, King`s College London, UK
Understanding cell heterogeneity in multi-layered epithelia

Prof. Vatsala Thirumalai
NCBS, India
Follow the beat: Brain mechanisms for learning time intervals

Prof. James J Collins
Broad Institute of MIT and Harvard, The Wyss Institute
Synthetic biology: Life redesigned

Prof. Eric Vivier
Centre d'Immunologie de Marseille-Luminy (CIML), Marseille, France
Harnessing innate immunity in cancer therapy

Dr. Erwin London
Stony Brook University, USA
Using lipid exchange to understand membrane organization and function

Prof. Amitabh Joshi
JNCASR, Bangalore
The Illusion of mechanism in biology

Dr. Mary Gehring
Associate Professor of Biology, MIT, USA
Genetic Conflicts and Seed Biology

Prof. Vidyanand Nanjundiah
Centre for Human Genetics, Bangalore
Biology: An autonomous science?

Dr. Michael Rape
University of California, Berkely, USA
CCMB Biologue: The Code to Decide Fate

Prof. John Mattick
Garvan Institute of Medical Research
Genomes are .zip files of transcriptomes

2.2 G Events & Conferences

Independence Day (August 2021)

CCMB celebrated 75th Independence day on August 15, 2021. Following the flag hoisting by Dr.Vinay Nandicoori, Director, CCMB, a prize and certificate distribution programme to the staff was organized by CCMB club which conducted various activities on the occasion of Independence day.

CCMB Foundation Day (November 2021)

CCMB organized its Foundation Day celebrations on November 26, 2021 and Dr. Shekhar C Mande, Secretary, DSIR and Director General, CSIR, delivered the 34th CCMB foundation day lecture on "Big Data Analytics: Waiting to be tapped by Life Sciences" followed by a flute recital by Pandit Ronu Majumdar. As part of students' symposia, senior PhD students and postdocs presented their work to their peers at CCMB. Anindya Ghosh memorial award for Best coursework seminar 2021 was presented to Mr. Sohail Rafiq Mansuri and Mr. Nallamotu Krishna Chaitanya.

Republic Day (January 2022)

On the occasion of Republic day on January 26, 2022, Dr. Manjula Reddy, Acting Director hoisted the flag followed by address by the Chief guest, Dr Rajat Kumar, IAS, Spl. Chief Secretary to Govt., Irrigation & Command Area development department, Govt. of Telangana, as its Chief guest. In his address to the CCMB family, Dr. Rajat Gupta appreciated CCMB's contribution in universal primer technology to its involvement in testing and training during COVID pandemic.

Founder's Day (February 2022)

CCMB celebrated its 6th Founder's day on February 22, 2022. Day began with the alumni talks delivered by Dr Rana Anjum on "Navigating my career path in oncology drug development" and Dr Suresh Chintalapati on "True North". Founder's day distinguished guest lecture was delivere by Dr.VijayRaghavan, Principal Scientific Adviser, Govt. of India, on "Combining small, collaborative, interdisciplinary, and big: Indian Life Sciences research in the next 25 years" followed by a cultural event by Carnatic vocalist Shri M Sudhakar.

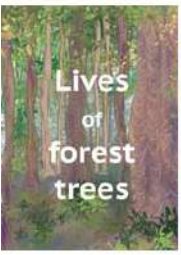
Science Leaders' Conclave (March 2022)

As a part of 75 years of India's independence celebrations – Azadi ka Amrut Mahotsav, Science Leaders Conclave involving Directors of 160 research institutes across disciplines of science and technology all over India was jointly organized by CCMB, IICT and NGRI from March 24 to 26, 2022. They discussed challenges and opportunities for India under the five broad categories: Climate Change, One Health, Energy Security, S&T for Sustainable Development Goals, and Applications of Artificial Intelligence in Agriculture, Water and Environment. These deliberations identified the issues relevant to India, proposed a future roadmap and S&T vision 2047 for the country. Shri Kishan Reddy, Hon'ble Union Minister for Culture and Tourism, attended the conclave and addressed the gathering.

2.2 H Science Outreach & Popularization Programs

Zines

We made small, easy to print, visually rich booklets, called as zines. Our zines focus on scientific questions that our scientists address as well as their life journeys. Our previously made zines on climate change were translated to Bangla by other science communication initiatives such as Bigyan and Sobuj Prithibi.



Milo CCMB

CCMB made a series of animated videos for students of Telangana Social Welfare Residential Educational Institutes Society (TSWREIS), spread across the state of Telangana. The videos were made on topics that are aligned to high school curricula, with social relevance and within CCMB's scientific expertise. The videos were made in English, Telugu and Hindi. These videos were shared with the students via their teachers. We then collected questions from the students on the topic of each video. This was shared with the respective CCMB scientist to design a follow-up interactive session with the scientists. Each session was attended by 300-500 students.

The videos made for this program can be accessed here: https://www.youtube.com/playlist?list=PL6FAIj7XldHt1jeTl9fpfINBZGCFp_FB8

Young Innovators Program

CCMB conducted its 8th Young Innovators Program. The program started with an online public lecture by Dr Raghunand Tirumalai on Resisting Antibiotic Resistance. This was followed by an online screening test, in which around 200 high school students from Hyderabad participated. 20 of them were selected to spend a week at CCMB. During this week, they had hands-on experimental sessions and interactions with scientists.

