RGCB

DISCOVERIES FOR A BETTER TOMORROW

Azadi Ka Amrit Mahotsav

ANNUAL REPORT 2021-22

www.rgcb.res.in

Rajiv Gandhi Centre For Biotechnology

CONTENTS

DIRECTORS' PAGE

After the two years of COVID 19 crisis, RGCB has seen transformative changes in all aspects of its academic and educational activity in the year 2022. In addition to the commendable scientific research capability and academic activity visible from our publications and technology transfer efforts, we have also responded to the national call by our Honourable Prime Minister to promote Make in India, Start-up India and Azadi ka Amrit Mahotsav initiatives with various programmes mobilising scientific / students community within institute and also the general public. Responding to the call for Start-up initiative, we have strengthened our start-ups effort in supporting more start- up incubates at our Biotech Incubator Facility BioNest, for the development of Covid 19 solutions and biotech process/ product development , with an aim of promoting industrial growth and creating job opportunities in Biotechnology. We have also continued our research and service intervention for the management of Covid 19. LMMD, the diagnostic wing of RGCB has completed 13000 SARS CoV2 sequencing as part of INSACOG activity and continue to support regular Covid 19 diagnosis service for the state of Kerala.

The two major developments of the year worth mentioning are the establishment of BSL3 Plus and Next Generation Sequencing facility at RGCB. We are proud to become the first R& D centre in Kerala to have a fully equipped BSL3 facility for supporting research involving high containment requiring pathogens including SARS CoV2. With this, the ongoing research programme on antiviral discovery, assay development against key viral and host targets are expected to reach new heights. This year, we have also strengthened our genomics facility with the addition of a new NGS equipment , Illumina Novaseq 6000 through the special support from DBT. I would like to place on record the timely financial support and encouragement received from the Secretary, Department of Biotechnology in establishing these two unique model facilities , first of its kind in Kerala. RGCB will be offering live virus neutralisation assays, vaccine efficacy testing services and drug screening services using live SARS CoV2 virus for the academia and industries soon with these new developments.

Through our team driven activity for social empowerment of tribal community using scientific interventions, we have documented traditional knowledge of livestock, ethno-veterinary practices, traditional paddy varieties, and cultivation practices. This ongoing research done as part of 'Center for Excellence in Inclusive Technology Interventions for Tribal Heritage Resilience of Kerala', led to the development of many value added products based on tribal knowledge in ethno-veterinary medicine. We have also completed one of the best science museum in our country at Wyanad, the aspiration District identified by the Govt of India, with an aim of promoting science culture among school students and public in line with the azadi ka amrit mahotsav call.

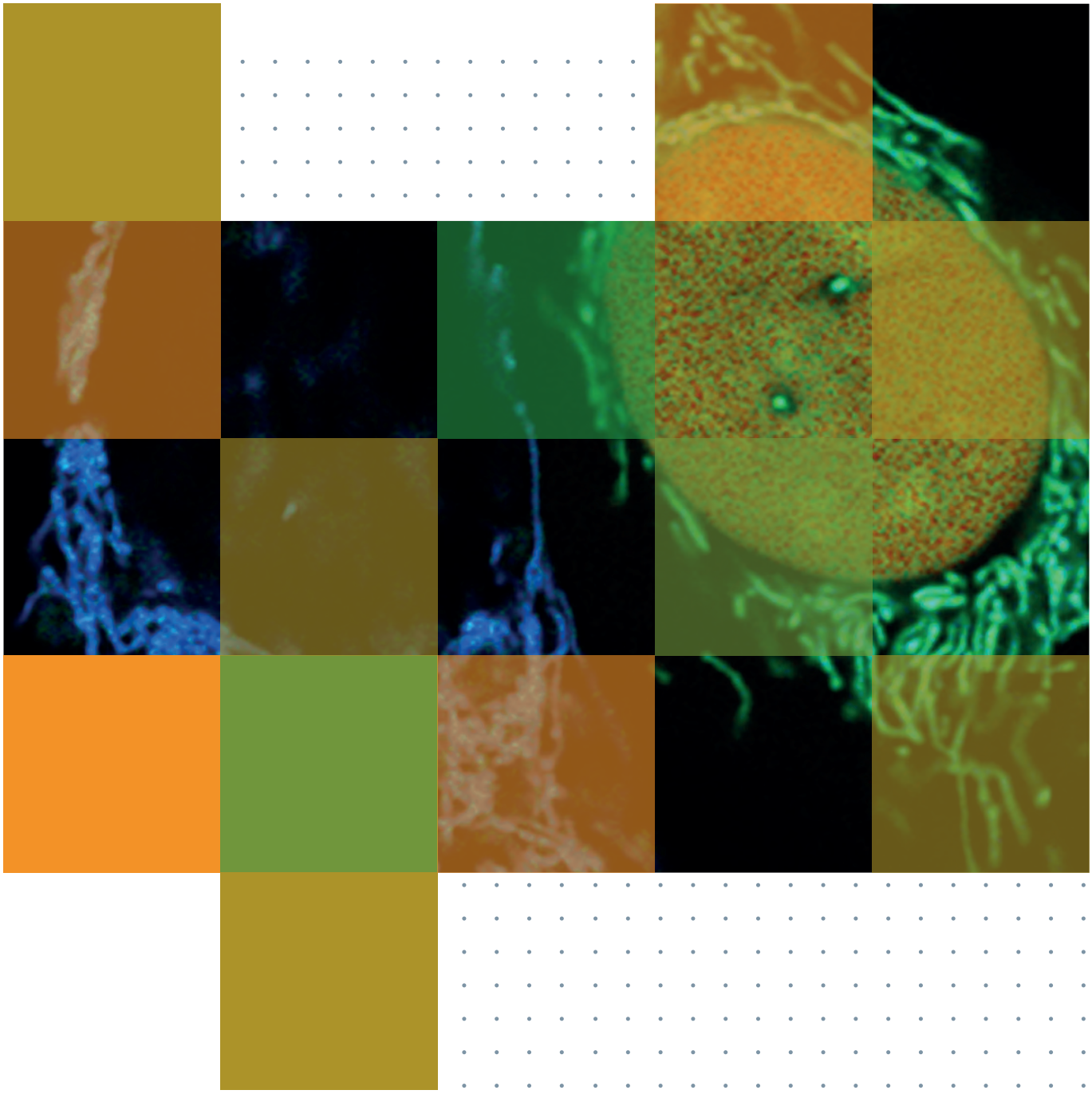
Our publications have increased and several of our academic research collaborations with many National and International Institutions yielded appreciation from public and academia. The key exciting examples are translational research work on HPV vaccine trail, that received attentions and has helped in radical policy change in vaccine scheduling, with a great social and economic impact on vaccination drive. Similarly, RGCB has played a significant role in determining the efficacy of Cervavac, Indias first indigenously developed vaccine developed for preventing the second most common cancer among women in the country. This is an illustrious example of our commitment to the Make in India concept and capability to support high end socially relevant research. The Bioinformatics Group has also launched a well-structured training programme for researchers that received increased attentions during this year.

The other exciting development of the year is the partial functioning of new campus at Akkulam with world word class facilities and infrastructure.

WE LOOK FORWARD TO DEDICATING THE SECOND CAMPUS TO THE NATION SOON. THIS MARKS THE BEGINNING OF THE NEXT PHASE OF RGCB'S PLEDGE TO DELIVER RESEARCH AND DISCOVERIES TO THE PEOPLE AND THE COUNTRY.

We are very much grateful to the DBT Secretary for the sustained support both for the newer initiatives and also for the ongoing research programmes.

JAI HIND
Professor Chandrabhas Narayana
DIRECTOR, RGCB



CANCER RESEARCH

Dr. T.R.SANTHOSH KUMAR

Scientist G, Cancer Research Program

BRIEF THEME OF LABORATORY

The thrust area of research is to understand molecular mechanisms of chemo resistance and tumour recurrence in solid tumours. Another important focus of the laboratory is the development of live cell-based assays and preclinical models for identifying molecules that specifically target key pathways in cancer such as cell cycle, proteasome-Ubiquitin pathway, angiogenesis, HIF, and tumor stem cells.

SPATIO-TEMPORAL ANALYSIS OF PROTEIN-PROTEIN INTERACTIONS USING FRET- FLUORESCENT LIFETIME IMAGING TO UNDERSTAND CELL CYCLE PROGRESSION AND CELL DEATH RESPONSE

Complex response heterogeneity in seemingly homogenous single-cell clones is a dynamic signalling and is poorly understood despite its importance in tumor biology. Functional heterogeneity of cells could be mediated by rapid changes in protein-protein interaction that in turn regulate the cell-cycle progression of cells. Studying realtime fast protein-protein interaction in live-cells offers great potential to unravel response heterogeneity of cancer cells and complex forms of nongenetic resistance mechanisms. Does this response heterogeneity determine cell-cycle and death decisions under stress and the dynamics of cell survival? To address this, we have developed real-time interaction visualisation approaches simultaneously with cell-cycle and cell death.

Bax and BclxL are key regulators of apoptosis and have antagonist effects in regulating cell death. We have attempted to study the dynamics of interaction between Bax and BclxL in live cells during the cell-cycle progression and death. We have developed stable cells expressing these two proteins as fusion with donor-acceptor fluorescent pairs. FRET-acceptor bleaching and FRET-FLIM confirmed the dynamics of interaction between Bax and BclxL. To visualise the interaction simultaneously with cell-cycle, the cells were engineered to express G1-sensor cdt1 with Kusabira orange and G2-probe Geminin with miRFP tag. The realtime imaging revealed the dynamics of interaction is highly dependent on the cell-cycle status and rapid alterations in their interaction while undergoing cell death. Overall, we have developed a cell-line model and method to analyse protein interactions with cell-cycle progression using FRET-FLIM and its potential applications in understanding the changes in protein-protein interaction in live cells under physiological and diverse stress responses.

Front Row From Left: Jain Tiffee PJ, Akshit Jain, Dr. Aneesh C, Dr. Shine VJ, Aswathy G Raj, Aparna GJ
Back row From Left: Dr. Shankara Narayana V, Halikar Aman, Shivanshu Kumar Tiwari, Arun C

From left: Jithu TG, Prakash R, John Sam SM, Visakh Nath VR

LABORATORY STRENGTH

Postdoctoral Fellows: 4
Ph.D Students: 6 | Technical Assistant: 2 | Project Associate: 2

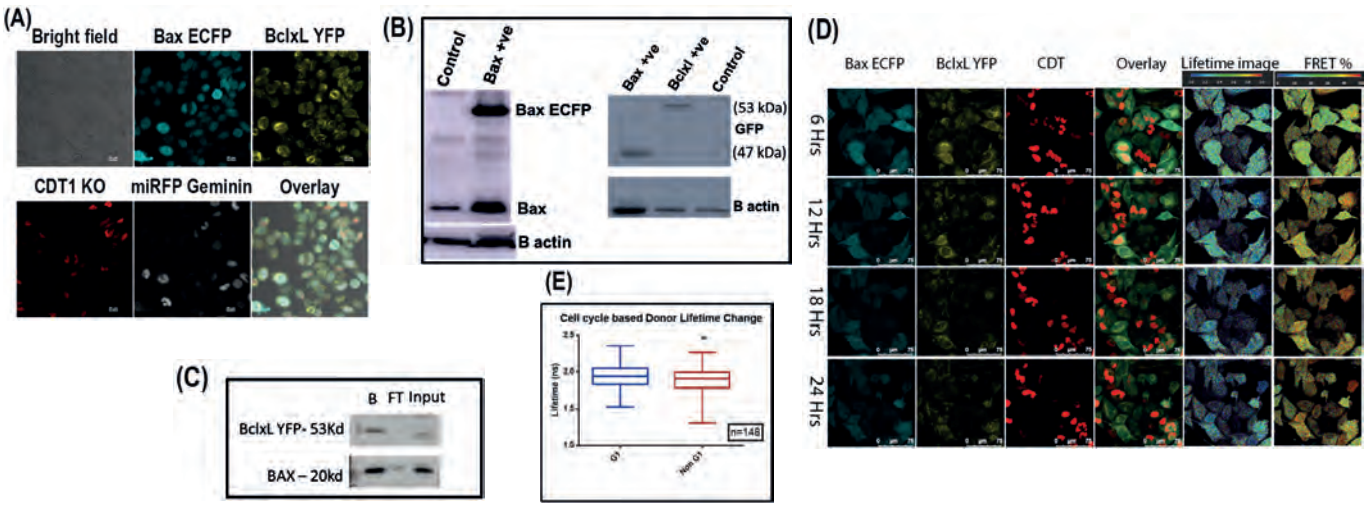


FIGURE LEGEND

Fig. (A)-The U251 cells stably expressing Bax ECFP/BclxL YFP/CDT1-KO/miRFP-Geminin; (B) Respective WB for overexpression of the proteins; (C) GFP trap pull-down of BclxL YFP shows interaction with Bax; (D) Realtime FRET-FLIM imaging with cell cycle progression probes for 24 Hrs, revealed the difference between G1 and NonG1 phases of the cell cycle represented in (E) (p= 0.0352)

PUBLICATIONS

- **Varadarajan SN, Mathew KA, Chandrasekharan A, Lupitha SS, Lekshmi A, Mini M, Darvin P, Santhoshkumar TR.** Real-time visualization and quantitation of cell death and cell cycle progression in 2D and 3D cultures utilizing genetically encoded probes. J Cell Biochem. 2022; 123(4):782-797.
- **Lupitha SS, Darvin P, Chandrasekharan A, Varadarajan SN, Divakaran SJ, Easwaran S, Nelson-Sathi S, Umasankar PK, Jones S, Joseph I, Pillai MR, Santhoshkumar TR.** A rapid bead-based assay for screening of SARS-CoV-2 neutralizing antibodies. Antib Ther. 2022; 5(2):100-110.

Dr. RUBY JOHN ANTO

Scientist G, Cancer Research Program

BRIEF THEME OF LABORATORY

My lab focuses on bioprospecting for anticancer products. My team has evaluated natural products as chemotherapeutics, chemosensitzers, and chemopreventives. We have identified three plant-derived anti-cancer principles, uttroside B from S.nigrum, tryptanthrin from W.tinctoria, and kaempferide from C.odorata. Utt-B is exceptionally active against hepatocellular carcinoma and the invention has received multi-national patents. Tryptanthrin shows remarkable potency against melanoma and non-melanoma and kaempferide exhibits therapeutic efficacy against cervical cancer.

BIOPROSPECTING FOR CHEMOPREVENTIVES, CHEMOTHERAPEUTICS AND CHEMOSENSITIZERS

The invention on the anti-HCC effect of Utt-B has been granted multinational patents, the compound received 'Orphan drug' designation against liver cancer by the US FDA, and the technology has been transferred to the multinational Pharma company, Q Biomed, for clinical trials. Utt-B also promotes pro-survival autophagy in hepatic cancer cells and inhibition of autophagy significantly enhances Utt-B-induced apoptosis of HCC. The study revealed that inhibition of autophagy using the antimalarial drug, Chloroquine, a well-known autophagy inhibitor, significantly enhances the antitumor efficacy of Utt- in NOD-SCID mice bearing HCC xenografts (Lekshmi et al, 2022, Frontiers in Oncology). We have validated the superior anti-HCC efficacy of Utt-B over sorafenib, the first-line treatment option against HCC in vitro and in vivo models of HCC. Our data indicate that apart from the superior therapeutic benefit over sorafenib, Utt-B is a pharmacologically safer molecule, and the drug-induced undesirable effects can, thus, be substantially alleviated in the context of HCC chemotherapy (Swetha et al, 2022, Pharmaceuticals).

Tpn was found to be very effective against melanoma and non-melanoma skin cancers. Microarray analysis of Tpn treated-melanoma cells followed by a STRING protein association network analysis revealed that differential expression of genes in melanoma converges at MITF-M, a melanocyte lineage-specific transcription factor. Key findings indicate that the anti-melanoma activity of Tpn is decisively contingent on its efficacy in down-regulating MITF-M expression and the study reveals Tpn as a promising anti-melanoma drug, by virtue of its attributes to impede melanoma invasion and metastasis through the attenuation of MITF-M (Shabna et al, 2022, Cellular and Molecular Life Sciences).

From Left: Aiswarya US, Jannet S, Keerthana CK, Rayginia P Tennyson, Shifana C Sadiq, Dr. Kalishwaralal Kalimuthu

LABORATORY STRENGTH

Postdoctoral Fellows: 2 | Ph.D Students: 2 | JRF: 2
Technical Assistant: 1 | Lab Assistant: 2

FIGURE LEGEND

Figure 1: Co-treatment of Cqn enhances the antitumor efficacy of Utt-B against HCC, in NOD-SCID mice bearing HepG2 xenografts.

Figure 2: Utt-B triggers apoptotic mode of cell death in HCC, exhibiting better therapeutic efficacy compared to sorafenib.

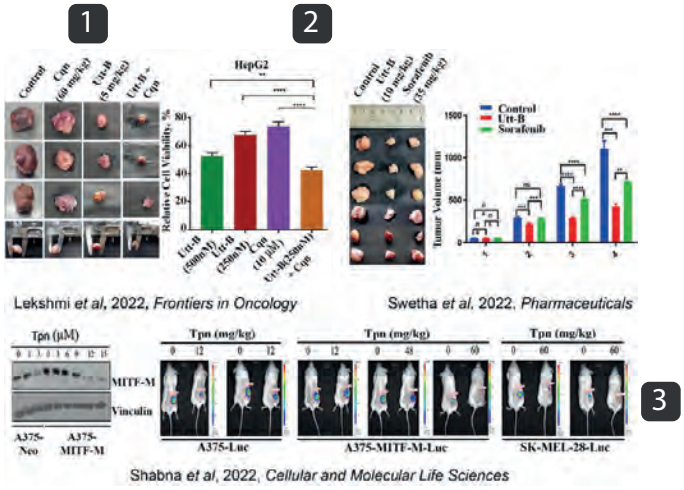


Figure 3: The anti-melanoma activity of Tpn is decisively contingent on its efficacy in down-regulating MITF-M expression.

PUBLICATIONS

- **Shabna A, Antony J, Vijayakurup V, Saikia M, Liju VB, Retnakumari AP, Amrutha NA, Alex VV, Swetha M, Aiswarya SU, Jannet S, Unni US, Sundaram S, Sherin DR, Anto NP, Bava SV, Chittalakkottu S, Ran S, Anto RJ.** Pharmacological attenuation of melanoma by tryptanthrin pertains to the suppression of MITF-M through MEK/ERK signaling axis. Cell Mol Life Sci. 2022;79(9):478.

- **Haritha NH, Nawab A, Vijayakurup V, Anto NP, Liju VB, Alex VV, Amrutha AN, Aiswarya SU, Swetha M, Vinod BS, Sundaram S, Guijarro MV, Herlevich T, Krishna A, Nestory NK, Bava SV, Sadasivan C, Zajac-Kaye M, Anto RJ.** Targeting thymidylate synthase enhances the chemosensitivity of triple-negative breast cancer towards 5-FU-based combinatorial therapy. Front Oncol. 2021;11:656804.

Dr. SUPARNA SENGUPTA

Scientist G, Cancer Research Program

BRIEF THEME OF LABORATORY

The cytoskeletal proteins have several functions including cell division, placement of cell organelles and movement of several vesicles and molecules. We are looking for the role of cytoskeletal and associated proteins in mitosis, centrosome organization and trafficking. Their role in cancer is also being looked upon.

ROLE OF BETA TUBULIN ISOTYPE TUBB4 IN STEM CELL MAINTENANCE AND THE CYTOSKELETAL PROTEIN FODRIN IN CANCER AND APOPTOSIS

α-fodrin in cancer and apoptosis

Fodrin is a cytoskeletal protein with a conventional function of maintaining cellular integrity. We utilized a global protein expression analysis approach to detect underexplored functions of fodrin. Depletion of α-fodrin in glioblastoma cells results in upregulation of genes affecting the regulation of the cytoskeleton, cell cycle and apoptosis. We validated the results by real-time PCR studies and western blotting. Further, based on our earlier results that α-fodrin regulates chromosome congression and mitosis, its effect on cancer and apoptosis was studied. Fodrin levels are changed differently in different tumors but the mechanism is not known. It can be anticipated that the mitotic defects caused by fodrin are one of the causes for its level change in cancer. In vitro analysis of the effect of α-fodrin depletion in the presence of an apoptosis inducing agent taxol followed by xenograft models of pancreatic cancer indicate that fodrin has a tumor suppressor role in pancreatic cancer.

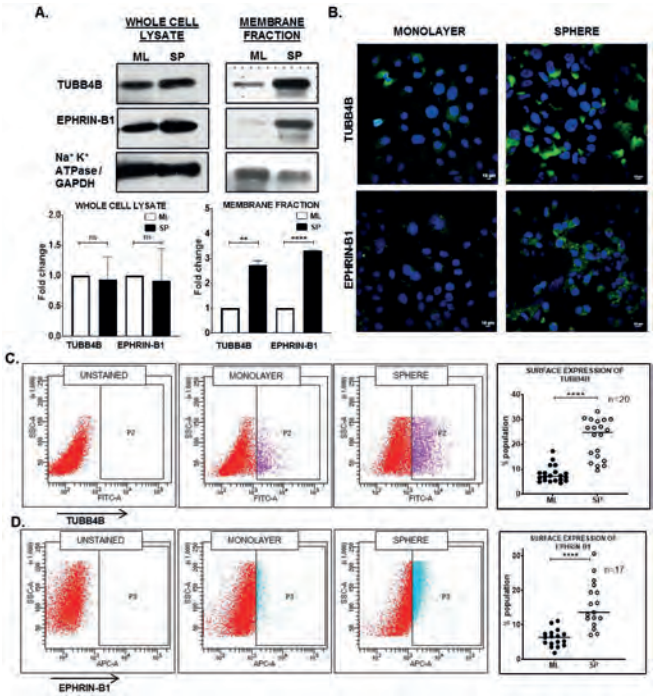
From Left: Athira SS, Athira Jyothy, Julfequar Hussain

LABORATORY STRENGTH

Ph.D Students: 2 | JRF: 1

β-Tubulin Isotype, TUBB4B, Regulates The Maintenance of Cancer Stem Cells

Cancer stem cell niche (CSC) is a crucial factor modulating



tumor progression and treatment outcomes. We have investigated the role of tubulin isotype TUBB4 in sustaining CSCs in oral cancer. TUBB4B was overexpressed in stem cell enriched cultures and sustaining CSC activity. Knockdown of TUBB4B downregulates the expression of pluripotency markers, decreases sphere formation, and diminishes the tumor initiation potential in vivo. The pattern of its expression in tissue sections made us believe that its membrane trafficking function plays a role in constituting a CSC niche. Further, analysis of TCGA datasets, clinical and xenograft samples as well as downregulation studies in stem cells implicate that the dynamics of TUBB4B is decisive for the surface localization of proteins, like Ephrin-B1, that sustain CSCs by their concerted signaling.

FIGURE LEGEND

Sphere culture enriches the surface expression of TUBB4B and Ephrin-B1. (A) Membrane fractions of sphere and monolayer cultures of HSC-3 cells. The fold changes were represented graphically. (B) shows membrane expressions of TUBB4B or Ephrin-B1. (C) HSC3 sphere or monolayer cultures probed for (C) TUBB4B or (D) Ephrin-B1 and the surface expressions analyzed. The graphs represent the quantitation of percentages of cells. Ns: non-significant data.

PUBLICATIONS

- **Sreeja JS, Jyothy A, Sengupta S.** α-Fodrin in cytoskeletal organization and the activity of certain key microtubule kinesins. Genes (Basel). 2021;12(5):750.
- **Dharmapal D, Jyothy A, Mohan A, Balagopal PG, George NA, Sebastian P, Maliekal TT, Sengupta S.** β-Tubulin Isotype, TUBB4B, regulates the maintenance of cancer stem cells. Front Oncol. 2021;11:788024.

Dr. S.ASHA NAIR

Scientist G, Cancer Research Program

BRIEF THEME OF LABORATORY

The Clinical research program target stem cell markers in Colorectal Cancer (CRC) and their manifestation of probable molecular pathways for chemotherapeutic intervention as prognostic indicators of CRC and Early-Onset of CRC. Pertaining to basic research, molecular targets relevant to the cell cycle machinery are being studied. The program on photodynamic therapy is on screening of photosensitizers and evaluation of biological property of Graphene & Molybdenum Quantum Dots.

STIL - A MOLECULAR REGULATOR OF SHH AND WNT SIGNALING, MEDIATING DRUG RESISTANCE IN COLORECTAL CANCER.

Colorectal cancer (CRC), ranking third in incidence and second in cancer associated mortality worldwide, is one of the most deadly cancers in late stage of diagnosis. Discovery of a potent gene regulating tumorigenesis and drug resistance is of critical clinical importance. Previous studies from our lab have shown that STIL is crucial for maintenance of stem cell population and silencing STIL reduced proliferation and tumor growth in CRC. Since stem cell population attributes to therapy resistance, we have looked at the role of STIL in drug resistance and also the molecular mechanism by which STIL regulates different

Back Row From Left: Anjana Soman,Samu John, Meera R Nair, Rajashree R Nair,
Front Row From Left: Evangeline Surya Hermon, Ketakee Mahajan, Krishna R

LABORATORY STRENGTH

Ph.D scholars: 5 | Project Assistant: 1
Lab Assistant: 1

proteins involved in CRC progression. STIL was found to regulate stemness markers CD133 & CD44 and drug resistant markers Thymidylate synthase (TS), ABCB1 & ABCG2, both in in-vitro and in-vivo CRC models. Treatment with 5-FU led to an increase in STIL in HT29 cells, suggesting a possible role of STIL in CRC drug resistance. STIL silencing was found to sensitize CRC cells towards Oxaliplatin, as shown by two-fold increase in cell death in STIL-silenced HT29 cells after oxaliplatin treatment. STIL has been considered as a positive regulator of Sonic hedgehog (Shh) signalling as evidenced by numerous studies till date, where interaction of STIL with SUFU inhibits the repressor function of SUFU towards GLI1 resulting in activation of Shh-Gli1 cascades. Interestingly, we perceived STIL mediated regulation of stemness and drug resistant genes, CD133, ABCG2 and TS to be independent of Shh signalling. Remarkably, we found STIL to regulate β-catenin levels through p-AKT, independent of Shh pathway. This partially answers Shh independent regulatory mechanism of CSC markers by STIL. Further, we found that STIL also regulate the cleavage and nuclear localization of β-catenin. Our study therefore suggests a dynamic role of STIL in molecular manifestation of CRC.

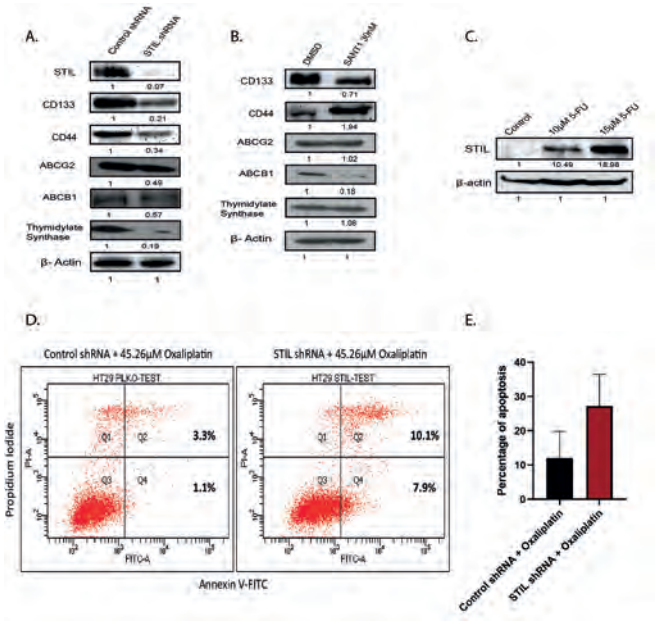


FIGURE LEGEND

Figure 1: Expression of CD133, CD44, ABCG2, ABCB1 and thymidylate synthase upon (A) STIL silencing, (B) Shh pathway inhibition. (C) Expression of STIL upon 5-FU treatment. (D & E) Annexin-V assay showing percentage of apoptosis upon oxaliplatin treatment.

Figure 2: Expression of β-catenin, AKT and p-AKT, upon (A) STIL silencing, (B) Shh pathway inhibition. (C) β-catenin protein levels in cytoplasm and nucleus upon STIL silencing. (D) Schematic representation of multifaceted role by STIL in CRC.

PUBLICATIONS

- **Pradhan T, Kumar V, Surya H E, Krishna R, John S, Jissa VT, Anjana S, Chandramohan K, Nair SA.** STIL endows oncogenic and stem-like attributes to colorectal cancer plausibly by Shh and Wntsignaling. Front Oncol. 2021;11:581671.
- **Anjana S and S Asha Nair.** Unfolding the cascade of SERPINA3: Inflammation to cancer. Biochim Biophys Acta Rev Cancer, 2022; 1877,5 188760.

Dr. PRIYA SRINIVAS
Scientist G, Cancer Research Program

BRIEF THEME OF LABORATORY

The major mandate of my laboratory is to understand the molecular mechanism of tumorigenesis in BRCA1 defective cancers and to identify diagnostic and therapeutic options. Other than this, my second major mandate is to develop non-invasive techniques for cancer diagnosis using body fluids.

βHCG MEDIATED IMMUNE SUPPRESSION IN BRCA1 DEFECTIVE BREAST TUMORIGENESIS

Since hCG has immunosuppressive action, we hypothesized that hCG might be skewing the immune response of the BRCA1 defective cells towards tumorigenesis. To examine the immunologic response of β hCG in vivo, we performed studies using Balb/C mouse models by orthotopically implanting BRCA1 wild-type, BRCA1 mutated, and βhCG overexpressed BRCA1 mutated breast cancer cells into the fourth mammary fat pad of the

mice. We used flow cytometry to characterize immune cell populations in lymphoid tissues and infiltrating the tumor. We observed induction of βhCG in BRCA1-mutated tumors with increases the population of MDSC and polarization of M1 macrophage phenotype to tumor promoting M2 macrophages M2 macrophages, thus inhibiting the host antitumor immune response. and promotes tumor growth in BRCA1 deficient breast cancers. βhCG promotes the expression of inhibitory molecules such as PD-L1 andPD- 1 and contributes to tumor aggressiveness. We proved for the first time that βhCG causes a decrease in the proportion of tumor-infiltrating cytotoxic CD8+ T cells with an increase in the proportion of FOXP3+ Treg cells, in BRCA1 mutant cancer cells. This study shows that resistance to immunotherapy shown by BRCA1 mutated breast cancers could be reverted by modulating βhCG in BRCA1-defective cancer patients.

From left: Arathy V Warrier, Neetha RL, Sheeja B, Dipyaman Patra, Priyanka Kumari, Aswathy Ashokkumar, Neethu Krishnan

LABORATORY STRENGTH

Postdoctoral Fellows: 1 | Ph.D Students: 7 | Technical Assistant: 1

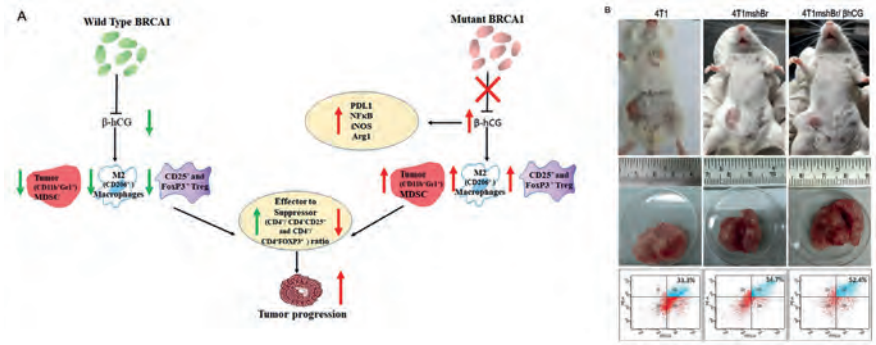


FIGURE LEGEND

A) Graphical abstract showing that βhCG overexpressed in BRCA1 deficient tumors increases tumor associated myeloid cells like MDSC and M2 macrophages contributing to tumor progression in vivo.B) Immunocompetent Balb/c mice injected with 4T1, 4T1mshBr and 4T1mshBr β tumor cells (first panel), tumors harvested respectively (second panel), flow cytometric analysis of CD11b+Gr1+MDSC in 4T1, 4T1mshBr and 4T1mshBr/ βhCG tumors (n = 4) (third panel).

PUBLICATIONS

- **Krithiga K, Arathi R, Geetu RV, Neetha RL, DipyamanPatra, Neethu KA Warrier and Priya Srinivas.** Partial genome analysis of Cox1 subunit-I region in mitochondrial DNA of canine mammary tumours.J Vet Anim Sci. 2021; 52(1): 95-98.
- **Arathi R, Geetu RV, I Yadev, Jaimie A, Neetha RL, D Patra, Neethu K, Krithiga K, Arathy VW, Satej Bhushan, Revathy N, Ram M Ram K, Priya Srinivas.** Modulation of BRCA1 mediated DNA damage repair by deregulated ER-α signaling in breast cancers. Am J Cancer Res. 2022; 12(1):17-47.

Dr. S.SREEJA
Scientist F, Cancer Research Program

BRIEF THEME OF LABORATORY

Our laboratory is interested in the mechanistic study of pathways involved in estrogen and progesterone action in hormone driven cancers and Selective estrogen receptor modulators (SERM). There are intricate signaling pathways that regulate the mechanism of these hormones and often these are interlinked. We are interested in understanding these complex mechanisms and signaling pathways involved in it.

INVESTIGATING THE THERAPEUTIC POTENTIAL OF UROLITHIN A AND DELINEATING ITS MECHANISM OF ACTION IN ORAL SQUAMOUS CELL CARCINOMA CELL LINES

Urolithin A (UA), a microbial metabolite of ellagic acid and allagitannins produced endogenously by human gut microbiome has been considered as a critical anti cancerous compound. In spite of this its anti tumorigenic effect in oral squamous cell carcinoma remains elusive. This led us to investigate the anti tumorigenic effect of UA in OSCC. Interestingly, our premliminary data on OSCC cell lines proved that UA could inhibit proliferation in OSCC cell lines significantly and induce the expression of apoptotic proteins. Previously, it is reported that UA induced autophagic cell death in many cancers. Henceforth, we proposed that UA could induce autophagic cell death via apoptosis and autophagy crosstalk. So we sought to determine whether Urlothin A also induced autophagic cell death in OSCC by assessing the expression of autophagic markers. Examination of autophagic and apoptotic specific proteins revealved that along with PARP cleavage UA progressively prompted the conversion of LC31 and LC3 11 and also downregulated the expression of p62 (SQSTM1) thus confirming the autophagosome formation and apoptosis. Taken together, our results suggests that UA induced cell death of OSCC via the induction of endoplasmic reticulum stress following the inhibition of AKT and mTOR signalling as revealved by reduced levels of phosphorylated mTOR and 4EBP1. Henceforth, we hypothesize that Urolithin A could be a potential anti cancer agent for oral squamous cell carcinoma.

Front Row From Left: Susmi TR, Ayswarya RS
Central Row From Left: Viji Remadevi, Swathy Ravindran, Vini Ravindran,Krishnedhu B
Back Row From Left: Juberiya M Azeez, Anjana SS

LABORATORY STRENGTH

Ph.D Students: 3 | JRF: 2 | SRF: 3 | Project Assistant: 1
Technical Assistant: 1 | Lab Assistant: 3

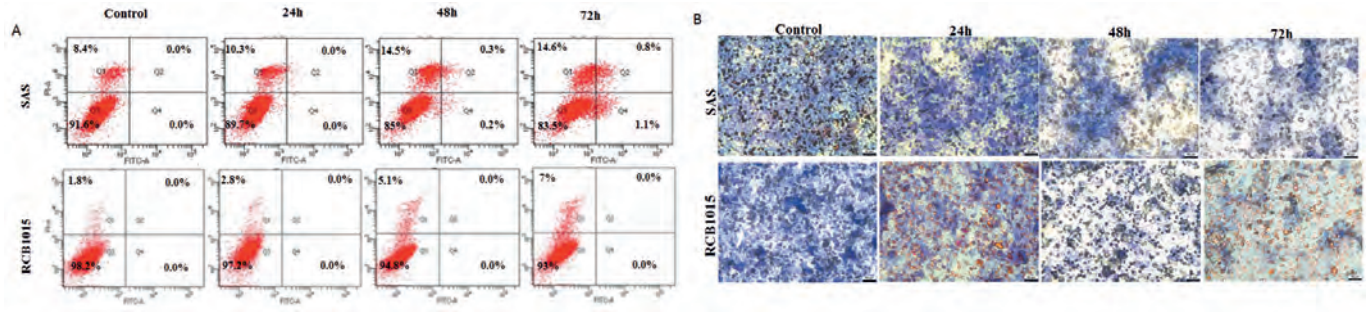


FIGURE LEGEND

A. Annexin V/FITC/PI flowcytometric analysis of SAS and RCB1015 cells treated with Urolithin A (40uM) for 24h, 48h and 72h. B. Cell invasion and migration assay: Matrigel invasion assay exhibited impaired migration and invasion in UA treated SAS and RCB1015 cells compared to its control cells.

PUBLICATIONS

- **Remadevi V, Muraleedharan P, Sreeja S.** FOXO1: a pivotal pioneer factor in oral squamous cell carcinoma. Am J Cancer Res. 2021;11(10):4700-4710.
- **Vini R, Rajavelu A and Sreeharshan S.** The Estrogen Receptor Modulator, Alters DNA Methylation in Breast Cancer. Front Endocrinol 2022; 13:783823.

Dr. G.S.VINOD KUMAR

Scientist F, Cancer Research Program

BRIEF THEME OF LABORATORY

Our group mainly focus on designing and development of peptide synthesis and multifunctional nanostructures for programmed drug delivery targeting systems in cancer. Several first and co-authored manuscripts are published in leading scientific journals and in addition hold key patents as inventor on Indian and US patents.

BIOPOLYMER DERIVED DRUG DELIVERY SYSTEM TO PLC/PRF/ 5 HEPATOCELLULAR CARCINOMA MODEL AND MALEIC-ANHYDRIDE BRIDGED POLYCAPROLACTONE-POLYETHYLENEGLYCOL FOR BREAST TUMOR TARGETING

This study aimed to design a prototypic drug delivery system made of an amphiphilic, Pullulan (Pull) derived biodegradable polymer for targeting the Asialoglycoprotein Receptor (ASGPR) overexpressed in Hepato Cellular Carcinoma (HCC). The study could develop an efficient drug delivery system to target hydrophobic drugs such as Sorafenib Tosylate to HCC. The drug entrapped nanoparticles (Pull-SA-SRFT) showed a sustained drug release pattern and accelerated drug-release in acidic pH. Cytotoxicity assay indicated that blank Pull-SA particles were non-toxic to cells and the drug entrapped nanoparticles could induce more death than free drug (SRFT) alone in a concentration-dependent manner. This was in accordance with the results obtained by the higher degree of chromosome condensation induced by Pull-SA-SRFT than free SRFT. Early and late studies conveyed that SRFT and Pull-SA-SRFT could induce apoptosis significantly in the later stages than in the earlier stages and a higher proportion of death was induced by the drug entrapped particles. The biodistribution study done in swiss-albino mice indicates that the system has more affinity and retention capacity to the liver and did not cause any acute toxicity. Hence a biocompatible, promisingly safe, and excellent nanocarrier to deliver hydrophobic drugs to HCC was developed (Figure).

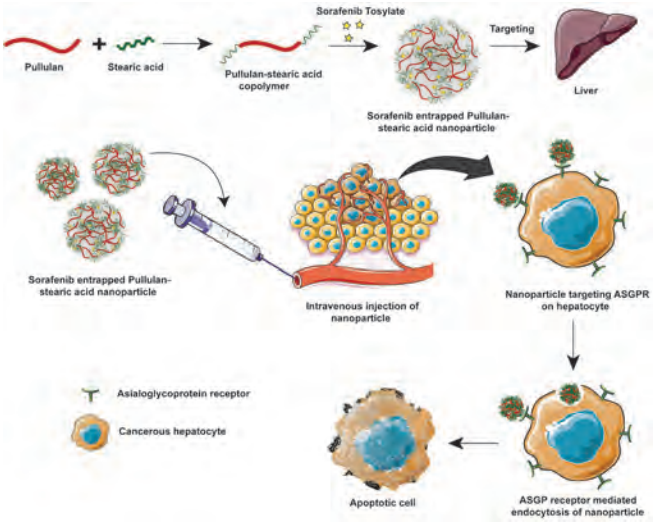
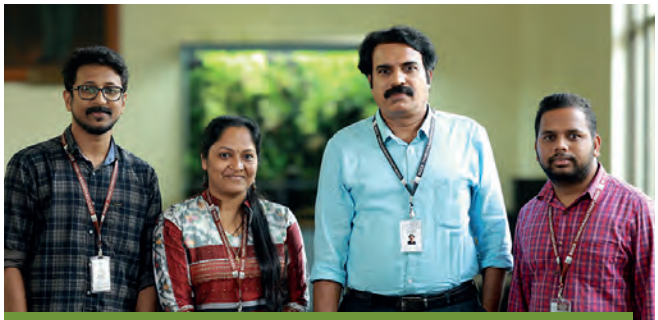


FIGURE LEGEND

Schematic representation of the preparation technique for Sorafenib Tosylate entrapped Pullulan-stearic acid nanoparticles for ASGPR targeting to the liver that leads to apoptosis of HCC cells.



From Left: Vipin CL, Teena Jacob Chirayil, Lenkapothula Naresh Goud

LABORATORY STRENGTH

Ph.D Students: 6 | JRF: 1

PUBLICATIONS

- **Vijayan A, C L V, Kumar GSV.** Dual growth factor entrapped nanoparticle enriched alginate wafer-based delivery system for suppurating wounds. Int J BiolMacromol. 2022;208:172-181.
- **Wanjale MV, Sunil Jaikumar V, Sivakumar KC, Ann Paul R, James J, Kumar GSV.** Supramolecular hydrogel based post-surgical implant system for hydrophobic drug delivery against glioma recurrence. Int J Nanomedicine. 2022;17:2203-2224.

Dr. DEVASENA ANANANTHARAMAN

Scientist F, Cancer Research Program

BRIEF THEME OF LABORATORY

Our lab investigates the contribution of HPV infections in several cancers with the aim of understanding cancer aetiology. Additional thrust areas include head and neck cancers where we focus on biomarker discovery for oral cancer risk prediction and correlates of B and T cell-mediated long term immune memory response to HPV vaccination. These are achieved through epidemiologic studies integrated with high-throughput lab data (e.g. multiplex HPV testing methods and whole-exome sequencing).

EFFICACY OF SINGLE DOSE HPV VACCINATION: INDIAN MULTI-CENTRE STUDY

The current recommendation of HPV vaccine dosage is age-dependent; two-doses for girls below 15 years of age and three-doses for women over 15 years and for immunocompromised. A one-dose HPV vaccination schedule will have substantial facilitate logistics of vaccine delivery. The objective of this study was to compare vaccine efficacy at 10 years post vaccination of single dose compared to the standard three/ two dose schedules. Vaccine efficacy was measured as the rate of persistent HPV 16 and 18 infection measured by the Luminex type-specific E7 PCR multiplex assay. Persistent infection was defined as detection of the same HPV type in two consecutive samples taken at least 10 months apart. Vaccine efficacy was calculated as one minus HPV infection rate in the vaccinated group divided by HPV infections rate in the unvaccinated group. Persistent HPV infections were tested in 6673 (73%) women. Similar frequencies of persistent HPV16/18 infections were observed in the single and three dose groups (Single doseN persistent infections/ Total women tested: 1/2135; Three doseN persistent infections/ Total women tested: 1/1460). The adjusted vaccine efficacy of a single dose against persistent HPV 16/18 infection was 95·4% (95% CI: 85·0–99·9), which was not significantly different from that observed with three doses (93·3%; 95% CI: 77·5–99·7). Based on systematic follow-up of more than 4000 adolescent girls receiving a single dose, our study has demonstrated very high efficacy of one dose of the quadrivalent vaccine against persistent infection from HPV 16/18, which is sustained until 10 years post vaccination. The data from this study played a pivotal role in deliberations in WHO Strategic Advisory Group of Experts on Immunization (SAGE) in April 2022 leading to the conclusion that, "One-dose Human Papillomavirus (HPV) vaccine offers solid protection against cervical cancer".