Games on Science

CCMB has made two games on science. One, called Fastest Protein First, explains how DNA is translated to proteins and the resources a cell needs for this. The other, called Climaze, is made based on the climate-related problems that urban young people of India relate with, and possible solutions towards them.

Podcast - India Asks Why

Dr Megha Kumar mentored a new podcast series called IndiaAsksWhy. They focus on common questions that we have on life by observing things around us. The podcast answers those questions through a conversation with an Indian scientist who works in the field.

Their work can be found here: https://www.indiaaskswhy.org

SciTales by CCMB

CCMB has a dedicated website called the SciTales by CCMB for its science communication content and events. You can access here: https://scitales.ccmb.res.in/

Open Day(s)

CCMB celebrated online Open Days from Sept 23-26. During these days, CCMB students and scientists put together 24 lab sessions, panel discussions and competitions for the participants. Due to the ongoing pandemic, the sessions happened online.

Wildlife Week Celebrations

In the first week of October, CCMB celebrated Wildlife Week with best nest making and painting competitions for local students at LaCONES-CCMB.

Superheroes Against Superbugs

CCMB is the scientific partner of the Superheroes Against Superbugs (SAS) initiative.

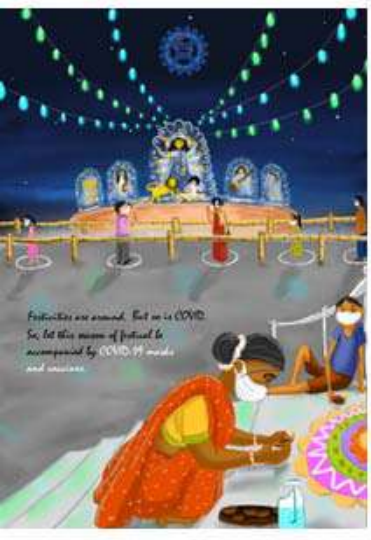
To celebrate the World Antimicrobial Awareness Week, CCMB students coordinated an interview series with experts working in India on various aspects of infection and antimicrobial resistance control. This series of interviews was published on the SAS website.

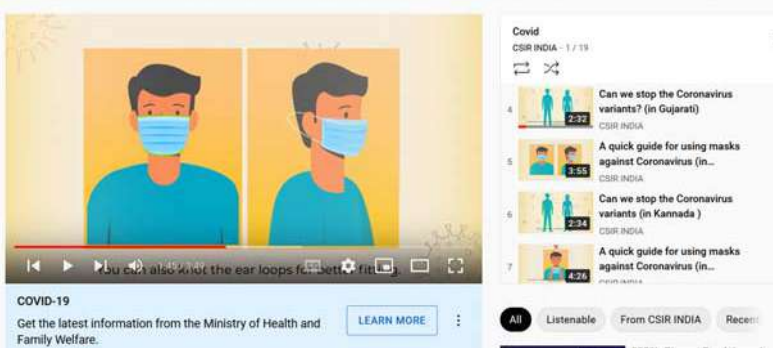
Study Tours

CCMB receives a number of requests from universities, colleges and schools every year for guided tours to the various facilities. CCMB took up this activity since its inception with an objective of keeping the young minds informed about the ongoing activities of CCMB in general and advances in frontier areas of modern biology in particular that they read in their text books in graduate and post-graduate studies. For this, a guided tour is organized for the visiting students groups. During the year, about 1000 students visited the institute from several colleges and universities of Karnataka, Tamil Nadu, Kerala, Maharashtra and Goa, in addition to student groups from local colleges and schools from Telangana and Andhra Pradesh.

COVID-19 Awareness

CCMB, with IICT and CSIR, made videos in multiple Indian languages and posters on how to use masks, to understand coronavirus variants and urging public to take vaccines and avoid crowds to fight the COVID-19 pandemic. CCMB conducted several webinars and actively interacted with press to keep them aware of the new findings of the pandemic our work showed us.





2.2 I Media coverage

THE HINDU
MONDAY, NOVEMBER 29, 2021

Tap big data analytics i
life sciences, CCMB tol
34th Foundation Day celebrated
SPECIAL CORRESPONDENT
HYDERABAD
students, staff and th
hlic and cow research

हिन्दी मिलाप

CSIR-CCMB to collaborate with Institut Pasteur
Research for personalised medicines
SPECIAL CORRESPONDENT
HYDERABAD
jects mentioned above. This is also a joint effort to tackle

Brahmin link to Roman Catholics: CCMB
U.Sudhakarreddy
@timesgroup.com
Hyderabad: Centre for Cellular and Molecular Biology (CCMB) scientists' study found that the Roman Catholics of Goa, Kumta and Mangalore regions are the
dia. Till date, no genetic study was done on this group to infer their origin and genetic history. This is the first high throughput study by CCMB and DST of Birbal Sahni Institute of Palaeosciences, Lucknow."
Researchers analysed DNA of 110 individuals from Roman Catholic community of Goa, Kumta and Mangalore, and compared the genetic information of the Roman Catholic group with previously published DNA data from India and West Eurasia.
The other institutes involved in this study are Mangalore University, Canadian Institute for Jewish Research and Institute of Advanced Materials, Sweden.

Telangana Today
Saturday, December 18, 2021
CCMB researcher, team identify key transporter protein in brain

పశ్చిమ తీరంలో రోమన్ క్యాథలిక్స్ మూలాలు
CCMB
CSIR-CENTRE FOR CELLULAR AND MOLECULAR BIOLOGY

रोमन कैथोलिक ब्राह्मणों के वंश

Efforts on to refine testing methods for Omicron detection
'Focus should be on inoculating unvaccinated population'
S. GEETHANJALI
HYDERABAD
Council Of Scientific And Industrial Research Centre For Cellular And Molecular Biology (CSIR-CCMB) is working on specific primers for in-
variant or the new Omicron," said director Vinay Kumar Nandicoori.
"As per the data available, Delta is still dominant across the country. Whether Omicron will replace it, we will see in the coming days. We should know that in South Africa where it was first detected, the Delta wave was waning when this new variant took over, which shows better infectivity and natu-
Omicron shows better infectivity and naturally, the unvaccinated are
patient to patient depending on many parameters, however, we should know that in addition to B-mediated im-
deaths," he said.
India having experienced the worst second 'Delta' wave with significant vacci-

Hydroxyurea gets approval for SCA
CITY BUREAU
CCMB had approached the Drug Controller General of India for approval of hy-
The approval to market hydroxyurea for treatment of SCA is a landmark achievement. This adds to the advantages of identifying the patients through a targeted screening programme, said Dr Giriraj R Chandak, Chief Scientist, at CCMB and Mission Director, leading the
fecting the red blood cell
is rampant among tribal an
general populations in M
harashtra, Madhya Pradesh
Chhattisgarh and Odish
Like most genetic disorder
SCA too has no cure but ha
symptomatic treatments f
pain, anaemia and vaso-o
clusive crisis, which mear

కేన్సర్ చికిత్సలో పసుపు సాయం
సీసీఎంబీ శాస్త్రవేత్తల అధ్యయనం వెలికి

వ్యవసాయ పరిశోధనల

CCMB celebrates Foundation Day
CITY BUREAU
Hyderabad
Hyderabad-based CSIR-Centre for Cellular and Molecular Biology (CCMB) celebrated its 34th Foundation Day here on Friday.
Multiple activities were organised by the authorities for CCMB students, staff and public, which included research scholars presenting their work.
The Foundation Day lecture was delivered by Dr Shekhar Mande, Director-General, Council of Scientific and Industrial Research (CSIR). In his talk, he spoke of how scientists understand structures of protein
complexes and their functions — a field where a large amount of biological data is generated.
Big question
Thus, the next big question lies in finding meaningful inferences from these large datasets. He pointed out this study is extremely important for the pharma and life science industry.
The day ended with a flute recital by Pandit Ronu Majumdar, an exponent from Maihar Gharana of Hindustani classical music. The recital followed by discussion with artists on their traditions and practices in the music community.

MAJOR BREAKTHROUGH
Y chromosome plays vital role in evolution, finds CCMB
EXPRESS NEWS SERVICE
A study conducted by the CSIR-CCMB has given fresh insights into the role played by the Y chromosome in the DNA. The study done by a team of researchers headed by Professor Rachel Jesudasan, Adviser (Research) at the Department Genetics of Osmania University, throws light on novel regulatory functions of the Y chromosome. Published in BMC Biology, the research suggests that beyond determining the gender of a person, the Y chromosome also regulates genes on other chromosomes involved in male reproduction.
According to scientists from the CCMB, the Y chromosome is known to be the male-determining chromosome. It is smaller in comparison to the X chromosome : its partner. It was not known to have any function except sex determination.
"Our previous studies had shown that sex and species-specific repeats on the Y chromosome regulate a reproductively important protein-coding RNA transcribed from chromosome number 1. Along with this study, there are reports of interaction between the Y chromosome and other chromosomes. Thus, consolidating the two studies, we see a more pervasive regulation of genes associated with reproduction by the Y chromosome," said Prof Jesudasan.
"As the species evolve, these repeats also co-evolve. Gradually, they are no longer able to regulate the reproduction of the species. Thus, it appears that these repeats are at the crux of species identity evolution," she added.
The new study is crucial as generally the DNA sequences on the Y chromosome are repetitive and large present in multiple copies and very few of them code for proteins. Given the previous function, most parts of DNA of Y chromosome considered junk.

కొవిడ్ అంకుర కేంద్రాలకు తోడ్పాటు

ఈనాడు, హైదరాబాద్: కొవిడ్ మహమ్మారిని ఎదుర్కొనేందుకు యంగా కొత్త ఆవిష్కరణలు, సాంకేతికతలను అభివృద్ధి చేసే అంకుర స లను ప్రోత్సహించేందుకు సెక్యూరిటీ ప్రింటింగ్ అండ్ మింటింగ్ కార్పొరే ఆఫ్ ఇండియా లిమిటెడ్(ఎస్‌పీఎంసీఐఎల్) ముందుకొచ్చింది. బయోటె లజీలో అంకుర సంస్థలకు ఇంక్యుబేటర్‌గా ఉన్న సీసీఎంబీలోని అ ఇంక్యుబేషన్ కేంద్రానికి రూ.2.3 కోట్ల సాయాన్ని ఈ సంస్థ ప్రకటించి కొవిడ్-19 ఎదుర్కోవడంలో స్వదేశీ సాంకేతికతన జిక బాధ్యతగా సహకారం అందిస్తున్నామని బు చిన ఎస్‌పీఎంసీఐఎల్ సీఎండీ త్రిప్తి పత్ర మోష్ మరింత ముందడుగు పడుతుందని కేంద్రం సీ