Front Row from left: Purnima Kartha, Lekshmy SR, Sinumol George, Shreya Sara Ittycheria, Manju V
Back row from left: Kannan TR, Jinu Austin, Devika VA, Aishwarya Ajith, Subha Sankaran

LABORATORY STRENGTH

Ph.D Students: 3 | JRF: 2 | Project Assistant: 1
Technical Assistant: 3

Table: Analysis of persistent HPV16/18 infections

	HPV infection status in participants with two or more samples tested		
	Women assessed	Women with persistent infections	Proportion of persistent infection (95% CI)
Women with samples tested	7938	..	..
HPV 16 and 18 infections			
Three-dose cohort	1460	1	0·1% (0·0–0·4)
Two-dose cohort	1452	1	0·1% (0·0–0·4)
Single-dose default cohort	2135	1	0·0% (0·0–0·3)

FIGURE LEGEND

Table represents the proportion of persistent HPV16/18 infections. Proportion and 95% CI estimated as number of persistent HPV16 or HPV18 positives/ total number of women tested.

PUBLICATIONS

- **Basu P, Malvi SG, Joshi S, Bhatla N, Muwonge R, Lucas E, Verma Y, Esmy PO, Poli URR, Shah A, Zomawia E, Pimple S, Jayant K, Hingmire S, Chiwate A, Divate U, Vashist S, Mishra G, Jadhav R, Siddiqi M, Sankaran S, Prabhu PR, Kannan TPRA, Varghese R, Shastri SS, Anantharaman D, Gheit T, Tommasino M, Sauvaget C, Pillai MR, Sankaranarayanan R.** Vaccine efficacy against persistent human papillomavirus (HPV) 16/18 infection at 10 years after one, two, and three doses of quadrivalent HPV vaccine in girls in India: a multicentre, prospective, cohort study. Lancet Oncol. 2021;22(11):1518-1529.
- **Simoens C, Gorbaslieva I, Gheit T, Holzinger D, Lucas E, Ridder R, Rehm S, Vermeulen P, Lammens M, Vanderveken OM, Kumar RV, Gangane N, Caniglia A, Maffini F, Rubio MBL, Anantharaman D, Chiocca S, Brennan P, Pillai MR, Sankaranarayanan R, Bogers J, Pawlita M, Tommasino M, Arbyn M**; HPV-AHEAD study group. HPV DNA genotyping, HPV E6*I mRNA detection, and p16INK4a/Ki-67 staining in Belgian head and neck cancer patient specimens, collected within the HPV-AHEAD study. Cancer Epidemiol. 2021;72:101925.

Dr. TESSY THOMAS MALIEKAL

Scientist E-II, Cancer Research Program

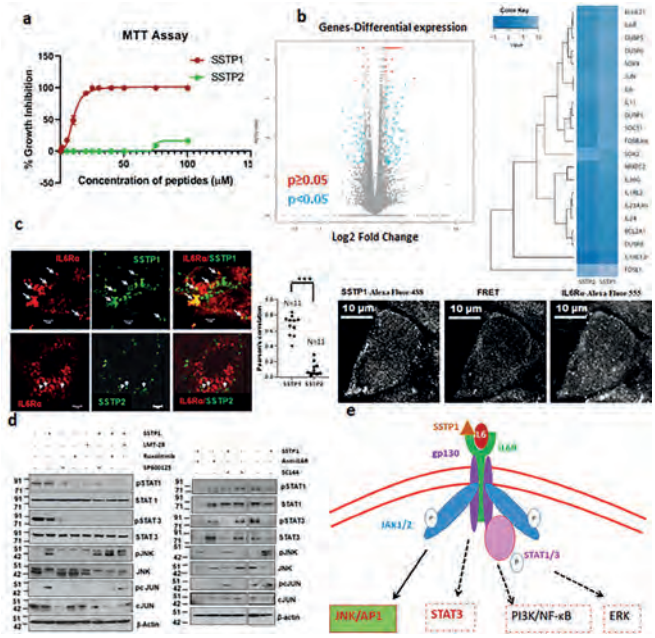
BRIEF THEME OF LABORATORY

My lab focuses on the signaling pathways required for the maintenance of self-renewal ability in cancer stem cells. We also exploit the use of peptides in cancer biology for various purposes. Recently we identified a host defense peptide that induces apoptosis in cancer cells. Understanding its molecular mechanism revealed the role of immunomodulatory pathways in the antitumor activity of host defense peptides This property offers a therapeutic potential to this peptide in cancer therapy.

SSTP1, A NOVEL TEMPORIN, INDUCES APOPTOSIS IN CANCER CELLS BY ACTIVATING JNK/AP1 PATHWAY

Host defense peptides (HDPs), which fight microorganisms and modulate immune system of the host, possess antitumor activities through membranolytic as well as non-membranolytic activities. we found that one of the temporins, SSTP1, binds to an immune-modulator, IL6Rα, on cancer cells to induce apoptosis, explaining a mechanism for nonmembranolytic activity. RNASeq analysis suggested the involvement of IL6 pathway. While co-localization studies and pull-down experiments showed that SSTP1 binds to IL6Rα, in silico docking and dynamic simulation analysis revealed that it's binding on the active IL6/IL6R α/gp130 complex. SSTP1 shifts the proliferative IL6/JAK/STAT signaling to apoptotic IL6/JNK/AP1 pathway. In contrast to IL6 blockers that inhibit JAK/STAT activity, SSTP1 activates JNK/AP1 pathway with concomitant inhibition of STATs.

Majority of the reported antitumor HDPs function by



From Left: Amrutha Mohan, Reshmi raj K, Padmaja KP, Gayathri Mohan

LABORATORY STRENGTH

Ph.D Students: 4 | Lab Assistant: 1

membranolytic activity, which is non-specific leaving them unfit for in vivo application and clinically irrelevant. Contrary to the expectation that the efficiency of the antitumor peptide is proportional to the membranolytic activity, we provide an evidence to show that HDPs can modulate signaling pathways, like cytokine signaling, to induce apoptosis in cancer cells. The sensitivity of cells to the peptide SSTP1 was found to be dependent on IL6R alpha levels, and it was effective for triple negative breast cancer, which is resistant to chemo/radiotherapy. So the peptide might have a potential for clinical application, which needs further investigation. Since the mode of action of the peptide is different from the conventional IL6 blockers, which do not activate JNK/AP1 pathway, this molecule might have therapeutic application in other contexts, where there is aberrant IL6 pathway activation and conventional Il6 blockers fail to be effective. Thus, our observations have high impact on the basic knowledge as well as drug discovery.

FIGURE LEGEND

SSTP1 interacts with IL6Rα to induce apoptosis in cancer cells by the activation of JNK/AP1 pathway. a) IC50 of SSTP1 is 15 μM. b) RNAseq data identifies IL6 pathway components as differentially regulated. c) confocal and FRET data showing the interaction of SSTP1 and IL6Rα. d) Specific inhibitors confirm the dependence of IL6, IL6Rα and gp130 for the activation of JNK/AP1 pathway e) model depicting the mode of action of SSTP1.

PUBLICATIONS

- **Mohan A, Raj Rajan R, Mohan G, KollencheryPuthenveettil P, Maliekal TT.** Markers and reporters to reveal the hierarchy in heterogeneous cancer stem cells. Front Cell Dev Biol. 2021;9:668851.
- **Mohan A, Raj R R, Mohan G, PadmajaKP ,Maliekal TT.** Reporters of cancer stem cells as a tool for drug discovery. Front Oncol. 2021;11:669250.

Dr. SUNIL MARTIN

Scientist E-II, Cancer Research Program

BRIEF THEME OF LABORATORY

Emerging evidence from curiosity-driven explorations revealed specific and durable immune responses against tumor cells at all stages of progression. Grounded on these foundational principles of cancer immunosurveillance, the laboratory envisions engineering αβ and γδ T cells with CARs to target refractory/relapsed malignancies using the tools of synthetic immunology. Retrospectively, we also would explore the interactions between the tumor and the engineered immune effector cells using multidisciplinary approaches.

ENGINEERING ANTI-TUMOR IMMUNITY

We have initiated three different approaches toward targeting tumor cells by adoptive immunotherapy. In the first approach, we aim to develop a cGMP-compatible protocol to expand γδ T cells with multivalent anti-tumor functions to make this therapy available to the clinic. There is an unmet need in India to develop such a universal therapeutic immune cell product that controls tumor burden with a better safety profile. Establishing such a protocol is a prerequisite for the generation of engineered cell therapeutics such as CAR γ9δ2 T cells. We have optimized a protocol for expansion of peripheral blood-derived fresh γ9δ2 T cells in a serum-free media to possibly treat multiple hematologic malignancies in autologous settings. Importantly, we will will use this system for exploring the immuno-biology of tumor-γ9δ2 T cell interaction as well.

The second project aims to generate αβ CAR T cells for targeting refractory or relapsed pediatric acute lymphoblastic leukemia (r/r B-ALL). Although CAR Therapy provided outstanding results against aggressive B Cell malignancies, the therapy is unaffordable in the current FDA-approved formats. Furthermore, neurologic toxicities due to hypercytokinemia is a major clinical side effect of CAR Therapy. To resolve this issue, we embarked on streamlining a protocol for the in vitro generation of CAR T cells with various molecular configurations to reduce toxicity and cost of production. We have generated and characterized αβCAR T cells targeting CD19 in vitro. We will now test CD19 CAR T cells in vivo using the NSG model followed by the scale-up studies.

The third project involves sensitizing the tumor cells to immune effector cell-mediated lysis. Towards this end, we are screening multiple epigenetic regulators that modulate the immune effector molecules on tumor cells.

LABORATORY STRENGTH

Ph.D Students: 1 | JRF: 1

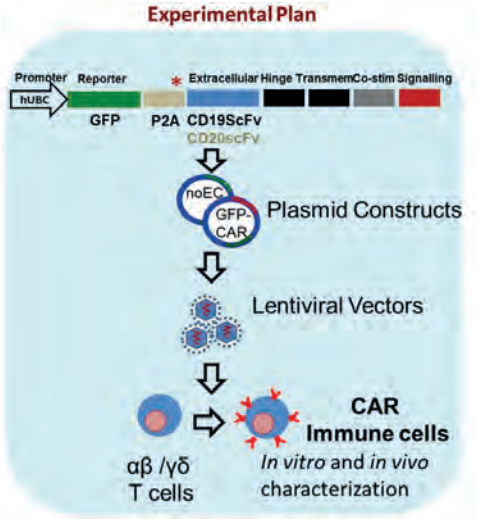


FIGURE LEGEND

Generation of CAR–Immune Cells: αβ or γδ T cells are generated from the peripheral blood mononuclear cells (PBMC). We will then stimulate the T cells with Zoledronic Acid (ZA) in presence of rhIL-2 to expand γ9δ2 T cells. αβ T cells will be stimulated with anti-CD3 and CD28 in presence of rhIL-2 before extensive characterization. These immune cells will then be engineered by the lentiviral transduction of CAR vectors.

PUBLICATIONS

- **Ganapathy T, Radhakrishnan R, Sakshi S, Martin S.** CAR γδ T cells for cancer immunotherapy. Is the field more yellow than green? Cancer Immunol Immunother. 2022 (Epub ahead of print)
- **Muthuvel M, Srinivasan H, Louis L, Martin S.** Engineering off-the-shelf universal CAR T cells: A silver lining in the cloud. Cytokine. 2022;156:155920.

Dr. K.B.HARIKUMAR

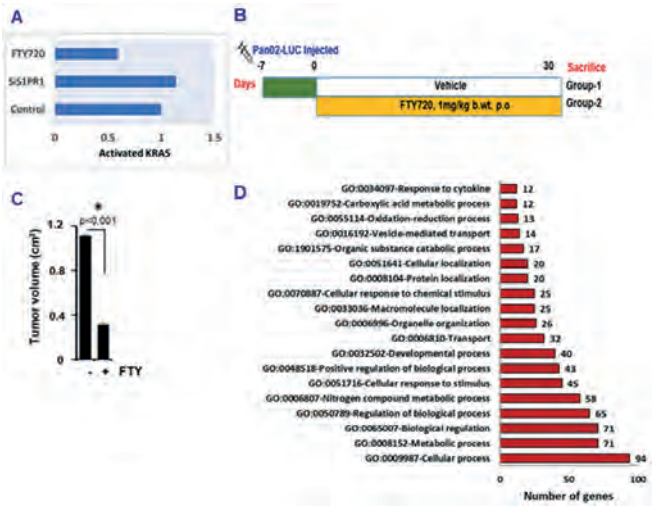
Scientist E-II, Cancer Research Program

BRIEF THEME OF LABORATORY

The main focus of the laboratory is understanding the role of inflammation in physiology (innate immune response) and pathophysiology (cancer). We are particularly interested in the roles of Sphingosine 1-phosphate (S1P) in inflammation and carcinogenesis.

CROSS TALK BETWEEN S1PR1 AND K-RAS IN PANCREATIC CANCER

S1PR1 and KRAS are two independent signalling pathways which regulate many characteristic properties like cell proliferation and survival, migration and invasion. They also contain common downstream signalling molecules like ERK1/2, PI3K/AKT etc. Few reports showed the link between bioactive sphingolipid metabolism and KRAS. There is no direct evidence between S1PR1 and KRAS relationship, and so we asked a question whether they are linked. We noticed that S1PR1 and KRAS does not influence each other at transcription or translational level. Further we analyzed the effect of S1PR1 on K-RAS activity. Interestingly genetical silencing of S1PR1 did not alter the K-RAS activity, however FTY720, a functional antagonist of S1PR1 inhibited the K-RAS activity (Figure A). Next we did an in vivo syngeneic orthotopic model of pancreatic cancer in mice and observed that FTY720 inhibited the tumor formation. The PAN 02-Luc cells were used to test the anticancer potential of FTY720. On Day 0, orthotopic implantation were performed (figure B). Animal subjects were monitored for



From Left: Yadu Vijayan, Rajeev J Thampi, Aparna JS, Anu B, Shirley James, Arun V, Prameela Kumari TK

LABORATORY STRENGTH

Ph.D students: 3 | SRF: 1 | Project Assistant: 1
Technical Assistant: 2

any side effects to the compounds during the treatment tenure. All animals were sacrificed on the day 35 and gross necropsy was conducted to make out any differences between the groups. The tumor was resected from each animal and tumor volume was noted. The tumor volume was statistically decreased in the FTY720 group as compared to control group (Figure C). We performed a proteomic analysis of the tumor samples and a total of 4457 protein hits were identified and sorted based on their p-Values (Figure D). Gene ontology using string was used to detect the localisation of altered proteins. Majority of proteins were localised in the intracellular organelle followed by membrane bound organelle. Further analysis is ongoing.

FIGURE LEGEND

(A) K-RAS pull down assay: Quantification of data showing the effect of silencing of S1PR1 in K-RAS activity; (B) Schematic representation of experimental procedure; (C) The final tumor volume represented as mean ± S.D; (D) GO distribution of identified proteins from proteomics analysis.

PUBLICATIONS

- **Kiran S, Parvathy J, Sukumaran T, Varghese J, Lakshmi S, Kumar SS, Babu A, Harikumar KB and Ragupathy L.** Immunomodulatory properties of D-sorbitol/D-mannitol incorporated linear step-growth Co-polymers, Int J Polym Mater. 2022 (In Press).
- **Manu KA, Harikumar KB, Ishimoto T.** Editorial: Targeting Pancreatic Cancer: Strategies and Hopes. Front Oncol. 2022. 12:873682.

Dr. ANI V DAS

Senior Program Scientist, Cancer Research Program

BRIEF THEME OF LABORATORY

The main focus of my research is to understand the involvement of non-coding RNAs and associated proteins in the stem cell maintenance and also their correlation with HPV-mediated tumorigenesis in cervical cancer. My research also involves elucidation of epigenetic mechanism behind the regulation of multidrug resistance in germ cell tumours.

RXR AGONIST, BEXAROTENE , EFFECTIVELY REDUCES DRUG RESISTANCE VIA PLEOTROPIC REGULATION OF NRF2 AND RFX1 IN EMBRYONIC CARCINOMA CELLS

Cancer stem cells (CSCs) are a subset of cancer cell population having enhanced chemotherapy resistance and pose a big challenge to current treatment regimens. A key factor responsible for their high resilience against therapy is the increased expression of multidrug resistant (MDR) proteins. Targeting these MDR proteins has shown to be very fruitful against drug resistance. Therefore, a key strategy to identify factors involved in the regulation of MDR proteins in CSCs. We found that transcription factors, RFX1 and Nrf2 could differentially regulate MDR genes. While Nrf2 positively regulated MDR genes, RFX1 acted strictly as a negative regulator. Our preliminary data suggested a possible interlinked activity between Nrf2 and RFX1 in NT2 cells which led us to check for agents that could simultaneously upregulate RFX1, while inhibiting NRF2.

Bexarotene, a selective activator of retinoid X receptor (RXR), is known to be regulating a number of genes that are involved in various cellular processes. Though Bexarotene has shown potential to be used in chemotherapy, either alone or in combination with other drugs, the mechanism by which it imparts its effect is not yet clear. We found that Bexarotene could target both RFX1 and NRF2 in combating multi-drug resistance. It could block NRF2-mediated effects and CSC-associated properties in NT2 cells. Bexa could sensitize cells more effectively than Cisplatin, a well-known cancer therapeutic drug (Figure). Interestingly, we found that Bexa could increase the expression of RFX1 in NT2 cells, while inhibiting NRF2-ARE binding-mediated transcriptional regulation. Further analyses proved that Bexa accentuated RFX1 promoter activity which is mediated via RXRa binding. Our data suggest that Bexarotene can act as a double-edged sword by targeting NRF2 and RFX1 and counter MDR-mediated drug resistance in CSCs and could be used alone or in combination with other drugs.

From Left: Pooja SR , Midhuna Raj K , Reshma Murali , JayaSree R

LABORATORY STRENGTH

Ph.D students: 2 | JRF: 1 | Lab Assistant: 1

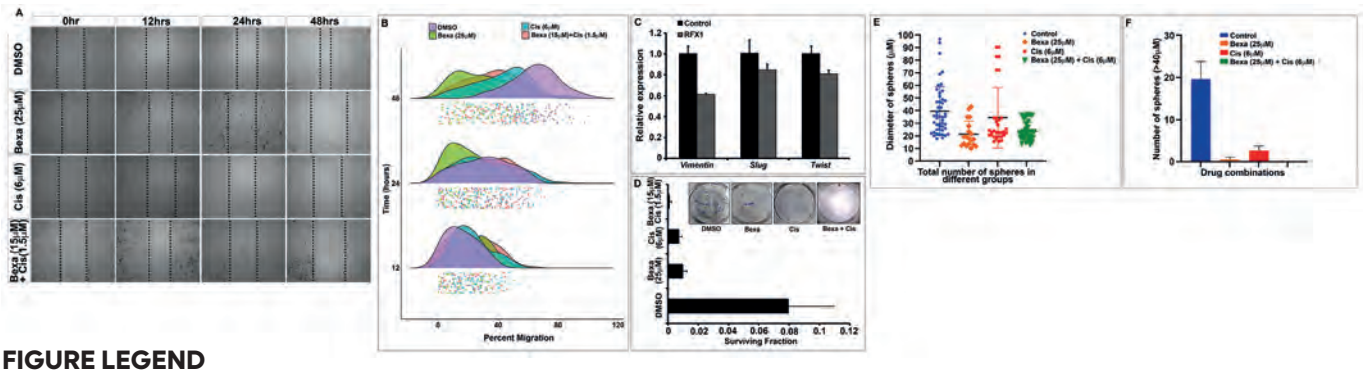


FIGURE LEGEND

Bexarotene targets CSCs hallmarks: Bexarotene alone and in combination prevented cell migration (A, B, C), colony formation (D) and tumorosphere formation (E,F) and to a great extent while cisplatin treatment was the most efficient in preventing colony formation.

PUBLICATIONS

- **Midhunaraj K, Mary Angelin & Ani V Das**. PIWI proteins and piRNAs in cervical cancer: A propitious dart in cancer stem cell targeted therapy. Human Cell. 2021; 34(6):1629-1641.

Dr. RADHIKA NAIR
Program Scientist, Cancer Research Program

BRIEF THEME OF LABORATORY

Comprehending the mechanisms that allow a tumour cell to survive and thrive in a hostile new environment of a distant organ is vital to deciphering the complexity underlying metastasis. The hypothesis underpinning our work is that breast cancer cells form metastases utilizing a combination of cell autonomous ('intrinsic') programs and microenvironmental ('extrinsic') changes. This has implications for understanding the critical molecules in metastasis and identifying its "Achilles' heel", which can be exploited for therapeutic purposes.

DECIPHERING THE COMPLEXITY OF BREAST CANCER METASTASIS

Metastasis or the spread of cancer from the primary site to other parts of the body is a silent killer in breast cancer, with 90% mortality rate for women with metastatic disease. Therapeutic targeting requires a deeper understanding of this complex cascade of events eventually leading to metastasis. I aim to comprehend the cell intrinsic and extrinsic mechanisms that allow a tumour cell to survive, remain in a state of dormancy and then thrive in a hostile new environment of a distant metastatic organ.

Approach 1- Investigating the role of known molecular mediators of metastasis in breast cancer

I have focused on the Inhibitor of differentiation (or Id) family of bHLH transcriptional repressor proteins which play a critical role in the metastatic spread of breast cancer cells to distant organs especially the lung. I have gone onto identify two potential pathways by which Id proteins control key cancer phenotypes – via negative transcriptional regulation of the Robo1 pathway and cell cycle pathway by impacting Kif11 and Aurka.

Approach 2: Identifying the molecular mediators involved in breast cancer metastasis using an unbiased approach

I plan to expand this work to identify pathways which are critical for the metastatic phenotypes hardwired into the metastatic cells with the aim of discovering new potential therapeutic targets. I have isolated two phenotypically distinct tumor cell populations with differing metastatic potential. Resolving the molecular drivers behind the intratumoral heterogeneity revealed critical players which are druggable (Preprints doi:10.20944/preprints202202.0133.v1). Using a validation cohort of 20 matched primary and metastatic tumors will allow me to further understand the genetics underlying the metastatic process and drive my work into more translational avenues in an Indian context.

LABORATORY STRENGTH

Ph.D Students: 1

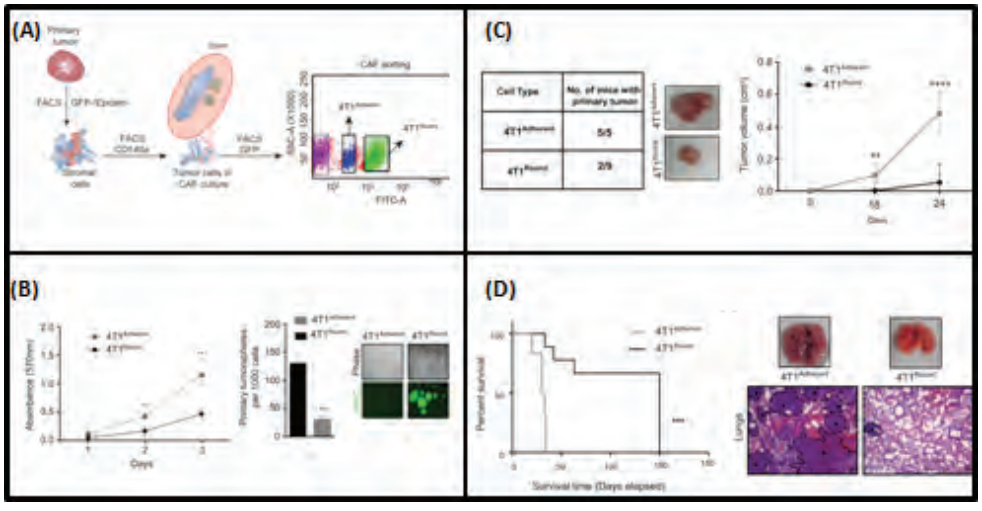


FIGURE LEGEND

Isolation of phenotypically distinct tumor cells from a heterogeneous population. (A) Schematic showing the sorting of primary tumor. (B) Proliferation and tumorsphere assay. (C) The 4T1Adherent cells are highly aggressive. (D) Kaplan-Meier survival curves and representative H&E staining of lungs from two groups of mice. Magnification 10x. Data are expressed as mean ± standard deviation. n=3, p <0.05 are considered statistically significant with *p<0.05, **p<0.01, ***p<0.001, ****p<0.0001

PUBLICATIONS

- **Thankamony AP, Murali R, Chakraborty P, Karthikeyan N, Varghese BA, Jaikumar VS, Jolly MK and Nair R.** Phenotypic heterogeneity drives differential disease outcome in Triple Negative Breast Cancer (Preprints doi:10.20944/preprints202202.0133.v1)
- **Thankamony AP, Subbalakshmi AR, Jolly MK, Nair R.** Lineage plasticity in cancer: the tale of a skin-walker. Cancers (Basel). 2021;13(14):3602.

Dr. ANANDA MUKHERJEE

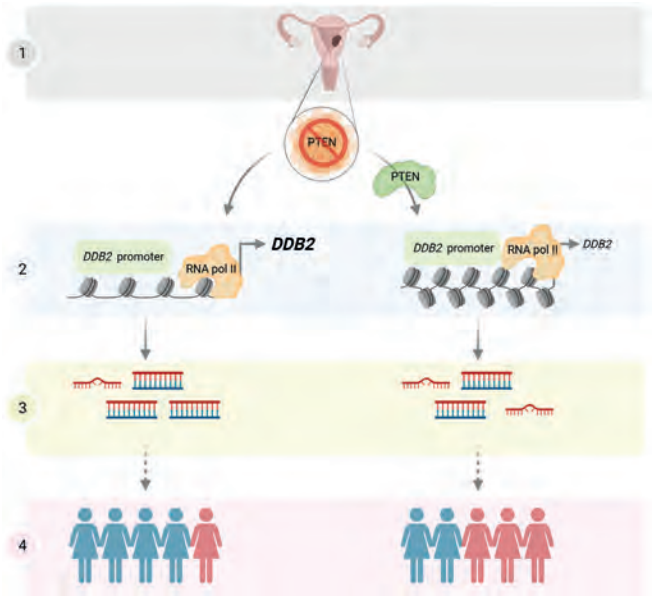
DBT Ramalingaswami Fellow, Cancer Research Program

BRIEF THEME OF LABORATORY

My group studies genomic instability and DNA repair defects in tumor initiation, progression, and therapy. Every day, external and internal agents damage our DNA (70,000 lesions/cell/day). Several DNA repair and damage tolerance pathways can rectify most of these. But if damage remains unrepaired, it kills cells or causes cancer-causing mutations. Using modern biochemical and genomic tools, we examine how genome-wide instabilities affect tumour suppressor mechanisms in malignancies.

NUCLEOTIDE EXCISION REPAIR IN ENDOMETRIAL CANCER

The most prevalent cancer of the female reproductive system in developed nations is endometrial cancer (EC), which develops from the endometrium tissue of the uterus. The rate of EC is expected to rise globally, in part because of its positive correlation with lifestyle and economic development. The majority of EC manifested with endometrioid histology and genetic changes that rendered the tumor suppressor gene PTEN inactive. PTEN serves as a barrier against the development of tumors by negatively regulating the PI3K/Akt/mTOR axis of cell proliferation. Through its chromatin-related activities, PTEN is also connected to DNA repair procedures. However, we do not fully comprehend how DNA repair takes place in the absence of PTEN activity in EC. The expression of PTEN in EC was found to be negatively correlated with the damage sensor protein of nucleotide excision repair (NER), DDB2, based on the Cancer Genome Atlas (TCGA). We established a link between increased DDB2 expression and enhanced NER activity without PTEN through several biochemical studies and cellular endpoint assays using EC cell lines. The mechanism of transcriptional activation of DDB2 is mediated by the binding of RNA polymerase II to the DDB2 promoter in PTEN-null EC cells. Our research showed NER and EC to be causally related, suggesting a possible target for treating the illness.



From Left: Anjali Devarajan, Ahel Bhattacharyya
Fathima Hameed JS

LABORATORY STRENGTH

Ph.D students: 1 | JRF: 1 | Project Assistant: 1

FIGURE LEGEND

A model depicted a probable mechanism and consequence of high DDB2 expression in PTEN-null EC. The PTEN-negative EC (1) induces the transactivation of DDB2 by facilitating the recruitment of active RNA polymerase II at the DDB2 promoter (2). Higher expression of DDB2 leads to augmented repair synthesis and protects the genome more efficiently (3), presumably contributing to the better survival of those patients (4). Women in blue represented live patients; women in red represented deceased patients.

PUBLICATIONS

- **Misra S, Chowdhury SG, Ghosh G, Mukherjee A, Karmakar P.** Both phosphorylation and phosphatase activity of PTEN are required to prevent replication fork progression during stress by inducing heterochromatin. Mutat Res. 2022;825:111800.

Dr. RAM MOHAN RAM KUMAR

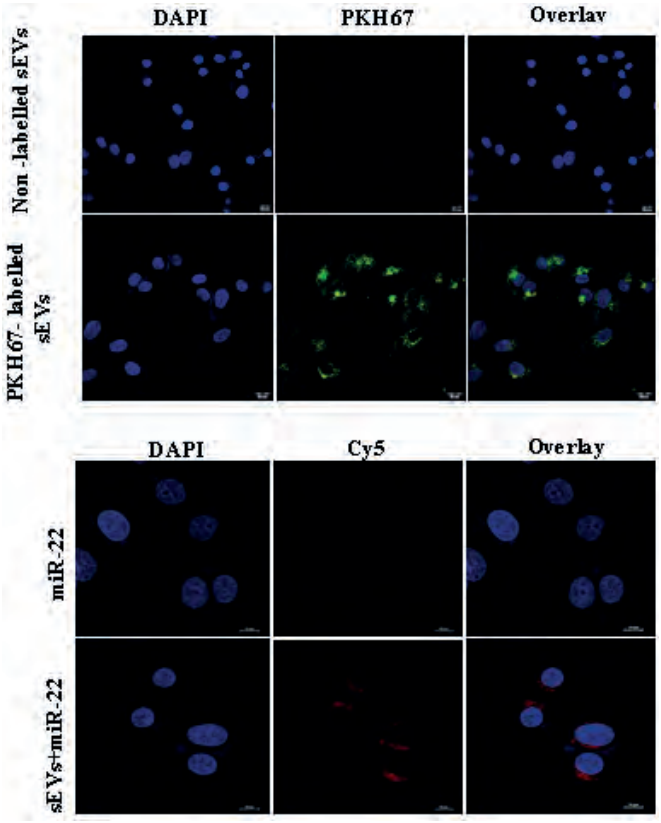
DBT-Ramalingaswami Fellow, Cancer Research Program

BRIEF THEME OF LABORATORY

One of our research themes focuses on the greatest challenges facing modern therapeutics: the delivery of small molecules or drugs. Despite the unprecedented knowledge of diseases and their mechanisms due to advances in biomedical sciences; many promising therapeutic approaches are still clinically unavailable. This is because there are no efficient and safe means of delivering therapeutics to the tumour target sites. The lab focuses on diagnostics and therapeutic aspects of extracellular vesicles in human diseases.

SMALL EXTRACELLULAR VESICLE BASED CANCER THERAPY

Cervical cancer (CC) is the third leading cause of cancer mortality amongst females. The early metastasis of the primary tumor results in poor prognosis and poor therapeutic outcomes. Specifically, an increasing amount of research has revealed that long-lasting infections of high-risk human papillomavirus (HPV), such as HPV-16 and HPV-18, mainly compose the majority of CC cases, however, the infection alone may not be sufficient to induce malignancy. About 45% of women with CC are diagnosed at an early stage. If CC is metastasised to the surrounding tissues, organs or the regional lymph nodes, the 5-year survival rate is 56%3. The therapy prospect for CC patients has not improved significantly and treatment



1

2

From Left: Dr. Ram Mohan Ram Kumar, Sreebharathi R

LABORATORY STRENGTH

Ph.D Students: 1 | Project Assistant: 1

regimens for CC are highly toxic, and 5patients with metastatic disease are rarely cured. Strategies to deliver small RNA molecules such as tumour suppressor miRNAs (miRs) are an exciting and potential therapeutic option for controlling the growth of malignant CC.

The ability of miRs to down-regulate the expression of genes involved in cancer progression makes them an excellent candidate for developing a miR-based therapeutic strategy. Delivery of these molecules to the target site is another area of concern since most of the carriers such as gold nanoparticles, viral vectors etc. cause immunogenicity and lack inherent targeting ability. We focus on delivering those miRNA molecules using surface-engineered non-toxic carriers such as small extracellular vehicles (sEVs) which will exhibit inherent targeting ability and deliver the tumour suppressor miRs to the target site without affecting the normal cells. The surface of sEVS will be conjugated with cervical cancer-specific peptides and loaded with miRs targeting the tumour cells.

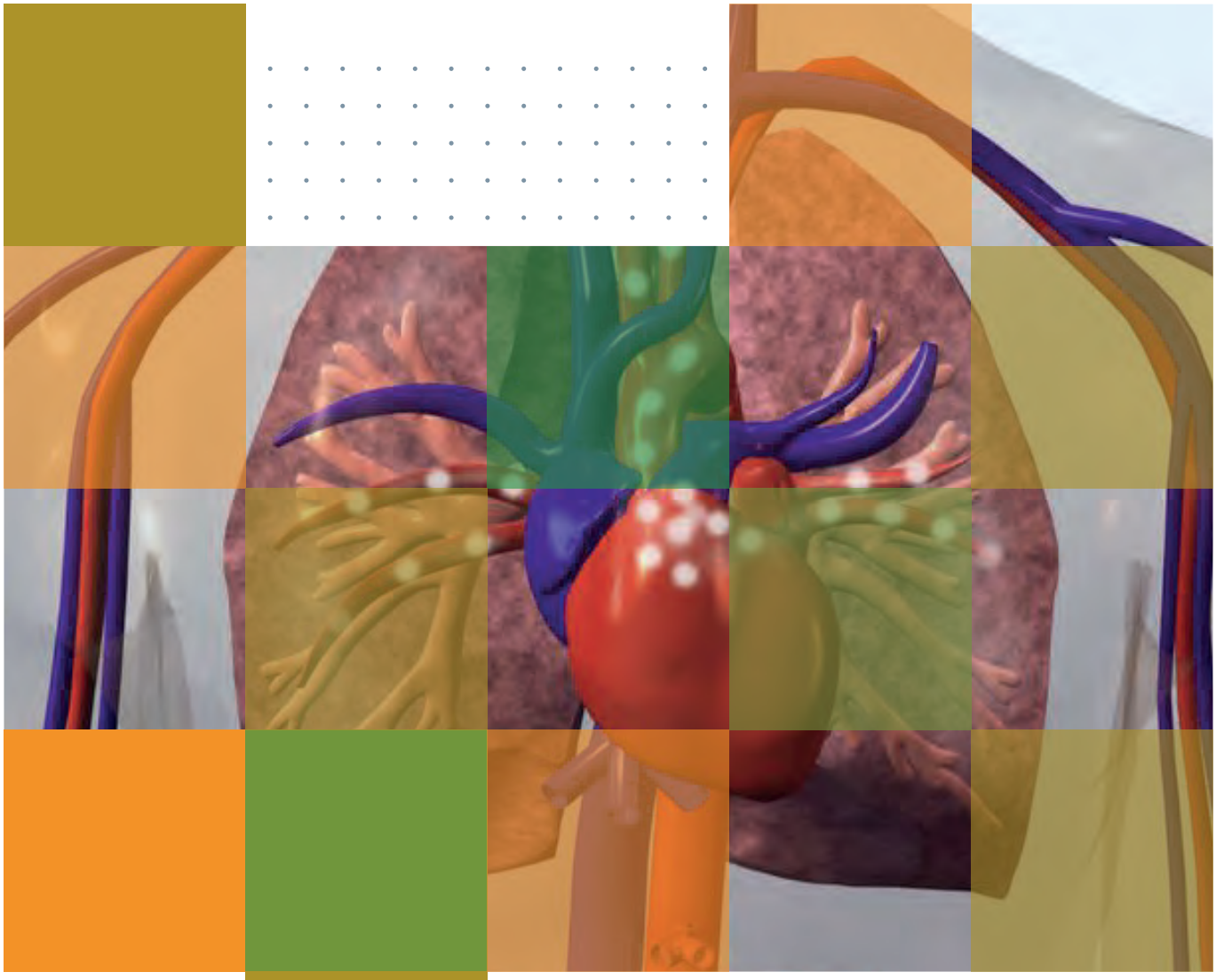
FIGURE LEGEND

Fig 1: Cell Uptake of sEVs: sEVs are readily taken up by SiHA cells after 16h.

Fig2: cy5-miR-22 incorporation in sEVs. miR22 is readily incorporated in SiHa cells by sEVs.

PUBLICATIONS

- **Rajan A, Varghese GR, Yadev I, Anandan J, Latha NR, Patra D, Krishnan N, Kuppusamy K, Warrier AV, Bhushan S, Nadhan R, Ram Kumar RM and Priya Srinivas.** Modulation of BRCA1 mediated DNA damage repair by deregulated ER-α signaling in breast cancers.Am J Cancer Res. 2022; 12(1): 17–47.



CARDIOVASCULAR DISEASES & DIABETES BIOLOGY

Dr. ABDUL JALEEL

Scientist G, Cardiovascular Diseases & Diabetes Biology

BRIEF THEME OF LABORATORY

We investigate how independent risk factors for type 2 diabetes evolve over time in developing insulin resistance using tools of mass spectrometry based omics tools. This is executed through human studies in a population cohort, and confirming the findings through animal studies using various models of obesity and type 2 diabetes.

Comprehensive mass spectrometry based Lipidomics & metabolomics platforms for promoting biomedical research & advanced training for Indian researchers

ASSESSMENT OF TYPE 2 DIABETES RISKS IN HUMAN AND ANIMAL MODELS

Our earlier data shows that people, who are having diabetes risks, despite being healthy, have altered metabolism, and that alteration is different between various risks such as family history of diabetes and overweight. This project is to follow-up of those earlier study participants (longitudinal study) to see how many of them contract T2DM or prediabetes to determine their metabolic alterations retrospectively. If such metabolic alterations/signatures are detectable in a healthy population, early interventions can be utilized for prevention of disease. So far 94 participants have been recruited and performed human study on them. We found that out of 94 participants 9 (9.6%) people became diabetic and 35 (45%) became prediabetic. There is a significant increase in BMI and insulin resistance among the study participants after 5 years. We performed the LC/MS/MS runs for the plasma metabolomics of samples from before and after 5 years to find out metabolic alterations and the risk for diabetes mellitus retrospectively. The data analyses are going on at present.

In another study under the same theme, we challenge the physiology of female and male animals with high-fat diets and fructose. Metabolic alterations associated with insulin resistance is studied by biochemical measurements, untargeted metabolomics analysis of plasma, liver and adipose tissue samples and label-free proteomics analysis of liver and tissue samples. Understanding the development of metabolic disorders in the background of dimorphism will help to tackle the disease in a more effective manner. The study is being conducted by feeding C57BL/6J mice for 10 weeks grouped into four diet categories; 1) Chow diet, 2) Chow plus Fructose, 3) High fat diet & 4) High fat diet plus fructose. After treatment, mice were euthanized and liver, abdominal and epididymal fat pads were collected for quantitative real time-PCR, metabolomics, and proteomics analysis.

From Left: Akhila Suresh SS, Gopika Satheesh, Dr. Kalaivani V, Dr. Nandini RJ

LABORATORY STRENGTH

Postdoctoral Fellows: 2 | Students: 3 | SRF: 1
Project Assistant: 1

	NORMAL	PREDIABETIC	DIABETIC	TOTAL
MALE	17	18	6	41
FEMALE	18	32	3	53
COMBINED	35	50	9	94

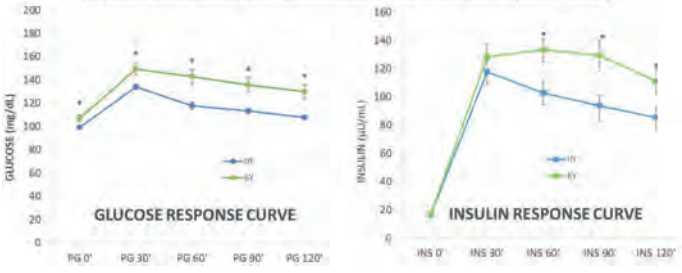


FIGURE LEGEND

Our earlier results showed that there are metabolic alterations in healthy young adults, if they are having the risk for type 2 diabetes (T2DM). Continued investigation in this study cohort after 6 years showed that both glucose curve and insulin curve are higher indicating already developed insulin resistance.

PUBLICATIONS

- **Anandan V, Thulaseedharan T, SureshKumar A, Karthika CL, Amjesh R, Mullasari AS, Kartha CC, Jaleel A, Ramachandran S.** Cyclophilin A impairs efferocytosis and accelerates atherosclerosis by overexpressing CD 47 and down-regulating calreticulin. Cells 202; 10: 3598.
- **Aneesh Kumar A, Ajith Kumar GS, Satheesh G, Surendran A, Chandran A, Kartha CC, and Jaleel A.** Proteomics Analysis Reveals Diverse Molecular Characteristics between Endocardial and Aortic-Valvular Endothelium. Genes 2021; 12: 1005.

Dr. RAKESH S. LAISHRAM

Scientist E-II, Cardiovascular Diseases & Diabetes Biology

BRIEF THEME OF LABORATORY

RNA mediated gene regulation: Role of untranslated and non-coding RNAs

CLEAVAGE HETEROGENIETY IN GENE EXPRESSION AND THE ROLE OF NON CANONICAL POLYMERASE, STAR-PAP IN CLEAVAGE AND POLYADENYLATION OF TARGET MRNAS

Processing at the 3′-untranslated region (UTR) is an essential step in the generation of eukaryotic mRNAs. It involves two coupled steps – cleavage and polyadenylation. Global cleavage site analysis shows a heterogeneity averaging 6 cleavage sites per poly(A) site (PA-site) on an mRNA. The two nuclear poly(A) polymerases (canonical PAP and Star-PAP) have similar cleavage site distribution on target mRNA PA-sites. Mutational analysis of cleavage site(s) on Star-PAP target PA-sites revealed specific but stuttering cleavage pattern where the number of cleavage site is inversely related to the protein expression. Intriguingly, each PA-site contains a primary cleavage site, having the highest efficiency such that increased cleavage events on non-primary sites reduce cleavage efficiency limiting the protein expression. Our study demonstrated that increased expression of stress response proteins during oxidative stress involves reduction in cleavage heterogeneity and increase in the primary site cleavage. Our study establishes a signaling regulation of cleavage heterogeneity that controls stress response gene expression.

Recent studies have shown that Star-PAP regulates 3′-end processing of mRNAs involved in cancer. We show that miRNAs that targets oncogenes are dependent on

Front Row From Left: Ciji Varghese, Dr. Ganesh Ram Koshre, Dr. Dhanya R, Nimmy Francis, Malaya Ranjan Behera
Back Row From Left: Dr. Sumayya Shahzad, Feba Shaji, Neeraja KM, Diksha Singh, Sneha Sandra

LABORATORY STRENGTH

Postdoctoral Students: 2 | Ph.D Students: 6 | JRF: 1
Project Associate: 1

Star-PAP and that Star-PAP controls pri-miRNA generation in the miRNA biogenesis pathway. Consistently, Star-PAP depletion resulted in decreased expression of target miRNAs leading to induced expression of targeted oncogenes in MCF-7 cells. Conversely, Star-PAP re-expression in MDA-MB-231 (where Star-PAP expression is marginal) induces miRNA expression and downregulates targeted oncogenes. As a result, we observed an increased cell proliferation in MCF-7 cells on Star-PAP depletion, and a consequent reduction in tumour formation on Star-PAP overexpression in SCID mice xenograft models. Our results establish a novel mechanism of oncogenic protein expression via Star-PAP control of pri-miRNA cleavage and polyadenyation.