Mystery of Covid senses unlocked

Suppressed genes behind loss of smell, taste, says CCMB

The functioning of genes related

Norms for ancient DNA study formed

CITY BUREAU

A group 64 scholars from 31 countries including senior

priate for diverse local contexts. Our discussion with a truly international and diverse set of scholars was key to identify principles

Genetic inbreeding CCMB sees success

Lost smell & taste due to Covid? This CCMB study can tell you why

SUNITA JOSE

A new study to the Centre for Cellular and Molecular Biology (CCMB) gives insights into why

No signs of genetic inbreeding in captive-bred pygmy hogs: CCMB

Collaborative study to vet reproductive and genetic fitness of these animals

SPECIAL CORRESPONDENT
HYDERABAD

Pygmy hogs are among the rare and endangered animals listed by the International Union for the Conservation of Nature and the Indian Wildlife Protection Act. The present population is estimated to be less than 300 in wild and the original population may be less than 50 and restricted to Manas National Park in Assam.

The Pygmy Hog Conservation Program (PHCP), a collaborative project with

A pygmy hog breeding and conservation centre in Guwahati. • ARRANGEMENT

SPMCIL pledges ₹2.3 cr. to 6 start-ups on COVID

To identify and implement short and long-term solutions

CCMB, IICT collaborating on indigenous mRNA vaccine

Two such COVID-19 vaccines are currently in use across the world

Y has another function oth than sex determinatior

TIMES NEWS NETWORK

Hyderabad: A study by Centre for Cellular and Molecular Biology revealed that the Y chromosome has another function apart from sex determination. The novel finding indicates

NOT JUST SEX DETER

• A novel finding by CCMB indicates that Y chromosome regulates other chromosomes related to male

జన్యుమార్పులతోనే గుండెజబ్బుల ముప్పు?

• భారతీయుల్లో అత్యధిక మందికి ప్రతిదీ కార్డియా మయోపతి
• సీసీఎంబీ సీనియర్ శాస్త్రవేత్త బాబై తంగరాజ్

వైరస్ కొత్త రకాలపై ముందుగానే అంచనా

• ఐఎస్‌ఎస్‌వీ క్రూడింగ్‌తో సాధ్యమే
అంటున్న సీసీఎంబీ పరిశోధకులు

Research on COVID gets CCMB award

Award received at the hands of Vice-President

2.2 J Staff, Research Students, Project Staff

SCIENTIFIC RESEARCH GROUPS

A S Sreedhar Group

A S Sreedhar	Senior Principal Scientist
A Vijaya Lakshmi	Senior Principal Scientist
K R Paithankar	Principal Technical Officer
Akhil Kotwal	Ph.D. student
Shrikant Dharaskar	Ph.D. student

Karthik Bharadwaj Group

Karthik Bharadwaj	Scientist
Wasimuddin	Project Scientist-III
Lamuk Zaveri	Project Scientist-II
Sree Sankar D	Project Scientist-I
Chandreswara Raju K	Senior Project Associate
Manish Ranjan	Senior Project Associate
Surya Narayan Mishra	Senior Project Associate
Vidhyadhari Methuku	Senior Project Associate
Pramada Prasad	Senior Project Associate
Bishwadip Singha	Project Associate-II
Jandhyala Sai Krishna	Project Associate-II
Sumedha Avadhanula	Project Associate-II
Sneha N	Project Associate-II
Payel Mukherjee	Project Associate-II
Rachiraju Hema Sindhuja	Project Associate-I
Victor Banerjee	Project Associate-I
Aman Kumar Suryan	Project Associate-I
Himasri B	Project Associate-I
Kottapalli Srividya	Project Associate-I
N Uma Venkata Sai Malini	Project Associate-I
Banda Lavanya	Project Associate-I
Sreelekshmi M S	Project Associate-I
Neha Singh	Project Associate-I
Gulafsha Khan	Project Associate-I
Vodapalli Amareshwar	Project Associate-I
Devavrat Santosh Desai	Project Associate-I
A Vasanthakumar	Laboratory Assistant
Neha Sharma	Laboratory Assistant

Purnima Bhargava Group

Purnima Bhargava	Emeritus Scientist

Venkata R Aditya Chalamcharla Group

Venkata R Aditya Ch	Senior Scientist
Anubhav Bhardwaj	Sr. Technical Officer (1)
Harsh Kapoor	Ph.D. student
Annapoorna K P	Ph.D. student
Sauvik Dasnaskar	Ph.D. student
Kabila N	Project Associate-I
Hanuman Kale	Project Associate-II