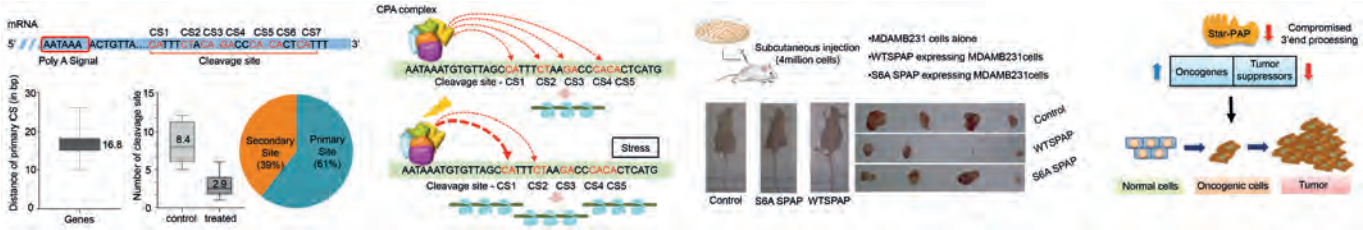


FIGURE LEGEND

Figure showing cleavage heterogeneiety and its regulation of oxidative stress resposne and role of Star-PAP pri-miRNA control in oncogene expression in breast cancer

PUBLICATIONS

- **Neeraja KM, Shaji F, Koshre G and Laishram RS** Alternative polyadenylation: an enigma of transcript length variation in health and disease. Wiley Interdiscip Rev: RNA . 2021. e1692.
- **Koshre GR, Shaji F, Mohanan NK, Mohan N, Ali j and Laishram RS.** Star-PAP RNA binding landscape reveals novel role of Star-PAP in mRNA metabolism that requires RBM10-RNA association. Int J Mol Sci. .2021 .22(18), 9980

Dr. SURYA RAMACHANDRAN

Program Scientist, Cardiovascular Diseases & Diabetes Biology

BRIEF THEME OF LABORATORY

The research focus is on developing approaches to understand how hypercholesterolemia and hyperglycaemia interferes with key genetic, inflammatory and cellular pathways to accelerate atherosclerotic lesion progression.

MATERNAL HYPERCHOLESTEROLEMIA INDUCES FETAL PROGRAMMING CAUSING INCREASED RISK OF ATHEROSCLEROSIS IN OFFSPRING

Maternal hypercholesterolemia during pregnancy has long been given less clinical relevance. Fatty streak formation in the aortas of 6-month-old fetuses of hypercholesterolemic mothers indicated that hypercholesterolemia during pregnancy is pathogenic. We hypothesized whether atherogenic programming in maternal hypercholesterolemia is due to differential expression of LDL receptors across the placenta. The study was performed in High Fat Diet fed pregnant New Zealand white rabbits and human subjects. Pregnant rabbits were fed with 0.3%cholesterol for hypercholesterolemia and the control group with normal chow diet. Lipid profiling was performed in mothers throughout gestation. At the end of each trimester, placenta and fetal tissues were collected. Histological analysis (Figure 1) and differential expression of these receptors were analyzed in the placenta of pregnant New Zealand white rabbits in all three trimesters. Offsprings of such animals were allowed to attain adulthood and were identified with atherogenesis in early adulthood with high lipid profile . Biosynthesis of cholesterol by the offspring liver was also studied to understand the role of endogenous cholesterol sources in developing hypercholesterolemia in offspring.

Back Row From Left: Aswathy S, Jagannath RS, Jeeva Prasannan, Vinitha A
Front Row From Left: Jayalekshmi VS, Rajeswari Gopal G

LABORATORY STRENGTH

Ph.D Students: 3 | JRF: 1

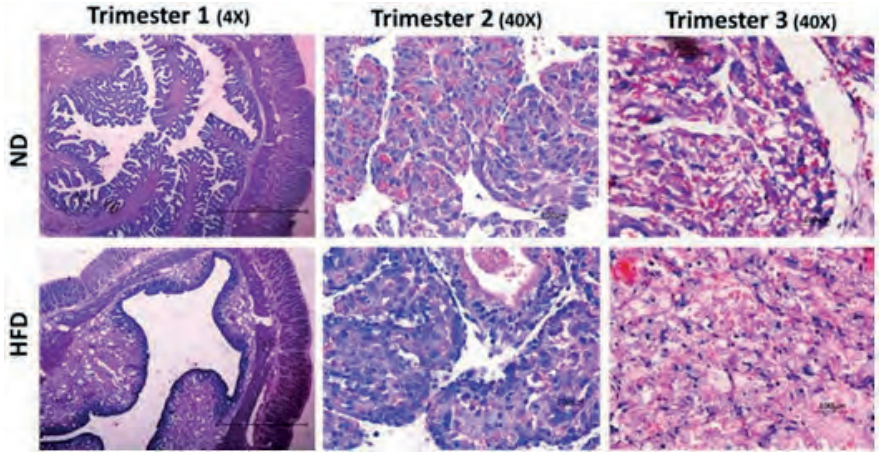


FIGURE LEGEND

Hematoxylin and Eosin staining of placenta of New Zealand white rabbits in different trimesters

PUBLICATIONS

- **Anandan V, Retnabai, SKT, Jaleel A, Thulaseedharan T, Mullasari A, Pillai MR, Kartha CC, Ramachandran S.** Cyclophilin A induces macrophage apoptosis and enhances atherosclerotic lesions in high-fat diet-fed hyperglycemic rabbits. FASEB BioAdvances. 2021; 3(305).
- **Anandan V, Thulaseedharan T, Suresh Kumar A, Chandran Latha K, Revikumar A, Mullasari A, Kartha CC, Jaleel A, Ramachandran S.** Cyclophilin a impairs efferocytosis and accelerates atherosclerosis by overexpressing CD 47 and down-regulating calreticulin. Cells. 2021; 10(12):3598.

Dr. S.SUMI
Program Scientist, Cardiovascular Diseases & Diabetes Biology Program

BRIEF THEME OF LABORATORY

The association between blood flow and endothelial signal programming is very complex. We focus on mechanotransductive pathways activated in luminal endothelium in response to altered shear stress in vascular diseases such as cerebral arteriovenous malformations and varicose veins. We believe that this approach would empower us to explore hemodynamics-associated endothelial signalling under disease conditions, and could translate into the delineation of drug targets and development of pharmacotherapeutic strategies in these diseases.

ALTERED SHEAR STRESS INDUCE NOTCH3-INDUCED ENDMT IN CEREBRAL ARTERIOVENOUS MALFORMATIONS

Arteriovenous malformations (AVM) are tangles (nidus) of dysplastic blood vessels which shunt blood from arteries to veins with no intervening capillary bed. Cerebral AVM, are important causal factors of intracranial hemorrhage which result in permanent disability or death, if not detected early and corrected surgically. A strong genetic basis and hemodynamic modulation is presumed in the AVM pathogenesis. The pathogenesis of these malformations still remains an enigma thus complicating therapeutic strategies.

Studies from our research group have demonstrated the presence of active angiogenesis and vascular remodelling postnatally in AVM. We have demonstrated an upregulated expression of angiogenesis-related factors in human brain AVMs. We found increased expression of mesenchymal markers in endothelial layers of AVM indicating the activation of endothelial mesenchymal transition (EndMT). AVMs are high shear stress systems due to the direct connection of feeding artery to drainer veins. We hypothesize that disturbed fluid shear stress induce differential expression of shear sensitive signaling cascades such as Notch signalling that have prominent role in the induction of EndMT.

EndMT-like phenotype switching with a gain of mesenchymal markers such as αSMA, Calponin1, N-Cadherin and Transgelin as well as transcriptional factor TWIST1 was observed in AVM nidus in comparison to control neural vasculature. Notch3, a critical mediator of EndMT was found to be localized to large vessels in cerebral AVM nidus (Figure 1). To understand the role of altered shear stress in inducing EndMT in cerebral microvascular endothelial cells, we exposed them to various flow regimes such as static, arterial shear stress and oscillatory shear stress. Endothelial cells exposed to oscillatory flow produced Notch3 and EndMT markers compared to normal arterial shear stress. Progress in elucidating these mechanisms may provide insights into the factors that determine postnatal growth of these lesions and their recurrence after resection.

From Left: Karthika CL, Sreelakshmi BJ, Ahalya Sreekumar, Suvarna CM, Vani Venugopal

LABORATORY STRENGTH

Ph.D Students: | JRF: 1 | SRF: 2

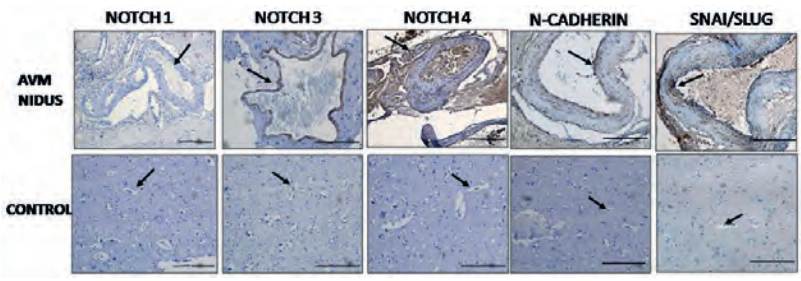


FIGURE LEGEND

Immunohistochemical staining shows the expression of Notch- 1, Notch-3 and Notch -4, N-Cadherin and SNAI/SLUG ,in AVM nidus tissues compared to normal brain tissues (Scale bar 100 µM, magnification 20×). Notch3 and EndMT markers were found to be localized to large vessels in cerebral AVM nidus. There was no significant difference in the expression of Notch1 and Notch4 between control and AVM nidal tissues.

PUBLICATIONS

- **Karthika CL, Ahalya S, Vyshna Beena, BinilRaj SS, RaviKumar B Lakkappa, Ravi Kalyani, Radhakrishnan N, Kalpana SR, Kartha CC, Sumi S.** Shear stress alterations activate BMP4/pSMAD5 signaling and induce endothelial mesenchymal transition in varicose veins. Cells. 2021; 10(12), 3563.
- **Venugopal V, Sumi S.** Molecular biomarkers and drug targets in brain arteriovenous and cavernous malformations: where are we? Stroke. 2022;53(1):279-289.

Dr. ANANTHALAKSHMY SUNDARARAMAN

DBT-Ramalingaswami Fellow, Cardiovascular Diseases & Diabetes Biology Program

BRIEF THEME OF LABORATORY

Intracellular Trafficking in Cardiovascular Health and Disease

MITOCHONDRIA-DERIVED VESICLE TRAFFICKING IN MITO-NUCLEAR COMMUNICATION AND QUALITY CONTROL IN THE CARDIOVASCULAR SYSTEM

Mitochondria-derived vesicles (MDVs) represent a pathway that operates at the intersection of quality control and vesicular trafficking. MDVs are the first line of defence against oxidative damage and upon failing to degrade oxidised proteins, the cells further resort to whole organelle degradation through mitophagy. Cardiomyocytes are crucially dependent on healthy mitochondria for their bioenergetics. Dysfunctional mitochondria are a center of ROS production and oxidative damage leading to cell death. Mitochondrial quality is maintained through several mechanisms like mitophagy and regulated fission and fusion. In adult cardiomyocytes, however, mitochondria embedded within the myofibrils rarely undergo fission and fusion4, suggesting that these cells are likely to be crucially dependent on other forms of mitochondrial quality control. We hypothesise that MDV trafficking is crucial to maintaining cardiomyocyte health.

Additionally, a previous study revealed that functional pyruvate dehydrogenase complex is present in the nucleus, and provides acetyl CoA for the acetylation of histones. We therefore hypothesised that a new mito-nuclear shuttle system operated by MDVs carrying key cargo to the nucleus. To enable an unbiased approach to understanding mito-nuclear transit, we have undertaken mito-targeting of the mutant biotin ligase, TurboID to different mitochondrial compartments (Image 1A) and detecting biotinylated proteins in the nucleus by nuclear lysate pulldowns. We have also detected two novel MDV cargo proteins that are also present in the nucleus (data not shown). We are presently trying to understand if MDVs are a trafficking route for direct mito-nuclear communication, a line of research funded by the SERB POWER grant. As an endosymbiont with 2 billion years of evolutionary history, it would be surprising if vesicles from mitochondria specifically target lysosomes and peroxisomes, and have no role in mito-nuclear communication. If this hypothesis is true, we will be the first group to demonstrate mito-nuclear vesicular trafficking.

From Left: Dr. Ananthalakshmy Sundararaman, Thejaswitha Rajeev

LABORATORY STRENGTH

Ph.D Students: 1 | JRF: 1 | Project Assistant: 1

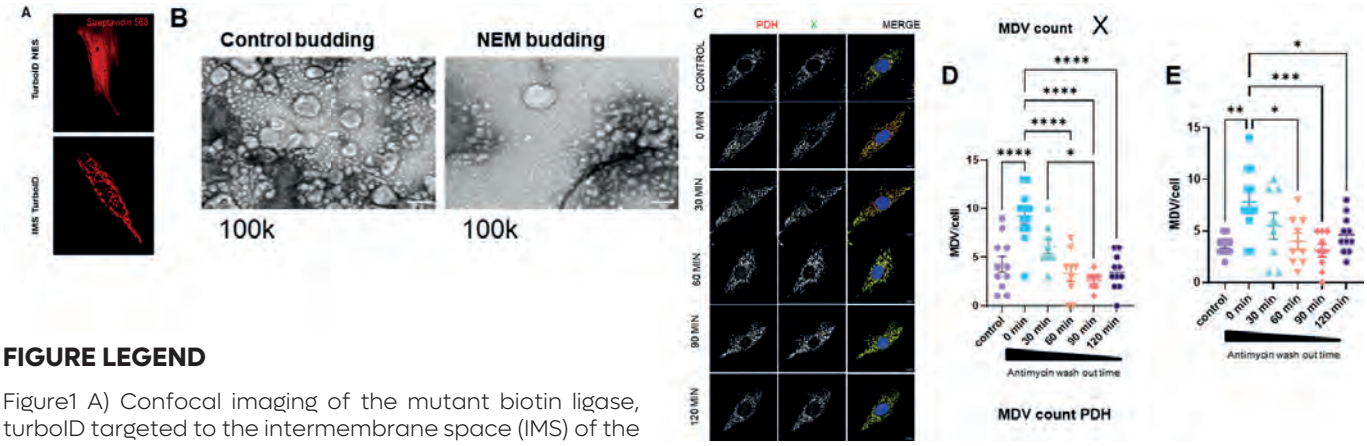
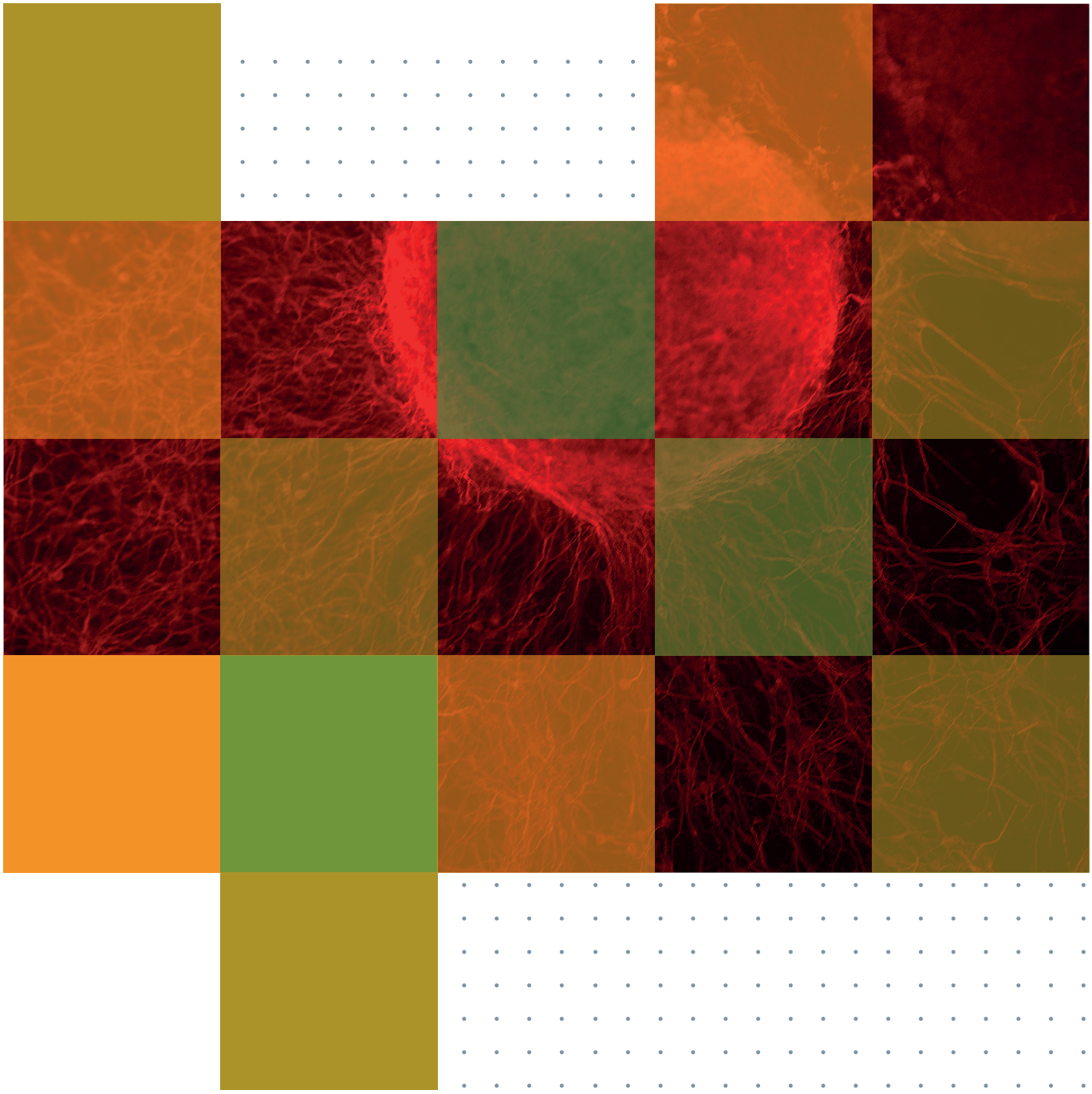


FIGURE LEGEND

Figure1 A) Confocal imaging of the mutant biotin ligase, turboID targeted to the intermembrane space (IMS) of the mitochondria in H9C2 cardiomyocytes. B) TEM imaging of isolated MDVs showing drastic reduction after N-ethyl maleimide treatment C) Antimycin washout assay of PDH (reported cargo) and a novel cargo (X) in H9C2 cells. D) Quantification of MDVs from confocal images show that (X) and PDH are incorporated into MDVs in an antimycin-sensitive manner.

PUBLICATIONS

- **Nidhi Nair and Ananthalakshmy Sundararaman;** In Vitro Reconstitution of Mitochondria-derived Vesicle Formation from Rat Hearts, STAR Protocols (In preparation)
- **Nidhi Nair, Lariza Ramesh, Areeba Marib and Ananthalakshmy Sundararaman,** Actin Cytoskeleton in Angiogenesis, Biology Open (In Press)



NEUROBIOLOGY & REGENERATIVE BIOLOGY

Dr. R.V.OMKUMAR
Scientist G, Neurobiology Program

BRIEF THEME OF LABORATORY

Calcium signaling in neurons underlie several brain functions. Impairment in these mechanisms contribute to the pathophysiology of several diseases. Hence, proteins such as the calcium conducting NMDA receptor (NMDAR), voltage gated calcium channel (VGCC) and the calcium activated enzyme, CaMKII, are pursued as drug targets for the management of such diseases. We study these proteins in vitro and in vivo under normal and diseased conditions towards developing therapeutic strategies by targeting these proteins.

NEURONAL CALCIUM SIGNALING IN HEALTH AND DISEASE

Several rodent models have been established for studying calcium signaling mechanisms and also to test the efficacy of neuroprotective drug candidates in vivo. When rats were administered a single dose of okadaic acid (OA) into the cortex by stereotactic injection, they developed hyperactivity and reduced anxiety like behaviour compared to normal animals as observed in open field test (OFT). However they did not show cognitive impairment in novel object recognition test (NORT). Acute treatment with OA may be causing alterations in the levels of neurotransmitters like dopamine, involved in locomotion or γ-aminobutyric acid (GABA), involved in the control of emotional responses. Sustained changes in the levels of proteins involved in cell survival and apoptosis such as tropomyosin receptor kinase B (TrkB), brain-derived neurotrophic factor (BDNF), protein kinase B (PKB/Akt), B-cell lymphoma 2 (Bcl-2), apoptosis-inducing factor (AIF) and caspase 9 were also observed. Further analysis of the neuronal connectivity in this model by immunohistochemical staining is being pursued towards understanding circuitries and mechanisms involved in emotional regulation.

From Left: Reena Sara Jacob, Devaraj TP, Veluthai G

LABORATORY STRENGTH

Ph.D Students: 2 | JRF: 2 | Technical Assistant: 1
Lab Assistant: 1

We also found that brief activation of VGCC in primary cortical neurons causes neuronal death, probably due to calcium overload. The calcium influx through VGCC induces phosphorylation of AMPA receptor, probably by activating CaMKII. Further analysis of the pathways involved in these phenomena are underway.

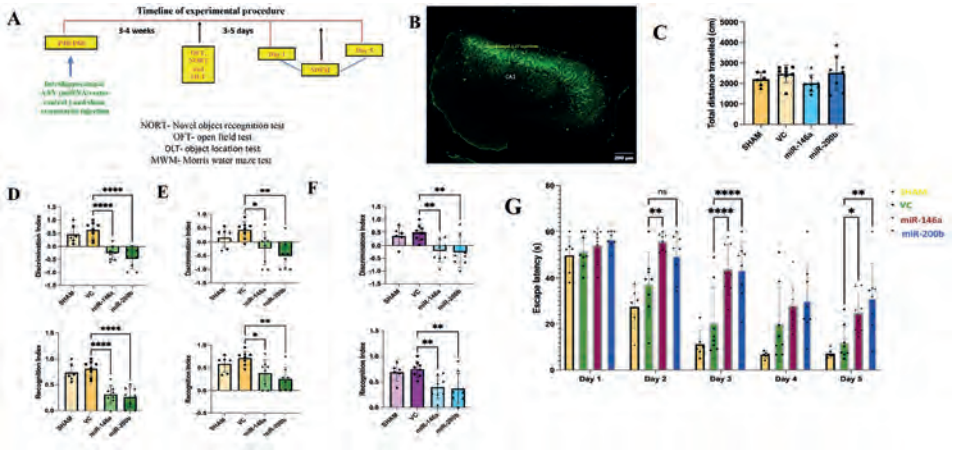


FIGURE LEGEND

Animals injected with miRNAs show impaired learning and memory A: Timeline of the experimental procedures. B: Fluorescence image of a coronal section of the brain of rat 4 weeks after injection of AAV-mir-200b. C-G: Behavioural analysis of animals injected with AAV-miR-146a or AAV-miR-200b or VC constructs. C: OFT. D and E: NORT conducted at 1 hr (D) and 24 hrs (E) after training. F: OLT. G: MWM test

PUBLICATIONS

- **Remya C, Dileep KV, Koti Reddy E, Mantosh K, Lakshmi K, Sarah Jacob R, Sajith AM, Jayadevi Variyar E, Anwar S, Zhang KYJ, Sadasivan C, Omkumar RV.** Neuroprotective derivatives of tacrine that target NMDA receptor and acetyl cholinesterase - Design, synthesis and biological evaluation. Comput Struct Biotechnol J. 2021;19:4517-4537.
- **Gunasekaran S, Jacob RS, Omkumar RV.** Differential expression of miR-148b, miR-129-2 and miR-296 in animal models of schizophrenia-Relevance to NMDA receptor hypofunction. Neuropharmacology. 2022;210:109024.

Dr. MOINAK BANERJEE
Scientist G, Neurobiology Program

BRIEF THEME OF LABORATORY

The laboratory studies the intricacies of neuropsychiatric, neurodevelopmental and neurological disorders including diagnosis & therapeutics of these diseases from genetic, pharmacogenetic, immunogenetic and epigenetic perspectives.

GENETICS AND EPIGENETICS OF COMPLEX DISEASE

Deep Learning model in Biology

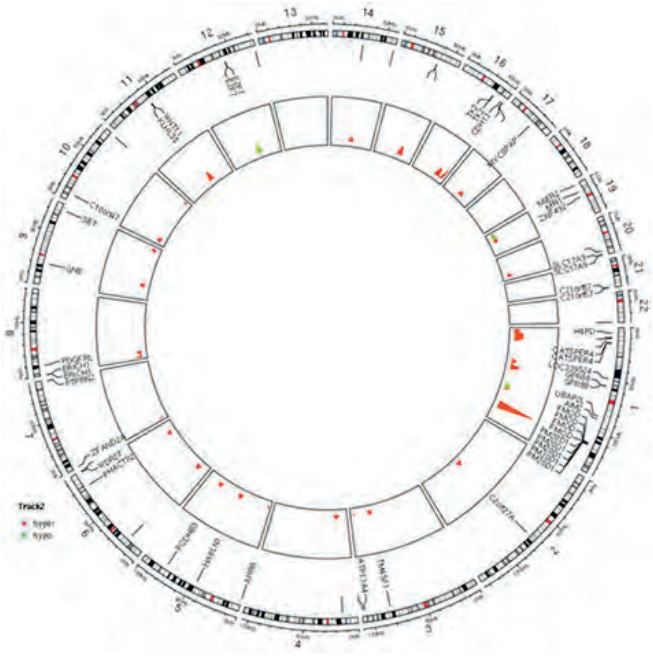
Artificial intelligence has resulted in advanced prediction of complex biological models. Deep learning, a type of AI, learns complex interactions by mimicking the learning process of the human brain. We developed a robust deep learning model for predicting regulatory feature interaction using block Self-attention and attention-attribution model

Pharmacoepigenetics of Antihypertensives

Antihypertensives can have adverse side effects. We assessed the epigenetic modification induced by Calcium channel blocker, Amlodipine, through global DNA methylation assay and gene expression of genes implicated in methylation maintenance in HepG2. We observe time and dose dependent gene expression with increased expression of DNMT1 and decreased expression of DNMT3B and TET2.

Pharmacoepigenetics of Antiepileptics

AEDs in pregnancy can induce major congenital malformations. We assessed the epigenetic modification



Front Row From Left: Dr. Krishna Priya EK, Binithamol K. Polakkattil, Ardra M
Back row From Left: Rashmi Sukumaran, Anil Prakash, Samyukta Bhass, Neethu Mohan, Alfiya F

LABORATORY STRENGTH

Post Doctoral fellows: 1 | Ph.D Students: 7

induced by AEDs in HEK293 and SH-SY5Y through global DNA methylation and expression of genes implicated in methylation maintenance. The carbamazepine and Phenytoin, show increased global DNA methylation changes which were further reflected with increase in expression of DNMTs and decrease in TETs expression.

Methylation signature of treatment response in schizophrenia

We performed 850K methylomic analysis in responder and non-responder schizophrenia patients. We observe that in responders, the methylomic variations were associated primarily with immune system whereas in nonresponders it impacted nervous system development, synaptic functions, cell adhesion, migration and cytoskeleton organization.

DeNovo mutations in Epileptic Encephalopathies (DEE)

DEE are rare neurodevelopmental disorders characterized by the co-occurrence of epilepsy, intellectual disability, autism spectrum disorder and developmental delay. We performed Whole Exome Sequencing of 42 trios consisting of well-defined or unclassified phenotypes of DEE. We identified 59.52% (25/42) de novo mutations including 7 novel variants in our cohort. Probands with known DEE phenotypes had de novo P/LP variants in genes of SCN1A,TSC2, KCNT1,IDH2 while in unclassified phenotypes, the P/LP de novo variants were in genes of CHRNA4,SLC2A1,MCTP2,DCX,TUBA3E,TUBB3,CHRNA2,CDKL5,SCN8A,GABRB2.

PUBLICATIONS

- **Banerjee M** Pharmacoepigenomics a key determinant in resolving epigenomic parameters in pathogenesis, and treatment response. Pharmacogenomics, 2022; 23 (2), 81-84.
- **Anil Prakash, Moinak Banerjee,** Genomic selection signatures in Autism identifies cognitive genomic tradeoff and its relevance in paradoxical phenotypes of Autism., Sci Rep 2021; 11, 10245.

Dr. JACKSON JAMES

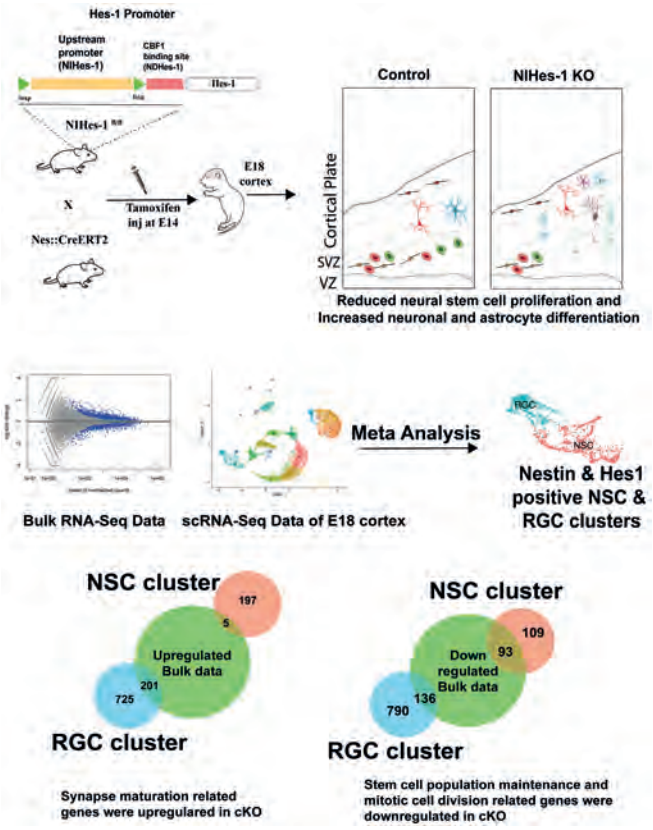
Scientist G, Regenerative Biology Program

BRIEF THEME OF LABORATORY

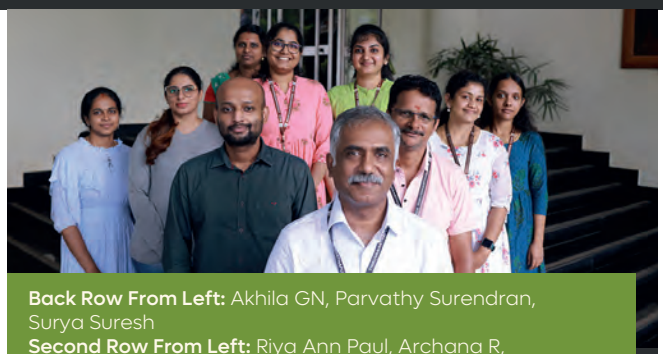
The main focus of our lab is to understand the early developmental cues that promote neural stem cell maintenance and fate specific differentiation which will shed light in developing possible therapeutic strategies against neurodegenerative diseases.

DIFFERENTIAL HES-1 PROMOTER ACTIVATION REGULATES STEMNESS DURING NEOCORTICAL DEVELOPMENT

We have previously demonstrated the existence of a new subclass of Notch Independent Hes-1(NIHes-1) expressing neural stem cells within the pool of Notch Dependent Hes-1 (NDHes-1) expressing neural progenitors/Radial Glial Cells (RGCs) in the developing neocortex. To understand the relevance of NIHes-1 expression in terms of neural stem cell maintenance during development we have generated a new conditional Knockout mouse i.e., Nestin CreERT2: NIHes-1fl/fl for knocking out NIHes-1 promoter region from Nestin positive neural stem cells.



From our immunohistochemical (IHC) and transcriptomic analysis it appears that knocking out Hes-1 from the NIHes-1 expressing cells did not alter the Hes-1 gene expression. Here, the canonical Notch target Hes5 was upregulated in the cKO neocortex which indicated a possible shift from non-canonical Notch activation to canonical Notch activation that was evident from the increased radial glial morphology. More specifically, we were interested in the fate of neural stem cells (NSCs) and radial glial cells (RGCs) upon knocking out the NIHes-1 promoter region. From meta-analysis of a published single cell RNA-Seq data, we found that there was a significant reduction of embryonic cortex neural stem cell population whereas radial glial markers and Cajal Retzius neuron were upregulated. IHC of control and cKO embryos showed a decrease in proliferating Ki67 positive cells in cKOs. We also observed a decrease in proliferating AUKB positive cells which was reported as the decision maker gene in choosing quiescence or proliferation. Moreover, our data showed a prominent decrease in GFAP positive glial cells than of mature neurons. Thus, we conclude that NIHes-1 promoter activation at the embryonic stages maintains the cycling neural stem cell population and in the absence of NIHes-1, early maturation of the primitive stem cell pool mostly towards an astrocyte or glial fate is taking place.



Back Row From Left: Akhila GN, Parvathy Surendran, Surya Suresh
Second Row From Left: Riya Ann Paul, Archana R, Budhaditya Basu, Binu S Nair, Sreedevi LR, Meera V

LABORATORY STRENGTH

Ph.D Students: 6 | Project Assistant: 1 | Technical Assistant: 1
Lab Assistant: 1

FIGURE LEGEND

Schematic representing the breeding strategy, transcriptomic and meta-analysis used in the study. Data revealed that the NIHes-1 promoter activation at the embryonic stages maintains the cycling neural stem cell population and in the absence of NIHes-1, early maturation of the primitive stem cell pool is taking place.

PUBLICATIONS

- **Wanjale MV, Sunil Jaikumar V, Sivakumar KC, Ann Paul R, James J, Kumar GSV.** Supramolecular hydrogel based post-surgical implant system for hydrophobic drug delivery against glioma recurrence. Int J Nanomedicine. 2022;17:2203-2224.

Dr. DEBASREE DUTTA
Scientist E- II, Regenerative Biology Program

BRIEF THEME OF LABORATORY

Development and disease biology.

PKC SIGNALING INHIBITION REPRESENT A NEW STATE OF PLURIPOTENCY-DEVELOPMENTAL CONTINUUM EXPLORED

Inhibition of Protein Kinase C siganling (PKCi) maintains pluripotency across different mammalian embryonic stem cell lines. However, the position of PKCi maintained ESCs in the pluripotency continuum is largely unknown. In that pursuit, after the maintenance of mouse ESCs for a significantly long time (75 days), the cells retained a naïve-like pluripotent state, closer to the ground state of pluripotency than that of conventional Serum+LIF (S/L) maintained naïve ESCs. At the molecular level, induction in phosphorylation of PKCζ isoform during ESC to Epiblast-Like Cell transition and in pre-implantation blastocyst to post-implantation embryo was observed. Our data suggest that PKCi-controlled DNMT3B expression is a major axis for this regulation. Interestingly, PKCi-mediated DNMT3B loss is a reversible phenomenon, indicating genomic integrity maintenance in PKCi ESC. Our proteomics and phospho-proteomics analysis further elucidated the mechanisms underlying the naïve state maintenance in PKCi ESCs, which is very different from LIF maintained naïve state of pluripotency. The proteomics analysis shaded light on pathways enriched in PKCi ESCs like pathways related to RNA metabolism, glutathione metabolic process, cell-cell adhesion. Phospho-proteomic analysis revealed a unique phospho-peptide profile in PKCi ESCs compared to LIF ESCs. Epigenetic factors like DNMT3B, KDM4C, CHD4, MeCP2, SNW1, and other genomic factors like YAP, RAF1, cMYC, have a differential enrichment for phospho-peptides in both the ESCs, which might be responsible for the maintenance of a state of pluripotency intermediate to ground and naive states of pluripotency. As ground state represent the totipotent to 2-cell state whereas the naive one represent the morula to blastocyst stage of development, we predict that ESCs mainatined in PKCi might represent a state in between 2-cell to morula stages of embryonic development.

Front row from left: Bindu MS, Sruthy MR, Ishita Baral Debparna Nandy
Back row from left: Pallavi Chinnu Varghese Mayur Balkrishna Shirude

LABORATORY STRENGTH

Ph.D Students: 5 | JRF: 1 | Lab Assistant: 1

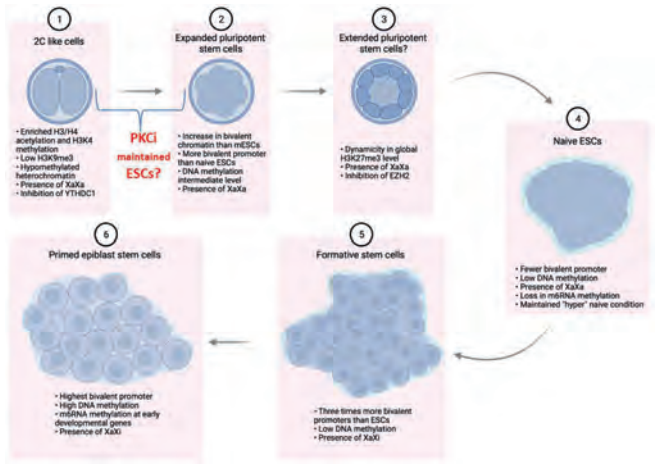


FIGURE LEGEND

Developmental continuum and different states of plruipotency of embryonic stem cells

PUBLICATIONS

- **Rajam SM, Varghese PC, Dutta D.** Histone Chaperones as Cardinal Players in Development. Front Cell Dev Biol. 2022 ;10:767773.
- **Varghese PC, Rajam SM, Nandy D, Jory A, Mukherjee A, Dutta D.** Histone chaperone APLF level dictates the implantation of mouse embryos. J Cell Sci. 2021; 134(1):jcs246900.

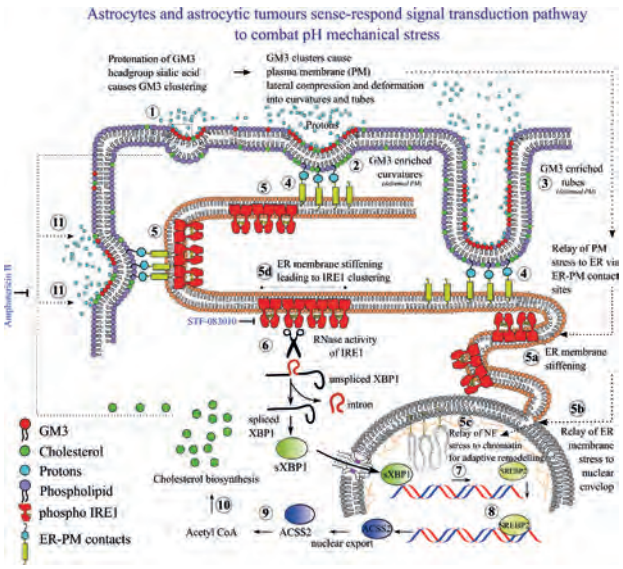
Dr. RASHMI MISHRA
Scientist E-II, Neurobiology Program

BRIEF THEME OF LABORATORY

The major goal of the lab is to understand 'how cells sense and respond to mechanical microenvironment' with a therapeutic implications to cancers, neuro and cardio degenerative diseases as well as aging. The research involves examining the mechanical stressors at a cellular level by engaging physico-chemical assays and multi-omics analysis. The results obtained are escalated to the relevant animal models for validation and to the patients' samples for the examination of clinical relevance.

DISCOVERY OF THE SENSE AND RESPOND STRATEGIES GENERATED BY ASTROCYTES AND ASTROCYTIC TUMOURS TO COMBAT PH MECHANICAL STRESS: THERAPEUTIC IMPLICATIONS ON BRAIN'S PATHOPHYSIOLOGICAL MANAGEMENT

Brain pH crucially impacts its functions. We unveiled the molecular steps by which the astrocytes sense and respond to the extracellular pH stress. As shown in the figure, in both brain astrocytes and astrocytic tumour cells, 1) high microenvironmental proton concentrations induces protonation of sialic acid headgroup of GM3 glycosphingolipid leading to ligation with neighboring GM3 molecules. 2) GM3 homo-ligations leads to extensive GM3 clustering on the plasma membrane, inducing lateral membrane compression and mechanical imbalances, thereby deforming the membrane into curvatures. 3) Membrane curvatures transforms into tubes in intense GM3 clustered areas. 4) GM3 enriched curvatures and tubes interacts with the peripheral ER via ER-PM membrane contact sites, through which the mechanical stress in GM3 force foci is relayed to the ER network. 5a-b) Stiffened ER then relays membrane mechanical stress to the nuclear envelope (NE), which is continuous with the ER, and 5c) resultant nuclear stiffening allows appropriate chromatin-remodelling, as chromatin is in direct contact with NE, to permit transcription of anti-pH stress adaptation machinery. 5d) On the parallel platform, ER lipid bilayer stress causes IRE1 transmembrane protein oligomerization and activation of RNAase activity 6) which triggered splicing of the intron in XBP1 mRNA, generating sXBP1 mature RNA, which is translated and translocated to the nucleus. 7-11) In the nucleus, sXBP1 promotes the synthesis of SREBP2, which in turn synthesizes ACSS2. ACSS2 enables cholesterol synthesis in the cytoplasm, which is trafficked to the surface to provide mechanical tenacity.



From Left: Puja Shinde, Gayathri KG

LABORATORY STRENGTH

Ph.D Students: 3 | JRF: 1 | SRF: 1

GM3-IRE1-sXBP1-ACSS2-cholesterol axis is deduced as a unique anti-acid stress survival mechano-machinery in astrocytes which can be clinically translated by potentiating IRE1 activation, through known small molecules, in brain injuries and neurodegeneration involving acidosis. Conversely, suppressing IRE1 and depletion of surface cholesterol via STF-083010+Amphotericin B drug combination will be helpful in anti-astrocytoma therapeutics.

FIGURE LEGEND

A working model of the sense and respond strategies generated by astrocytes and astrocytic tumours to combat extracellular pH (pHe) mechanical stress.

PUBLICATIONS

- **John S, Gayathri KG, Krishna AP, Mishra R.** Neurotherapeutic implications of sense and respond strategies generated by astrocytes and astrocytic tumours to combat pH mechanical stress. Neuropathol Appl Neurobiol. 2022;48(2):e12774.
- **Krishna AP, John S, Shinde PL, Mishra R.** Proteo-transcriptomics meta-analysis identifies SUMO2 as a promising target in glioblastoma multiforme therapeutics. Cancer Cell Int. 2021;21(1):575.