G R Chandak Group

G R Chandak	Chief Scientist
Seema Bhaskar	Principal Tech. Officer
Inder Deo Mali	Lab Assistant
P Ashok	Lab Assistant
Ashutosh Singh Tomar	Ph.D. student
Prachand Issarapu	Ph.D. student
Sara Sajjadi	Ph.D. student
Swati Bayyana	Ph.D. student
Sohail Rafik Mansuri	Ph.D. student
Alagu Sankareswaran	Ph.D. student
Harsha Lad	Project Scientist-II
Suraj Singh Nongmaithem	Project Scientist-I
Rajnish Kumar Singh	Project Scientist-I
Ajay Deepak Verma	Senior Project Associate
Shoma Kumaresh Naskar	Project Associate-II
Arumalla Manisha	Project Associate-I
Riya Dogra	Project Associate-I
Palav Ashwini Dhaku	Project Associate-I
Anushri U	Project Associate-I
Bernadette Mathew	Project Associate-I
Punya Sri PSKDB	Project Assistant
ShaguftaTasneem	Project Assistant
Varsha Kolaria	Project Assistant

Amitabha Chattopadhyay Group

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

Ch Mohan Rao Group

Ch Mohan Rao	CSIR-Distinguished Scientist
Kamakshi Dandu	Ph.D. student

Saikat Chowdhury Group

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

Mandar V Deshmukh Group

Mandar V Deshmukh	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

Jyotsna Dhawan Group

Jyotsna Dhawan	Emeritus Scientist
Sujoy Deb	Ph.D. student
Debarya Saha	Ph.D. student
Swetha S	Ph.D. student
Priti A S	Ph.D. student
Ananga Ghosh	Ph.D. student

G Umapathy Group

G Umapathy	Senior Principal Scientist
Vinod Kumar	Technical Officer
Mihir Trivedi	Ph.D. student
Manu S	Ph.D. student
Krupa Vinay Teja P	Ph.D. student
G Anusha	Ph.D. student
Gopikrishnan P	Ph.D. student
Manisha Ray	Ph.D. student
Khan Aamer S Zafarullah	Project Associate-I

Ajay Gaur Group

Ajay Gaur	Senior Principal Scientist
V Purushottam	Technical Officer

H H Krishnan Group

H H Krishnan	Principal Scientist
M Mohan Singh	Technical Officer
Haripriya Parthasarathy	Ph.D. student
Divya Gupta	Ph.D. student
Vishal Sah	Ph.D. student
Dixitkumar Nanubhai T.	Ph.D. student
P. Sai Poojitha	Ph.D. student
Prangya Paramita Sahoo	Ph.D. student
Anoop B S	Senior Project Associate
Abdul Hamid Siddiqi	Project Associate-I

K Thangaraj Group

K Thangaraj	Chief Scientist (*on lien*)
Nitin C Tupperwar	Principal Scientist
G Mala	Principal Tech. Officer
S Deepa Selvi Rani	Sr. Technical Officer (3)
Jagamohan Chhatai	Technical Officer
Jaydeep A Badarukhiya	Ph.D. student
Lomous Kumar	Ph.D. student
Deepak Kumar Kashyap	Ph.D. student
Partheusa Machha	Ph.D. student

Arvind Kumar Group

Arvind Kumar	Senior 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
Unis Ahmad Bhatt	Project Associate-II

Lekha Dinesh Kumar Group

Lekha Dinesh Kumar	Senior Principal Scientist
Rohitesh Gupta	Senior Research Associate

Megha Kumar Group

Megha Kumar	DST-INSPIRE Faculty
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
Naman Goswami	Project Associate-I
Kashmiri Manish Lande	Project Associate-I

Mukesh Lodha Group

Mukesh Lodha	Principal Scientist
Preethi Jhampala	Ph.D. student
Akanksha Garhewal	Ph.D. student

M Mohammed Idris Group

M Mohammed Idris	Senior Principal Scientist

Rakesh Kumar Mishra Group

Rakesh Kumar Mishra	AcSIR Disting. Emer. Professor
Rashmi Upadhyay Pathak	Senior Principal Scientist
Phanindhar K	Ph.D. student
Nikhil Hajirnis	Ph.D. student
Ashish Bihani	Ph.D. student
Ravina Saini	Ph.D. student
Avvaru Akshay Kumar	Ph.D. student
Soujanya M S	Ph.D. student
Sonu Yadav	Ph.D. student
Saketh Murthy	Ph.D. student
Puja Singh	DST-INSPIRE Faculty
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
Yogita Kapoor	Ph.D. student
Priyadarshini Sanyal	Ph.D. student
Abhishek Saha	Ph.D. student
Amit Chakraborty	Ph.D. student
Saba Naz	Project Scientist-I

P Chandra Shekar Group

P Chandra Shekar	Principal Scientist
Vishnu Vijay	Ph.D. student
Mansi Srivastava	Ph.D. student
NiharikaTiwary	Ph.D. student
Elarani Majhee	Ph.D. student
Debabrata Jana	Senior Project Associate

Anant B Patel Group

Anant B Patel	Senior Principal Scientist
K S Vardarajan	Sr. Technical Officer (1)
Dipak Roy	Ph.D. student
Bedaballi Dey	Ph.D. student
Kamal Saba	Ph.D. student
Ajay Sarawagi	Ph.D. student
Prajakta Pramod Biyani	Ph.D. student
Chaynita Dashora	Ph.D. student
Akila Ramesh	Ph.D. student
Sanjana Sinha	Project Associate-I
Navleen Kour Anand	Project Associate-I