Dr. RAJEEVE SIVADASAN
DBT-Ramalingaswami Fellow, Neurobiology Program

BRIEF THEME OF LABORATORY

Neurodegenerative Diseases lab

ELUCIDATE THE ROLE OF RNA BINDING PROTEINS AND RNA IN NEURODEGENERATIVE DISEASES

The nervous system is a highly evolved and sophisticated biological system. The backbone of the neuronal system comprises of an enormous array of neuronal and glial cell subtypes. ALS (Amyotrophic Lateral Sclerosis) and FTLD (frontotemporal lobar degeneration) are linked by several lines of evidence with respect to clinical and pathological characteristics. Interestingly, some of the proteins, such as TDP-43 and FUS/TLS, have common relations with ALS-FTLD and SMA (Spinal muscular atrophy). Research advances in neurodegenerative diseases have pointed to novel mechanisms to protein aggregation that revolve around the unique biology of RNA binding proteins. RNA binding proteins are predominantly present in the nucleus. Cellular stress induced due to neurodegeneration shows these RNA binding proteins translocate to the cytoplasm. Resent studies have shown that pathological aggregates occurring in ALS, Alzheimer's disease, and other dementias co-localize with stress granules. TDP-43 is a significant component of tau-negative and ubiquitin-positive inclusions. TDP-43 is predominantly nuclear in normal tissues, in disease, TDP-43 is mislocalized to the cytoplasm, ubiquitinylated, and hyperphosphorylated. Other RNA binding proteins are like (FUS/TLS) and other heterogeneous nuclear ribonucleoproteins (hnRNPs) that are also mutated/or aggregated in diseased brains. Similar findings for FUS/TLS and C9ORF72 (chromosome 9 open reading frame 72) (Sivadasan et al 2016) has opened up the entire field of RNA binding proteins (RBPs) and RNA metabolism, a new and promising area of research in neuroscience. My lab would investigate in understanding the function of the RNA binding protein-like TDP-43, Fus/TLS in their role in axonal RNA control, by purifying axonal RNA and proteins from primary neurons with the help of compartmental cultures. This will help us understand the role of RNA and RNA binding proteins (RBP) in different disease conditions and better understand the modulator of the disease phenotype.

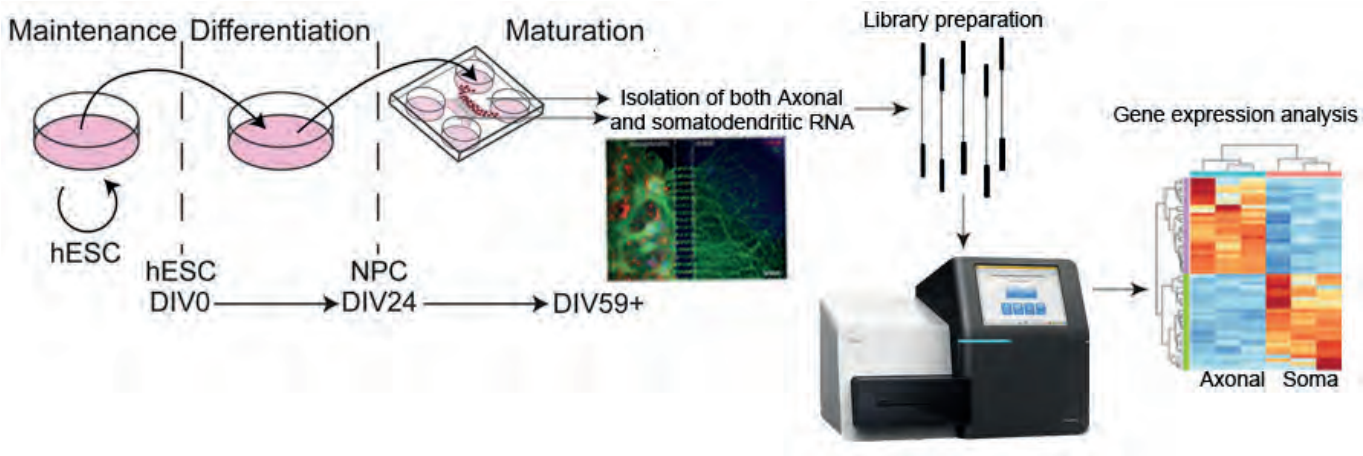
From Left: Dr. Rajeeve Sivadasan, Udhaya Bharathy S

LABORATORY STRENGTH

Ph.D Students: 1 | Project Assistant: 1

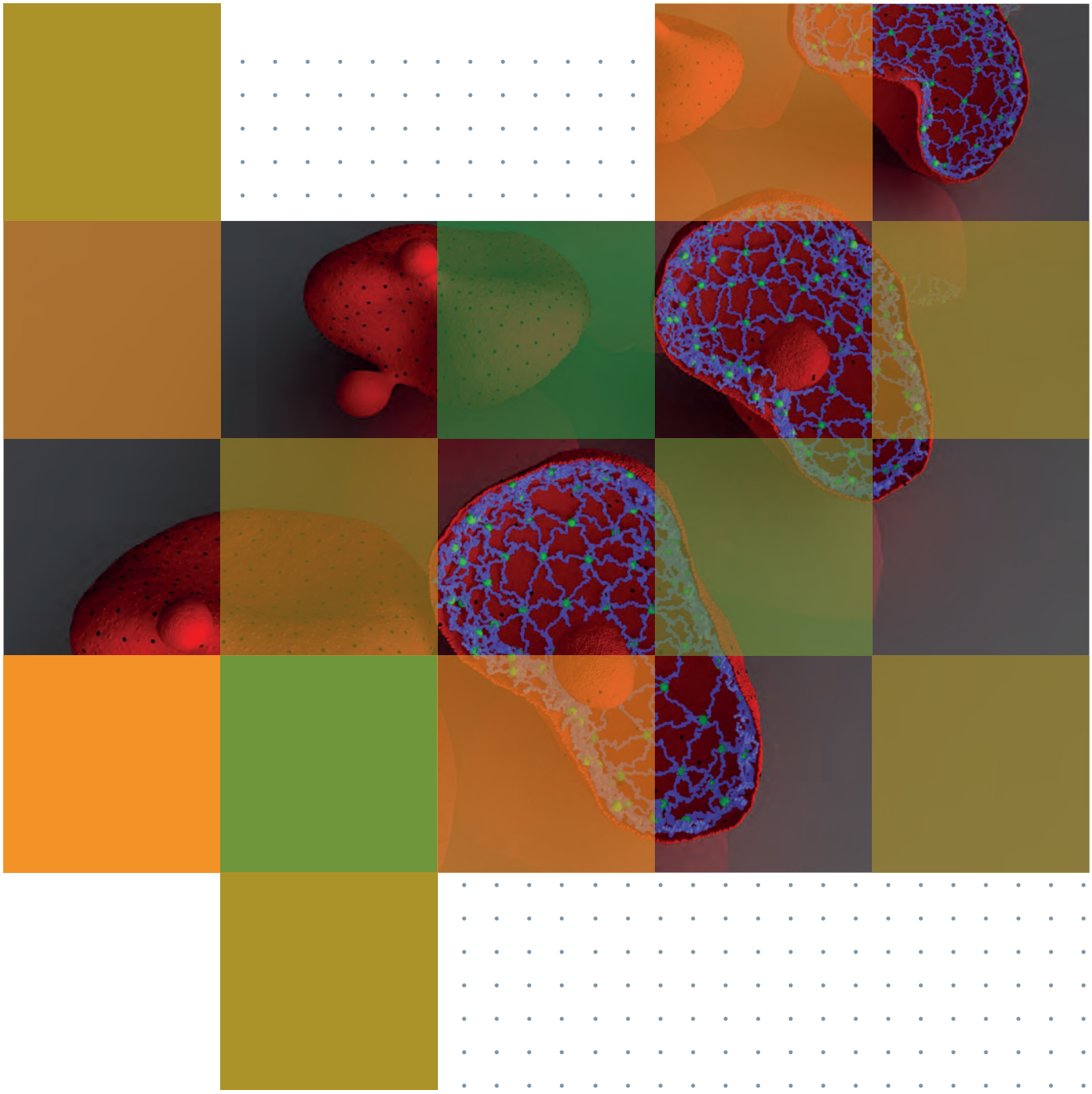
FIGURE LEGEND

Overview of the experimental setup to understand the role of RNA and RNA binding proteins (RBP) in patient-derived neuronal cells.



PUBLICATIONS

- **Ghanawi H, Hennlein L, Zare A, Bader J, Salehi S, Hornburg D, Ji C, Sivadasan R, Drepper C, Meissner F, Mann M, Jablonka S, Briese M, Sendtner M.** Loss of full-length hnRNP R isoform impairs DNA damage response in motoneurons by inhibiting Yb1 recruitment to chromatin. Nucleic Acids Res. 2021;49(21):12284-12305.
- **Hansen JP, Ali WM, Sivadasan R, Rajeeve K.** Bacteria-cancer interface: awaiting the perfect storm. Pathogens. 2021;10(10):1321.



PATHOGEN BIOLOGY

Dr. R.AJAY KUMAR

Scientist G, Pathogen Biology Program

BRIEF THEME OF LABORATORY

Gene regulation in Mycobacterium tuberculosis.

MYCOBACTERIUM TUBERCULOSIS TRANSCRIPTIONAL REGULATOR RV1019 IS UPREGULATED IN HYPOXIA AND NEGATIVELY REGULATES RV3230C-RV3229C OPERON ENCODING ENZYMES IN THE OLEIC ACID BIOSYNTHETIC PATHWAY.

The main obstacle in eradicating tuberculosis is the ability of Mycobacterium tuberculosis to remain dormant in the host, and then to get reactivated even years later under immuno-compromised conditions. Transcriptional regulation in intracellular pathogens plays an important role in their adapting to the challenging environment inside the host cells. Previously, we demonstrated that Rv1019, a putative transcriptional regulator of M. tuberculosis H37Rv, is an autorepressor. We now show that Rv1019 is cotranscribed with Rv1020 (mfd) and Rv1021 (mazG) which encode DNA repair proteins, and negatively regulates the expression of these genes. Further, Rv1019 also regulates the expression of Rv3230c and Rv3229c (desA3) which form a two-gene operon in M. tuberculosis. Overexpression of Rv1019 in M. tuberculosis significantly downregulates the expression of these genes. Employing Wayne's hypoxia-induced dormancy model of M. tuberculosis, we show that Rv1019 is upregulated 3-fold under hypoxia. During hypoxia Rv1019 is recruited to the promoter of Rv3230c-Rv3229c and negatively regulates this operon which is involved in the biosynthesis of oleic acid. Thus, we show that Rv1019 is a key regulator molecule in M. tuberculosis and is an ideal candidate for therapeutic intervention to treat tuberculosis.

From Left: Jijimole GR

LABORATORY STRENGTH

Ph.D students: 1

PUBLICATIONS

- **Muralikrishnan B, Edison LK, Dusthackeer A, Jijimole GR, Ramachandran R, Madhavan A, Kumar RA.** Chrysomycin A inhibits the topoisomerase I of Mycobacterium tuberculosis. J Antibiot (Tokyo). 2022;75(4):226-235.
- **Akhil Raj P, Lakshmi K Edison, Ramakrishnan Ajay Kumar.** Mycobacterium tuberculosis transcriptional regulator Rv1019 is upregulated in hypoxia and negatively regulates Rv3230c-Rv3229c operon encoding enzymes in the oleic acid biosynthetic pathway. 2022. FEBS J. (accepted).

Dr. SABU THOMAS

Scientist F, Pathogen Biology Program

BRIEF THEME OF LABORATORY

The laboratory focuses on molecular mechanisms involved in pathogenicity and multidrug resistance of top priority bacterial pathogens. Studies involve the alternative strategies such as biofilm inhibition, phytochemical-antibiotic combinations and probiotics of human origin to control bacterial infections and emerging antimicrobial resistance. Another major focus is on exploring the human microbiome for beneficial health impacts and to study the effect of therapeutic interventions on the gut microflora.

LEVERAGING GUT MICROBIOME TO TACKLE MULTIDRUG RESISTANT BACTERIAL PATHOGENS

Bacterial infections and the emerging antimicrobial resistance is a global threat and its devastating effect on commensal gut microbiota is a major concern. The rampant use of prophylactic antibiotics in the postpartum period leads to intestinal dysbiosis in infants and exacerbates the threat of antimicrobial resistance. The team has analysed the impact by conducting an observational cross-sectional pilot study by performing shot gun metagenomics on infant gut microbiomes and resistomes wherein mother-infant dyads were grouped as: antibiotic group comprising mothers who had administered prophylactic antibiotics after delivery and non-antibiotic group comprising mothers not resorted to antibiotics. Variations in bacterial diversity were observed between the groups in lower taxonomic levels. Total abundance of genes encoding resistance to aminoglycoside, fluoroquinolone, cephalosporin, and peptide antibiotics were higher in antibiotic group. The LEfSe analysis indicated the characteristic presence of Citrobacter werkmanii, an emerging MDR uropathogen in the antibiotic treated cohort, and beneficial genera Bifidobacterium in non-antibiotic group (Fig 1). Furthermore, the study highlights considerable adverse effects of an overlooked time-point in peripartum antibiotic administration and emphasises the need to strengthen policies regarding antibiotic prescription across the health sectors.

Gut microbes are a potential source of bioactive metabolites including antimicrobial molecules. The team has isolated and characterized a probiotic strain of infant gut origin against drug resistant strains of Staphylococcus aureus, Vibrio cholerae and Klebsiella pneumoniae. The nature of antimicrobial substances produced was determined by pH neutralization, heat inactivation and trypsinisation of supernatant and identified to produce a bacteriocin like compound. Cell adhesion and co-culture experiments in CaCo-2 cells with K.pneumoniae showed its competitive exclusion property and its efficacy is well proved in BALB/c mice model. The selected isolate of infant gut origin can be taken forward as a promising probiotic candidate for prophylactic applications against infectious pathogens.

From Left: Geetha SL, Devika Das J, Karthika S, Merin Paul, Divya R, Deepa Mathew P

LABORATORY STRENGTH

Postdoctoral Fellows: 2 | Ph.D Students: 2
Project Assistant: 2 | Technical Assistant: 1 | Lab Assistant: 1

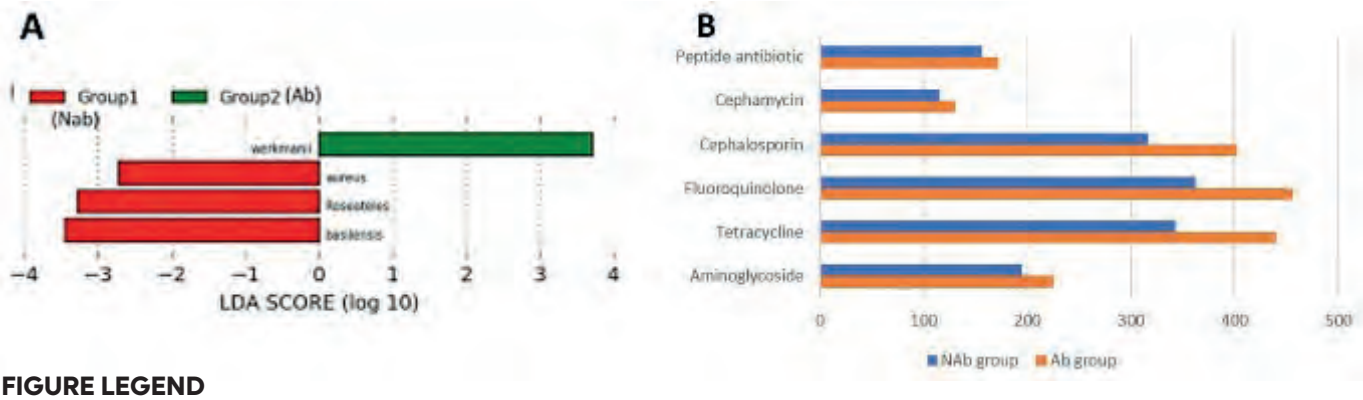


FIGURE LEGEND

Fig. 1. A) LefSe plot representing beta diversity between Non-Antibiotic and Antibiotic groups. B) Relative abundance of genes encoding resistance to a major class of antibiotics in Antibiotic and Non-Antibiotic groups

PUBLICATIONS

- **Divya MP, Hardip RP, Sivakumar KC, Sabu Thomas.** 2021. Genomic attributes differ between Vibrio parahaemolyticus environmental and clinical isolates including pathotypes. Environ Microbiol Rep. 14(3):365-375.
- **Lekshmi N, Gopinathan A, Sreekrishnan TP, Asokan A, Kumar A, Kumar G, & Sabu Thomas.** 2021. The bane of coastal marine environment: A fatal case of Vibrio vulnificus associated cellulitis and septicaemia. Indian J Med Microbiol. 39(2021):386-388.

Dr. E.SREEKUMAR

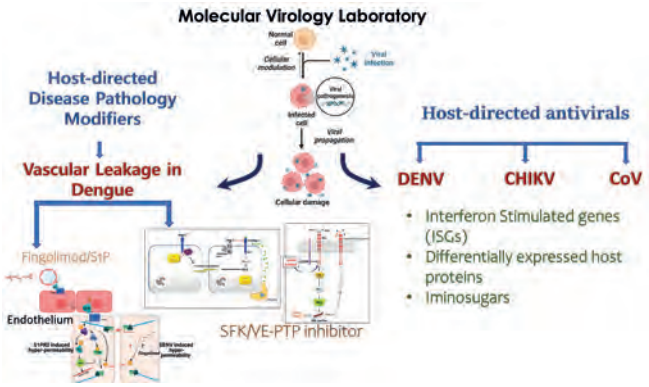
Scientist F, Pathogen Biology Program

BRIEF THEME OF LABORATORY

The research theme of Molecular virology laboratory is on understanding host-pathogen interactions with respect to emerging viral infections, focusing particularly on Dengue, Chikungunya and SARS CoV-2. We attempt to identify and develop host-targeted antivirals and disease modifiers. Specific aim is to understand the host-proteins involved in restricting virus infections including Interferon-stimulated genes, and also signaling pathways that play key role in disease manifestation such as vascular leakage.

MOLECULAR STUDIES ON EMERGING POSITIVE-STRANDED RNA VIRUS INFECTIONS TO UNDERSTAND HOST-PATHOGEN INTERACTIONS TO DEVELOP NOVEL ANTIVIRALS AND DISEASE MODIFIERS

In our pursuit to identify host-directed antivirals and disease-modifiers, we found that Nucleophosmin I is a host-protein that plays significant role in restricting Chikungunya virus infection. We also found that it interacts with CHIKV non-structural proteins to effect its antiviral action. Further we identified a number of interferon-stimulated genes that are modulated in response to CHIKV infection, which are being further characterized for their antiviral action. Since ISGs are key players in host-antiviral response, we hypothesised that ISG modulators can have potential as antiviral agents and to identify such modulators, we have developed cell-based assays for screening. We have successfully developed screening assays of eight ISGs that are key players in antiviral response to a number of emerging viruses. Screening a library of natural products we have identified five molecules that can modulate the ISG response. Studies on their antiviral activity is being pursued. Recently, a family of antiviral cellular proteins named the Surface-Hinged, Rigidly-Extended Killer (SHREK) was identified. These proteins are also reported to demonstrate broad-spectrum host antivirals by blocking the infection of a diverse family of viruses. The mechanism underlying the action of the SHREK family of proteins is being explored. Further, we will explore the regulatory pathways and molecules involved in the antiviral mechanism of these proteins during infection.



From Left: Ayan Modak, Srishti Rajkumar Mishra, Parvanendhu Pradeep, Seethalakshmi S, Mansi Awasthi, Ariya Ajay, Guhan KS

LABORATORY STRENGTH

Postdoctoral trainees: 1 | Ph.D students: 6

Dengue is a major problem in the tropics. We carried out identification of direct acting antivirals against dengue as well search for disease modifiers that can specifically focus on alleviating the vascular leakage, the major complication in severe dengue. Screening of synthetic derivatives of iminosugars for their direct-anti-Dengue viral activity has given promising leads. Further assays are being planned to elaborate the antiviral function of these compounds. We developed in vitro assays for elucidating the endothelial cell permeability upon dengue infection using Trans-endothelial electrical resistance measurement and FITC-dextran leakage assays. Using these assays we identified that several kinase inhibitors and Sphingosine-receptor modulators are promising as agents to prevent permeability changes in DENV-infected endothelial cell-monolayers. We have successfully developed an animal model for Dengue virus serotype 2 using a non-mouse adapted virus to test these compounds. The experiments are progressing.

PUBLICATIONS

- **Mudaliar P, Pradeep P, Abraham R, Sreekumar E.** Targeting cap-dependent translation to inhibit Chikungunya virus replication: selectivity of p38 MAPK inhibitors to virus-infected cells due to autophagy-mediated down regulation of phospho-ERK. J. Gen Vir. 2021; 30;102(7):001629.
- **Arun Sankaradoss*, Suraj Jagtap, Junaid Nazir, Shefta E. Moula, Ayan Modak, Joshuah Fialho, Meenakshi Iyer, Jayanthi S. Shastri, Mary Dias, Ravisekhar Gadepalli, Alisha Aggarwal, Manoj Vedpathak, Sachee Agrawal, Awadhesh Pandit, Amul Nisheetha, Anuj Kumar, Mahasweta Bordoloi, Mohamed Shafi, Bhagyashree Shelar, Swathi S. Balachandra, Tina Damodar, Moses Muia Masika, Patrick Mwaura, Omu Anzala, Kar Muthumani, Ramanathan Sowdhamini, Guruprasad R. Medigeshi, Rahul Roy, Chitra Pattabiraman, Sudhir Krishna, Easwaran Sreekumar.** Immune profile and responses of a novel dengue DNA vaccine encoding an EDIII-NS1 consensus design based on Indo-African sequences. Mol Ther. 2022; 30 (5): 2058-2077.

Dr. R.RADHAKRISHNAN

Scientist F, Laboratory Medicine & Molecular Diagnostics

BRIEF THEME OF LABORATORY

Laboratory Medicine and Molecular Diagnostics is the public service arm of RGCB upholding the social commitment of an Institute. Molecular Diagnostics of infectious and non-infectious diseases performed in the division along with next generation sequencing support has helped the clinician as well the Dept of Health, Govt of India for planning their treatment strategies as well as having an upper hand in controlling epidemics.

TRANSLATIONAL RESEARCH OUTCOMES

My laboratory at RGCB in addition to the normal duties in enhancing the public outreach program of RGCB through advanced molecular diagnostics, is also engaged in translational research. Absorbing confidence from the previous translational research activities like snake venom detection LFA and dengue multiplex analysis, in which technology transfer was completed, newer frontiers in viral/bacterial diagnostic testing is initiated at LMMD. LMMD has partnered with Microbio® of Australia and has co-developed a melt curve-based detection system to differentiate between actively replicating and nonreplicating COVID-19 virus. This helps the clinician to differentiate between disease transmitters and non-transmitters. The test can be completed under one hour post isolation of the RNA. The developed platform is currently commercialized in Australia and has obtained clearance from CDSCO to be deployed in India as well.

Sepsis usually proves fatal in very young and very old who are affected. This primarily is attributed to the delay in accurate diagnosis which usually takes days. LMMD along with Microbio® has developed and validated a PCR-based multiplexing kit which can identify the organism causing sepsis under one hour post DNA isolation. The test covers 39 of the most known microorganisms which is inclusive of bacteria and fungi. The test kit is in the final stages of regulatory approval in India.

LABORATORY STRENGTH

Postdoctoral Fellows: 1 | Project Assistant: 2
Technical Assistant: 5 | Lab Assistant: 3 | Project Associate: 3

Gut microbiome plays an important role in the disease progression of colon cancer, it is also widely believed that the gut microbiome plays an important role in colon cancer incidence. Additionally, the gut microbiome also has farfetched effects in the general wellbeing of a person. With additional resources such as next generation sequencer and downstream computational analysis pipeline existing in LMMD, the Department has initiated gut microbiome analysis with identification and metabolomic reporting of the organisms. The work is being utilized extensively by the Regional Cancer Centre. Other major hospitals are also utilizing this NGS-based testing which is done at a fraction of the cost of private service providers.

Left ventricular failure is a major cause of sudden death which usually goes undiagnosed. LMMD has partnered with SCTIMST and is in the final stages of completing a detection of NTProBNP (left ventricular failure marker) as an early detection system for impending heart failure. This test is performed at the patient's bedside using only a drop of blood. The detection system is ready and only a strip reader development is pending which is in the final stage. This project is supported by ICMR.

PUBLICATIONS

- **Srinivas L, Gracious N, Nair RR.** Pharmacogenetics based dose prediction model for initial tacrolimus dosing in renal transplant recipients. Front Pharmacol. 2021;12:726784.
- **Seetha D, Pillai HR, Nori SRC, Kalpathodi SG, Thulasi VP, Nair RR.** Molecular-genetic characterization of human parvovirus B19 prevalent in Kerala State, India. Virol J. 2021;18(1):96.

Dr. K.HARI KRISHNAN

Scientist E-II, Pathogen Biology Program

BRIEF THEME OF LABORATORY

Primary focus of the laboratory is metagenomics, specifically characterizing a novel L-Asparaginase from the soil metagenomic library, having potential in leukemia therapy. Studies also look at characterizing novel antifungal molecules from metagenomic libraries generated from various soil environments and identification of the gut microbiome in Kerala populations.

PROTEOME ANALYSIS OF PHOSPHATE SOLUBILISING PANTOEA SP., ISOLATED FROM EICHHORNIA RHIZOSPHERE

Bioavailability of essential nutrient such as phosphorus is a limiting factor on primary production. Salinity of soil is a prominent abiotic stress for crops and has detrimental effect on productivity. Apart from affecting the soil quality in general, it incurs salinity induced phosphorous deficiency to crops. Microbial interactions at the root rhizosphere help in solubilization of this major nutrient and facilitate its uptake and serve as an alternative mechanism of stress tolerance by plants. Saline tolerant root microbes that survive under osmotic and ionic stress can be a promising biological agent for improved agricultural production. Aquatic weeds like Eichhornia sp. are well documented for their stress tolerance towards various parameters. The biomolecules from their root microbial community may have higher stress tolerance, plant growth promoting potential. A comprehensive understanding of proteome of these microbes will help to develop them as potential plant growth promoting bacteria and hence the study focuses on elucidating the mechanism of salt tolerance of Pantoea sp., a phosphate solubilising bacteria isolated from root rhizosphere of Eichhornia sp. through a quantitative proteomic approach.

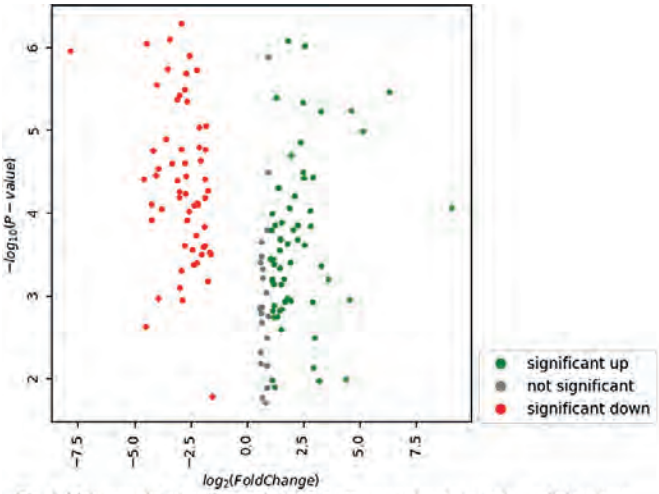


Fig. 1 Volcano plot showing variations in expressed protein under salinity stress

From Left: Athira SS, Geetha SL, Priya P

LABORATORY STRENGTH

Post doctoral fellow: 1 | Laboratory assistant: 2

Pantoea sp. showing comparatively higher phosphate solubilization Index (2.5 + 0.02 under 1M NaCl) was cultured under saline stress. The total protein from the cell pellets were extracted quantified and subjected to proteome analysis by LC-MS/MS and performed bioinformatics analysis. The protein profile revealed variations in expressed bacterial protein due to saline stress (Fig. 1). The proteins identified are primarily involved in amino acid and organic acid metabolism, carbohydrate metabolism, energy metabolism, antioxidant activities, peptidoglycan synthesis and stress adaptive mechanisms. Amino acid-dependent stress response systems are a major response of bacterial cells under stress and glutamine amidotransferase, a glutamine synthesizing protein was upregulated under osmotic stress. Survival mechanisms such as protein RecA, LexA repressor and iron-sulfur cluster synthesis were also found to be upregulated under saline stress, showing the improved salt stress defence mechanism.

FIGURE LEGEND

Fig 1. Volcano plot of differentially expressed protein in Pantoea sp., (p = < 0.05)

PUBLICATIONS

- **Priya P, Aneesh B and Harikrishnan K.** Genomics as a potential tool to unravel the rhizosphere microbiome interactions on plant health. J Microbiol Methods. 2021; 185: 106215.

Dr. RAJESH CHANDRAMOHANDAS

Scientist E-II, Pathogen Biology Program

BRIEF THEME OF LABORATORY

Our lab studies host-pathogen interactions in microbial infectious diseases to understand molecular mechanisms underpinning host invasion, manipulation and cytolysis towards therapeutic development.

LABORATORY OF RED CELL DISEASES

Plasmodia are host-specific at the organism and cellular levels, although emerging trends of zoonoses indicate progressive changes in such preferences. While P. falciparum (Pf) is able to infect all stages of RBCs (but with a preference to young blood cells), it's benign counterparts, P. vivax (Pv) and P. ovale display a predilection for young reticulocytes. Our laboratory is interested in identifying molecular determinants of host tropism and explore their viability as drug or vaccine targets.

Another facet of our research explores how chemically induced phenotypes can be utilized as indicators of the cellular pathways perturbed by the molecule of interest. P. falciparum and T. gondii, two well studied parasites, offer a good choice to undertake such phenotypic screens, since complementary experimental tools and reagents are available to dissect cellular phenotypes in these organisms. For instance, phenotypic features associated with impaired growth kinetics (i.e., fast vs delayed killing), host cytolysis (the end point of an intracellular replicative cycle), and host invasion (first step to establish a new infectious cycle), are well characterized in both parasites by us and others, and their therapeutic potential has been validated.

From Left: Aravind, Christeen Davis, Akhila TP

LABORATORY STRENGTH

Ph.D Students: 2 | JRF: 1 | Project Assistant: 1

Our laboratory studies these processes using a combination of small molecule screening, activity-based protein profiling and quantitative mass spectrometry to unravel novel small molecule inhibitors acting via hitherto un-explored mechanisms and their cellular targets for translational interventions against protozoan parasites and pathogenic viruses.

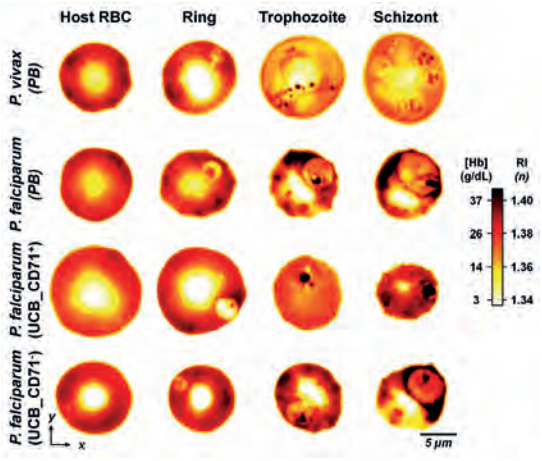


FIGURE LEGEND

Figure 1. Plasmodia employs different host manipulation mechanisms, as captured by Optical Tomography technique which measures 3 Dimensional Refractive Infdex (3D-RI) Distribution across the cell. The image illustrates infection of Plasmodium falciparum and Plasmodium vivax into mature and immature human red blood cells (Ong et al, Spectrochimica Acta A, in Press)

PUBLICATIONS

- **Reghunandanan K and Chandramohanadas R.** Chemically induced phenotypes during the blood stage development of Plasmodium falciparum as indicators of the drug mode of action. Front Drug Discov. 2022; 2:920850.
- **Jessica J.Y. Ong, Jeonghun Oh, Xiang Yong Ang, Renugah Naidu, Trang T.T. Chu, Jae Hyoung Im, Umar Manzoor, Tuyet Kha Nguyen, Seok-Won Na, Eun-Taek Han, Christeen Davis, Won Sun Park, Wanjoo Chun, Hojong Jun, Se Jin Lee, Sunghun Na, Jerry K. Y. Chan, Yong-Keun Park, Bruce Russell, Jin-Hee Han and Rajesh Chandramohanadas.** Optical Diffraction Tomography and Image Reconstruction to measure host cell alterations caused by divergent Plasmodium species. Spectrochim Acta A Mol Biomol Spectrosc, (in Press)

Dr. JOHN BERNET JOHNSON

Scientist E- I, Pathogen Biology Program

BRIEF THEME OF LABORATORY

RNA viruses constitute a large group of viruses of both human and veterinary significance. Using Rhabdoviruses (vesicular stomatitis, Chandipura and rabies viruses) and Alphaviruses (chikungunya virus) as model pathogens we focus on unraveling the complex interplay between the host and the pathogen with a special emphasis on the potent host innate immune barrier the complement system. Our goal is also to tap the potential of these viruses to develop novel oncolytic and vaccine vectors.

TAMING WILD TYPE RNA VIRUSES TO TAP THEIR ONCOLYTIC POTENTIAL.

Cancer is well recognized as a grave health crisis with the estimated number of cases standing at 19.3 million in 2020 as per WHO with the numbers projected to be around 28.9 million by 2040. Revolutionary approaches over the decades have impacted the way cancer is looked at and treated improving prognosis in many types of cancer. However cancer treatment is challenging and therefore novel approaches are required to circumvent cancer. An emerging area gaining prominence in the West is the strategy to employ viruses with cell killing property (cytopathic) to target cancer, which is very much underrepresented in our country. We have embarked on unravelling the oncolytic potential of Chandipura virus (CHPV), a cytopathic virus which is mostly endemic to India.

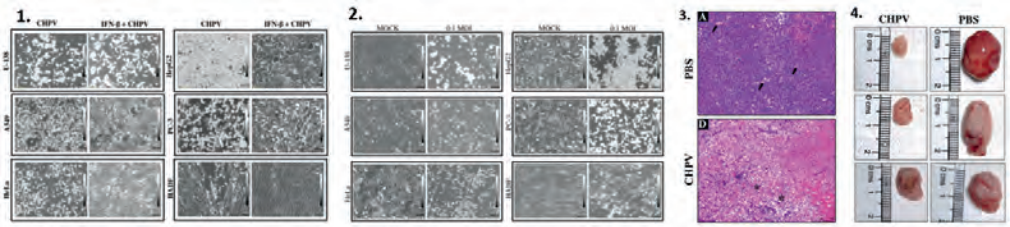
The overall premise of this approach is that viruses are generally restricted in normal cells due to their antiviral properties, which is however skewed in cancer cells. Thus CHPV can readily target cancer cells and in the due course of replication will not only directly lyse cancer cells but will also help attract other immune players to effectively target these cells. Our studies involving a panel of cancer cell lines of human origin and normal human adult dermal fibroblasts (HADF) showed that while the cancer cells were highly susceptible to low doses of CHPV (0.1 MOI), the HADF cells had limited susceptibility. Interferon sensitivity assays showed that in normal cells both virus output and sensitivity to CHPV was significantly reduced while it was the opposite in cancer cells. Since the glioblastoma cell line U138 was highly susceptible to CHPV, in vivo tumor explants were established and challenged with CHPV. Compared to the PBS control marked tumor regression was observed in the CHPV treated tumors. Thus our study offers the exciting proposition of exploiting the oncolytic potential of CHPV.

Front Row From Left: Karthika Rajeevan, Aranya Anunaya
Central Row From Left: Umerali K, Reshma Balan, Sivaja M
Back Row: Ashik Francis

LABORATORY STRENGTH

Ph.D Students: 4

FIGURE LEGEND



Cancer cell lines of human origin are sensitive to Chandipura virus both in vitro and in vivo. (1) Human origin cancer cell lines are differentially sensitive to CHPV with (2) interferon sensitization protecting HADF cells but not cancer cells like U138. In vivo CHPV could regress U138 tumor explants (3) which is quite evident from the histopathological sections which show less cell density in the CHPV treated compared to PBS controls (4D and A).

PUBLICATIONS

- **Kumar NA, Suma SM, Kunnakkadan U, Nag J, Mukesh RK, Lyles DS, Johnson JB.** Functional dissection of the dominant role of CD55 in protecting vesicular stomatitis virus against complement-mediated neutralization. Viruses. 2021; 13(3),373.
- **Mukesh RK, Kalam AA, Nag J, Jaikumar VS, Kunnakkadan U, Kumar NA, Suma SM, Rajavelu A and Johnson JB.** Chandipura virus induces cell death in cancer cell lines of human origin and promotes tumor regression in vivo. 2021; Mol Ther Oncolytics. 23:254-265.

Dr. KARTHIKA RAJEEVE

Scientist E-I, Pathogen Biology Program

BRIEF THEME OF LABORATORY

We study the pathogenesis of Chlamydia infections. My group focuses on the infection-cancer interface and investigates how the pathogen evades the immune system.

Our laboratory also focuses on the world's top infectious killer, Mycobacterium tuberculosis, the causative agent of tuberculosis. We investigate the fundamental mechanisms by which the bacteria evade the host immune system and create a protective niche in the human body.

c-MYC PLAYS A KEY ROLE IN IFN-γ-INDUCED PERSISTENCE OF CHLAMYDIA TRACHOMATIS

Chlamydia trachomatis (Ctr) can persist over long periods of time within their host cell and thereby establish chronic infections. One of the major inducers of chlamydial persistence is interferon-gamma (IFN-γ) released by immune cells as a mechanism of immune defence. IFN-γ activates the catabolic depletion of L-tryptophan (Trp) via indoleamine 2,3-dioxygenase (IDO), resulting in persistent Chlamydia. Here we show that IFN-γ depletes c-Myc, the key regulator of host cell metabolism, in a STAT1-dependent manner. Expression of c-Myc rescued Chlamydia from IFN-γ-induced persistence in cultured cell lines, but also in human fallopian tube organoids. L-tryptophan concentrations control c-Myc levels via the PI3K-GSK3β axis. Unbiased metabolic analysis revealed that Chlamydia infection reprograms the host cell tricarboxylic acid (TCA) cycle to support pyrimidine biosynthesis. Addition of TCA cycle intermediates or pyrimidine/purine nucleosides to infected cells rescued Chlamydia from IFN-γ-induced persistence. Thus, our results challenge the longstanding hypothesis of L-tryptophan depletion through IDO as the major mechanism of IFN-γ-induced metabolic immune defence and significantly extends the understanding of the role IFN-γ as a broad modulator of host cell metabolism.

Front Row From Left: Smitha RP, Paridhi Agarwal
Back Row From Left: Rahul Jose, Soumyanil Chatterjee

LABORATORY STRENGTH

Ph.D Students: 3 | JRF: 1 | Technical Assistant: 1

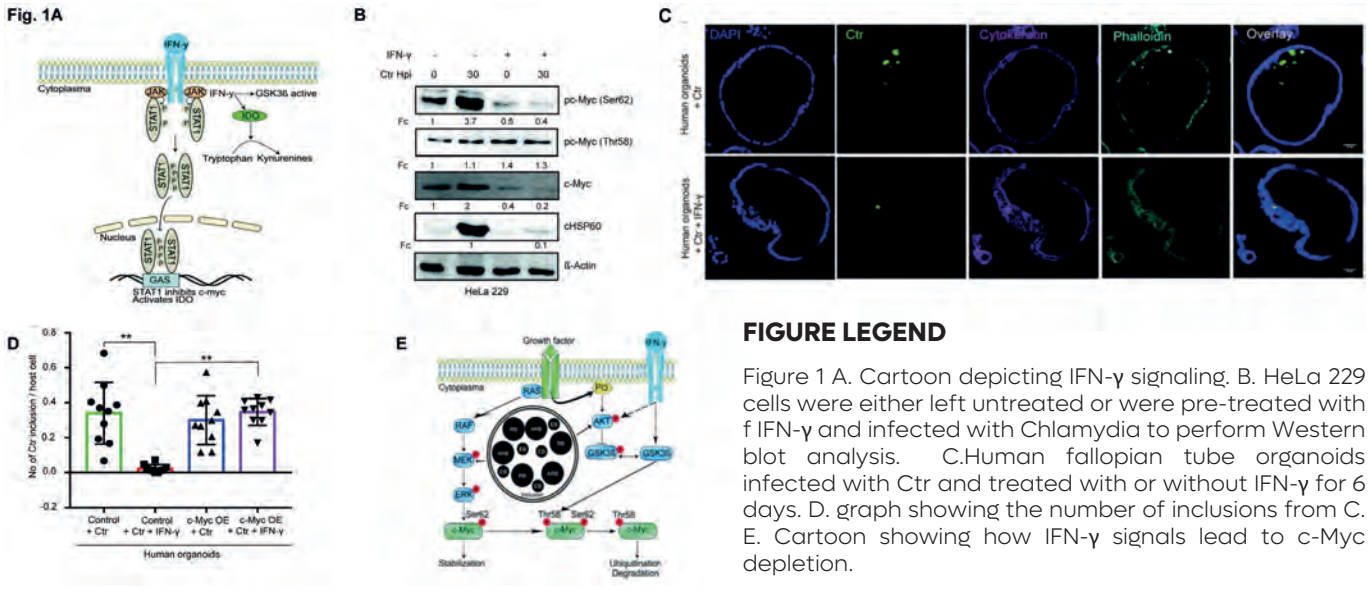


FIGURE LEGEND

Figure 1 A. Cartoon depicting IFN-γ signaling. B. HeLa 229 cells were either left untreated or were pre-treated with f IFN-γ and infected with Chlamydia to perform Western blot analysis. C.Human fallopian tube organoids infected with Ctr and treated with or without IFN-γ for 6 days. D. graph showing the number of inclusions from C. E. Cartoon showing how IFN-γ signals lead to c-Myc depletion.

PUBLICATIONS

- **Vollmuth N, Schlicker L, Guo Y, Hovhannisyan P, Janaki-Raman S, Kurmasheva N, Schmitz W, Schulze A, Stelzner K, Rajeeve K, Rudel T.** c-Myc plays a key role in IFN-γ-induced persistence of Chlamydia trachomatis. Elife. 2022;11:e76721.

Dr. KARTHIK SUBRAMANIAN

Scientist C, Pathogen Biology Program

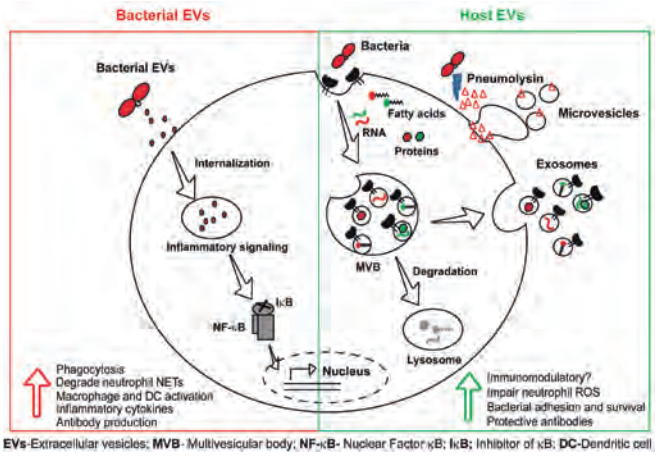
BRIEF THEME OF LABORATORY

Streptococcus pneumoniae is the major causative of fatal diseases such as pneumonia, septicemia, and meningitis accounting for 600000-800000 deaths every year in children below 5 years. Hence, WHO classified it as a priority pathogen that needs urgent research into pathogenesis and the development of new and effective antibiotics. The major focus of my laboratory is to study the molecular pathogenesis of pneumococcal infections and investigate the mechanisms underlying bacterial immunoevasion.

ISOLATION AND CHARACTERIZATION OF EXTRACELLULAR VESICLES SECRETED BY HUMAN MONOCYTES CHALLENGED WITH THE PNEUMOCOCCAL PORE-FORMING TOXIN, PNEUMOLYSIN

Streptococcus pneumoniae colonizes the human upper respiratory tract and is a major cause of life-threatening diseases such as pneumonia, septicaemia and meningitis, resulting in death of over 800,000 children annually. Pneumococci express several virulence factors such as the polysaccharide capsule and the cholesterol dependent pore-forming cytotoxin, pneumolysin (PLY) to evade immune response and establish disease. Pneumolysin toxin binds to cholesterol present in the plasma membrane of host cells, oligomerizes and form trans-membrane pores, which eventually lead to Ca2+ influx and cell death. Cellular membrane repair mechanisms limit the extent of damage and shed the toxin-damaged membrane in the form of extracellular vesicles (EVs). During an infection, variety of EVs are released from infected cells and contain both bacterial virulence factors such as toxins as well as host factors that could modulate the course of the infection and host immune response (Figure 1). The biological composition and pathophysiological functions of EVs shedded from pneumolysin-challenged cells are unknown.