Hitendra Kumar Patel Group

Hitendra Kumar Patel	Principal Scientist
Raju Madanala	Sr. Technical Officer (2)
B Kranthi	Technical Officer
Vinoth Kumar	Technician
Vishnu Narayanan M	Ph.D. student
Komal Ashok Awalellu	Ph.D. student
Gokulan C G	Ph.D. student
Donald James	SERB National PDF
Rajkanwar Nathawat	Sr. Project Associate
Kamal Kumar Malukani	Sr. Project Associate
Jamaloddin	Sr. Project Associate
Bipin Kumar K	Sr. Project Associate-I
Rennya P R	Project Associate-I
Gattu Niranjan	Project Associate-I
Maliha A	Project Associate-I
Deepak Niranjan	Project Associate-I
Vutukuri Rani	Project Field Worker

R Nagaraj Group

R Nagaraj	INSA Senior Scientist

Swasti Raychaudhuri

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
PallaviRao T	Ph.D. student
Sristi Chakraborty	Project Associate-I
Richa Singh	Project Associate-I

Manjula Reddy Group

Manjula Reddy	Chief Scientist
G S N Reddy	Principal Tech. Officer
M B Madhavi	Sr. Technical Officer (2)
Nilanjan Som	Ph.D. student
Raj Bahadur	Ph.D. student
Shambhavi Garde	Ph.D. student
Ashis Kumar Pradhan	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
Mangayarkarasi Nivaskumar	Project Scientist-II
Balaji V	Prl. Project Associate
Krishna Leela J	Job contract

Kumaraswamy Regalla Group

Kumaraswamy Regalla	Senior Scientist
Abishek Bharadwaj	Ph.D. student
Priyanka Pant	Ph.D. student
Disha Nanda	Ph.D. student
Garima Slathia	Project Associate-I
Hariharan K	Project Associate-I

Rajan Sankaranarayanan Group

Rajan Sankaranarayanan	Outstanding Scientist
P Shobha Krupa Rani	Senior Principal Scientist
Biswajit Pal	Principal Scientist
P Sambhavi	Sr. Technical Officer(1)
Jotin Gogoi	Ph.D. student
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
K Priyadarshan	Senior Project Associate
Dinesh Babu K S	Senior Project Associate
Akshay Bhatnagar	Senior Project Associate
Ankit Roy	Project Associate-I
Bapin Kumar Panda	Project Associate-I
Raja Rathinam Viola Valamathi	Project Associate-I
Nikita Shukla	Project Associate-I
Pujaita Banerjee	Project Associate-I

Yogendra Sharma Group

Yogendra Sharma	J C Bose Fellow
Syed Sayeed Abdul	Lab Attendant (2)
R Phanindranath	Sr. Technical Officer(1)
Asmita Pawar	Ph.D. student

Amrutha H C	Ph.D. student
Sai Uday Kiran P	Ph.D. student
Venu Sankeshi	Prl. Project Associate

Imran Siddiqi Group

Imran Siddiqi	CCMB Emeritus Scientist
Frank Keith Max	Ph.D. student
Sivakumar P	Ph.D. student
Survi Mahesh	Ph.D. student
Aswan Nalli	Project RA-I
Jayesh Kumar Davda	Project RA-I
Vishakha Bhardwaj	Project Associate-I
Avinash Kumar Singh	Project Associate-I
Chandan Kumar	Project Associate-I
Ginkuntla Saikiran Goud	Project Associate-I
Kaladhar Bethoju	Job Contract
Prashanthi Saini	Job Contract

Puran Singh Sijwali Group

Puran Singh Sijwali	Sr. Principal Scientist
Manish Bhattacharjee	Ph.D. student
Deepak Kumar	Ph.D. student
Zeba Rizvi	Ph.D. student
Srinivas Reddy G	Ph.D. student
Somesh Machhindra Gorde	Ph.D. student
Kanika Saxena	Ph.D. student
Manash Kumar Behera	Ph.D. student
Gayatri Pratyusha M	Ph.D. student
Renu Sudhakar	Sr. Project Associate
Angel Nivya M	Project RA-I

Divya Tej Sowpati Group

Divya Tej Sowpati	Scientist
Nitesh Kumar Singh	Sr. Technical Officer (1)
Sofia Banu	Ph.D. student
Abhijeet Karan	Project Associate-I
Archana Verma	Project Associate-I
Onkar Vasantrao Kulkarni	Project Associate-I
Priya Singh	Project Associate-I
Liza Changkakoti	Project Associate-I
Sangepu Jyothi	Scientific Admin. Asst.