In my laboratory at RGCB, we aimed to isolate, characterize and investigate the functional effects of EVs shedded from human monocytes challenged with purified pneumolysin. The EVs were isolated from the cell-culture supernatant by polymer precipitation and characterized using electron microscopy and dynamic light scattering. The majority of the EVs ranged in size from 50nm to 600nm with a spherical structure resembling exosomes and microvesicles. We found that the EVs shedded from PLY-challenged cells contained membrane-embedded PLY by performing western blotting using monoclonal antibody against pneumolysin. Besides, the PLY-containing EVs also induced hemolysis in a dose-dependent manner and were internalized by dendritic cells. By LC-MS, we found that PLY-induced EVs also harbour a repertoire of proteins that mediate antimicrobial as well as immunomodulatory functions in target cells upon cellular internalization.



EVs-Extracellular vesicles; **MVB**- Multivesicular body; **NF-κB**- Nuclear Factor κB; **IκB**; Inhibitor of κB; **DC**-Dendritic cell

From Left: Dr. Karthik Subramanian, Chinmayi V Bhat

LABORATORY STRENGTH

Project Assistant: 1 | Technical Assistant: 1

FIGURE LEGEND

Bacterial membrane vesicles containing virulence factors are internalized by host cells and activate macrophages and dendritic cells. Host EVs harbor bacterial and host macromolecules that enhance bacterial invasion and intracellular survival by transmitting virulence factors to bystander cells. Pores induced by the pore-forming toxin, pneumolysin are extruded as microvesicles during membrane repair. EVs, host extracellular vesicles; MVs, bacterial membrane vesicles; MVB, multivesicular body; NF-kB, nuclear factor kB; IkB, inhibitor kB; DC, dendritic cell.

PUBLICATIONS

- **Parveen S, Subramanian K.** Emerging roles of extracellular vesicles in pneumococcal infections: immunomodulators to potential novel vaccine candidates. Front Cell Infect Microbiol. 2022;12:836070.

Dr. SARA JONES
Program Scientist, Pathogen Biology Program

BRIEF THEME OF LABORATORY

Our Lab focuses on understanding how influenza viruses evolve in a population exposed to natural infection compared to being vaccinated. We also investigate molecular factors involved in measles vaccine failure.

MEASLES VACCINE FAILURE (AND SUCCESS) IN SOUTHERN INDIA

Measles is a highly contagious viral infection causing significant mortality and morbidity globally. In India, measles vaccination coverage is only 81.1% compared to other childhood vaccines resulting in more than 20% of susceptible children and can contribute significantly to the total burden of the measles virus outbreaks worldwide. In the present study, we screened for measles-specific IgG antibodies to understand the seroconversion rate in children who had received two doses of the measles vaccine. We observed rare cases of measles in those who have had multiple vaccine doses and that children under the recommended vaccination age of nine months are highly susceptible to measles. The IgG titers in the children aged 4-16 ranged between 2.8 to 58.2 NTU (Novatech unit) (Fig A). Of a total of six hundred and ninety-nine children recruited, 640 individuals (91.5%) were found to be protective, 23 (3.3%) were borderline, and 36 (5.2%) were susceptible (Fig B). There was no gender-specific variation in IgG titers. We further checked for measles-specific IgG titers in mothers of these children. Our data suggest that most mothers have pre-existing immunity to the measles virus. The higher titers in the mothers compared to the children may also reflect immune boosting due to repeat measles exposure, most probably from the child. For genotyping of the measles virus circulating in Kerala, throat swab was collected from suspected measles cases. Each sample was subjected to the measles virus N gene amplification and sequencing. During the 2021-2022 periods, the highly prevalent genotype circulating in Kerala was found to be segregated with clade D. The sequence identity of D8 genotypes circulating in south India with the WHO reference genotype D8 ranged between 96%- 99%. In-depth investigations into the immune profile of these individuals are further being studied.

Front Row From Left: Remya VS, Remya Raveendran, Aakriti Langeh
Back Row From Left: Usman Ghani, Jayalekshmi D, Archana MA,Vishnu VM

LABORATORY STRENGTH

Ph.D Students: 1

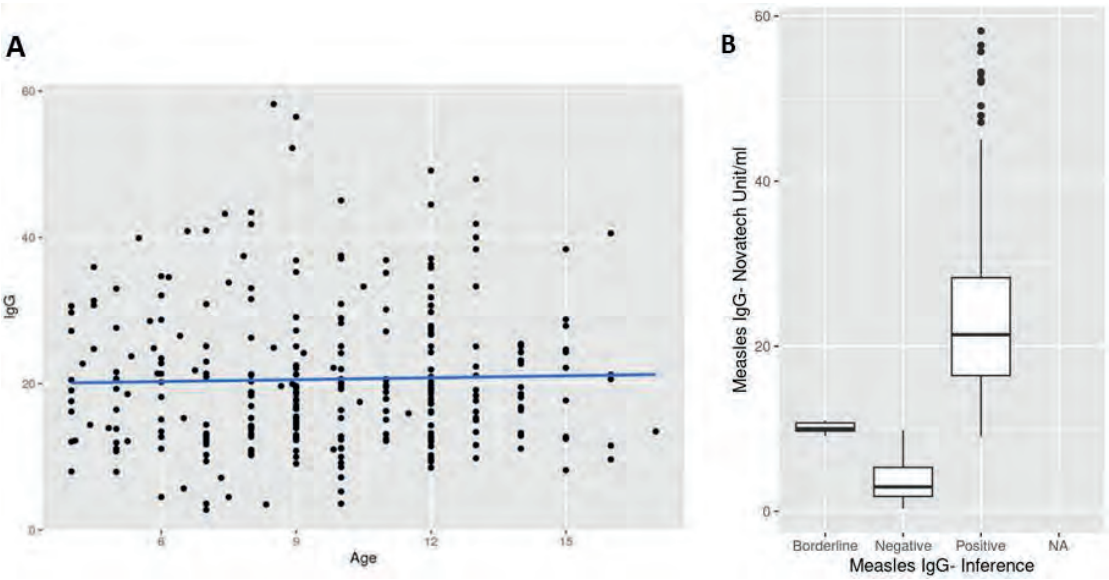


FIGURE LEGEND

Figure. (A) Correlation between measles-specific IgG antibody levels and age, (B) Measles-specific IgG antibody levels in the serum samples from study subjects

Dr. IYPE JOSEPH

Program Scientist, Pathogen Biology Program

BRIEF THEME OF LABORATORY

Epidemiology support to scientists in RGCB.

CLINICAL EXPERIENCE IN COVID-19 MANAGEMENT

All waves of COVID-19 had affected the staff, students and their relatives. About 400 persons with COVID-19 were supported through the medium of telephone calls. This gave us a unique opportunity to follow-up many patients from the point of first symptom onset till full recovery.

We could make few observations which consistently lead to predictable outcomes. Increased likelihood of requiring supplementary oxygen support during the clinical course was closely linked to the amount of physical exertion taken by the patient. Excessive talking over mobile phone, climbing stairs, walking fast within room, cleaning up the room, scrubbing the bathroom are usual activities taken up by patients as soon as they start to recover. But, we found them to be very detrimental to health. Characteristically, hypoxia developed after a delay of about 36 - 48 hours. In our small sample of persons whom we could counsel to avoid even minor exertions, especially in the period immediately after the reduction of early phase symptoms, we never had any clinical worsening.

Other beneficial interventions included slight over hydration with added table salt during times of fever (it helped in limiting giddiness on getting up from bed and in managing fever) and sleeping as much as possible (without blankets). During the second week of illness, oxygenation and pulse rate were monitored 3 – 4 times daily. Patients got 24-hour support in interpreting the pulse oximeter readings over SMS/WhatsApp. The common practice of steam inhalation for blocked nose was found to cause occasional acute deterioration. An alternative in smelling crushed orange outer covering was found to be safe and effective in clearing the blocked nose.

It is proposed that drugs which can induce tolerance to hypoxia (leading to reduction in the consequent inflammatory reaction) may help in recovery of hypoxic patients. Such drugs merit attention.

PUBLICATIONS

- **Lupitha SS, Darvin P, Chandrasekharan A, Varadarajan SN, Divakaran SJ, Easwaran S, Nelson-Sathi S, Umasankar PK, Jones S, Joseph I, Pillai MR, Santhoshkumar TR.** A rapid bead-based assay for screening of SARS-CoV-2 neutralizing antibodies. Antib Ther. 2022;5(2):100-110.

Dr. KRISHNA KURTHKOTI

DBT Ramalingaswami Fellow, Pathogen Biology Program

BRIEF THEME OF LABORATORY

The major focus of the lab is to understand the role of iron homeostasis in mycobacterial dormancy and reactivation. Another area of interest is to identify mechanisms that confer antimicrobial resistance in mycobacteria

EXPRESSION OF MYCOBACTERIAL ERROR-PRONE POLYMERASE IMPEDES GROWTH AND CONTRIBUTES TO GENETIC DIVERSITY IN BIOFILM

LABORATORY STRENGTH

JRF: 1 | Project Assistant: 1

Biofilms are multicellular communities held together by an extracellular matrix. Due to the complex architecture of the biofilm, the availability of nutrients will not be uniform among the bacterial population in the biofilm resulting in heterogeneity among the bacterial cells. In this study, we have used Mycobacterium smegmatis as a model organism to further understand the emergence of genetic heterogeneity within the biofilm. RNA-Seq analysis of biofilm culture revealed that DNA repair pathways were downregulated in biofilm while the expression of the mutasome consisting of dnaE2, imuA, and imuB was upregulated. Furthermore, when the biofilm cultures were subjected to planktonic growth the DNA repair was induced while mutasome expression was repressed- a complete reversal of the biofilm expression. We reasoned that the synergy between reduced DNA repair and induction of mutasome would lead to mutagenesis.

Although there was no significant increase in mutation in the biofilm culture compared to the planktonic forms in the wild-type strain, we observed higher mutation frequency in the biofilm culture of the wild-type strain in comparison to the biofilm culture of the dnaE2 mutant. Additionally, we observed that expression of dnaE2 reduced bacterial multiplication most likely by interfering with the normal DNA replication and its downregulation following planktonic growth would enable bacterial multiplication. Deletion of dnaE2 resulted in fitness defect of the mutant strain when competed against the parental strain in a biofilm environment. Our study uncovers the multiple outcomes of expression of dnaE2 such as increased mutagenesis and reduced growth rate both of which could be necessary for bacterial survival and adaptation within biofilms.

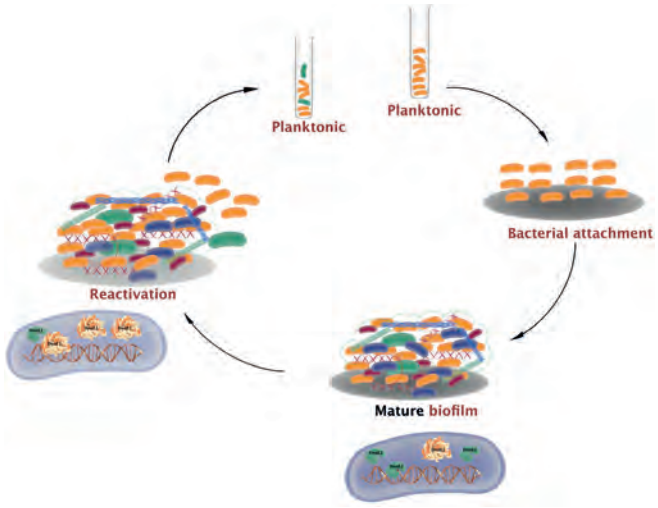


FIGURE LEGEND

Impact of DnaE2 expression in mycobacterial biofilms: Mycobacterial biofilm consists of a heterogenous population such as dead cells (red), growth-arrested (blue), and cells harboring genetic mutation (green) due to expression of DnaE2, and normal cells (orange) within an extra-cellular matrix. The growth arrest is due to the occupancy of DnaE2 on the genomic DNA conflicting with DnaE1. During reactivation, the balance of polymerase shifts in favor of DnaE1 allowing bacterial multiplication.

PUBLICATIONS

- **Salini S, Bhat SG, Naz S, Natesh R, Kumar RA, Nandicoori VK, Kurthkoti K.** The Error-prone polymerase DnaE2 mediates the evolution of antibiotic resistance in persisterMycobacterial cells. Antimicrob Agents Chemother. 2022;66(3):e0177321.
- **Salini S, Balaji M, Sinchana G Bhat, Ajay Kumar and Krishna Kurthkoti.** Mycobacterial membrane protein complex MSMEG_1381 and MSMEG_1382 functions as a novel efflux pump in conferring resistance to multiple antibiotics. Preprints doi: 10.20944/preprints202204.0003.v2

Dr. SANTANU CHATTOPADHYAY
Program Scientist, Pathogen Biology Program

BRIEF THEME OF LABORATORY

Our aim is to understand virulence and antibiotic resistance of the gastric pathogen Helicobacter pylori and its interaction with various microbes in gastrointestinal microbiome in the context of severe gastric diseases. We use next-generation sequencing (NGS) based approaches to study microbial genomics and metagenomics, which are typically followed by in vitro microbe-microbe interactions and antimicrobial susceptibility assays. Our results show promises for developing novel microbiome based therapies against peptic ulcer and gastric cancer.

GENOME ANALYSIS REVEALED UNIQUE WESTERN AS WELL AS EAST-ASIAN TRAITS IN THE VIRULENCE AND IN THE HOUSEKEEPING GENES OF THE HELICOBACTER PYLORI STRAINS ISOLATED FROM NORTH-EAST INDIAN STATE SIKKIM THAT SHARES BORDERS WITH BHUTAN, NEPAL AND CHINA

Helicobacter pylori causes long-term colonization before causing peptic ulcer and gastric cancer and gets ample opportunities for acquiring adaptive mutations suitable for surviving within a specific gastric niche. The pathogen shows remarkable variability with geography since it co-evolves with respective hosts. H. pylori cytotoxin associated gene A (cagA), which is present in a horizontally acquired pathogenicity island (PAI) and encodes a potent oncoprotein (CagA), has two major variants— Western (e.g. Europe, India) and East-Asian (e.g. Japan, China), which are also different in their oncogenic potentials— East-Asian CagA is the more potent between the two. Sikkim, a Himalayan state in North-East India, shares borders with West Bengal, Nepal, Bhutan and China. We have isolated 25 H. pylori strains from all 4 districts of Sikkim and characterized them by whole genome sequencing (WGS) using Illumina NovaSeq6000 and Oxford Nanopore MinION. Our WGS analysis revealed that the Sikkim H. pylori strains carry unique features in both their housekeeping and virulence genes, which also includes the cagA gene and the type IV secretion system encoding genes in the cagPAI. To the best of our knowledge, this is the first study that shows the coexistence of both Western and East-Asian cagA types within a small Indian state. More importantly, we were able to detect the amino acid sequences that are typical markers of the Western type CagA in the East-Asian type CagA and vice versa (Figure 1), suggesting Sikkim is a perfect geographical region that serves as the hotspot for H. pylori genetic exchange. This is probably linked to the exposure of the Sikkim population to Subcontinental, Western as well as East-Asian people since ancient time due to silk trades and human migrations.

From Left: Retnakumar RJ, Angitha N Nath

LABORATORY STRENGTH

Ph.D Students: 1 | JRF: 1

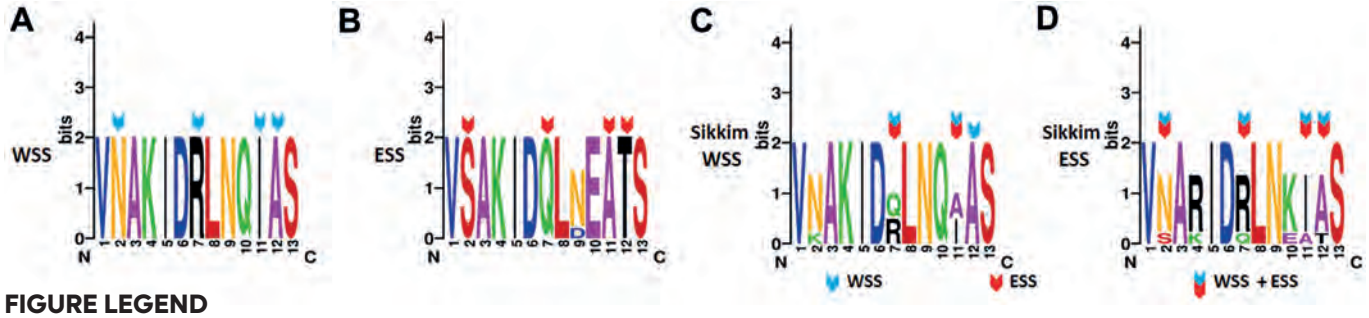


FIGURE LEGEND

Figure 1. Uniqueness of the Sikkim CagA. (A) Amino acid (AA) sequences of the conventional Western (WSS)-type CagA and (B) the conventional East-Asian (ESS)-type CagA. (C) Sequences of the Sikkim WSS-type CagA and (D) the Sikkim ESS-type CagA. The Sikkim H. pylori strains not only carry both CagA types, but also their WSS-types show AAs that are usually present in ESS-type, and vice versa.

PUBLICATIONS

- **Mehrotra T, Devi TB, Kumar S, Talukdar D, Karmakar SP, Kothidar A, Verma J, Kumari S, Alexander SM, Retnakumar RJ, Devadas K, Ray A, Mutreja A, Nair GB, Chattopadhyay S*, Das B*.** Antimicrobial resistance and virulence in Helicobacter pylori: Genomic insights. Genomics. 2021; 113 : 3951–3966. *Co-corresponding authors.

- **Alexander SM, Retnakumar RJ, Chouhan D, Devi TNB, Dharmaseelan S, Devadas K, Thapa N, Tamang JP, Lamtha SC, Chattopadhyay S.** Helicobacter pylori in human stomach: the inconsistencies in clinical outcomes and the probable causes. Front Microbiol. 2021;12:713955.

PLANT BIOTECHNOLOGY & DISEASE BIOLOGY

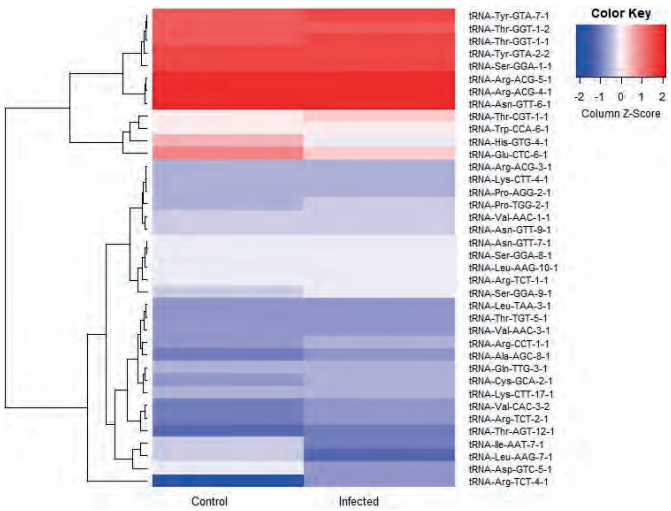
Dr. E.V.SONIYA
Scientist G, Plant Biotechnology & Disease Biology Program

BRIEF THEME OF LABORATORY

Our Lab is interested in developing an insight in to the molecular mechanisms underlying the interactions of plants with both biotic and abiotic stimuli, with a particular focus on Black pepper-Phythophthora capsici interaction as well as the molecular intricacies of metabolic pathways for the generation of secondary metabolites in medicinal plants.

INTEGRATED OMICS APPROACH FOR REVEALING THE DEVELOPMENT AND DEFENCE REGULATION IN PIPER NIGRUM L. AND TO UNVEIL THE NOVEL TYPE III POLYKETIDE SYNTHASES INVOLVED IN THE PRODUCTION OF MEDICINALLY IMPORTANT NATURAL COMPOUNDS

Piper nigrum, which is more often referred to as black pepper, is an medicinally and economically significant spice crop that is cultivated in most of the tropical regions. Phythophthora capsici, an oomycete pathogen in black pepper causing severe yield loss is a major threat to this medicinally important crop. Our Laboratory focuses on developing Phythophthora capsici resistant black pepper through various molecular approaches. We have identified and validated novel miRNA, lncRNAs and N6-methyladenosine modifications involved in fighting off the pathogens. A high throughput tRF-target cleavage validation was also done to understand the implication of tRFs in stress response. Concurrently, we are also exploring the function of small RNAs generated by Phythophthora capsici during the encounter in an effort to uncover methods of reducing disease severity. We are also investigating the metagenomic profile of Piper spp. to understand its impact on disease resistance induction in resistant cultivars to susceptible cultivars to explore root rhizosphere and endospheric bacterial microbiome. Attempts were also made to manage the disease condition using green nanoparticles. The effect of colonisation by P. indica in Piper nigrum on growth advantages, floral induction, and evocation is also being carried out. Thus, our lab's extensive molecular discoveries will give unique strategies for combating this dreadful oomycete pathogen. Our lab also investigates on identifying and modulating type III polyketide synthases that are involved in the production of therapeutically relevant secondary metabolites from medicinal plant Strobilanthes alternata and its endophytes. The genes involved in the synthesis of type III PKS will be studied using RNA sequencing methods, and the endophytic composition of microorganisms will be investigated using a metagenomic approach. Novel Type III PKS identification from endophytes widens the area of research by opening a pavement for understanding the crosstalk and correlation of type III PKS in endophyte and its host.



Front Row From Left: Pooja Visvam, Preetha Chandran P
Central Row From Left: Apsara IG, Hima Parvathy A, Dr. Lekshmi R.S
Back Row From Left: Akash P, Dr. Santhoshkumar R

LABORATORY STRENGTH

Postdoctoral Fellows: 1 | Ph.D Students: 5 | JRF: 1
Project Assistant: 3 | Technical Assistant: 1 | Lab Assistant: 2
Project Associate: 1

FIGURE LEGEND

The differential expression of tRNAs in black pepper during Phythophthora capsici infection. The heatmap shows the significant (p-value ≤ 0.05) differential expression of 38 tRNAs in the infected samples when compared to control samples

PUBLICATIONS

- **Kattupalli D, Srinivasan A, Soniya EV**. A Genome-Wide analysis of Pathogenesis-Related Protein-1 (PR-1) Genes from Piper nigrum reveals its critical role during Phytophthora capsici infection. Genes (Basel). 2021;12(7):1007.
- **Santhoshkumar R, Hima Parvathy A, Soniya EV**. Phytosynthesis of silver nanoparticles from aqueous leaf extracts of Piper colubrinum: characterisation and catalytic activity. J Exp Nanosci. 2021; 16:1, 295-309,

Dr. GEORGE THOMAS

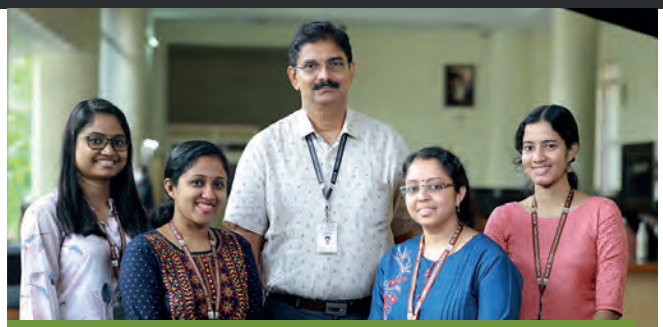
Scientist G, Plant Biotechnology & Disease Biology Program

BRIEF THEME OF LABORATORY

We focus on molecular characterization of Zingiber-Pythium pathosystems. The pathogenicity factors produced by a pathogen decide the nature of the host's response to an invading pathogen. In compatible pathosystems, the pathogenicity factors secreted by the pathogen target certain genes in the host (susceptibility genes) and exploit host cellular machinery for its colonization. Our interest is to identify and characterize susceptibility genes in spice crop ginger targeted by Pythium myriotylum during soft rot disease development.

MOLECULAR CHARACTERIZATION OF ZINGIBER-PYTHIUM PATHOSYSTEMS AND THE IDENTIFICATION OF HOST SUSCEPTIBILITY TARGETS

The species of the necrotrophic oomycete genus Pythium, particularly P. myriotylum Drechsler, cause the soft rot disease in the spice crop ginger (Zingiber officinale). The obligate asexuality together with the uniform susceptibility of ginger cultivars to soft rot disease deters the application of conventional crop improvement protocols for improving soft rot disease tolerance in ginger. This necessitates looking for unconventional methods for managing soft rot disease in ginger. The recent advances in gene editing methods have triggered an upsurge of interest among crop scientists to identify the susceptibility genes in the host and to evaluate their disease suppression efficiency by gene silencing experiments. We envisaged a dual approach to investigate the genes in ginger that innately support the infection process of P. myriotylum. The first approach involved the comparative examination between the transcriptome data generated in P. myriotylum susceptible ginger and the resistant Z. zerumbet and the identification and validation of putative susceptibility genes. The presumptive functions of the highly upregulated ginger transcripts were examined by KEGG pathway analysis and literature survey, and a set of 42 highly upregulated ginger transcripts with known susceptibility functions in other plants were identified. In the other approach, we determined the pathogenicity factors secreted by the pathogen into the host, by subjecting the P. myriotylum transcriptome data obtained by dual sequencing to various computational methods. In the process, we developed a pool of 10512 transcripts produced by P. myriotylum during the process of infecting ginger, of which the expression of 1896 transcripts is modulated, either up or down, during the process of infection. A repertoire of 187 effectors was predicted from the P. myriotylum transcriptome. In addition, we validated the role of putative resistance genes identified in Z. zerumbet by transcriptome analysis in conferring P. myriotylum resistance by virus-induced gene silencing approaches.



From Left: Dr. Joyous T Joseph, Lini Varghese, Vinitha MR, Jiya Rose

LABORATORY STRENGTH

Postdoctoral Fellows: 1 | Ph.D Students: 2
JRF: 1 | SRF: 1 | Technical Assistant: 1

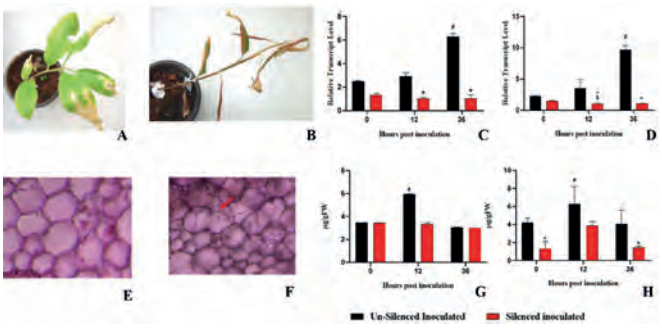


FIGURE LEGEND

Gene silencing experiments suggest a key role for Jasmonic acid (JA)-Salicylic acid cross-talk in determining host response in Zingiber-Pythium pathosystems. A- gene silenced Zingiber plant; B-gene silenced and Pythium inoculated plant; C-reduced expression of the silenced gene; D- reduced expression of a downstream gene; E-uninoculated silenced plant; F- Pythium inoculated silenced plant; G-SA content; and H-JA content in the silenced plant.

PUBLICATIONS

- **Satheesh GR, Koyyappurath S, Varghese L, Thomas G.** Genome and Transcriptome Sequence Resources and Effector Repertoire of Pythium myriotylumDrechsler. Mol Plant Microbe Interact. 2022;35(8):715-718.

- **Alex TE, Nath VS, Varghese L, Geetha KA, Augustine L, Ramaswamy VM, Thomas G.** Transcriptome-wideidentification and transcriptional profiling reveal remarkable expression modulation of redox genes in Zingiberzerumbet against Pythium myriotylum. PhysiolMolPlant Pathol. 2022; 121: 101885

Dr. V.V.ASHA
Scientist F, Plant Biotechnology & Disease Biology Program

BRIEF THEME OF LABORATORY

Plants have been used as an abundant repository of medicines for a long time and our Indian traditional systems of medicine rely heavily on these medicinal plants for the prevention and cure of many diseases. Phytopharmacological investigations are scientifically validating the pharmacological properties of traditionally valuable herbs and then focus on the characterization of active ingredients responsible for the activity.

COMPARATIVE LABEL FREE LC-MS/MS ANALYSIS OF HEPG2 CELLS TREATED WITH CHLOROFORM EXTRACT OF CUSCUTA REFLEXA ROXB.

To examine the effect of Chloroform extract of Cuscuta reflexa (CRCE) in hepatocellular carcinoma cells, a label-free mass spectrometric strategy was used and protein quantification was achieved by spectral counting. Proteins with 2 fold higher level of expression in the CRCE treated cells were considered to be up-regulated and proteins with 2 fold lower levels of expression were considered to be down-regulated. Proteomic changes were evident in CRCE treated cells. A total of 1102 different proteins were identified using LC-MS/MS analysis when HepG2 cells were treated with CRCE. Out of these, the number of proteins which showed significant difference in expression levels in CRCE treated cells were 126. Upon CRCE treatment expression of 50 proteins were found to be up regulated and 76 proteins were down regulated.

Among the down regulated proteins the highest fold change (34.7 fold lower) was observed in protein Importin subunit alpha-4 encoded by KPNA3 gene. KPNA3 is a key mediator in promoting growth and aggressiveness of HCC. It is involved in many signalling pathways that are highly activated in HCC like Adipocytokine signaling pathway Prolactin signalling pathway, IL-17 signaling pathway etc.

Further CRCE treatment also reduced the expression level of E3 ubiquitin-protein ligaseTRIP1, Actin-depolymerizing factor Phosphodiesterase, LanC-like protein 2, Homeoboxprotein DBX2, which promotes the growth of liver cancer cells.

The prediction database, STRING was employed to get to the PPIs (Protein-Protein Interactions) relevant in the list of proteins identified to be differentially expressed during CRCE treatment. The interactome of the significantly up-regulated and down-regulated proteins in cells treated with CRCE, helped to arrive at the various clusters to which these proteins fall. This mapping realised using STRING database, is illustrated below. The network was subjected to k-means clustering, which groups the proteins into a specified number of clusters.

From Left: Dr. VV Asha, Gayathri LT

LABORATORY STRENGTH

Technical Assistant: 1 | Lab Assistant: 1

FIGURE LEGEND

Figure 1 : String network analysis for down-regulated proteins in CRCE treated cells

Figure 2: String network analysis for up-regulated proteins in CRCE treated cells

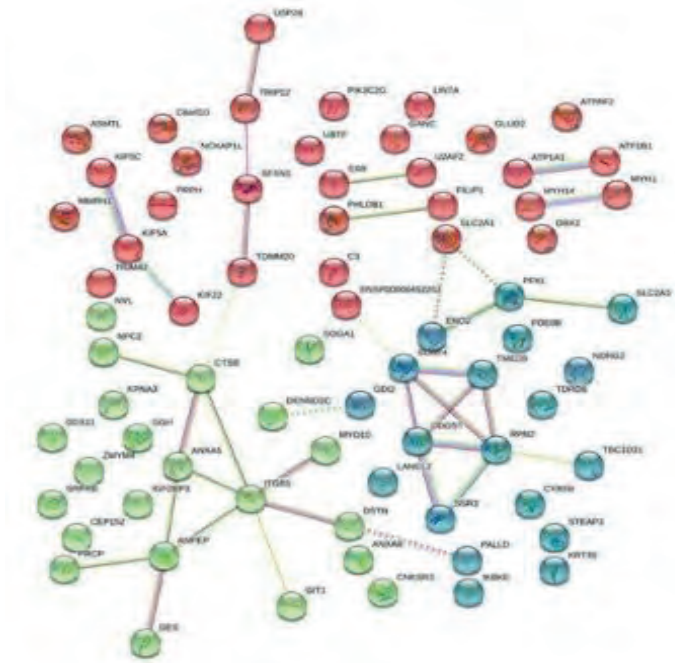


Figure 1

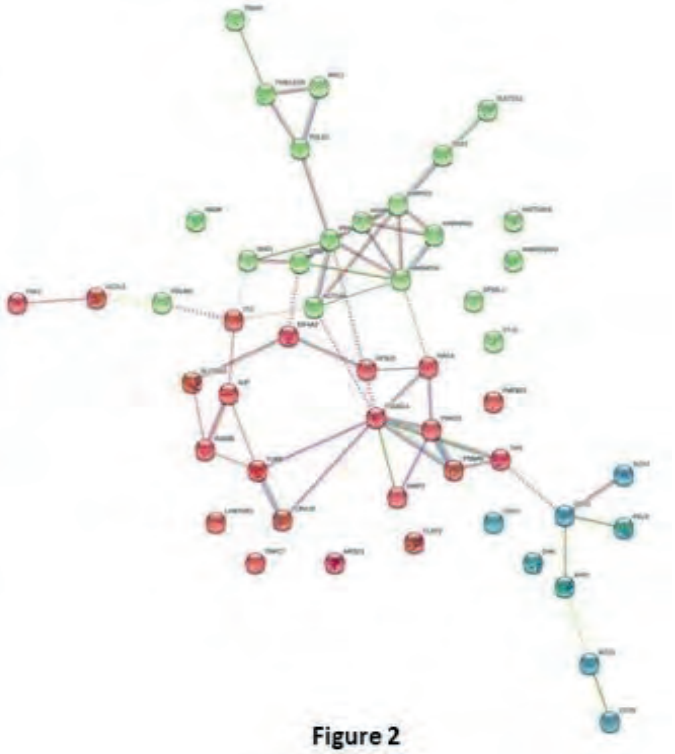


Figure 2

Dr. S.MANJULA
Scientist F, Plant Biotechnology & Disease Biology Program

BRIEF THEME OF LABORATORY

My laboratory focuses on developing priming-based crop protection strategies for crop improv ement in Piper nigrum and gaining insights on the mechanism of priming through molecular approaches including gene functional studies and metabolite pathway analysis.

ELUCIDATING THE MOLECULAR MECHANISMS OF DEFENSE PRIMING IN PIPER NIGRUM AS A CROP PROTECTION STRATEGY

To compensate for their sessile life, plants have evolved a wide range of survival and adaptation strategies. 'Priming' is one such phenomenon with practical field application. Piper nigrum, is under severe threat by Phytophthora capsici and all released varieties of P.nigrum are highly susceptible to this pathogen. Negative impact of currently used chemical fungicides on the environment and the ecosystem has urged the need for adopting more sustainable 'greener' practises for crop improvement. The consequence of priming in modulating Piper nigrum defense against Phytophthora capsica was tested using the known plant defense elicitor- Glycol Chitosan (GC), which was used at a concentration of 1mg/mL to infiltrate detached leaves of young P.nigrum leaves. It was observed that pre-treatment of GC for 24h resulted in significant reduction of disease symptoms in infected leaves, as evidenced by the marked decrease in size of necrotic lesions and also delayed the appearance of symptoms up to 72 hpi. An ROS-mediated manifestation of Hypersensitive Response (HR) induced by Chitosan was also evident in pre-treated leaves observed by DCFDA staining, which was accompanied by overexpression of ROS producing and antioxidant genes. A corresponding visual indication of increased lignification was obvious, with a correlated enhancement in lignin content of GC treated leaves. This was further supported by significantly high RNA expression levels of key genes in the lignin biosynthesis pathway. Enhanced callose deposition was apparent in

Front Row From Left: Gayathri GS, Saranya V
Central Row From Left: Liya Kurien, Geetha S Nair, Indu M, Meera B
Back Row From Left: Mookul Samader

LABORATORY STRENGTH

Ph.D Students: 4 | JRF: 2 | SRF: 2 | Technical Assistant: 1

GC infiltrated leaves along with overexpression of Callose synthase gene transcripts. A noteworthy finding was the significant quantitative enhancement in Piperine content of GC infiltrated leaves which also indicated an associated increase in phenolic acids. These findings provide strong molecular evidences endorsing the twofold advantage of defense priming in P.nigrum by improving crop protection along with enhanced Piperine biosynthesis, which has evident practical relevance.

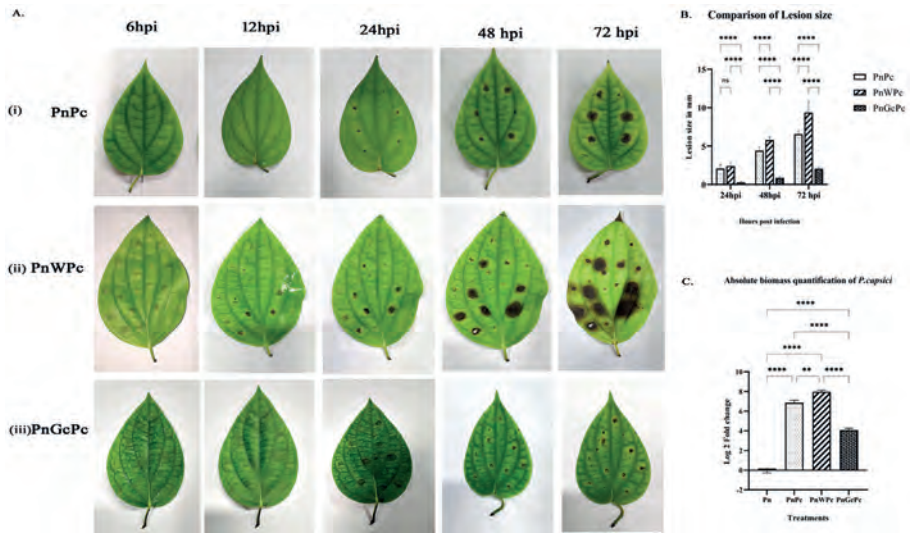


FIGURE LEGEND

(A): P. capsici infection progression in (i)control (ii) water infiltrated (iii) GC infiltrated P. nigrum leaves at different time points, (B): Comparison of P. capsici infection lesion size before and after GC and mock(water) treatments (PnPc: P. nigrum infected with P. capsici, PnWPc: Water infiltrated P. nigrum infected with P. capsici & PnGcPc: GC infiltrated P. nigrum infected with P. capsici (C) Quantification of the relative growth & absolute biomass of P. capsici

PUBLICATIONS

- **Rajeswari Gopal Geetha, Sivakumar Krishnankutty Nair Chandrika, Gayathri G Saraswathy, Asha Nair Sivakumari and Manjula Sakuntala.** ROS dependent antifungal and anticancer modulations of Piper colubrinum Osmotin.Molecules.2021;26:2239

Dr. SARASWATI NAYAR

Program Scientist, Plant Biotechnology & Disease Biology Program

BRIEF THEME OF LABORATORY

The focus of the laboratory is studying hormone related genes and transcription factors in unicellular green algae.

CSUBMADS1 REGULATES STARVATION STRESS RESPONSE IN COCCOMYXA

Previously in my lab, we have successfully characterized and continuing to characterize the role of a MADS-box transcription factor (CsubMADS1) from a unicellular green microalga Coccomyxa subellipsoidea C-169. C-169 is an alga which survives the harsh conditions of Antarctica, where it was first isolated (Blanc et al, 2012). In our previous study, the overexpressors of CsubMADS1 were found to be tolerant to starvation stress (Nayar et al, 2021). By RNA sequencing, it was found that the overexpression of CsubMADS1, activated expression of an entire set of Chlorophyll related genes. These genes thus seem to be the downstream targets of CsubMADS1. The binding of CsubMADS1 to the motif in the promoter of these genes was confirmed by EMSA. The CsubMADS1 overexpressors were tolerant to nitrogen starvation and stress induced during stationary phase. The lipid droplet formation was reduced in case of overexpressors when compared to the wild type which shows that the overexpressors are tolerant to starvation stress. These results show that CsubMADS1 has an important role during stress tolerance in nutrient limiting conditions.

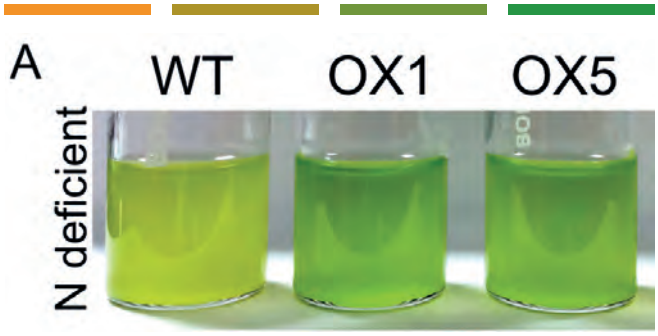
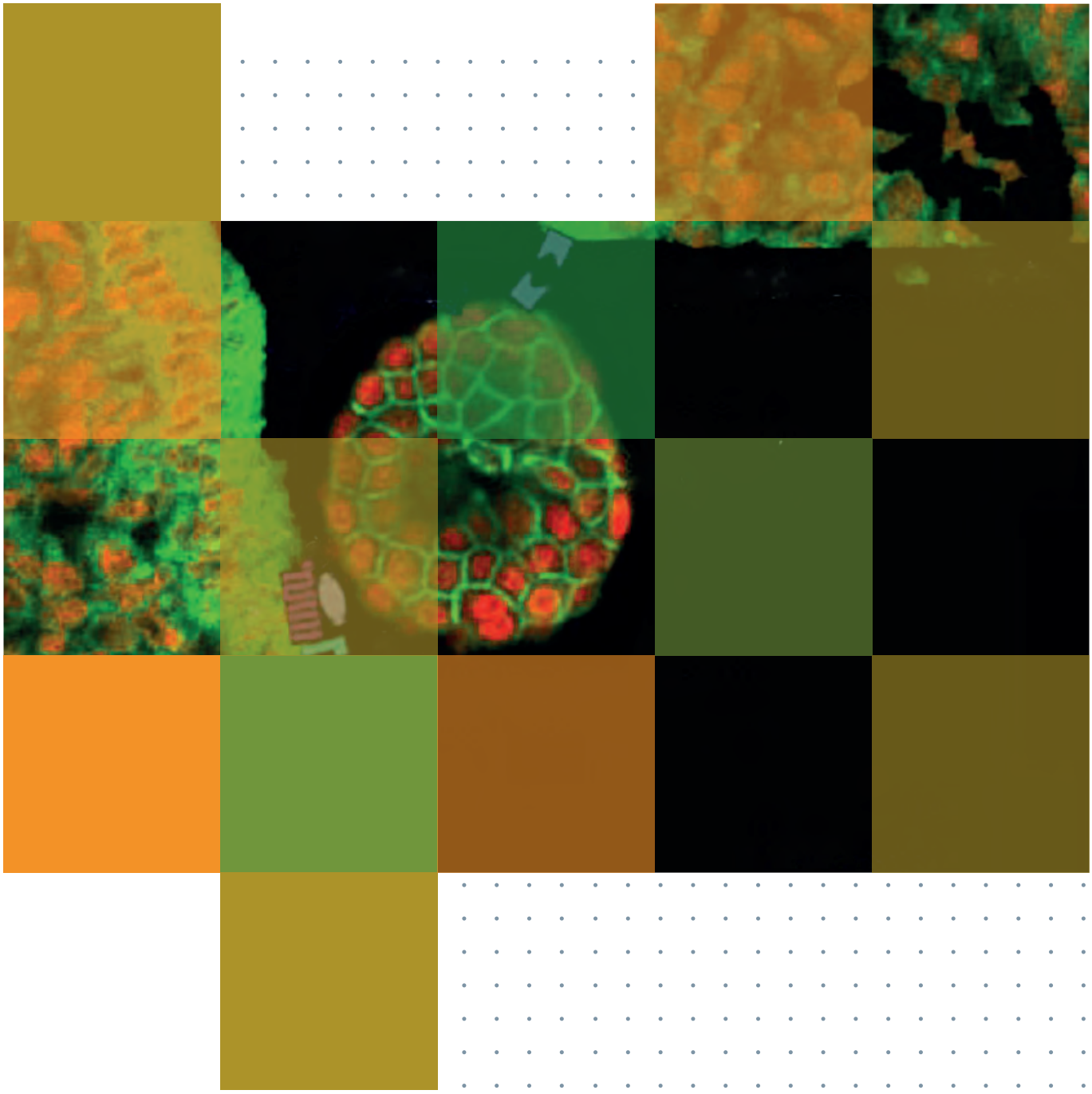


FIGURE LEGEND

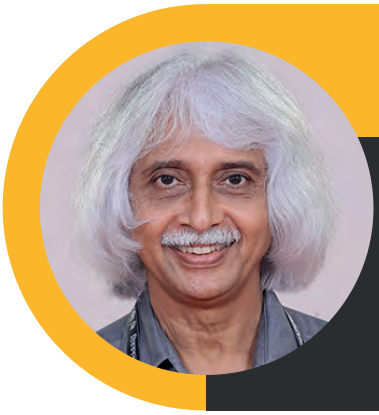
Growth of wild type and CsubMADS1 overexpressors in nitrogen deficient medium. The overexpressors are tolerant to nitrogen starvation compared to the wild type. The wild type has entered the death phase whereas the overexpressors are still bright green in colour.