Ghanshyam Swarup Group

Ghanshyam Swarup	INSA Senior Scientist

Raghunand R Tirumalai Group

Raghunand R Tirumalai	Principal Scientist
Ravi Prasad Mukku	Ph.D. student
Korak Chakraborty	Ph.D. student
Shiela Chetri	Research Associate-I
Kokavalla Poornima	Project Associate-I
Muskan Gupta	Project Associate-I

Shrish Tiwari Group

Shrish Tiwari	Principal Scientist
Prachi Singh	Senior Scientist
P Ramesh	Prl. Technical Officer
Deepti Rao	Ph.D. student
Ruby Srivastava	Project Investigator
Tummala Nikhila Sai	Project Associate-I

Tushar Vaidya Group

Tushar Vaidya	Chief Scientist
Sanjay Kumar Suman	Technical Officer
Loka Ram Prasad	Ph.D. student
Pradyumna Swanand P.	Ph.D. student
Aayushi Arora	Project Associate-I

Karthikeyan Vasudevan Group

Karthikeyan Vasudevan	Senior Principal Scientist
B Sambasiva Rao	Principal Scientist
S Harika	Technical Officer
K Rajya Lakshmi	Technical Officer
Afsar Sogra	Lab Assistant
Siddharth Bhatia	Ph.D. student
Gayathri Sreedharan	Ph.D. student
Ravi Kumar Singh	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
Tanushree Srivastava	Sr. Project Associate
Javaid Hameed	Project Associate-I
Moomin John	Project Associate-I
Sripuram Srinivas	Field Assistant
Anand Meharwade	Field Assistant
Dheeravath Sarika	Field Assistant
Ranjith Kumar	Field worker
Guna Sekaran M	Field worker
Shaik Shaheen	Field worker
Narsing Rao N	Job contract

P Anuradha Reddy Group

P Anuradha Reddy	Principal Scientist

V Radha Group

V Radha	Emeritus Scientist
Gowthaman G	Project Associate-I

Vasant Shinde Group

Vasant Shinde	CSIR Bhatnagar fellow
Vasundhra	Project Associate-I

Sonal N Jaiswal Group

Sonal N Jaiswal	Senior Scientist
J Nandan	Ph.D. student
K Aishwarya Arun	Ph.D. student
Priyanka Pandey	Ph.D. student
Brinda Palliyana	Project Associate-I
Reshmi Varghese	Project Associate-I

Pavithra Chavali Group

Pavithra Chavali	Senior Scientist
Sourav Ganguli	Ph.D. student
Deena T David	Ph.D. student
Dhruv Kumar Shakyawar	Prl. Project Associate
Aswathy G Krishnan	Project Associate-II
Rajashree Ramaswamy	Project Associate-II

B Kiran Kumar Group

B Kiran Kumar	Senior Scientist
Mohammed Ghalib	Project Associate-I
Parekh Yash Rajendra	Project Associate-I
Jessie Thomas	Project Associate-I

Meghna Krishnadas Group

Meghna Krishnadas	Senior Scientist
Vinayak Prakash Saini	Ph.D. student
Rishiddh Jhaveri	Ph.D. student
Nadendla Leela Prasad	Project Associate-I
Soumyashri Bhoi	Project Associate-Ina

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
Mihir R Kulkarni	SERB National PDF
Bharti K Dharapuram	Sr. Project Associate
Pooja Pawar	Project Associate-I

Director's Group

Sriram Varahan	DBT-Wellcome India Alliance Early Career fellow
Ishwariya Venkatesh	Ramanujan fellow

S&T Resource Group

K Lakshmi Rao	Sr. Principal Scientist
P Kavin Kennedy	Sr. Principal Scientist
V Vijaya Bhaskar	Principal Scientist
Suman Siddharth Thakur	Principal Scientist
Manoj Balyan	Senior Scientist
S Thanumalayan	Sr. Technical Officer (3)
Sandeep Shrivastava	Sr. Technical Officer (1)
M Sanjeev Chavan Nayak	Technical Officer
G Vidyasagar	Lab Attendant (2)

Innovation Cell

V Srinivas	Prl. Technical Officer
Y V Subba Lakshmi	Sr. Technical Officer (3)
Hemalatha	Senior Steno
K Srinath	Lab Attendant (2)

CCMB-Atal Incubation Centre

N MadhusudhanaRao	Chief Executive Officer
Ramjee Pallela	Chief Operating Officer
Ritika Marrampalli	Commun. 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 (1)
M Nageswara Rao	Lab Assistant
K Raju	Lab Assistant
M Rajeshwari	Multitask Staff
Lalaiah B	Job contract
Pacha Ravi	Job contract

Bioinformatics

Surabhi Srivastava	Sr. Technical Officer (2)

BSL 2/3 facility

Amit Kumar	Technical Officer

Cryo EM facility

Harikrishna Adicherla	Sr. Technical Officer (2)

Diagnostics Facility

M K Kanakavalli	Sr. Technical Officer (1)

Drosophila Facility

V Bharathi	Sr. Technical Officer (2)
K Ramachandra Rao	Sr. Technical Officer (1)

Imaging Facility

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

Next Generation Sequencing Facility

Mohammad Jafurulla	Sr. Technical Officer (2)
A Sreenivas	Sr. Technical Officer (1)

Proteomics Facility

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

SAXS Facility

R Rukmini	Prl. Technical Officer
K Mallesham	Technical Officer

Tissue Culture Facility

Avtar Singh Meena	Scientist
Ch Varalakshmi	Prl. Technical Officer
V R Sundereswaran	Prl. Technical Officer
Zareena Begum	Prl. Technical Officer
B V V Pardhasaradhi	Prl. Technical Officer
D Partha Sarathi	Sr. Technical Officer (2)
S Easra	Senior Technician (2)
T Dayakar	Lab Attendant (2)

Transgenic Knockout Facility

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

Wildlife Forensics Facility

O V Padmalatha	Sr. Technical Officer (2)
Raghavendra Babu	Technician (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)
Sushmitha Raj Nitta	Project Associate-I
Varnali Acharya	Project Associate-I
Manchala Santosh Kumar	Data Entry Operator
Harinarayanan Rao	Job contract

Engineering Services

G C Thanu	Senior Suptd Engineer
Ch Bikshamaiah	Senior Suptd Engineer
Ashok Baswa	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)
K Mohan	Senior Technician (2)
M TirumalaRao	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
P Venkatarama Rao	Lab Assistant
T Venkateswar 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

Y Rama Dasu	Prl. Technical Officer
Kishore Joshi	Prl. Technical Officer

Information Technology Group

GeethaThanu	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 (2)
K Rama Chary	Sr. Technical Officer (2)
Sreekanth Mamidala	Sr. Technical Officer (1)
M Srinivasa Rao	Lab Assistant

Instrumentation Group

I Asha Ramesh	Prl. Technical Officer
U S T R B Bapi Raju	Prl. Technical Officer
B Venkata Narayana	Prl. Technical Officer
N Ravindra Chakravarthi	Sr. Technical Officer (3)
Dattatrya N Gurkhel	Sr. Technical Officer (2)
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 (1)
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	Sr. Principal Scientist
Mani Ramana Rao	Senior Steno
P Gyaneshwar	Lab Assistant
L Laxman Dora	Lab Assistant
M A Jaleel	Lab Assistant
B Sanjeeva Rao	Lab Assistant
Y V Rama Rao	Job contract
M M Rajendran	Job contract
Sasi Bhushan A N	Project Associate-II

Planning, Monitoring and Evaluation (PME)

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

Research Grants Office

Sravanti Vaidya	Project Scientist –III
Shailaja Kanumuri	Laboratory Technician

Science Communication & Public Relations

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
K Lakshmi Rao	Senior Principal Scientist
D Lavanya	Sr. Technical Officer (2)
S Madhuri	Staff Officer & I/c Academic Cell
Somdatta Karak	Science Communications and Public Outreach Officer
B V N Naveen Kumar	Technical Officer

Administration

Pooja P. Kulkarni	Controller of Administration
Ram Kumar Singh	Administrative Officer
Sudhanshu Kumar	Administrative Officer
Anirudh Manwal	Section Officer (G)
N C Vamshi Krishna	Section Officer (G)
Noopur Rani Prasad	Hindi Officer
N Naveen Kumar	Private Secretary
J Venu	I/c Transport
S Kanchanamala	Assistant Section Officer (G)
R Gopal	Assistant Section Officer (G)
Manju Singh	Assistant Section Officer (G)
T Rajani	Sr. Secretariat Assistant (G)
Ch Sridevi	Sr. Secretariat Assistant (G)
Ashok Kumar Swasani	Sr. Secretariat Assistant (G)
Abdul Raheem Qureshi	Jr. Secretariat Assistant (G)
Savita Kumari	Jr. Hindi Translator
K Madhavi	Receptionist
Mohd Pasha	Senior Technician (2)
M Devendra Nath	Senior Technician (2)
D Ramesh	Senior Technician (2)
B Sadanandam	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 Attendant (2)
M Sharadha	Bearer (Adm)
Ambe Naveen Kumar	Multitask Staff
K Satyanarayana	Job contract

Finance & Accounts

Kolla Ramesh	Controller of Finance &Accounts
K Rama Krishna	Asst Section Officer (F&A)
Vimala Prakash	Assistant Section Officer (F&A)
P L Janaky	Assistant Section Officer (F&A)
V V L Prasanna	Assistant Section Officer (G)
M V Subba Rao	Senior Steno
G Anuradha	Junior Secretarial Assistant
W Sudhakar	Senior Technician (2)
M Vishnu Yadav	Technician (1)
K Venkateswarulu	Lab Assistant

Stores & Purchase

S Gnanaprakasam	Senior Controller of Stores & Purchase
Jai Singh	Stores &Purchase Officer
S Aruna	Assistant 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)
Maqsood Ali	Junior Steno
Preethi Arjunan	Jr. Secretariat Assistant (S&P)
MohdYakubAkheel	Lab Attendant (2)
Shareef Abdul Aleem	Job contract

RTI Cell

Tushar Vaidya	Appellate Authority
BV Ramakrishna	Central Public Information Officer
T Rajani	Assistant Public Information Officer

Medical Services

V Venugopal Rao	Medical Officer
T Nagalakshmi	Senior Technical Officer (1)
A Mahesh	Technical Officer
U V Sitaramamma	Senior Technician (2)
R Palnitkar	Consultant
G Sujatha	Consultant
Ravinder Reddy D	Job contract
Nusrath Banu	Job contract

Security

C V Tirumala Rao	Senior Security Officer
Raveendra Kumar K V V S	Senior Security Officer (On deputation)

Guest House

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

Canteen

Vikram Kumar	Senior Technical Officer (1)
M Venkatesan	Senior Technician (2)
P M Mani Maran	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

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