PUBLICATIONS

- **Nayar S, Thangavel G.** CsubMADS1, a lag phase transcription factor, controls development of polar eukaryotic microalga Coccomyxasubellipsoidea C-169. Plant J. 2021;107(4):1228-1242.



REPRODUCTION BIOLOGY



Dr. PRADEEP KUMAR G
Scientist G, Reproduction Biology Program

BRIEF THEME OF LABORATORY

To understand molecular networks regulating germline stem cell maintenance, division and differentiation in mammalian testis

PKC SIGNALING INHIBITION REPRESENT A NEW STATE OF PLURIPOTENCY-DEVELOPMENTAL CONTINUUM EXPLORED

We identified fourteen common target genes of miR-34c and miR-449a using in silico approaches. Real-time PCR analysis revealed a strong negative correlation in their levels and that of miR-34c & miR-449a. A corresponding reduction in protein levels was observed for NONO, PPP2R5A, S1PR3, VAT1, and TBC1D2B. Using anti-miRNA approach in GC-1 spg cells, 10 selected target genes (Akap2, Gabra3, Marcks, Nav1, Nono, Padi2, Pkia, Ppp2r5a, Tbc1d2b, and Vat1) were confirmed as the bona fide targets of miR-34c and miR-449a. Elevated expression of Yamanka/ Thomson factors, EMT markers and altered cytokinesis/karyokinesis were observed in miR-34c/miR-449a silenced GC-1 spg cells. Global proteomic analysis following miR silencing showed upregulation of cytoskeletal, nucleic acid binding protein, metabolite interconversion enzymes and NMD pathway genes whereas structural proteins, scaffold adaptor, enzyme modulator and chaperone were downregulated.

We evaluated the expression of Cnnm1 in mice during embryonic germ cell development. We noted a significant increase in its expression after gonad development compared to Primordial Germ Cells, suggesting its role in the establishment of SSCs during the initial stages of development. The expression of Cnnm1 in C18-4 cells increased on treatment with a self-renewal factor (GDNF and rWnt3A) or proliferation-inducing agent (letrozole). CNNM1 knockdown altered the cell cycle progression in C18-4 spermatogonial cells. Two functionally active putative promoter sequences of mouse Cnnm1 were characterized.

Over-expression and knock models of Dynlt1 in GC1-spg cells were generated. Profiling of gene expression following these manipulations indicated perturbations in the expression of a range of stemness regulating genes including Yamanaka/Thomson factors and germline stemness markers. We are in the process of developing an antibody array to map the presence/absence of 74 critical proteins on human spermatozoa.

LABORATORY STRENGTH

Postdoctoral Fellows: 2 | Ph.D Students: 3
JRF: 2 | SRF: 2 | Lab Assistant: 1

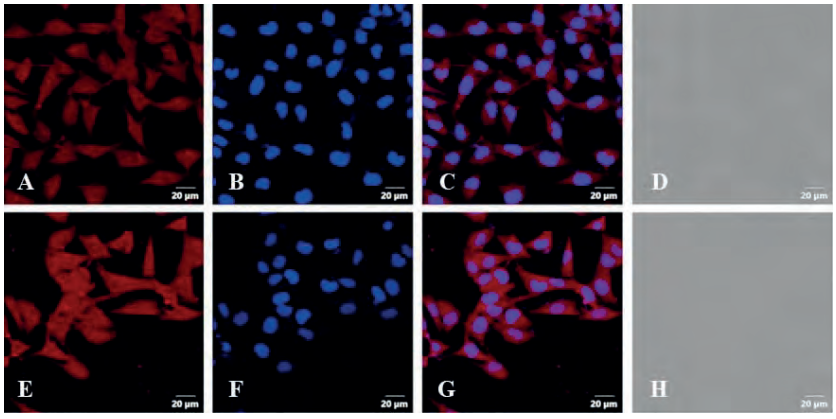


FIGURE LEGEND

Figure 1: Immunofluorescence analysis of CNNM1 expression in C18-4 cells before (A) and after (E) sGDNF treatment. Corresponding DAPI stained cells (B, F), merged images (C, G) and DIC pictures (D, H) are presented. Bar = 20 µm.

PUBLICATIONS

- **Sahadevan M and Kumar PG.** Peptidyl Arginine Deiminase 2 (PADI2) is Expressed in Post-Meiotic Germ Cells in the Mouse Testis and is Localized Heavily on the Acrosomal Region of Spermatozoa. J. Endocrinol. Reprod. 2021;25(1): 53-65.
- **Kutteyil SS and Kumar PG.** Spermatogonial stem cells: A story of self-renewal and differentiation. Front Biosci (Landmark Ed), 2021: 26:163-205.

Dr. MALINI LALORAYA

Scientist G, Reproduction Biology Program

BRIEF THEME OF LABORATORY

My laboratory mainly focuses on understanding molecular events crucial for embryo implantation leading to a successful pregnancy. Failed implantation represents a major obstacle in assisted reproduction and is called as the 'black-box of assisted reproduction'. We focus on understanding the impact of 'nidatory estrogen' leading to uterine receptivity acquisition via uterine reprogramming. Polycystic Ovarian Syndrome which is associated with sub-fertility due to higher risk of implantation failure, is our second focus of research.

INVESTIGATING THE ROLE OF SUPEROXIDE IN REGULATING ADHESION, A CRITICAL STEP REQUISITE FOR EMBRYO IMPLANTATION.

Our lab has pioneered the work on a beneficial role of superoxide radical in female reproduction as early as 1990's. We had found an estrogen sensitive spurt in NAD(P)H oxidase generated superoxide at the 'window of embryo implantation' which is important in 'tissue remodeling specifically the membrane fluidity' and 'zona hatching'. The abrogation of pregnancy by superoxide quenchers represents their novel therapeutic potential. Our recent interests now focus on mechanistic aspects of superoxide action on uterus tissue remodeling during implantation.

We hypothesized that superoxide could modulate endometrial epithelial surface adhesion molecule repertoire. Our work revealed that superoxide generation by PMA stimulation leads to increased E- CADHERIN expression on the cell membrane in Ishikawa cells when compared with control in immunofluorescence analysis. Superoxide inhibition by treatment with Naloxone and gp91ds-tat results in loss of E-cadherin expression. Interestingly, HEC-1A, the nonreceptive cell-line does not show efficient response to superoxide stimulation.

In vitro spheroid attachment assay was developed during this year using Ishikawa cell monolayers as the receptive endometrium layer and JAR cells which mimic the trophoblast to assess whether blocking superoxide could modulate embryo adhesion. Spheroid attachment capability to Ishikawa (a receptive endometrial cell-line) and HEC-1A (a non-receptive endometrial cell line) was addressed. Our results show that receptive Ishikawa cells exhibited a significantly higher percentage of spheroid attachment compared with HEC-1A. We further could demonstrate that superoxide treatment leads to improved JAR spheroid adhesion on Ishikawa monolayers while its blockade inhibited adhesion. This suggests superoxide modulates embryo adhesion as the rate of spheroid (embryo mimic) attachment to Ishikawa monolayer (endometrium mimic) upon the addition of superoxide inhibitors (Naloxone and gp91ds-tat) was significantly reduced. Thus, our results point to superoxide induced improved adhesion via increased E-cadherin expression.

Front row from left: Vani Manoharan Nair, Dr. Renjini AP, Anagha Balakrishnan, Beauty Rani Koch, Anjana MJ, Sangavi Murugesan
Central row from left: Lipika Priyadarsini Patra, Dr. Betcy Susan Johnson, Deepthi Prakash, Ajay Kumar Dhyani
Back row from left: Jeeva SE, Vysakh G, Shabith Raj K, Irfan Khan P, Dr. Mahitha Sahadevan, Rahul Singh

LABORATORY STRENGTH

Postdoctoral Fellows: 1 | Ph.D Students: 3 | JRF: 2
SRF: 2 | Lab Assistant: 1

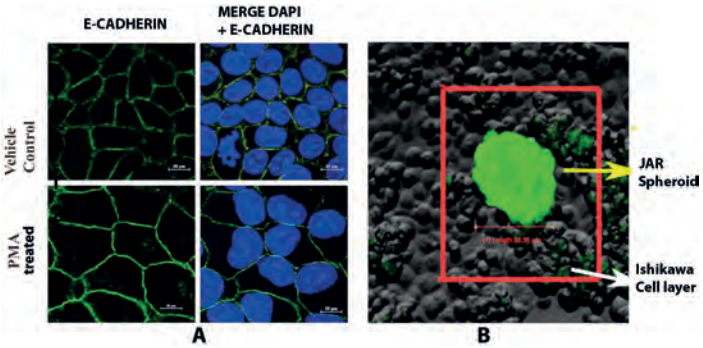
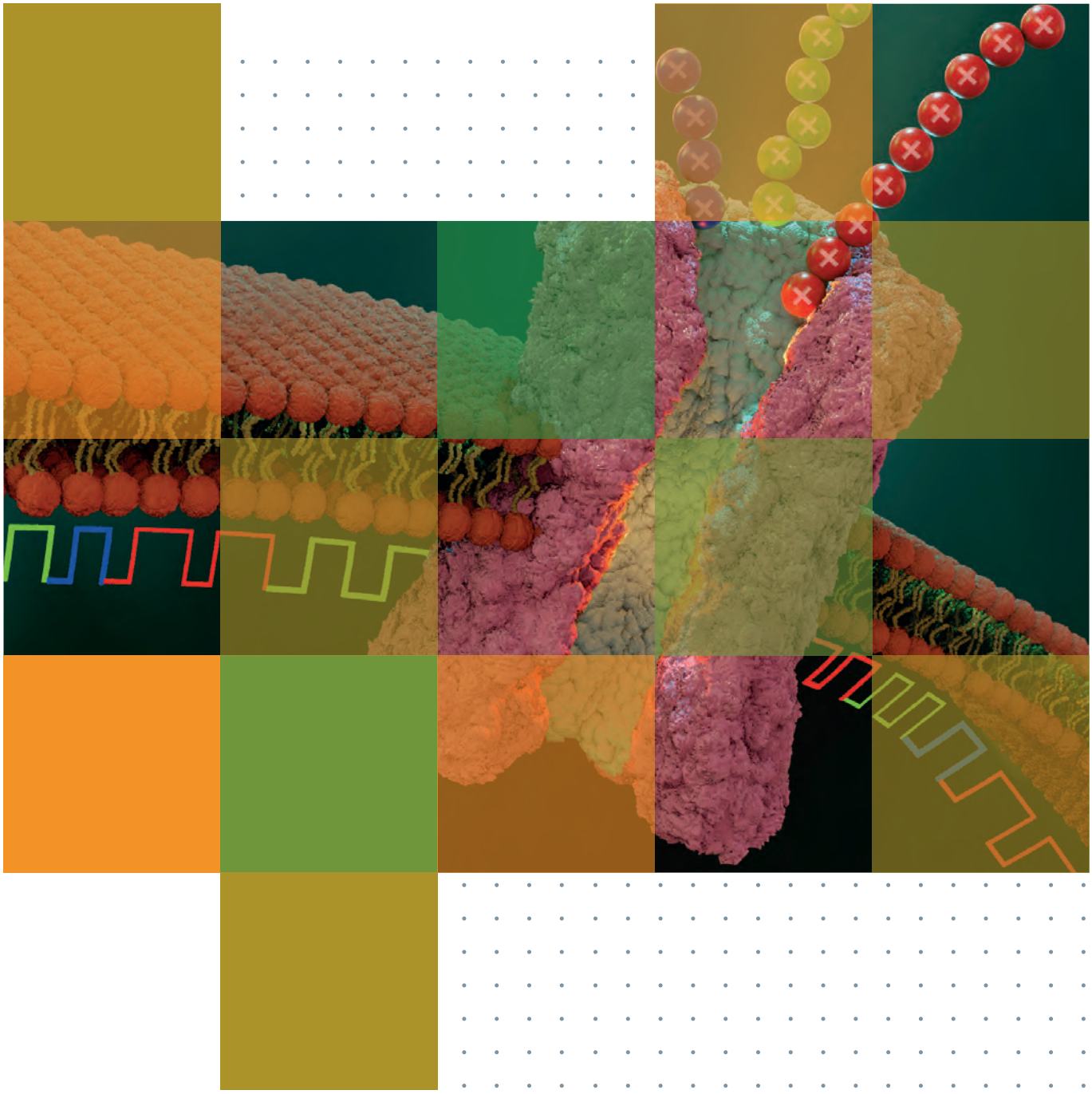


FIGURE LEGEND

Figure showing (A) E-CADHERIN expression in Ishikawa cells upon PMA treatment (B) JAR spheroid (green fluorescence) adhering to Ishikawa (receptive) cell monolayer.

PUBLICATIONS

- **Ghosh S, Parikh S, Nissa MU, Acharjee A, Singh A, Patwa D, Makwana P, Athalye A, Barpanda A, Laloraya M, Srivastava S, Parikh F.** Semen proteomics of COVID-19 convalescent men reveals disruption of key biological pathways relevant to male reproductive function. ACS Omega. 2022;7(10):8601-8612.



TRANSDISCIPLINARY BIOLOGY

Professor Chandrabhas Narayana
Director

BRIEF THEME OF LABORATORY

Surface enhance Raman studies (SERS) on biomolecules

INSIGHTS ON AGGREGATION OF HEN EGG-WHITE LYSOZYME FROM RAMAN SPECTROSCOPY & MD SIMULATIONS

As we age, we are more likely to suffer from neurodegenerative diseases such as Alzheimer's and Parkinson's, which result from the deposition of misfolded proteins and their aggregates. Protein aggregation can occur through several unique mechanisms/pathways such as the reversible association of the native monomer, aggregation of the conformationally altered monomer, aggregation of the chemically modified product, nucleation-controlled aggregation, and surface-induced aggregation. In the present work, the spontaneous aggregation of hen egg-white lysozyme (HEWL) in an alkaline pH 12.2 at an ambient temperature was studied to obtain molecular insights. This helps in elucidating the effect of pH without any other interferences. This aggregation process is directed by the isodesmic pathway. Hence, it can be studied at relatively dilute concentrations and provide insights into the protein aggregation mechanism. The time-dependent changes in spectral peaks indicated the formation of β sheets and their effects on the backbone and amino acids during the aggregation process. Introducing iodoacetamide revealed the crucial role of intermolecular disulphide bonds amidst monomers in the aggregation process. These findings were corroborated by Molecular Dynamics (MD) simulations and protein-docking studies. MD simulations helped establish and visualize the unfolding of the proteins when exposed to an alkaline pH. Protein docking revealed a preferential dimer formation between the HEWL monomers at pH 12.2 compared with the neutral pH. In this work we attempted to shed light on the nature of molecular interactions leading to dimerization and aggregation of HEWL monomers using MD simulations and Raman analysis. Our study also implicate that the combination of Raman spectroscopy and MD simulations is a powerful tool to study protein aggregation mechanisms.

Back Row From Left: Debanjan Bhowmik
Front Row From Left: Irfan Shafi Malik, Bhawna Kangotra, Abhirami Ajith

LABORATORY STRENGTH

Postdoctoral Students: 1 | Ph.D Students: 1

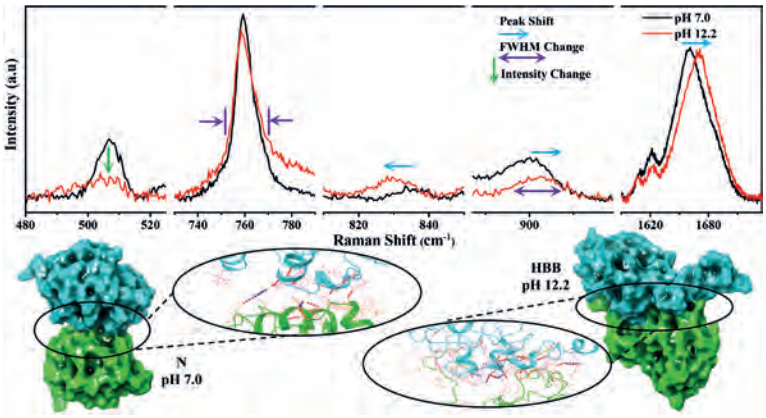


FIGURE LEGEND

Raman spectra of the pH 7.0 and pH 12.2 buffer using 532 nm laser (top panel). a visual representation of the docked protein dimers in N and HBB indicating a more significant number of interactions in HBB as compared with N (bottom panel)

PUBLICATIONS

- **Chalapathi D, Kumar A, Behera P, Sathi SN, Swaminathan R, Narayana C.** Insights on aggregation of hen egg-white lysozyme from Raman Spectroscopy and MD Simulations. Molecules. 2022; 27(20):7122.
- **Kamali K, Joseph B, Rajaji V, Narayana C.** Pressure-Induced Loss of Long-Range Structural Order in MFM-300 (Al): An X-ray Diffraction and Raman Spectroscopic Study. J Phys Chem C. 2021;125(28):15472-8.

Dr. SANIL GEORGE
Scientist E-II, Transdisciplinary Biology Program

BRIEF THEME OF LABORATORY

The laboratory focuses on molecular ecology of amphibians and discovery of natural antimicrobial peptides (AMPs) for new therapeutic applications including the AMPs present in the skin secretion of endemic and untapped frog species of Western Ghats.

THE COMPLETE MITOCHONDRIAL GENOME OF EUPHLYCTIS KARAAVALI (AMPHIBIA: ANURA)

The complete mitochondrial genome of skittering frog Euphlyctis karaavali (Karaavali Skittering Frog) was sequenced. The mitogenome is a circular molecule of 15,505 bp in length containing 13 protein-coding genes, two ribosome RNA genes, 21 transfer RNA (tRNA) genes and a non-coding D-loop region (control region). Its gene arrangements are similar to the typical neobatrachian-type except for the loss of tRNAPro gene. Our data which represent the first mitogenome for the species Euphlyctis karaavali is a newly reported species and known only from the type locality (coastal plain of Karnataka, India) at an elevation of 2 m Mean Sea Level. Our data revealed that the geographical distribution range of this species is extended up to the southern part of Kerala State and recorded at an elevation of 68 m from the Mean Sea Level. Our data will serve as a reference for further studies on the conservation genetics of the Euphlyctis genus in India.

From Left: Akhilnath PG, Anoop VS

LABORATORY STRENGTH

JRF:1

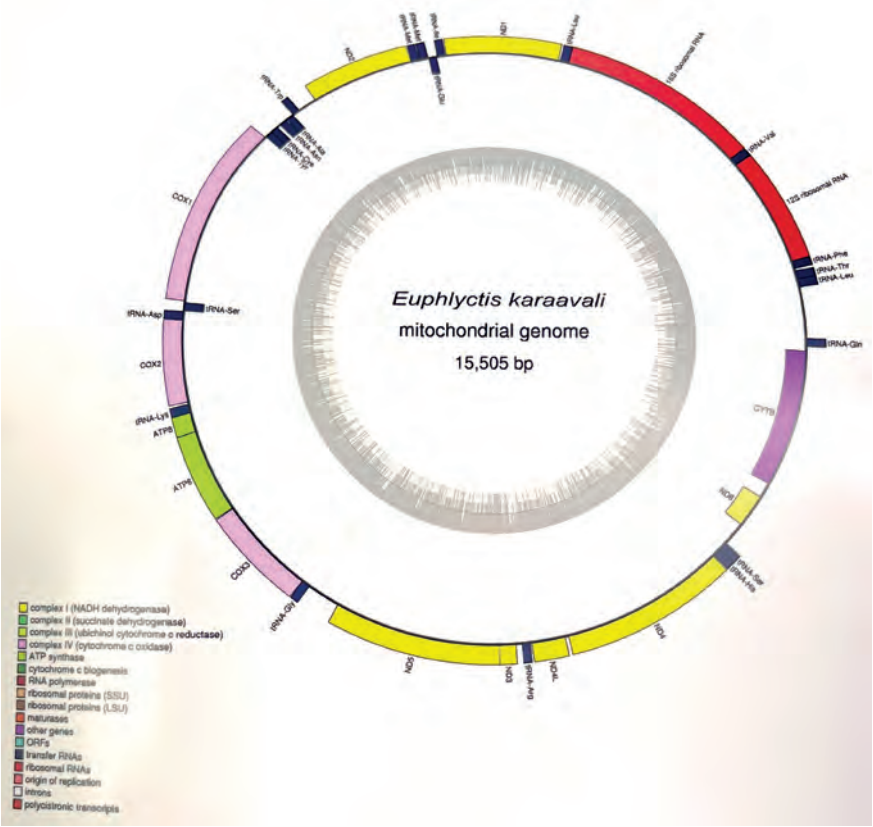


FIGURE LEGEND

Complete mitochondrial genome of Euphlyctis karaavali

Dr. K.R.MAHENDRAN
Scientist E-I, Transdisciplinary Biology Program

BRIEF THEME OF LABORATORY

Our lab mainly focuses on building sophisticated α-helix-based transmembrane protein pores for applications in nanobiotechnology. We suggest that this new class of pores will exhibit structural and functional versatility and can be expanded for the detection of folded proteins, peptides and polysaccharides. Our findings shed light on the mechanism of action of antimicrobial peptides and pore-forming toxins. Additionally, we focus on the molecular basis of substrate translocation across outer membrane bacterial membrane pores.

TRANSMEMBRANE PORES FOR NANOTECHNOLOGY AND MEDICINE

Membrane protein pores have demonstrated applications in nanobiotechnology. Most previous studies have focused on β-barrel protein pores, whereas α-helix-based pores are rarely explored. Here, we developed a synthetic transmembrane peptide pore, pPorA, built entirely from short synthetic α-helical peptides based on the porinACj of the Corynebacterium jeikeium. Using single-channel electrical recording, we define the structural properties of the pore and elucidate its assembly pathway. The peptide pore is ion-selective, functional, and capable of conducting ions and binding blockers. We determined the kinetics of differently charged peptides binding and translocation through the pPorA at single-molecule resolution. Further, we show that unnatural D-amino acids can be incorporated by chemical synthesis into the peptides to build stable transmembrane mirror-peptide pores. Such designed pores of unique architecture will be advantageous for single-molecule electrical sensing and related technologies. The D-peptide pores showed resistance to protease and were highly stable and functional. Notably, molecular dynamics simulations of the structural models of the mirror-image peptide pores revealed their specific alpha-helical packing and surface charge conformation consistent with the experimental observations. Our findings will shed light on the mechanism of action of antimicrobial peptides and aid the design of sophisticated dimeric pores in biotechnology.

From Left: Anjali Devi Das, Smrithi Krishnan R, Vidhu G, Smitha Devi, Remya S

LABORATORY STRENGTH

Ph.D Students: 4 | JRF: 1 | Technical Assistant: 1

Additionally, we focus on the molecular basis of substrate translocation across a specialized specific bacterial membrane pore CymA, which has the 15-residue segment inside the pore barrel, restricting its diameter and generating a sophisticated architecture. We elucidated the molecular mechanism of cyclic and linear carbohydrate polymer translocation through CymA and defined the dynamics of substrate transport through the pore. We emphasize that this pore can be used as a biotechnological sensor and our findings will answer the fundamental questions related to molecular membrane transport.

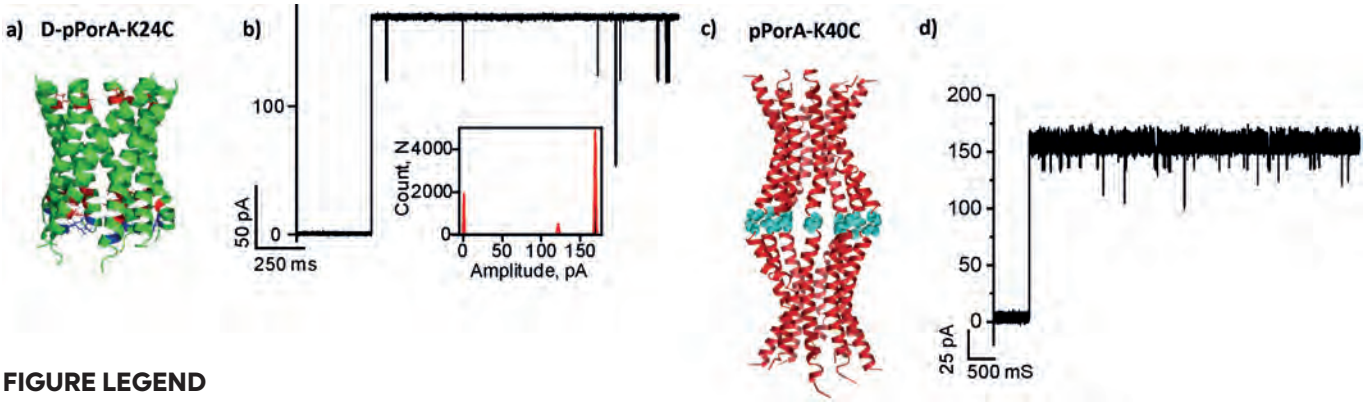


FIGURE LEGEND

a) The DpPorA stable structure is shown in cartoon representation. b) Single mirror image pore insertion at +100 mV and corresponding unitary conductance histogram by fitting the distribution to a Gaussian (n = 50). c) Dimeric alpha-helical pores shown in cartoon representation. d) Single dimeric alpha-helical pore insertion at +100 mV.

PUBLICATIONS

- **Krishnan RS, Jana K, Shaji A, Nair KS, Das AD, Vikraman D, Bajaj H, Kleinekathöfer K Mahendran KR.** Assembly of transmembrane pores from mirror-image peptides. Nat Commun. 2022. (In press).
- **Puthumadathil N, Krishnan RS, Nair GS, Mahendran KR.** Assembly of alpha-helical transmembrane pores through an intermediate state. Nanoscale. 2022; 14: 6507-6517.

Dr. SHIJULAL NELSON SATHI

Scientist C, Transdisciplinary Biology Program

BRIEF THEME OF LABORATORY

The Bioinformatics Laboratory is mainly focusing on highthoughput (Meta)genomics and evolutionary bioinformatics approches to unreveal the origin, adaptation, transmission and evolution of antibiotic resistance genes within pathogenic bacteria and development of strategies to slow down its further spread. In addition the laboratory is studying the structural and functional implications of non-synonymous mutations present in fast evolving rna viruses (SARS-CoV2).

STRUCTURAL AND FUNCTIONAL IMPLICATIONS OF NON-SYNONYMOUS MUTATIONS IN SARS-COV2 VARIANTS

Mutational landscape and in silico structure models of SARS-CoV-2 spike RBD

We analyzed 31,403 SARS-CoV-2 genomes randomly across the globe and identified 444 non-synonymous mutations in RBD that cause 49 distinct substitutions in contact and non-contact amino acid residues. Interactions mediated via N487 residue in cluster-I and Y449, G496, T500, G502 residues in cluster-III remained largely unchanged in all RBD mutants (Figure). Despite extensive changes in the interface, RBD-ACE2 stability and binding affinities were maintained in all the analyzed mutants.

Docking of peptide inhibitors against major drug targets of SARS-CoV-2 variants

We analyzed the effects of non-synonymous mutations in major targets of SARS-CoV-2 in response to potential peptide inhibitors, we have screened 12 peptide inhibitors against RBD and 5 peptides against Mpro of SARS-CoV-2 variants using molecular docking and simulation approaches. We found that LCB1 - de novo-synthesized peptide has the highest binding affinity to RBD and antimicrobial peptide; 2JOS, was identified against Mpro with high binding affinity as it interacts with key residues in dimerization sites, crucial for viral replication. Molecular Dynamics simulations affirm the stability of RBD-LCB1 and Mpro-2JOS complexes.

Hybrid genome assembly and annotation of multi-drug resistant Staphylococcus aureus genotype ST672-SCCmec type IVd (2B)

We analysed the complete genome of S. aureus SCCmec IVd(2B), which exhibit resistance against antibiotics - ciprofloxacin, oxacillin, kanamycin, erythromycin, azithromycin, methicillin, and vancomycin. We obtained a complete genome of S. aureus S145 having 79 virulence and 90 antibiotic resistance genes and has a ~17-kb SCCmec which encodes genes such as mecA, delta-mecR1, IS1272, ccrAB2, and SCCmec IVd(2B) subtype gene CG002 and a ~30-kb multidrug-resistant plasmid with eight AR genes forming three gene clusters for penicillin (blaI-blaZ-blaR1), macrolides (mphC-msrA), and aminoglycoside-streptothricin (aphA3-sat4-partial aadE).

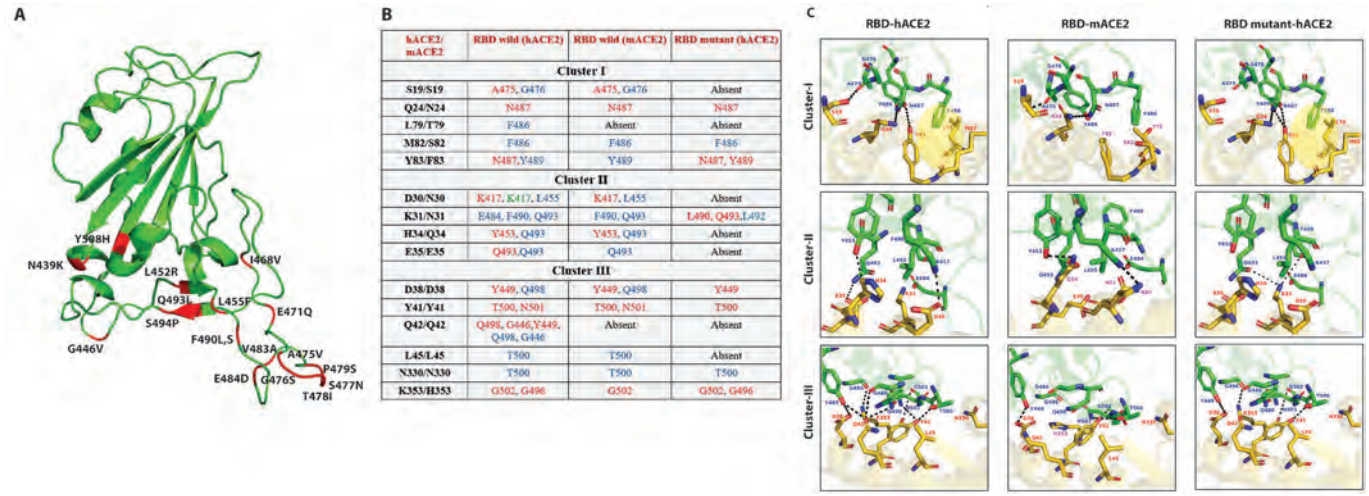
From Left: Elizabeth Philip, Kartik Rangari, Pawan K Khangar, Iwin K Joseph, Athira Mathew.

LABORATORY STRENGTH

Postdoctoral Fellows: 1 | Ph.D Students: 1 | JRF: 1
Project Assistant: 1

FIGURE LEGEND

(A) SARS-CoV-2 RBM highlighting mutated interacting residues and most frequent mutations in RBM. (B) List of cluster specific molecular interactions of hACE2, mACE2, and mutated RBD-ACE2 complexes. (C) Structural visualization of key interactions listed in (B). RBD is represented in green and ACE2 in gold. The hydrogen bond interactions between ACE2 and RBD are shown as dotted lines



PUBLICATIONS

- **Nelson-Sathi S, Umasankar PK, Sreekumar E, Nair RR, Joseph I, Nori SRC, Philip JS, Prasad R, Navyasree KV, Ramesh S, Pillai H, Ghosh S, Santosh Kumar TR, Pillai MR.** Mutational landscape and in silico structure models of SARS-CoV-2 spike receptor binding domain reveal key molecular determinants for virus-host interaction. BMC Mol Cell Biol. 2022;23(1):2.
- **Gopalakrishnan S, Uma SK, Mohan G, Mohan A, Shanmugam G, Kumar VTV, J S, Chandrika SK, Vasudevan D, Nori SRC, Sathi SN, George S, Maliekal TT.** SSTP1, a host defense peptide, exploits the immunomodulatory IL6 pathway to induce apoptosis in cancer cells. Front Immunol. 2021;12:740620.

Dr. N.G.LIGHTSON

Scientist C, Transdisciplinary Biology Program

BRIEF THEME OF LABORATORY

We are studying next generation biochip techniques for biomedical and environmental relevant biomarkers employing nanomaterials/biomolecules, micro/nanofluidics, and lab-on-a-chip techniques. Our interest extends to a wide range of fusion of nanotechnology and biotechnology, understanding the phenomena in micro & nano scale, and practical applications such as developing portable and cost-effective biosensors or bioanalytical devices.

ENZYME-LIKE CATALYTIC PROPERTY OF NOVEL CARBON NANOZYME FOR BIOSENSING APPLICATION

Biosensors as diagnostic and therapeutic point-of-care testing (POCT) devices have been applied in various fields. While developing biosensors, one of the components is the biorecognition element that has direct interaction with the target analytes. In the conventional biosensor, biorecognition elements such as antibodies, enzymes, proteins, peptides etc. are being employed because of their inherent physico-chemical and structural advantages such as specific and selective binding sites for the target analytes. For instance, enzyme-based biosensors are very sensitive, selective, and specific; but enzymes have low shelf-life, some are expensive, easily denatured, etc. that leads to the question - can we design efficient enzyme-mimicking biomaterials? Metal and metal oxide nanomaterials have shown the enzyme-like catalytic effect as per the reports. However, these nanoparticles (NPs) have certain limitations such as cytotoxicity, less biocompatible, challenging to prepare < 20nm size, no fluorescence, etc., so one of the objectives is to focus on biomaterials to prepare NPs.

Initially, we design carbon nanomaterials that mimic enzymes called 'carbon nanozymes' with carbon precursors such as L-pyroglutamic acid, thiourea, citric acid, 4-amino-3-hydrazino-5-mercapto-1,2,4-triazole, etc. Carbon dots (CDs) were synthesised following pyrolysis and

From Left: Aswathy Prasad, Aman Grewal, Smitha Devi S

LABORATORY STRENGTH

JRF: 1 | Technical Assistant: 1

hydrothermal methodologies. In the process, we synthesised novel CDs that have high peroxidase mimicking and catalytic properties. These CDs can replace the redox enzymes such as peroxidase in developing biosensors to detect biomarkers of clinical and environmental relevant biomarkers. In the next phase, we are mimicking other important enzymes such as oxidase, catalase, etc. by synthesising, engineering, and designing novel CDs. The enzyme-like CDs will be further applied in developing robust and high-performance microfluidic paper-based bioanalytical devices that can be used as personalized monitoring, surveillance, and quality assessment system.

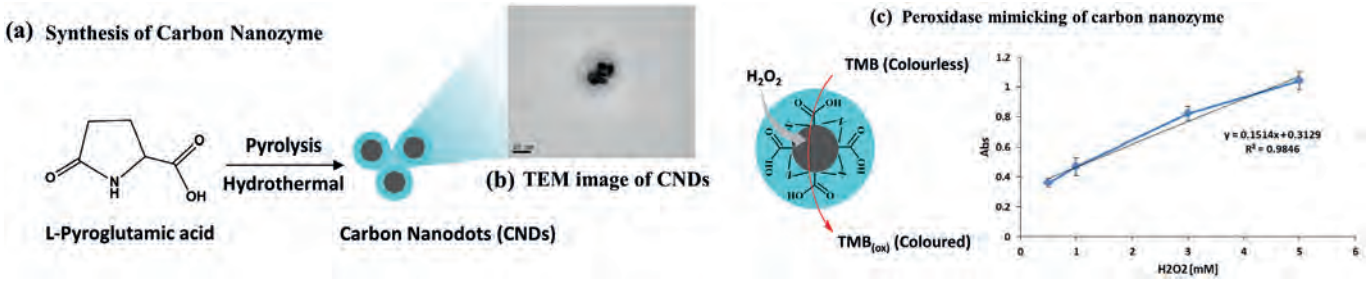


FIGURE LEGEND

Peroxidase-mimic carbon dots: (a) Synthesis of carbon nanozyme by pyrolysis or hydrothermal methodology, (b) TEM image of synthesized carbon nanodots, (c) Colorimetric determination of hydrogen peroxide (H2O2) reacting with chromogen tetramethyl benzidine (TMB)

PUBLICATIONS

- **Ngashangva L, Hemdan BA, El-Liethy MA, Bachu V, Minteer SD, Goswami P.** Emerging bioanalytical devices and platforms for rapid detection of pathogens in environmental samples. Micromachines (Basel). 2022;13(7):1083.
- **Das S, Ngashangva L, Goswami P.** Carbon dots: An emerging smart material for analytical applications. Micromachines (Basel). 2021;12(1):84.

Dr. KATHIRESAN NATARAJAN

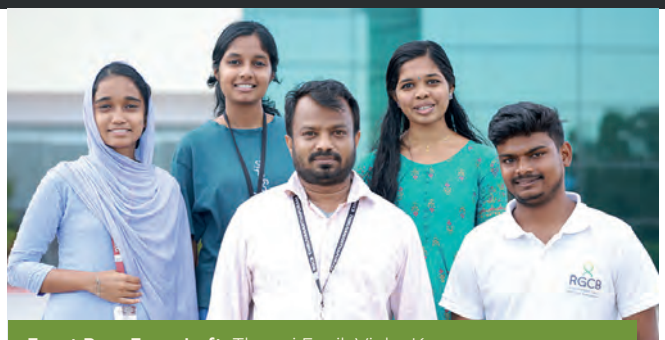
Scientist C, Transdisciplinary Biology Program

BRIEF THEME OF LABORATORY

Our laboratory is interested in nicotinic acetylcholine receptors that play important role in fast signaling throughout the body. It is critical to understand the structure-function connection of nicotinic acetylcholine receptors to comprehend their function in health and disease. Numerous nicotinic receptor subtypes may be specifically targeted, and various biological entities can regulate receptor function. Our research focuses on drugs and physiological modulators that act differently on these receptors and are potentially therapeutic.

UNRAVELING THE BINDING MODE OF CATESTATIN AND CURCUMIN ON A7 NICOTINIC RECEPTORS

Nicotinic acetylcholine receptors (nAChRs)are members of the superfamily of ligand-gated ion channels known as "Cysteine-loop". These receptors contain a central ion pore enclosed by a five-fold pseudosymmetry. Each receptor contains an extracellular ligand-binding domain and an ion-pore-containing transmembrane region. nAChR anomalies can lead to Alzheimer's disease, Parkinson's disease, epilepsy, schizophrenia, and smoking addiction. nAChR subtypes with varied pharmacological sensitivity and physiological distributions are created via diverse subunit combinatorial assembly. The majority of α7 nAChRs are in the human brain's hippocampus and cortical regions. These receptors participate in the transduction of Na+, K+, and Ca2+ ions and have a variety of physiological activities. Their important function in neurotransmitter release systems makes them a possible therapy target for drug addiction, neurodegenerative, and psychological diseases.



Front Row From Left: Thasni Fazil, Vicky Kumar
Back Row From Left: Athira J, Aruna Chandran

LABORATORY STRENGTH

Ph.D Students: 1

Deducing the molecular interactions between modulators and the α7 nAChR receptor can assist in comprehending their mode of action and involvement in molecular pathways. In this study, the binding mode of physiological peptide catestastin (CST) and its variants, phytochemical curcumin, and its analogues with neuronal α7 nAChRs was investigated. This was accomplished using in-silico approaches such as molecular docking and molecular dynamics simulations to comprehend the dynamics of the docked complexes. In addition, a comprehensive examination of the interactions and simulation trajectories provided insight into the design of pharmacological compounds capable of activating and inhibiting the receptor molecule. The wild type catestatin and the mutant CST-364S formed persistent connections with the receptor and occluded the pore region, suggesting that CST (WT and its variants) can function as a non-competitive inhibitor of the α7 nAChR binding to the membrane pore. The curcuminoids cyclo-curcumin and demethoxycurcumin stabilize the α7 nAChR by forming stable hydrogen bonds and ionic interactions at the extracellular-transmembrane junction, thus could act as an allosteric modulator.

Figure 1

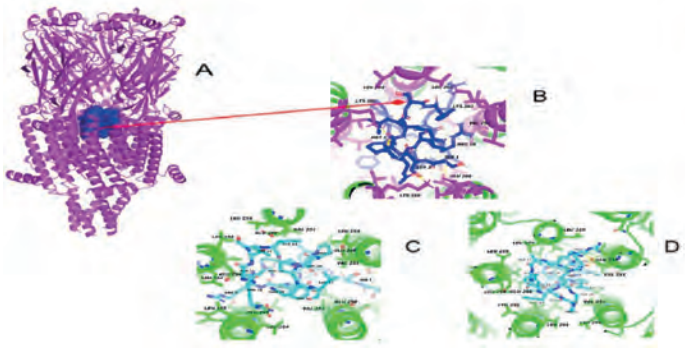


Figure 2

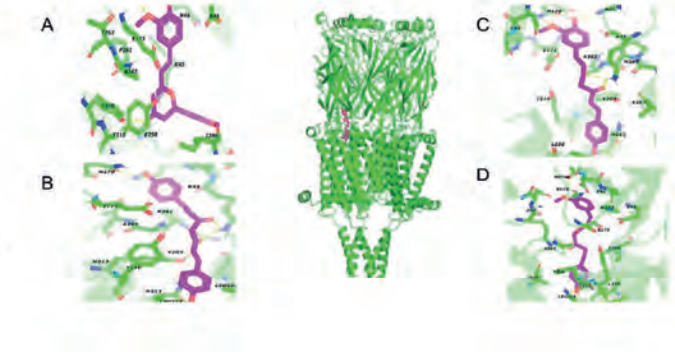


FIGURE LEGEND

Figure 1: Interaction of human catestatin and its variants on human α7 nAChR. (A, B) Binding mode of CST-WT (shown in blue; front and top view). (C) Binding mode of CST-364S (shown in cyan - bottom left). (D) CST-370L (shown in cyan - bottom right).

Figure 2: Interaction of curcumin and its analogues on human α7 nAChR. (A) Curcumin, (B) bisdemethoxycurcumin, (C) demethoxycurcumin, (D) cyclocurcumin

Dr. P.K.UMASANKAR
DBT-Ramalingaswami Fellow, Transdisciplinary Biology Program

BRIEF THEME OF LABORATORY

Our lab seeks to understand regulatory mechanisms of clathrin-mediated endocytosis (CME), a major protein trafficking pathway in all eukaryotes. In particular, we are interested in uncovering molecular switches involved in the initiation of CME with the hope to identify specific inhibitors and activators. We use an integrated approach combining cell biological, biochemical and gene-editing tools in cultured cells and in our chosen model organism, zebrafish.

REGULATORY MECHANISMS OF CLATHRIN-MEDIATED ENDOCYTOSIS

A major project in our lab is to understand the activation mechanisms of AP-2, the central adaptor protein complex in CME. Recently, we identified a novel BMP-2- inducible kinase (BMP2K) which phosphoregulates AP-2 both in vitro and in vivo. We also found that BMP2K localizes and stabilizes at clathrin-coated pits on plasma membrane via interaction of its unstructured C-terminus with AP-2. Depleting FCHO proteins, the allosteric activators of AP-2, via gene-editing ablated BMP2K-AP-2 interaction leading to loss of kinase and AP-2 phosphorylation. This in turn caused defects in clathrin-coat morphology and cargo uptake revealing functional significance of BMP2K-mediated AP-2 phosphorylation in CME. We also identified that BMP2K-AP-2 axis is pivotal for the proper formation of notochord (precursor of spine) in zebrafish embryos

From Left: Navyasree KV, Shikha Ramesh T

LABORATORY STRENGTH

Ph.D Students: 2

(Ramesh et al, 2021). Another project investigates molecular connections between CME and nutrient sensing pathways in mammalian cells. Along these lines, we have established a key role for cholesterol endocytosis in the activation and reactivation of mTOR, the master regulator of nutrient sensing and cell growth. Depletion of total cholesterol by methyl-β-cyclodextrin (MCD) inactivates mTORC1 by displacing the kinase from lysosomes to cytosol. In addition, we also identified that cholesterol along with insulin and autophagy sustains mTORC1 reactivation in starvation-induced cells. Consistently, the adverse effects on mTOR signalling can be reversed by repleting cholesterol in the form of LDL or free cholesterol. Interestingly, we discovered that Smith-Lemli-Opitz syndrome (SLOS) patients having defects in cholesterol biosynthesis and CME exhibit insufficient mTOR signalling (Navyasree et al, 2022). Future studies will focus on delineating the molecular mechanisms underpinning these defects and their implications in SLOS pathophysiology. Together, our findings imply novel functions of CME in human health and disease.

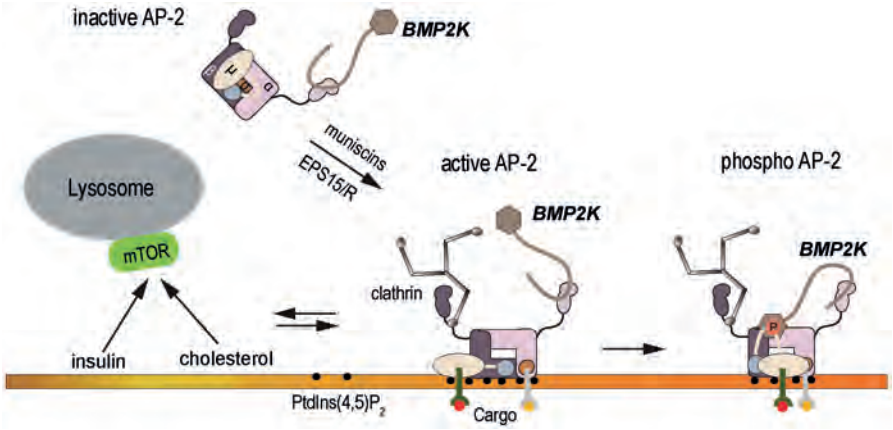


FIGURE LEGEND

Model depicting activation mechanisms of AP-2, the central adaptor protein in clathrin-mediated endocytosis (CME) along with the regulators (EPS15, muniscins, BMP2K) involved and the cross talk of CME with the mTOR nutrient sensing pathway on lysosomes via cholesterol-insulin axis.

PUBLICATIONS

- **Ramesh ST, Navyasree KV, Sah S, Ashok AB, Qathoon N, Mohanty S, Swain RK, Umasankar PK*.** BMP2K phosphorylates AP-2 and regulates clathrin-mediated endocytosis. Traffic. 2021;22(11):377-396.
- **Nelson-Sathi S, Umasankar PK*, Sreekumar E, Nair RR, Joseph I, Nori SRC, Philip JS, Prasad R, Navyasree KV, Ramesh S, Pillai H, Ghosh S, Santosh Kumar TR, Pillai MR.** Mutational landscape and in silico structure models of SARS-CoV-2 spike receptor binding domain reveal key molecular determinants for virus-host interaction. BMC Mol Cell Biol. 2022;23(1).

Dr. DEBANJAN BHOWMIK

DST Ramanujan Fellow, Transdisciplinary Biology Program

BRIEF THEME OF LABORATORY

Resolving how nanoparticle (NP)-properties affect their cellular interactions is critical for understanding nanoconstructs' design-activity-relationships. Questions like 1) Which NP-shape is most efficient in receptor targeting? 2) What ligand density is optimal? 3) How to ensure endosomal escapes? etc., require information at the single NP level. We focus on 1) nanoconstruct designing, 2) probing their cellular interaction via fluorescence and DIC imaging, Raman spectroscopy and SERS and 3) evaluating their effectiveness in therapeutic and diagnostic applications.

DESIGNING AND TESTING OF NANOCONSTRUCTS AS THERAPEUTIC, DIAGNOSTIC, AND IMAGING AGENTS.

Imaging of single nanoconstruct dynamics in live-cells: We test different nanoconstruct designs by visualizing the entire process of NP-cell interaction at single particle level. We focus on several different important events in nanoconstruct-cell interaction, starting from probing of NP-cell membrane binding at initial time periods to the tracking of NPs inside the live-cells with DIC, Raman and fluorescence imaging.

From Left: Abhirami Ajith, Bhawna Kangotra, Professor Chandrabhas Narayana, Irfan Shafi Malik

Targeting cancer specific plasma-membrane receptor with anti-cancer nanoconstructs. Many different cancer types have over-expressing of HER-2, a plasma-membrane receptor. Targeting of HER-2 with ligands have been shown to trigger apoptosis. We are designing nanoconstructs with these HER-2 targeting molecules as surface ligands and testing their performance in specific-killing of cancer cells. Gold nanoparticle (AuNPs)-based on their size and shape-can concentrate, protect, and project these targeting ligands on NP-surfaces and boost the over-all effect. We are testing different such functionalized AuNPs (as shown in the figure) for their performances.

Designing and building of a portable Raman spectrometer: We are designing and building an optical fibre based Raman spectrometer and SERS based platforms. With the development of such a portable system, we aim to take cost-effective diagnostics even to the remote areas of our country and out-side.

Designing of nanoconstruct to aid in cholesterol movement: Niemann-Pick disease type C (NPC) results from diseases causing mutations that leads to the accumulation of high amount of cholesterol in lysosomes. To aid the cholesterol movement from inside the cells, derivatives of cyclodextrin molecules (CDs) have been tried as carriers. These efforts, however, failed due to cytotoxicity resulting from unwanted interaction between CDs and plasma-membrane cholesterol, rather than the preferred interaction with lysosomal cholesterol. We are designing CD-functionalized AuNPs to stealthily deliver CDs specifically inside lysosomes.

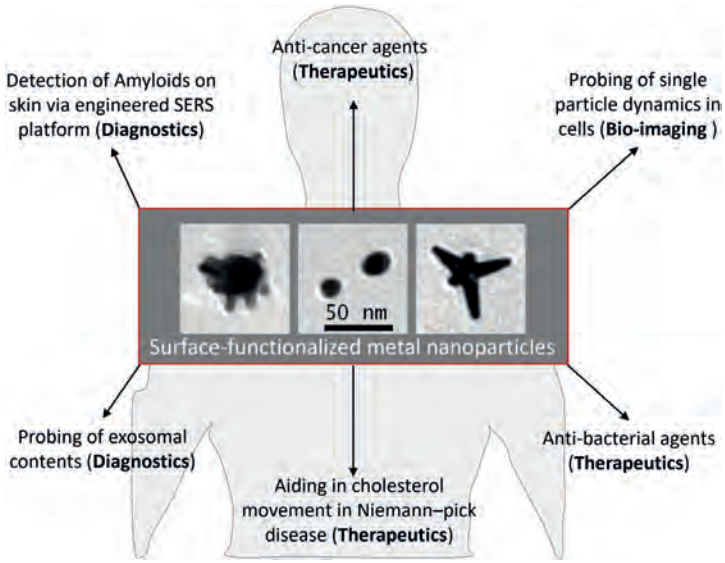


FIGURE LEGEND

Scheme depicting different applications of various nanoconstructs (TEM images at the middle panel) designed in the lab.

PUBLICATIONS

- **Gupta A, Dey S, Bhowmik D, Maiti S.** Coexisting ordered and disordered membrane phases have distinct modes of interaction with disease-associated oligomers. J PhysChem B. 2022;126(5):1016-1023.

GENERAL ADMINISTRATION, SUPPORT AND CORE FACILITIES

OFFICE OF DIRECTOR

Back Row From Left: Priya R, Venugopalan J, Jayalakshmi US
Front Row From Left: Professor Chandrabhas Narayana, Mohanan Nair S

The Office of Director is responsible for successful leadership and management of the organization according to the strategic directions set by the institute management. This office develops the vision and strategic plan to guide the organization, develop an operational plan which incorporates goals and objectives ensures that the operation of the organization meets expectations of its stakeholders and funding agencies. The Office of the Director also oversees efficient and effective day-to-day functions of the organization, draft policies for approval of the Governing Body; prepare procedures to implement organizational policies; review existing policies and recommend changes as appropriate; ensure that programs and services offered by the institute contribute to its mission; monitor day-to-day delivery of programs and services to maintain or improve quality, determine staffing requirements for organizational management and program delivery, recruit, interview and select staff that have the right technical and personal abilities to help further the organization's mission. The Office also is responsible to supervise preparation of a comprehensive budget and to secure adequate funding for the operation of the organization.

GENERAL ADMINISTRATION

The management of research and development (R&D) and innovation has emerged as a specialized area within both research and higher education institutions. New modalities of research and innovation have evolved over the last 10 to 20 years against a backdrop of major changes in the tertiary research and education sector as a whole. The Administration Group is backbone of any such organization. An effective administrator is an asset to an organization. The Administration Group is the link between various units and sections of the organization and ensures the smooth flow of information from one part to the other. The Administration Group also provides administrative & technical support in the areas of human resources management, budgetary, strategic planning, legal affairs, pay and allowances, medical benefits, leave management, purchase procedures, management of stores and facilitates security.

THE CONTROLLER OF ADMINISTRATION

S Mohanan Nair

Directs and coordinates the administrative, finance, purchase & stores activities at the Institute, business service functions & procedures of the Institute and ensures compliance with all applicable regulations & policies. The Controller of Administration is the primary link between the general administration groups and the Office of the Director. The Controller also provides leadership & supervision of business services, administrative duties, all recruitment & promotions, compilation and monitoring of revenue, expenditures etc. The Controller manages all procurements and provision of stores/stock. All legal matters are also supervised by the Controller. The Security, Vigilance, Disciplinary matters are all dealt with by the Controller of Administration.

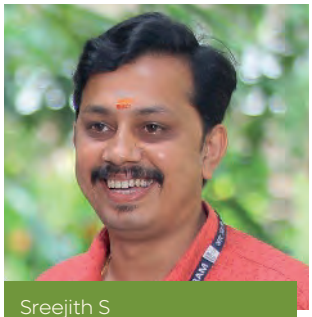
GENERAL ADMINISTRATION DIVISION

The main responsibility of general administration group is to ensure all requirements are implemented for the efficient performance of all research related services at RGCB. The General Administration Group serves as the connecting link between the senior management and employees. The major mandates of general administration include good coordination among all the departments ensuring attainment of organizational goals; optimum utilization of resources, minimization of cost, human resources and payroll, transportation, fulfilment of social and economic needs of the employees and organization as well as development and growth of the institute. The General Administration also implements work related to Estate Affairs, House Keeping & Welfare, Legal matters and implementation of various Acts (including RTI), Building Engineering & Construction, Security & Surveillance, Vigilance & Disciplinary matters and official language.

Front Row: Jayachandran Nair R, Mohanan Nair S
Second Row From Left: Edwin S, Jayakrishnan N, Priya R, Jayalakshmi US, Asha R Nair, Kumar R
Third Row From Left: Usha B, Sandhya SJ, Preetha R, Thankamany R, Reena Prasad, Vinod Lal K
Fourth Row From Left: Akhiljith S, Praveen B, Wilson T, Vishnu P, Santhosh S, Vishnu S

Nidheesh Raj R

Jayanandan J



Sreejith S

Anil Kumar R

INSTITUTE PROJECT PERSONNEL

First Row From Left: Bineesh Chandran SB, Harikrishnan S, Sarath SN, Dinesh Kumar S, Vysakh VR, Renjith Kurup, Akshay Kumar Nair
Second Row From Left: Navajit R Nair, Vinu S Nair, Pradeep TV, Abilal GO, Sreejith GS, Smitha LR, Asha VS, Sreevidya RC, Priya Aji
Third Row From Left: Anithakumari O, Kumari Geetha TR, Devika Menon GJ, Meena H, Chitra GS, Ambika P Kumar
Fourth Row From Left: Neethu SD, Athira VL, Athira Chandran, Vishnu Priya G, Jyothisri VT, Aryasri P, Arathy S

Suresh C

Anandhu Ashok

SUPPORTING STAFF

From Left: Hariharan S, Arun B Krishnan, Baiju R, Ashokkumar S, Pradeepkumar BS, Manukumar SK, Harikumar S

Rakesh SS

Vijayakumar S

PURCHASE & STORES DIVISIONS

From Left: Akhiljith S, Jayakrishnan N, Mohanan Nair S, Kumar R, Praveen B, Sujitha S

The Purchase & Stores Group occupies a vital and unique position in RGCB. This unit ensures procurement of the right material in right quantities and of appropriate quality. The section ensures procurement from right and reliable source or vendor as well as procurement of the material economically, i.e., at right or reasonable price. The RGCB Central Stores serves all four campuses of the institute. The most common yet major responsibilities that are carried by stores include receipt of incoming goods, inspection of all receipts, storage and preservation, identification of all materials stored, materials handling, packaging, maintenance of stock records, inventory control and stock-taking.

FINANCE & IFC DIVISIONS

From Left: Dileep Kumar R, S. Sathi Chandran, S. Mohanan Nair, R. Kumar

The Finance Division of RGCB has been inventive in budget planning and its real-time reporting, always in absolute synchronization with the scientific fraternity of the Institute. Preparation & Monitoring of Budget and Resource Generation are always aimed to acclimatize the available resources' utilization in achievement of its mandated science, thereby paving the way for productive application of all available resources. Prompt generation and submission of internal management information by the Finance Division always facilitates RGCB in taking accurate and apt decisions. Matters related to RGCB's Finance Committee, audit, processing of payments, TDS/GST and returns, accounting of receipts & disbursements, revenue refunds, reconciliation of bank accounts and rendition of utilization certificates and statements of expenditure are always promptly implemented by the Finance Division. The Final Accounts along with Audit Report are placed on the tables of both Houses of Parliament through the Department of Biotechnology. The dynamic contributions of Finance Division have always resulted in building organizational strength, enthusiastic and motivated personnel and hence a robust Institution.

A dedicated IFC enhances in all Financial as well as Administrative/Establishment works related to extra-mural funded projects of the Institute, all matters related to PhD, M.Sc, Summer training programs, Post-Doctoral Fellows etc. Accounting in respect of all service facilities of the Institute are exclusively done by this Group. This specialized Group plays an extremely important management role of all extramural and Institute generated funds. It is the connecting link between all funding agencies and RGCB. The vital duties of IFC includes implementation of procedures related to accounting, payment, preparation and rendition of Utilization Certificates and Statements of Expenditure in respect of all cases except the Core Grants, Ph.D Fellowships, Post Doctoral Fellowships, Program Scientist Fellowships and fund management of Extra Mural Projects. The IFC is also the internal link in respect of all matters pertaining to purchases in utilisation of such extra-mural funds & receipt and issue of stores.

OFFICE OF THE ACADEMIC AFFAIRS (OAA) AND MANAGEMENT

From Left: Briji S, Beena Nair L, Dr. Soniya EV, Dr. K Santhosh Kumar, Hareesh G, Bharath Krishnan JC

The Academic Council is the highest academic body of the institute, chaired by the Director and is responsible for the policies on maintenance of standards of instruction, student learning and experiences, examination and awards within the institute and advises the RGCB management on all academic matters. This committee is also responsible for structuring the course syllabus, admission procedures, program initiatives, faculty support, academic calendar, setting the timetables, the mode of valuation for the PhD course work and MSc programs. This committee also recommends suitable persons as faculty and adjunct faculty for these programs, decides on times and duration of specialty training and internships and ensures coordination between academic affairs management and all other administrative sections of the institute.

CONSTITUTION OF THE ACADEMIC COUNSEL		
Name	**Position**	**Designation**
Professor Chandrabhs Narayana	Director	Chairman
Dr. T R Santhosh Kumar	Scientist G & Dean (Research Administration)	Vice Chairman
Dr. E V Soniya	Scientist G & Dean (Academic Affairs)	Member
Dr. Jackson James	Scientist G & Associate Dean	Member
Dr. G S Vinod Kumar	Scientist F	Member
Dr. Debasree Dutta	Scientist EII	Member
Dr. Rajesh Chandramohanadas	Scientist EII	Member
Dr. K B Hari Kumar	Scientist EII	Member
Dr. K Santhosh Kumar	Senior Consultant (Academic Administration)	Member Secretory
Dr. S Sumi	Program Scientist	Special invitee

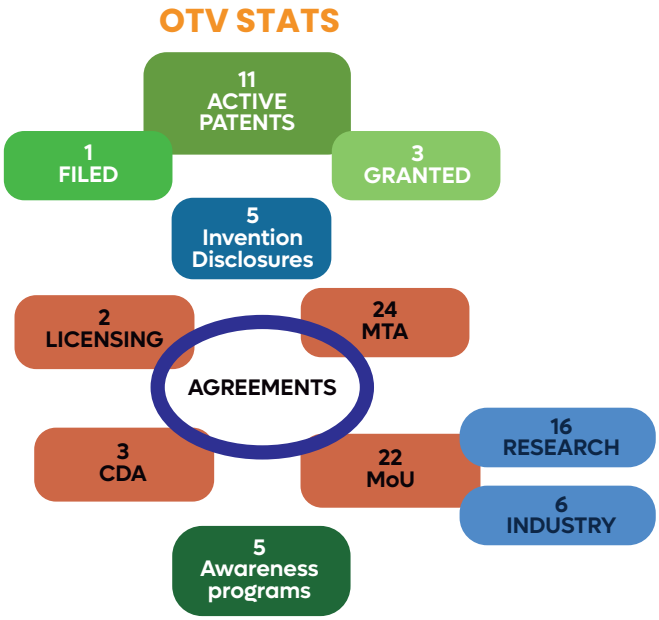
Office of Academic Affairs (OAA) supports the management of academic programs at RGCB including PhD program, MSc program, short term and long term training programs, Post-doctoral training, other specialized training programs and biotechnology skill development programs. The OAA assist the Academic Council to provide leadership roles for collaboration activities in curricular areas such as orientation, residence life, and student activities, while academic affairs tends to assume leadership roles for activities related to curriculum development, implementation, and policy.in development of a strong academic program, policy formulation, and program planning and student research progress evaluation. OAA keeps abreast of trends and changes in higher education; works for institutional vision, survival, stability, growth, and excellence; provides a connection between administration and faculty; serves as catalyst to create a climate conducive to scholarly research in an atmosphere committed to the mandates of the institute and the Department of Biotechnology. OAA's also responsible for the maintenance of all official records related to academics, conducting examinations and publishing results in a time bound manner and distribution of all certificates related to academic activities. The OAA's ensures coordination and collaboration to ensure quality learning for students and excellence in academic administration.

OFFICE OF TECHNOLOGY VENTURES

From Left: S Vivek Hari, Dr. Anish NP, Hima Sithul

The Office of Technology Ventures (OTV) at RGCB is primarily responsible for the Intellectual Property (IP) management of the institute. The roles of OTV include to assess, protect and License the IP developed by the institute's research community. OTV also manages to acquaint RGCB's researchers, students, technical personnel to be aware of generating and protecting the IP along with its commercialization. Apart from this, OTV also manages legal aspects of the research work which comprises of preparation, negotiation, reviewing and administering of the agreements such as Confidential Disclosure Agreements, Material Transfer Agreements, Memorandum of Understandings, sponsored research/consultancy service agreements and Technology Transfer Licensing Agreements to the in-house researchers. Thus we are committed to delivering the benefits of research to the society at large.

OTV is currently processing eleven patent applications and three patents were granted with jurisdictions of grant in Canada, Europe and South Korea. This year OTV received five Preliminary Invention Disclosure Forms (PIDF) from the scientists of RGCB and its evaluation procedures are in due process. We were also able to commercialise various recombinant cell lines developed by our various faculties to "CancerTools.org" managed by Cancer Research Technology, UK. In 2021-22, OTV conducted 3 brainstorming programs with domain experts for promoting Entrepreneurship Ecosystem in RGCB. The glimpses of activities conducted during 2021-22 are depicted in the pictogram.



ANIMAL RESEARCH FACILITY (ARF)

Back Row From Left: Dileep RK, Rajeev RV, Anwar KY
Middle Row From Left: Alex Anto A, Anil Kumar B, Vinod G
Front Row From Left: Sumaja V, Dr. Arya Aravind, Dr. Archana S , Govind V, Vinod VM

Animal Research Facility (ARF) is passionate about its role in providing quality services and expertise in animal research. The facility is registered with the "Committee for the Purpose of Control and Supervision of Experiments on Animals"(CPCSEA); 326/GO/ReBiBt/S/2001/CPCSEA for Research on Education purpose, Breeding for in-house use and Breeding for the purpose of trade. ARF is currently functioning at two campuses RGCB Main campus and RGCB Bio-Innovation Centre, KINFRA campus. It is a small animal facility housing mice, rats and rabbits which has been advancing over years since its establishment. ARF also has a zebra fish facility at RGCB Bio-Innovation Centre, KINFRA campus. At present ARF have 34 strains of mice 3 strains of rat and a strain of rabbit. Last year we expanded the mice stock by adding 7 new strains.

The animals are maintained in a well-controlled micro and macro environment according to their species specific preferences. The temperature, humidity and air changes in the animal holding rooms are controlled using air coolers and air handling unit. The mice are housed in Individually Ventilated Caging System (IVC) where the supply and exhaust air is filtered using HEPA filters. As part of improving the health status and quality of animals, ARF has remodeled the conventional rat rooms in to IVC rooms with controlled macro-environment. The zebra fishes are reared in Recirculating Stand Alone Housing system. ARF has the facility design, procedures and practices of Biosafety level II standards. The facility is equipped with most advanced equipments for various major and minor animal procedures including surgical procedures, imaging, euthanasia and sample collection. ARF also carry out hematological and biochemical analysis of blood and serum samples.

Animal welfare and ethics is given the same importance in

a balanced way along with animal experimentation with the immense support of the Institutional Animal Ethics Committee. The committee convenes meeting as per the guidelines of CPCSEA. The Animal House Management Committee supervises the overall activities of the animal house and takes decisions regarding the purchase activities, request for addition of new animals, expansion of animal house and other relevant matters associated with ARF.

ARF conducts "Certificate course on Laboratory Animal Science" for students and staff who wish to do animal studies. Only certified students are allowed to perform animal experiments. The facility also provides classes for PhD students in topics related to applications of animal research.

ARF believes in "Alacrity, Reliability and Fairness" as its values in its functioning.

BIO-IMAGING, FLOW CYTOMETRY, AND HISTOLOGY CORE FACILITY

FLOW CYTOMETRY CORE

The FACS facility of RGCB is equipped with the following flow cytometer sorters and analyzer. The facility support RGCB research programs requiring all application of cell analysis and sorting and is made available to external academia and industries as per the DBT SAHAJ guidelines. The facility also provides regular training and workshop to students and faculty in basic and advanced flow cytometer applications.

HIGH SPEED FLOWCYTOMETER SORTER SYSTEM: (FACSARIA III)

FACSAria III is a Bench top fixed aligned high speed 4-way sorter system from Becton Dickinson, USA and is equipped with the laser lines, 488 nm, 355 UV, 405 Violet, 561 yellow green and 633 nm red. The machine allows plate sorting. Also equipped with aerosol management system. Location: RGCB Main campus, Central Instrumentation.

HIGH SPEED FLOW CYTOMETER SORTER SYSTEM: (FACSARIA II)

FACS Aria II is a Bench top fixed aligned high speed 4-way sorter systems from Becton Dickinson, USA and is equipped with the laser lines 488 nm, 375 UV, 405 Violet lasers, and 633 nm. Also equipped with aerosol management system. Location: RGCB Main campus, Central Instrumentation.

HIGH SPEED FLOW CYTOMETER SORTER SYSTEM: (FACSARIA III)

FACS Aria III, Bench top fixed aligned flow cytometer is a high speed 4-way sorter system from Becton Dickinson, USA and is equipped with the following laser lines 488 nm Laser, 405 nm Violet lasers, 561nm laser and 633 nm laser. Location BIC, KINFRA, Central Instrumentation

HIGH SPEED JET IN AIR FLOW CYTOMETER SORTER SYSTEM: (ASTRIOS EQS)

This high-speed cell sorter is a six-way jet-in-air sorter from Beckman with 7 spatially separated lasers of 355 nm, 405 nm, 488 nm, 532 nm, 560 nm, 592 nm, 645 nm. Location: Akkulam Campus. The unit is housed in Custom Baker SterilGARD BSL2 cabinet to ensure sterile sorting applications. Location: Akkulam, Central Instrumentation

BIO IMAGING CORE

SPECTRAL CONFOCAL MICROSCOPE WITH RESONANCE SCANNER FOR FAST LIVE CELL IMAGING (A1RSI)

A1R si, NIKON is the most advanced and fully automated spectral confocal microscope from Nikon, capable of capturing high quality confocal images with high speed and sensitivity. This machine includes a 32 array spectral detector and high speed resonance scanner that can achieve more than 25 frames per second at 512x512 pixel dimension apart from motorized xy stage for multipoint confocal imaging. Available laser lines are 488nm Solid state, Diode laser 561 nm, HeNe 633 nm, Blue diode Laser 405nm, all with AOTF control. Also supported by live cell incubation chamber from Okolab for live cell imaging.

CONFOCAL LASER SCANNING MICROSCOPE WITH HIGH SENSITIVITY SPECTRAL DETECTOR (OLYMPUS FV3000)

Olympus FV3000 is equipped with a high sensitivity spectral detector (HSD) with GsAsP PMTs which enables it to view samples having weak emission. The desired emission range can be selected using the spectral detectors. The Diode Laser lines available are 405nm, 488nm, 514nm, 561nm and 640nm with 4x, 10x, 20x, 40x and 60x objectives.

CONFOCAL LASER SCANNING MICROSCOPE WITH GAASP DETECTOR FOR MULTIFLUORESCENCE AND LIVE CELL IMAGING (LEICA SP8 WLL CONFOCAL MICROSCOPE)

Leica SP8 Spectral Confocal with WLL is an advanced confocal microscope from Leica Microsystems, Germany. This equipment is configured with white light laser (WLL) that can support any laser lines between 470-670nm and AOBS for filter less emission tuning, in addition to the highly sensitive GaAsP detectors.

SP8 3X FLACON LIFETIME IMAGER WITH STED

This high end imaging device Leica SP8 3X FALCON is a fully configured Lifetime imaging unit with pulsed supercontinuum light source WLL that can support any laser lines between 470-670nm and AOBS for filter less emission tuning. Both spectral imaging and lifetime imaging is possible in thus system. The imager also supports super resolution STED imaging.

NIKON SPINNING DISC CONFOCAL IMAGER

The Nikon A1R confocal imager from Nikon, Japan is configured with a Yokogawa spinning Disc confocal unit with dual EMCCD camera from Andor to support ultrafast live cell confocal imaging. Most widely used laser lines such as 405, 488, 562 and 633 from Omicron is inbuilt in to the system to support most of the dyes and fluorescent proteins and simultaneous dual color imaging.

IVIS® SPECTRUM IN VIVO IMAGING SYSTEM

The In vivo animal imaging system from Perkin Elmer is located in both campuses. This is an ideal platform for non-invasive monitoring of disease progression and cell trafficking and able to perform high-sensitivity in vivo imaging based on fluorescence and bioluminescence.

HISTOLOGY CORE

The histology core facility is equipped with necessary infrastructure to help the ongoing research at RGCB. The core has a microtome, cryostst and automatic tissue processor and tissue embedder

Front Row From Left: Sanjai D, Dr. Santhosh Kumar TR, Laiza Paul, Surabhi SV
Back Row From Left: Ajith Gopal, Tilak Prasad, Anand Mohan, Vishnu S Sanjeev, Anurup KG

Viji S

Soumya SP

Arya VS

Saravana Kumar M

Jiji V

Indu Ramachandran

Tanima Toni

Ciji Varghese

BIOINFORMATICS FACILITY

The Bioinformatics Facility is located at the Bio-innovation Centre (Campus-II) of Rajiv Gandhi Centre for Biotechnology. Considering the growing demand for computational approaches to solve biological problems, the facility is offering various bioinformatics services and training programs to students and researchers from RGCB and academia. We provide i. Computational infrastructure (Servers and Storages) for performing large scale biological data analysis and storage ii. Short term (1 day) and long term (6-months/1year) training programs (The facility is conducting the training programs in online format) iii. Essential bioinformatics services to students and researchers from academics iv. Academic projects (Bioinformatics) to both internal and external students

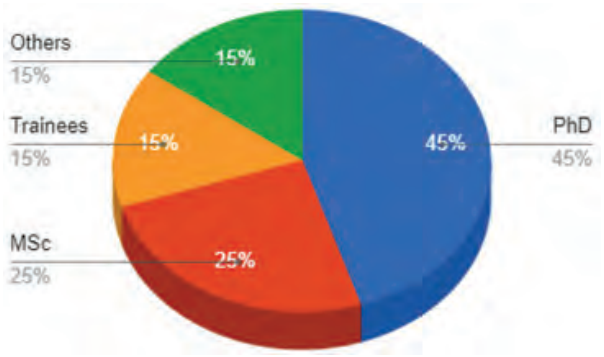
INFRASTRUCTURE

20 x computer terminals
1 x NVIDIA GPU Server with 40 GB RAM
2 x DELL Power Edge server with 128GB and 28TB
1 x NETGEAR storage device

COMPUTATIONAL INFRASTRUCTURE MANAGEMENT

The bioinformatics facility is providing computational servers and storage facility for both students and researchers at RGCB. Currently 2xCPU servers, 1x GPU server (NVIDIA DGX Station with 4xA100 GPUs- 40GB) and an NETGEAR storage device is available at the facility. During 21-22, over 75 server accounts were provided for students, trainees and researchers at RGCB.

Server usage



LIST OF SHORT TERM TRAINING PROGRAMS CONDUCTED DURING 2021-22

Sl.No	Title	Month	No. of Participants	Amount
01	Best practices on performing biological sequence analysis	05/2021	29	14500
02	Protein structure modeling and visualization	05/2021	44	26000
03	Programming for biologists	06/2021	35	19500
04	Practices in molecular docking	06/2021	36	20000
05	Introduction to r package	06/2021	30	15000
06	Introduction to phylogenetics	07/2021	49	35500
07	Jupyter notebook for python beginners	07/2021	15	9500
08	Computational Structure-Based Screening And Explicit Molecular Dynamics	08/2021	45	22500
09	Basics of Molecular Dynamic Simulations	08/2021	41	20500
10	Python Programming For Beginners	09/2021	7	5500
11	Protein Structure Modeling And Visualization	11/2021	33	16500
12	Protein Structure Modeling And Visualization	03/2022	75	39500
	Total		**439**	**2,44,500**

LONG TERM TRAINING PROGRAM (ONE YEAR CERTIFICATE PROGRAM)

	Duration	No. of participants	Amount
Part A	07/2021-12/2021	36	1080000
Part B	01/2022-06/2022	6	120000
Total		**36**	**12,00,000**

LIST OF BIOINFORMATICS SERVICES

	No. Requests	Accepted	Amount
NGS Analysis	10	0	
Protein Structural analysis	12	4	34220
Computer programming	1		
Others	2		
Total	**25**	**4**	**34220**

LIST OF ACADEMIC PROJECTS

Sl. no	Duration	No. of participants	Amount
01	1 months	10	150000
02	2-3 months	6	150000
03	6 months	6	210000
Total			**510000**

From Left: Amal V,Gowrisankar SP, Dr. Shijulal Nelson Sathi, Dr. Sivakumar KC

GENOMICS CORE FACILITY

RGCB genomics core facility offers comprehensive support for DNA-based genomic research methodologies to internal and outside researchers across India.

- The RGCB Genomics Team aspires to realize the vision of the RGCB's primary mandates (Technology Development, Translational Science, Training and Education).
- The Genomics facility is equipped to perform Sanger sequencing and genotyping on a variety of bacterial, viral, plant, and human samples using two Multicapillarry systems 3730 & 3730 XL DNA analyzers, for internal and external users, in order to fulfill the mandate of Technology Development with Innovation and on to business.
- On a fee-for-service basis, research divisions provide internal samples contributiing for sequencing and qRTPCR).
- Institutes like VCRC (Puducherry), JNTBGRI, Medical College Trivandrum, SCTIMST, Rubber Board (Kottayam), CSMCRI Gujarat, Lovely Professional University and many are our regular genomic service users, utilized our facility in 2021-2022 for their research needs, contributing Rs. 2,27,000.

- Fragment analysis: plant / animals samples were processed for SSR analysis, SNP genotyping and microsatellite analysis for various research laboratories.
- The facility is outfitted with Quantstudio 5 (both 96-well and 384-well) and RTPCR 7900HT for Q-PCR applications.
- Various internal and external investigators of research labs used the Real Time PCR facility for gene expression studies, in SNP analysis, absolute quantitation, relative quantitation, Allelic discrimination, & Taqman low Density (TLDA) array applications using SYBR green/Taqman chemistry.
- The affymetrix genechip microarray platform has been fully utilized with human and mouse arrays.
- The facility is also equipped with droplet digital PCR (BioRad) for copy number variation studies and genomic library quantitation.
- Illumina 'Novaseq 6000' is newly installed at the new RGCB campus at Akkulam and will be functioning shortly.
- Revenue generated from various training programs (Rs.14, 000), during the period.

Genomics lab is engaged in sequencing analyses for the Delta plus variant COVID mutation surveillance study to support the Molecular Infectious Virology Lab, screening multiple mutants in the Kerala population as part of the mandate of Translational Science to benefit individual, clinical, and public health sector.

RGCB's primary vision of developing a sustainable pipeline of biotechnology professionals (Training & Education), Genomics Team provided training in DNA Sanger sequencing / qPCR / Microarray to students and researchers of Amrita University (Kollam), VIT University (Vellore), and JSS Medical College, Mysore. Also numerous students from various institutes/colleges visited the facility during the period.

Fig: 1, Pie-charts showing 3730xl Sanger sequencing (left) & Quant Studio 5 qPCR (right), usage proportion and revenue generated from the RGCB genomics services. The total internal usage fee collected during the period is Rs. 4, 07,500 for Sanger sequencing/genotyping & Rs. 44,300 for qPCR. Genomic facility usage fee collected from external users is Rs. 2, 27,000 during the period.

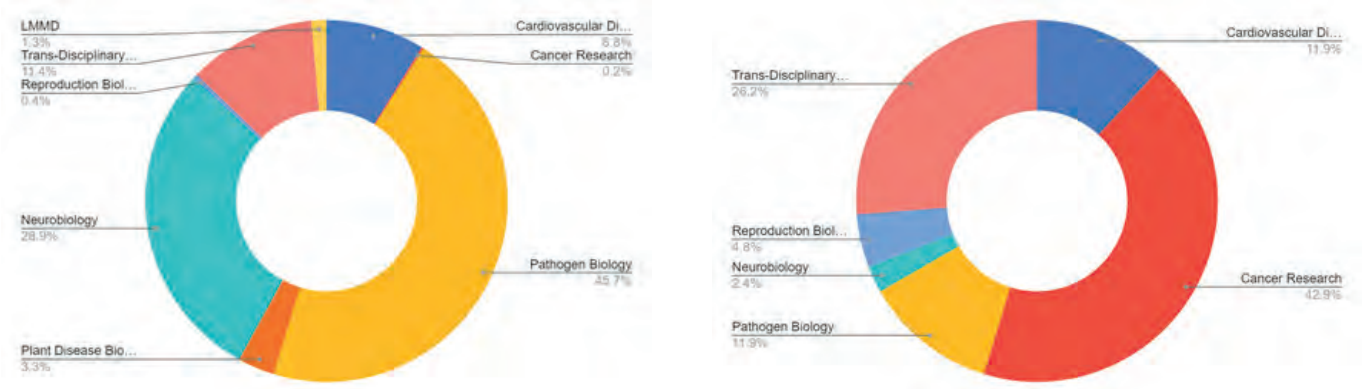
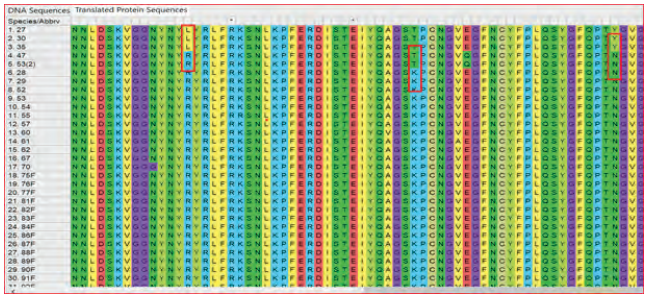


Fig: 2, multiple sequence alignment comparison between ORF1a sequences of COVID positive samples.

Multiple sequence alignment comparison between ORF1a sequences of COVID-positive individuals, showing strain and demography specific mutation detection [N501Y mutation (B.1.1.7), L452R mutant (Delta B 1.617 variant), and T478K (Alpha variant B1.1222)]



From Left: Dr. P Manoj, Dr. TR Barath Kumar

LABORATORY MEDICINE AND MOLECULAR DIAGNOSTICS (LMMD)

Laboratory Medicine and Molecular Diagnostics (LMMD) is a stand-alone laboratory under Rajiv Gandhi Centre for Biotechnology with worldwide recognition. The department was initiated to fulfil the social cause by handling molecular diagnostics, sequencing-based studies, and serology for different types of disorders in both infectious and non-infectious diseases. The Division currently performs over 250 parameters.

HISTORY

The Division had a very humble beginning under the ICMR Virology network program and was recognized as Grade 1 laboratory. The Division did initially concentrate on major infectious diseases such as HBV, HCV, H1N1, and Dengue virus. The Division gradually started expanding its portfolio from those four parameters to other infectious diseases in gastroenterology, transplant medicine, respiratory medicine, neurology, Ophthalmology, Pediatrics, Oncology, and Gynecology. With NGS-based detection for mutation and bacterial identification added to the current portfolio, LMMD now covers most of the Molecular Testing platforms. The Division has developed in-house PCR techniques for the identification of different organisms. The Division initiated non-infectious diseases at the beginning of 2013 by elaborating on the research in Hypertensive Hypertrophic Cardiomyopathy in association with KIMS Hospital. The lab attained the NABL ISO15189-2012, NABH, and ILAC accreditation in 2016 for its quality control.

INFECTIOUS AND NON -INFECTIOUS DISEASE INVESTIGATIONS

Currently, the Division has expanded its portfolio to nearly 250 investigations. The Division handles almost all Viral, Bacterial and Fungal diseases analysis. Whenever there is an emergence of new disease, the Division will start standardizing the test and will be ready for testing in the very first few weeks of the epidemic. This helps the government to take necessary preventive steps to circumvent further spread of the disease. The Division has included tests that are relied upon in identifying emerging infections, antibiotic resistance, exposure to toxic substances, and detection of chemical and biological threats into thrust areas of laboratory support. Except for five tests, all the remaining tests are developed and validated in-house. Non-Infectious diseases such as genetic disorders like Cardiovascular Diseases, Cancer markers, Autoimmune disease, transplant medicine, etc., are also screened. Personalized medical approaches for patients based on their needs were developed in the Division and are used nowadays by clinicians. The major highlight of investigations performed in the Division is turnaround time and cost-effectiveness, as a governmental institution the Division charges only a minimal amount for each investigation in comparison with other private diagnostic centers. Genotyping of HBV and HCV was an initiative by LMMD, which sheds light on antiviral therapy resistance. ELISA and Immunofluorescence assays were launched as testing platforms to rapidly detect major diseases such as scrub typhus and the Hanta virus. The reports generated for the Division are by a cloud-based system, Laboratory Information System (LIS). All the data received in the Division is uploaded on ICMR -NIE National Institute of Epidemiology.

SOCIAL SERVICES

The Division has initiated the screening of H1N1 during the pandemic in 2010. The Division was receiving samples from all over Kerala as well as Tamil Nadu and Karnataka states. More than 1000 samples per day were received in the Division during that period. The reports were sent to the Government of Kerala as well as ICMR for preventing the disease from further spreading. The Division in collaboration with the Govt of Kerala performed screening for the Dengue outbreak between 2012 and 2016. The technologists of the Division used to have peripheral posting for sample collection and point of care testing. The samples were bought back to the lab for detailed study such as genotyping, whole genome sequencing, etc. The lab has published the Dengue serotype 4 whole genome in NCBI, Seven Genebank® accession numbers KJ938501 through KJ938507 awarded for Dengue 4.2013, 4 papers were published in international journals from the Division based on the samples collected during epidemics. When the Nipah virus was reported in Kerala in 2019, LMMD initiated testing of suspected patient samples to screen for the possibility of an outbreak. The Division holds a huge repository of outbreak samples such as 7000 Dengue samples, 8000 H1N1 samples, etc.

SARS COV 2

SARS-CoV-2 was the major and deadliest pandemic that happened worldwide. The impact of the disease is persisting throughout the world. The screening of SARS CoV 2 was started on March 2020 as soon as the first case of SARS CoV 2 was reported in India. The lab started working 24 hours and still continues the process. The lab is working 365 days for the screening of SARS CoV 2. 25,6855 samples have been tested and among which 24,095 were positive. The positive samples are stored and are used for sequence-based studies for understanding the new mutations and viremia. LMMD, RGCB is the only participant from Kerala in INSACOG (Indian SARS-CoV-2 Genomic Consortia (INSACOG), coordinated by the Department of Biotechnology (DBT) along with MoH&FW, ICMR, and CSIR, the consortium will discover a new variant of SARS-CoV-2, in the country.

VALIDATION CENTER

LMMD is the Grade1 virology laboratory under ICMR and is an approved validation center for diagnostic kits and instruments. PCR, Antigen, Antibody, ELISA, and VTM used as a diagnostic tool for infectious diseases are validated in the Division. Disinfectants and instruments are also tested in the Division. The validation reports generated from this Division are approved by ICMR, CDSCO, and the Govt of India.

Antibody Kits	25
Antigen Kits	18
ELISA Kits	1
Isolation kits	9
PCR Kits	23
Disinfectants	5
Instruments	28
Batch Testing for CDSCO	7

▲ Table 1: Total number of kits validated in LMMD

RESEARCH

The Division concentrates on translational research. The lab has experience in developing point-of-care testing devices for many diseases such as swine flu, SARS CoV 2, etc. The lateral flow assay developed for snake bites is approved by Govt of India. The VTM, RTPCR kit, RAT kit, and RNA isolation kits jointly developed by the LMMD and industry partner for COVID-19 detection are approved by ICMR and CDSCO and are currently available in the market. The Division is a part of WHO KARS NET an initiation by WHO to study antibiotic resistance. Currently, the lab has an ICMR study on the Association of genes encoding APRIL and BAFF with IgA Nephropathy (2020-2023). LMMD along with SCTIMST is developing NTProBNP (left ventricular failure marker) lateral flow assay. This project is supported by ICMR

NEXT GENERATION SEQUENCING

The Division started next-generation sequencing on June 2022 based on Oxford Nanopore technology. The Division has performed whole genome sequencing of almost 11671 SARS CoV 2 samples and the data has been uploaded to GISAID (Global Initiative on Sharing Avian Influenza Data) and NCBI. LMMD also does gut microbiome analysis by deep sequencing the samples from the Regional Cancer Centre and other hospitals across India.

TRAINING

LMMD is an GMC-approved rotation center for medical PG students; 155 Medical Postgraduate students (MD Biochemistry, MD Microbiology, MD Pharmacology, MD Pathology, and MD Transfusion Medicine) have completed their training in this Division so far. The Division started a Skill development program, a 6-month program of hands-on training on molecular diagnostics, quality control, next-generation sequencing, etc.

REVENUE GENERATED

Total revenue generated from August 2021 till August 2022 is : 14597400 INR

Table 2: Total revenue generated Aug 2021- Aug 2022 ▼

Month	Revenue
April 2021	4427150
May 2021	1694350
June 2021	1262800
July 2021	1014600
August 2021	1303400
September 2021	1489200
October 2021	1446800
November 2021	1286800
December 2021	1244300
January 2022	3758300
February 2022	1559600
March 2022	529300

Front Row From Left: Rahul JL, Rabeeha AR, Sreelekshmi S, Akhila Jayan, Sanu Ghosh K, Surjith SB, Prasanth KP
Central Row From Left: Sarojam A, Manju S, Midhula SU, Vineetha PT, Heera Pillai R, Karthika V, Soumya Rafi, Chithra S, Soumya VK
Back Row: Visma S

LIBRARY AND INFORMATION SERVICES, CENTRAL LIBRARY, RGCB

From Left: Shibin SB, Balagopal S, Suma S Nair, Meera NV, Gopakumar G

The RGCB Central Library is a repository of a valuable collection of many sought-after international books and journals on life sciences. The library is well equipped and dedicated to cater to the needs of the diverse subscribers of its research/academia/general domains to meet the present and future needs of the centre. All in-house library procedures are fully automated through the open source library management software koha, and barcoding technology is applied for the circulation system. The library's committed aim of providing physical and online library & information-associated services is always harmonious in all respects to the current and envisioned educational and research information needs of the RGCB community.

LIBRARY RESOURCES

The library has a widely varied collection of traditional and digital resources. The printed resource collection of the library includes books, journals, magazines, standards, manuals, protocols, multi-lingual newspapers, etc. The library hosts a collection of more than 8500 printed documents, which contains a substantial number of internationally acclaimed books on life science, and a collection of national and international journals and magazines. Also, the library has a vast collection of standards, manuals, protocols, reports, reprints, back volumes of periodicals, theses & dissertations from RGCB, etc. Metadata of all these documents can be accessed globally through Online Public Access Catalogue (OPAC). Back volumes of more than a hundred international and national journals from 1995 onwards are preserved here. The library has a separate section on literature & popular science books. The documents are classified using the Dewey Decimal Classification (DDC), the globally-used classification scheme.

The e-resource collection of the library covers digital media references and various subscribed e-resources, including e-books, e-journals, e-databases, research support software, etc. Online resources in science and technology and related areas from national and international publishers are available for the user community. Majority of the e-resources were obtained through the DBT e-Library Consortium (DeLCON), which provides access to thousands of e-journals, e-books, databases, etc. RGCB library is a member of DELNET (Developing Library Network), the network that promotes resource sharing among libraries. The library has an institutional repository, IR@RGCB, hosted on the Science Central platform, which collects, preserves, and disseminates the institutional research outputs in digital format. The library has subscribed to JoVE (Journal of Visualized Experiments) Research Unlimited, a peer-reviewed scientific online video journal collection that publishes experimental methods in video formats. The digital library consists of several desktop computers with supporting audio-visual peripherals are available for maximum use of e-resources in the library. The additional requirements related to subscribers' queries were addressed using resource sharing from other institutes.

LIBRARY SERVICES

The library follows an open access system ensuring excellent service for all users. The library renders services such as OPAC services, digital library services, new arrivals alert, reference and consultation services, user orientations, reprographic services, media clipping service, citation and bibliographic analysis, document delivery services (print and electronic), CAS (Current Awareness Services) and SDI (Selective Dissemination of Information) services, etc., to update and support the user community with the latest information in their subject area.

RESEARCH SUPPORT TOOLS

The library has earned itself a key position with its professionalism and state-of-the-art infrastructural facilities. The library continuously updates technology to meet the demands of users. It facilitates access to the tools for the research activities of the RGCB Community. Some of the research supported tools are;

Turnitin - Software for plagiarism detection
FlowJo - Software for flow cytometry data analysis
GraphPad Prism - Software for statistical analysis
EndNote - Software for reference management
Grammarly - Academic writing tool
Quillbot - Academic writing tool

RGCB library continues its effort to respond positively to the diverse needs of the users. The library could discharge its onerous responsibilities with a sense of commitment to the expectations of all who seek assistance.

MASS SPECTROMETRY & PROTEOMICS CORE FACILITY

The Mass Spectrometry and Proteomic Core Facility at RGCB provides cutting edge mass spectrometry technology available to RGCB researchers as well as the wider academic and life science industry community across the country. While being a core facility, a major goal of the facility is to become a research environment for multidisciplinary research that utilizes mass spectrometry and other related technologies to understand the disease biology and molecular medicine in the post-genomic era. The facility has 1) Synapt G2 HDMS Quadrupole-TOF mass spectrometer (Waters Corporation), 2) MALDI-TOF-TOF (Ultraflextreme) from Bruker Daltonics, 3) Orbitrap Eclipse Tribrid Mass Spectrometer (Thermo Fisher Scientific), and 4) TSQ Altis-Plus Triple Quadrupole Mass Spectrometer (Thermo Fisher scientific). Together we provide services such as mass determination, polymer analyses, protein identification, high throughput proteomics protein profiling, relative quantification or protein expression, determination of post-translational modifications and Targeted and non-targeted metabolomics and lipidomics.

PROJECT TITLE

Comprehensive mass spectrometry based Lipidomics & metabolomics platforms for promoting biomedical research & advanced training for Indian researchers

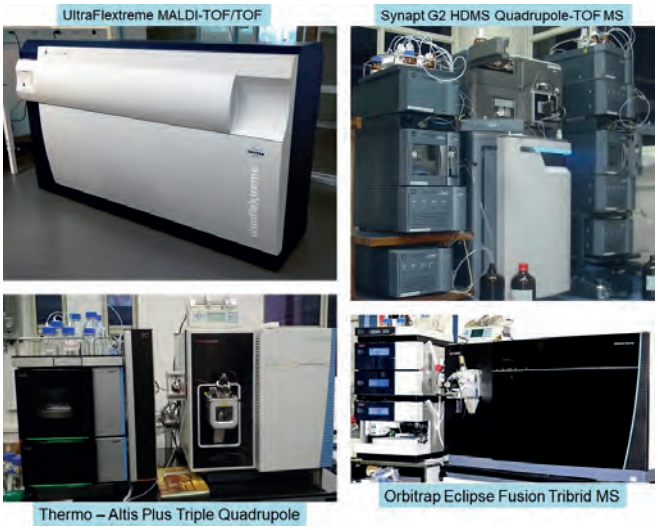
Project Leader/ PI	:	**Abdul Jaleel**
Funding Agency	:	**DBT (SAHAJ)**
Duration and Amount	:	**4 years (2019-2023)** **Rs. 995,48,800**
Date of starting work	:	**April 2021**
Envisaged date of completion	:	**March 2025**

From Left: Sudha B Nair, Arun Surendran, Anoop Krishna PN, Bindu Asokan, Lekshmi Padmakumar

SUMMARY

The overall aim is to establish a comprehensive mass spectrometry based Lipidomics & metabolomics platforms for promoting biomedical research & advanced training for Indian researchers. The platforms will be 1) a High Resolution Mass Spectrometer (HRMS) for discovery & characterization of molecules and 2) a Triple Stage Quadrupole Mass Spectrometer for absolute quantification of molecules. These platforms undertake clinical & biological studies of lipidomics & metabolites through identification and quantification of known and unknown lipids & metabolites in biological samples. The objectives of this project will be to;

- Develop a high-throughput, global, non-targted discovery type lipidomics profiling tools.
- Develop a comparative lipidomics approach that enables semi & absolute quantification of several lipid species across major lipid classes and subclasses (in hundreds) using the least minimum amounts of biological material.
- Implement stable isotope dilution (with different internal standards) approach to provide quantitative data on each of the several (various) lipid species.
- Development of panel of lipid metabolite species related to disease risks specific to the population of Kerala.
- Application of lipidomics to identify lipidomic signatures that can improve upon traditional risk factors for the prediction of diseases such as diabetes mellitus.



Our objectives will meet the stated goals of the SAHAJ-Infrastructure Programme of DBT such as; 1) Quantitative and qualitative expansion of the existing infrastructure, 2) To provide access to world class and state of the art facilities to users and investigators in the country, 3) To develop technology driven capacity building, 4) For the human resource development through training and finally 5) To improve the biotech infrastructure for educational and quality research leading to societal impact.

FIGURE LEGEND

Various Mass spectrometer systems housed in the MS and Proteomics Core Facility

RGCB MEDICAL LABORATORY SERVICES

RGCB Medical Laboratory Services (MLS) comes into the forefront with its unique translational capability in advanced laboratory and theoretical skills in disease biology as well as having a highly qualified and trained man power was initiated in 13-09-2017. RGCB MLS is an indispensable clinical laboratory professional partner that provides clinical lab information and services to the Public by use of optional but advanced levels of health care resources. Medical laboratory testing plays a crucial role in the detection, diagnosis and treatment of patients. Approximately 60 to 70 percent of all decisions regarding a patient diagnosis, treatment, hospital admission and discharge are based on laboratory test results. This permits maximizing effective delivery of care in today's complex health care system by accurate test results that enable providers to make the right diagnostic and therapeutic decisions. RGCB MLS provides all standard hematological, Clinical Pathological Biochemical, Immunological, Microbiological and Serological analysis performed on the latest state of the art analyzers, fully automated and interfaced platforms to cope up with the productivity of today's new technologies new diseases and disease epidemic that continue to drive the need for more innovative tests and testing methods drive the need for rapid diagnosis with stringent Internal and External Quality Control program. We are providing accurate reports by involving in strict internal control program for all sections and 2 External Quality Control Program of CMC Vellore and BIORAD USA.

While technology continues to improve the productivity of today's laboratories, new technologies new diseases and disease epidemics continue to drive the need for more innovative tests and analyzing methods.

We have Started many new generation post COVID analysis round the clock and doing analysis for all Govt. COVID centers. Using latest cloud based software, reports reach the persons immediately following the approval of reports.

RGCB MLS was awarded NABH accreditation for 5 main Centers separately on September 2018 and renewed up to September 2023. Labs are registered with Clinical Establishment Act 2018 also. RGCB MLS provides investigations on Central Govt. Rates (CGHS) with special concessions to BPL patients.

Started many new parameters and installed new analyzers like

1.Perkin Elmer DELFIA X PRESS 600 immunoanalyzer USA with life cycle software: For investigating Double marker and triple marker Test

2. Fully automated capillary electrophoresis system

3.Vapour pressure osmometer-Elitech USA

4. Magnus MX 21i LED microscope.

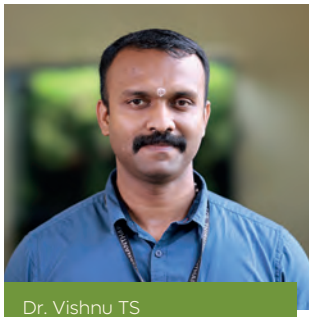
RGCB MLS is involved in investigating various types of analysis for many projects for RGCB Research program, for Cardiology, Ayurveda research Center and Home Research Division etc. Medical camps are conducted for doing various analysis panel required in Offices and Flats on CGHS rate.

Recently in this COVID -19 pandemic period, we have started Home Clinical Investigations service for all parameters including COVID 19 RT-PCR and COVID Antigen for Elders, Palliative care patients, pregnant ladies, children, persons under quarantine etc. to provide rapid information needed to triage patients and confirm the presence of communicable disease, on CGHS rates seems to be very helpful to the public.

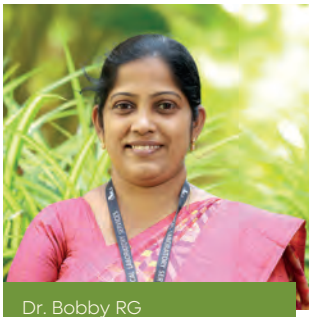
Now the GOVT. have encouraged us to provide advanced training in Medical Diagnostics and related areas to the staff and others engaged in the field of clinical investigations in Microbiology, Biochemistry, immunology and Haematolology. Short term training for two weeks and long term training for 3 months for DMLT, B.SC MLT, B.SC Biochemistry and Microbiology students as well as for M.SC Biochemistry and Microbiology students after completion of course.

Dr. Ashok R

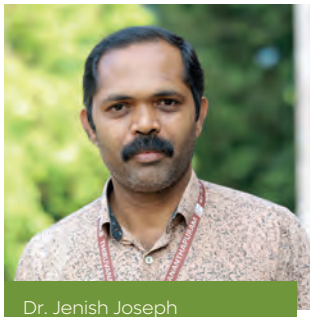
Padmavathy Amma B



Dr. Vishnu TS

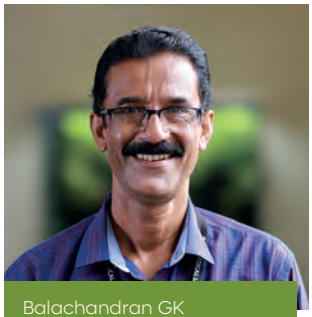


Dr. Bobby RG

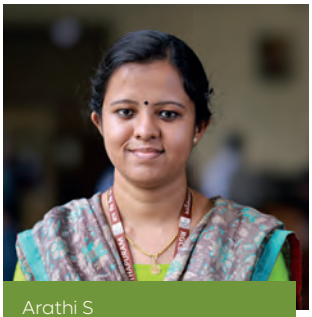


Dr. Jenish Joseph

Ambili S Nair



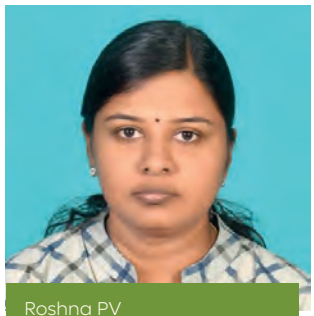
Balachandran GK



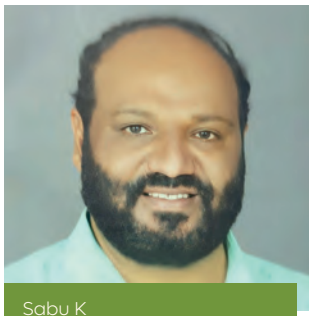
Arathi S

Arjun S

Sathiesh Kumar KB



Roshna PV



Sabu K

MOLECULAR FORENSICS & DNA TECHNOLOGIES (MFDT)

Front Row From Left: Rintu T Varghese, Dr. EV Soniya, George Varghese,Preetha V Rajan,Remya RC
Central Row From Left: Anilkumar P, Suresh Kumar U, Ratheesh RV, Renju Krishnan RV, Vinodkumar S, Johny G, Saptarshi Biswas
Back Row From Left: Abhilash MK, Anandhu A

MFDT offers DNA fingerprinting services to legal bodies, crime investigating and law enforcing agencies. The samples analysed at MFDT relates to maternity/paternity disputes, crime, rape incidents and cases involving man missing. CO1-based molecular identification and DNA barcoding of fauna especially for species identification in wildlife forensics is yet another service offered by MFDT. Other services offered by this facility include DNA fingerprinting of plants and animals in case-by-case manner using RAPD, AFLP or microsatellite markers and DNA barcoding of animals using CO1 gene and plants using matK and rbcL. The facility also offers hands on training on DNA fingerprinting and DNA barcoding techniques. Details about various DNA fingerprinting/barcoding services and training programmes are provided in our website.

In 2021-2022 we analysed more than 107 samples related to identification, maternity/paternity and relationship disputes forwarded by Courts from different districts of Kerala, Child welfare Committee and Kerala Women's Commission. In addition, we have analysed 10 forensic samples to identify the body recovered from the crime site.

We have also received more than 255 samples related to animal poaching forwarded from various forest range offices through court. Animal poaching is one of the major threats to the animals in wild. It is imperative to punish the offenders to prevent illegal poaching. Samples confiscated by forest officers in Kerala Forest Department are forwarded to our lab for identification of species, so as to enable them to charge the case and punish the offenders. DNA Barcoding helps to identify animals even from minute or cooked samples. But the exact identification of species from the Western Ghats region of Kerala, which is one of the hottest biodiversity hotspots, is often difficult or not possible due to the lack of reference sequences in databases.

Nine candidates were given training in DNA fingerprinting/barcoding during this period. We have received more than 2118 samples for DNA Barcoding/Fingerprinting/Sequencing analysis from various research institutions, colleges and universities from all over India.

RESEARCH ENGINEERING SERVICES

Front Row From Left: Soumya SP, Aswathy G Raj, Rajasekharan K, Sajan IX, Shaji V, Parvathy L
Back Row From Left: Ancy Prince, Ajith Kumar R, Prem Kumar V, Akhil Kumar T, Ullas Chandran CD, Aneesh B

Front Row From Left: Aneesh R, Sajin GS, Ajeesh SS, Bibin Dev, Jacob B, Sreekanth SL
Central Row From Left: Ajun babu SU, Shibin J ,Vijeesh T, Ajeesh Shaji, Sreenath, Ajeesh R, Desing
Back Row From Left: Ajith Kumar S, Rajasekharan K, Ancy Prince, Aneesh B

Research Engineering Service Department has been playing an important role since inception of the Institute, and its contributions in the growth of the Institute are not neglectable. Having operations in three campuses, it ensures uninterrupted supports, with no compromise on quality and standards at any level of its functioning, which directly contributes to the outcome of the various Research activities. The ultimate goal of the department is to support all divisions, striving to achieve the Mission & Vision of the Institute, impartially and upholding the highest standards of integrity.

The prime responsibility of The Department encompasses installation, care & maintenance as well as service of all sophisticated and general research Equipments, including that of Central Instrumentation Facilities at Main Campus and Bio Innovation Centres.

This Division also maintains a well equipped engineering workshop with facilities for repair of sophisticated instrumentation systems. It helps to curtail, the down time of the sophisticated instruments and heavy repair costs. Inhouse Engineer's expertise to fix highly complicated hardware issues helps the institute to save heavily on AMC and CAMC's to be signed with respective suppliers of the equipments. On top of the above, the Division also undertakes customisation by designing, fabrication & modification of components of research automations to meet end users requirements and convenience.

It also extends its support in procurement, by analysing the need of the user department, understanding the currently available technology, features and future upgradation/ customisation possibilities, and prepare necessary technical specifications within the budget, to initiate purchase processes through out the years.

Division has well equipped inhouse Calibration facilities, mainly for pipettes, electronic balances, centrifuges, autoclaves, freezers, incubators, PCRs etc., . This facility includes standards and measuring instruments with proper calibration certificates from Govt. recognised National Calibration and Acreditation Agencies. Department has been calibrating and certifying instruments of various laboratories aspiring for NABL accreditation.

Research Engineering Services has also been offering training programs for students of Engineering Degree & Diploma, on operation, application, calibration and maintanance of various instrumentation systems used in Biotechnology and Life Science Research. 35 students had undergone training program in research engeering Services division during the period 2021-22

Apart from the above, the division also maintains computers and security surveillance systems, biometric time attendance recorders, online conferencing facilities, communication systems, liquid nitrogen plant, auditoriums, convention centre, 11KV electrical substation & 340 ton AC plant which includes power transformers, distribution transformers, DG sets, protection & control equipments, medium & high voltage switchgears, chillers, UPS & batteries, passenger lifts and elevators. Department also takes a role in automation with PLC/DCS/Scada Control Systems.

Research Engineering services plays an instrumental role in recognizing and adapting cutting edge technologies to facilitate instrumentation systems to reduce man machine interface.

Research Engineering Services have set up new precedents and a bench mark for similar departments in other institutions in the country and this division can set up new goals while contributing silently and significantly to grow the institution to new heights in the days to come.

Front Row From Left: Lekshmi C, Arunima B
Back Row From Left: Renadeep CS Nair, Anoop ML, Sajith Kumar S, Vijaya Kumar AS

INFORMATION TECHNOLOGY AND DATA MANAGEMENT GROUP

From Left: Ramya Rajan, Rajasekharan K, Lekshmi R, Durga Prasad C, Radhika U

The IT infrastructure of RGCB's main campus includes 9 Servers, more than 400 Desktops, and Laptops, Network Printers, etc., and houses of one of the best computing networks with constant up-gradation in a bid to provide the students and staff with state-of-the-art facilities. The Institute has been connected to the National Knowledge Network, which provides a 1Gbps leased line with multiple redundant backups.

The highly distributed computing environment at RGCB uses sophisticated computer simulation to solve staff and research scholars' problems. It is managed and actively supported by experienced engineers in the IT Department. IT department is also responsible for maintaining and administrating Mail Servers. IT department provides technical support to staff and students within the Institute on LINUX, WINDOWS platforms and includes software development for research groups.

IT department design, develop, update, host and support RGCB Website, online admission portal, leave management system for PhD students/ project staff, laboratory management system, online training portal, online portal for various positions at RGCB, conference websites, intranet applications for various administration and scientific activities, yearly portals for updating annual reports, SAC and integrating payment gateway for various web applications. In the mid of Covid-19 pandemic, IT team supports the smooth functioning of onlineclasses for MSc and PhD students via moodle, hosted and fine tuned by IT Team.

Internet facilities are provided throughout the campus through 1 Gbps, and 100 Mbps leased lines from NKN and BSNL. Internet facility for Akkulam Hostel block also has the 100Mbps leased line.RGCB has invested in a high-speed Fibre Optic Backbone with high-end security for networking across the campus. Wireless connectivity is provided at strategic locations to provide Internet access to the faculty.
The Information Technology Division of Bio-innovation Centre at KINFRA,Kazhakuttom, uses cutting-edge technology to provide high-quality services and capabilities to different research groups. It includes servers with active directory domain infrastructure, secured network with state of the art firewall system,100Mbps leased line, and 100Mbps broadband line with failover backup connection

CAFETERIA

An exclusive well- maintained cafeteria is available in all our RGCB campuses offering tasty and hygienic food. In order to cater to all the students /staff and visitors from different parts of India and abroad, South Indian, North Indian and Chinese dishes are offered. Food quality and hygiene are the two most important factors in the cafeteria. There is regular quality control and quality checks at the cafeteria to ensure highest standards of hygiene. There is never a compromise on food quality, cleanliness, and overall hygiene at the cafeteria. Be it kitchen or raw materials used for preparation of food, everything goes through a stringent quality check. The "onam" feast with more than 20 different dishes is just one example of the culinary skills of the cafeteria chefs.

We aim to minimize the impact of catering operations on the environment and promote sustainable practices and consumption. The RGCB cafeteria runs on a "no profit no loss basis"

Main campus: Back Row From Left: Shivankutty Nair, K, Sajith C, Sureshkumar R, Manoj Kumar R,
Middle Row From Left: Najeem M, Sunil Kumar, Gopakumar, MS, Abinandh, PS, Arun Kumar, Deepu R V Nair
Front Row From Left: Sanshya R, Sailakumari, I, Meemna RP, Remadevi Amma BR, Prasanna TR

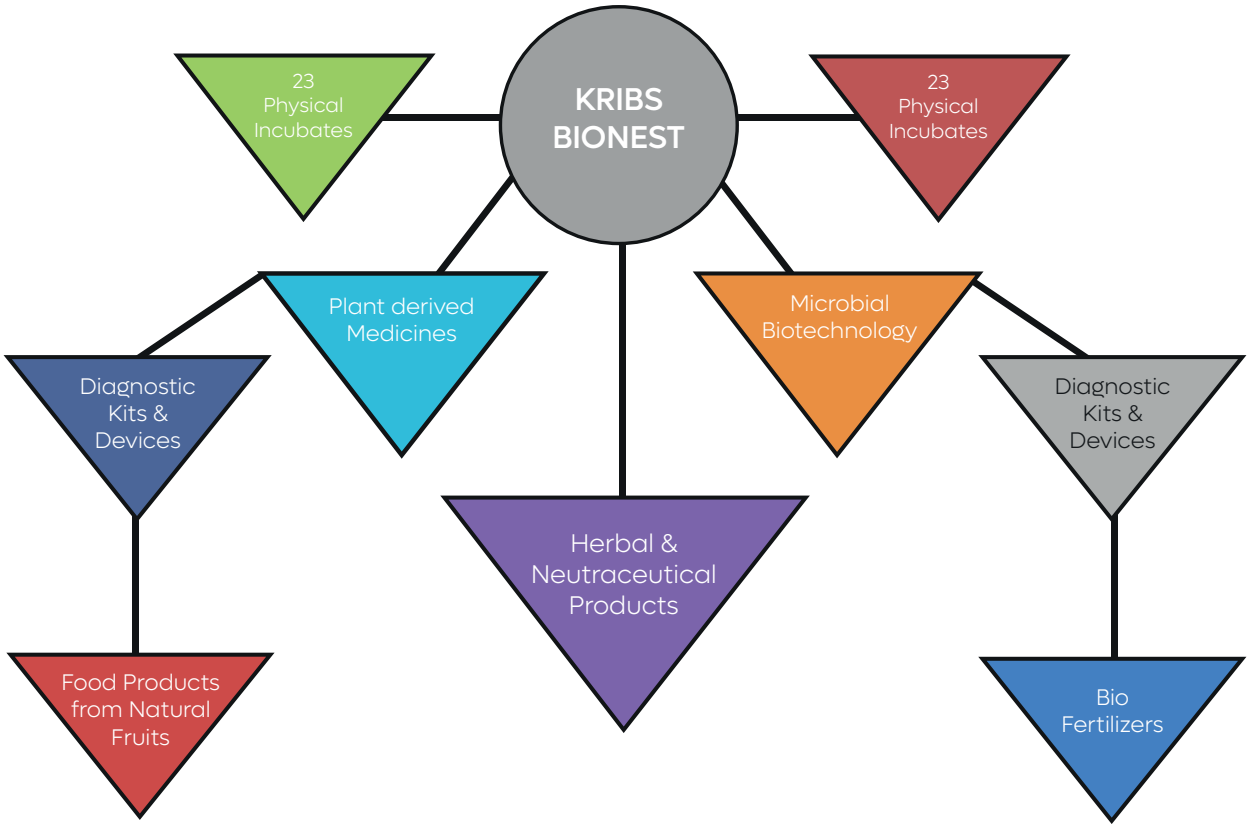
BIC campus: Back Row From Left: Rahul S, Anandhkumar, Baiju, Chandra Raj
Front Row From Left: Praveen Mohan, Nandha Kumar

Akkulam campus: Back Row From Left: Rajesh Kumar PS, Anoop KC, Manoj S
Front Row From Left: Baby saraswathy L, Bindhu, Jayakumari S,
Prathush P

KRIBS – BIONEST (2021-2022)

KRIBS-BioNest - Biotech Park - Kochi, the technology incubation centre of RGCB, operates in collaboration with Kerala Start-up Mission at Kerala Technology Innovation Zone, Kalamassery, This is a unique facility designed to provide infrastructure and scientific support to enable researchers and inverstors enterpreneurs looking to transform biology, medical based technologies and innovations into real and mature big business. With a total floor area of over 44,000 square feet, it offers over 17,000 square feet of bio incubation space and a common laboratory measuring 1000 square feet to the Start-ups housed within the facility.

The facility currently has 23 physical incubators and 7 virtual incubators. The number of new inquiries and applications for incubation based on biotechnology has significantly increased in the last year. Four of the incubators in their fourth year of incubation were permitted to lease land in the KINFRA Hi-Tech Park for the next 33 years. These companies can continue to utilize the cutting-edge technological platforms offered by KRIBS-BioNest.

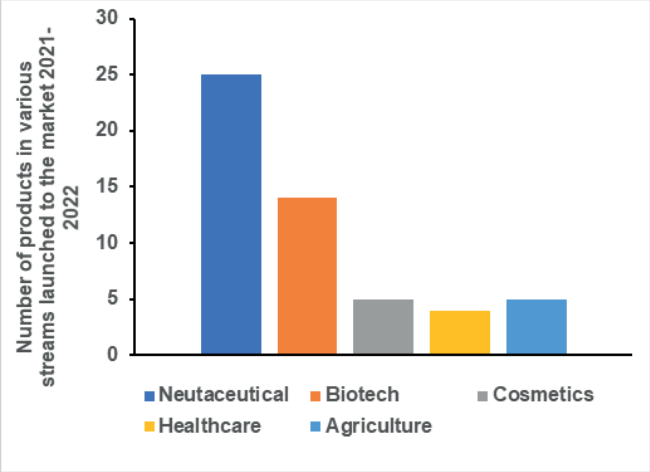


The broad business verticals/laboratories include Analytical Chemistry, Molecular Biology, Phytochemistry and Bioprocess Engineering conducts industry relevant research, supports upstream, downstream and testing facility to incubates and contract research operations. BioNest has been able to collaborate with a number of industries to set up Corporate Research Operations.

During last year, all the Start-ups launched different products in various streams; biotechnology, healthcare, nutraceuticals, cosmetics, agriculture, etc., and many of their products are under different stages of development. Many entrepreneurs explored various marketing strategies and succeeded in getting their products known in both national and international markets. The facility over the 4 years has witnessed growth in terms of number of incubates, creating employment opportunities, training students, and conducting industry-based contract research projects. Incubates have also made progress in terms of Patents, products launched and Technology Transfers.

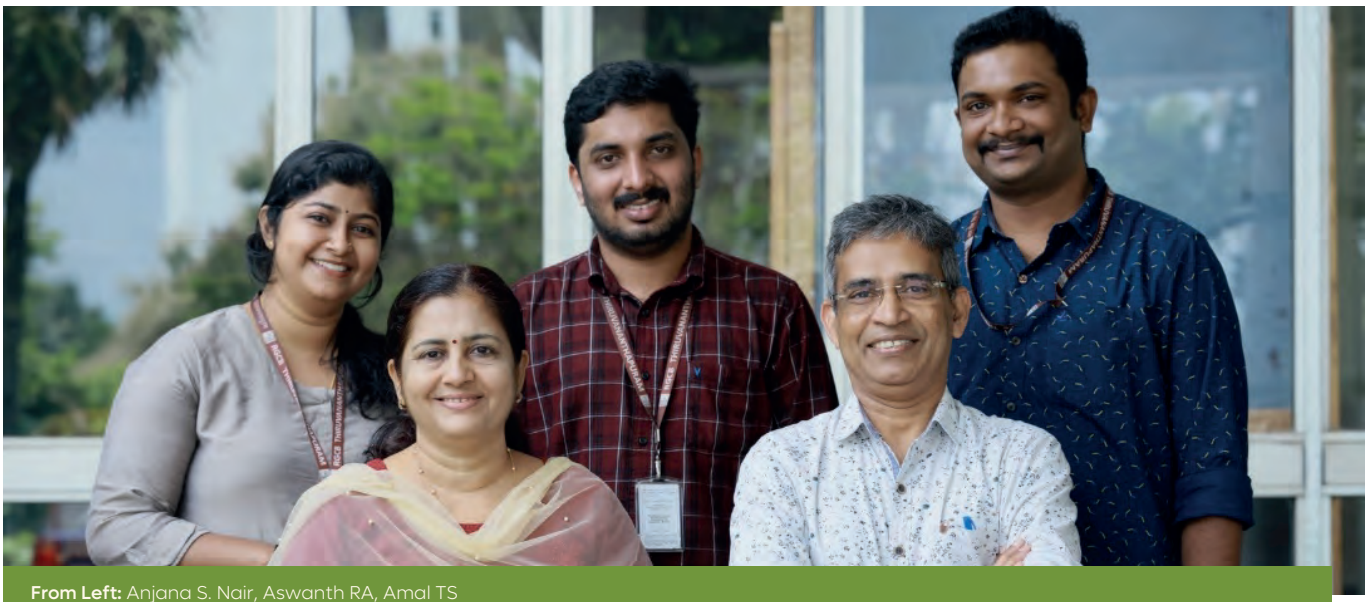
ACHIEVEMENTS BY START-UPS DURING THE PERIOD 2021-2022

YourStory Media's TechSparks 2021 (Tech50) selected as one among India's top 50 startups in 2021	M/s. Greenovative Foods Pvt Ltd
CDSCO liscense for RNA extraction kit for COVID	M/s. Primodia Lifesciences Pvt Ltd
Developed India's first Seaweed based Herbal Zerol Gargle with anti-viral and anti-bacterial properties	M/s. Bodina Naturals Pvt Ltd
Seed fund of 300,000 USD for the production of Melanin utilizing the fermentation and bioprocess facility housed in the Bionest	M/s. AVISA
Seed fund of INR 15 lakhs from Kerala Start-up Mission	M/s. Greenovative Foods Pvt Ltd
Seed fund of INR 7 lakhs from Kerala Start-up Mission for the productization of Seaweed based Herbal Zerol Gargle	M/s. Bodina Naturals Pvt Ltd
Productization grant INR 5 lakhs from Kerala startup mission	M/s. Primodia Lifesciences Pvt Ltd
Fund from DHWS and AEVAS	M/s. Scopeful Bioresearch
Patent for Melanin as protection against ionizing radiation [Patent No- WO2021/225657 A2 , International Patent classification- A61K31/407 (2006.01)]	M/s. AVISA
Two products filed for patent (Certificate No- IN-KA52591773592840S)	M/s. Scopeful Bioresearch



Back Row From Left: Manoj A, Antony KP
Front Row From Left: Jayakrishnan KS, Dr. Anish NP, Dr. Joby Jose, Charutha, Smitha S

GENOME LNDIA: CATALOGUING THE GENETIC VARIATION IN INDIANS.



From Left: Anjana S. Nair, Aswanth RA, Amal TS

"Genome India: Cataloguing the Genetic Variation in Indians" is a nationally important project to build an exhaustive catalogue of genetic variations for the Indian population. This would aid in the designing of genome-wide association chips which will facilitate further large-scale genetic studies in a cost-effective manner. As part of the Genome India Project, RGCB was assigned blood sample collection from healthy individuals of various large and isolated population groups of Kerala as well as secondary data analysis from the NGS sequence data. Commencing the sample collection on 10th August 2020, at RGCB, blood sample collection campaigns were arranged in different localities in Thiruvananthapuram, Ernakulum, Thrissur, Malappuram, Kannur etc. and samples were send to CBR (Centre for Brain Research Institute, Bangalore) for whole genome sequencing. We have almost completed the sample collection except for the two isolated communities.

NURTURING THE YOUNG MINDS: M.SC BIO-TECHNOLOGY PROGRAM

From Left: Dr. Rajeswari Gopal G, Dr. Lekshmy Srinivas. Dr. Aparna Shankar, Dr. Mahesh S Krishna

- August 2nd, Farewell of 1st batch MSc 2019. Ms Athira Menon was awarded the best outgoing student of the batch, with a citation and a cash prize of Rs. 10,000.
- 17th November 2021- 3rd batch of RGCB MSc student admission, followed by a day long orientation program.
- RGCB MSc students participated and won accolades at different functions organized by RGCB including Hindi Pakhwara diwas, GATI, Technology day and science day.
- MSc students qualified CSIR/UGC JRF NET 2022, BET 2022, GATE 2022

CSIR/UGC JRF NET 2022- Atriya Majumder, Victor Samuel, Ajay Pradhan, Ratulananda Bhadury, Saumya SK, Swarnabha Chowdhury , Vandana Sharma

BET 2022- Ratulananda Bhadury, Saumya SK, Swarnabha Chowdhury, Akshit Jain, Arvind, Priyanshu Priya, Baishali Chakraborty, Lakshay Garg

GATE 2022- 26 students from M.Sc 2020 batch and 1 student from MSc 2021 batch

- M.Sc 2019 and 2020 batch students successfully enrolled themselves in PhD programs both abroad and in India.

Athira Menon	:	Ph.D, University of Oxford, UK
P V Vinitha	:	Ph.D Neuroscience, NBRC, Haryana
Samrajni Banerjee	:	Ph.D, University of Liverpool, Institute of life courses and medical science
Fathima Hisana k Ferosh	:	Ph.D., BIOTEC, PoL, Technical University Dresden
Irene Infancy J	:	Ph.D, University of Illinois, Urbana-Champaign
Deepak Sahni	:	Ph.D, ACTREC,TMC, Navi Mumbai
Sudhanand M	:	Ph.D, National Centre for Biological Sciences
Devika S R	:	Ph.D, IIT Madras
Sreeparna Nath	:	Ph.D, ACTREC
Sampurno Banerjee	:	Ph.D, ACTREC
Asmita Datta	:	Ph.D, IISc, Bengaluru
Atriya Majumder	:	Ph.D, NCBS, Bengaluru
Saumya SK	:	Ph.D, IIT Hyderabad-Deakin University Joint Doctoral program
Ratulananda Bhadury	:	Ph.D, NII, New Delhi
Lakshay Garg	:	Ph.D, IISc, Bengaluru
Swarnabha Chowdhury	:	Ph.D, NBRC, Gurgaon
Victor Samuel	:	Ph.D, InStem, Bengaluru
Ajay Pradhan	:	Ph.D, NCCS, Pune

Joined in companies

Krishnendu CL, Shafnaz M, Aishwarya Sureshkumar

Joined as research fellow at esteemed institutes in India

Shifana C Sadiq, Anjitha R Vijay, Susi Mathews, Anshu, Sheri Vidya Ranl, Jiju P S, Ajay Narwade, Anjali Devarajan, Ahel Bhattacharyya, Ajay Pal, Samir Nandi, Lariza T R

NURTURING THE YOUNG MINDS: M.SC BIO-TECHNOLOGY PROGRAM

M.SC BIOTECHNOLOGY (2021-2023 BATCH)

Front Row From Left: Ayush Dave. Gaurav Nanakwani, Akshay Kumar, Swagato Bhattacharjee, Charanraj CA
Central Row From Left: Nirnisha Pramanik, Nandini Datta, Kamallata Chakraborty, Saurav Kumar, Vankudothu Swathi, Lavoori Ravindar, Nishant Kumar Suman
Back Row From Left: Sanjit Biswas. Kushala R, Shambhavi Mishra, Rashmi Rani, Rima Sarkar, Parvathi K, Arnab Kakati

M.SC BIOTECHNOLOGY (2022-2024 BATCH)

Front raw From left: Kajori Mahanta, Soma Banerjee, Tanaya Mukharjee, Krishna Sawarn, Nazmin Hussain, Pahil Sen, Sejal Sanjay Raskar, Soham Ghosh
Central raw From left: Tejas Meshram, Jyoti Ranjan Behera, Ajay Durve, Ritika Sachdeva, Zion Mercy M, AM Amrutha, Sachin Yadav
Back raw From left: Sreenath M, Shibam Dutta, Shreyansh Maurya, Sumit Singh, Kamal Narayan Chakraborty

TECHNOLOGY INTERVENTIONS FOR TRIBAL HERITAGE RESILIENCE OF KERALA

PROJECT TEAM

Prof. Chandrabhas Narayana, Director, RGCB
Dr. Anish N P, Scientist C & Assistant Registrar
Dr. Manoj P, Deputy General Manager (Technical Services)
Dr. Archana S. Manager, Veterinary Services
Project Staff: Project Associate-II: 2nos., Project Associate-I: 3nos., Project Assistants: 6 nos., Camp Office In-charge – 2 nos. and 1 Consultant

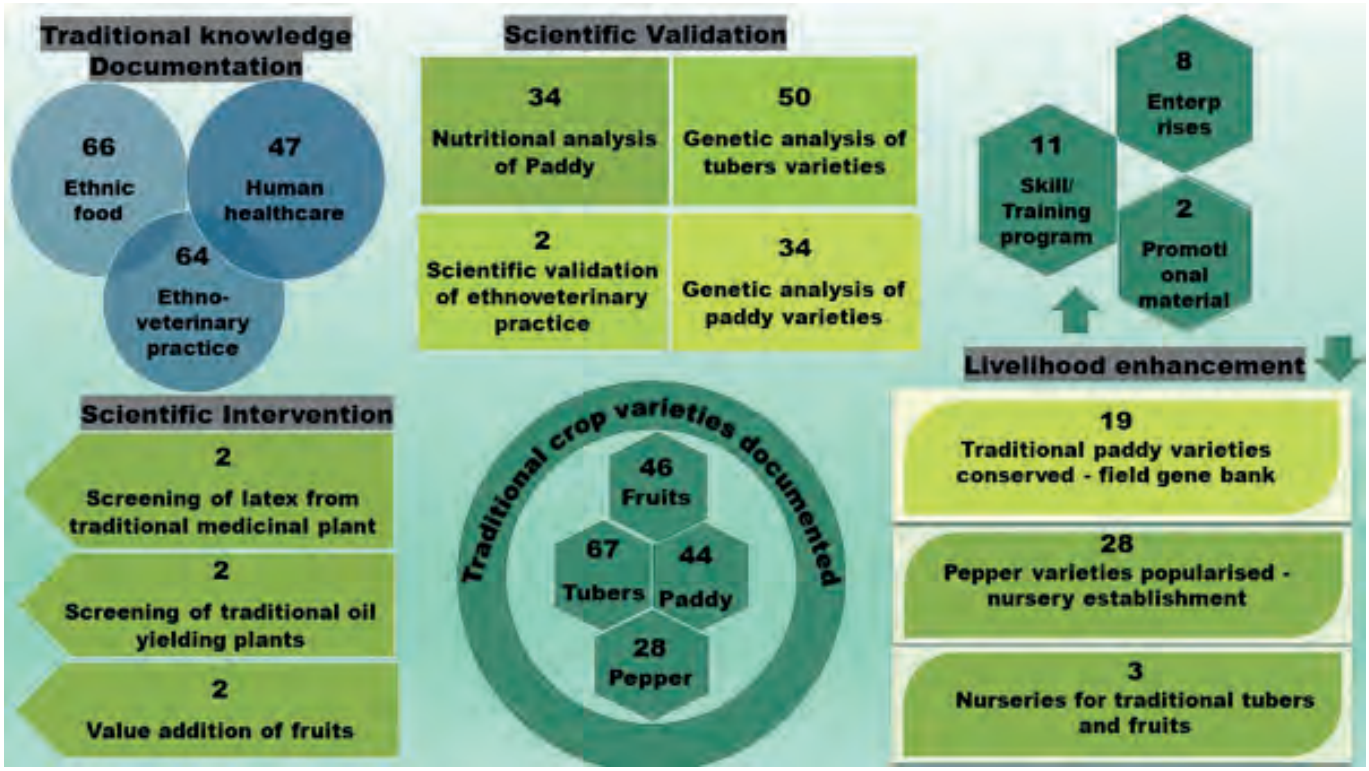
History, despite its lost roots, cannot be unlived, and it is advantageous in all ways to bring it back to life by restoring societal connections with cultural heritage. Preservation and valorization of legacy may be vastly augmented through scientific methods and technologies, thereby converting it into valuable resources for livelihood. With financial support from the Department of Science and Technology's SHRI program, we are conducting studies on the Tribal Heritage of Kerala.

Tribal traditional knowledge offers immense potential to serve national and global needs, therewith providing societal benefits as well as economic growth. We have achieved significant progress to document the traditional knowledge and identify the technology gaps and revitalize the tribal traditions in the three targeted districts, Thiruvananthapuram, Idukki and Wayanad. Twenty-five tribal healers were interviewed from nine tribal communities and documented 64 ethno-veterinary practices. Established two ethno-veterinary promotion clusters in Idukki and Wayanad districts and conducted awareness classes on traditional animal treatment and its contemporary relevance. Distributed 10 medicinal plants for 100 households in the Idukki and Wayanad districts for the formation of home herbal garden. We have developed a mobile application named 'Gau Mithra' with traditional remedies for 16 major diseases affecting livestock and made it available on Play Store. We also prepared a community knowledge register using the information collected from various traditional healers. This will help to avoid losing the traditional knowledge of tribal in veterinary medicine and animal health care. Scientific validation of the ethno-veterinary formulation for wound healing was performed through in silico, in vitro, and in vivo studies. Validation of another formulation for deworming of cattle is also progressing.

The Tribal heritage project team is documenting ethnic food recipes from different tribal communities and currently, 66 recipes were documented and conducted 5 demonstration programs for the promotion and popularization of ethnic foods. The establishment of community enterprises based on ethnic food and its value addition is progressing.

Traditional crop varieties are an integral part of tribal heritage. We have documented the native varieties of paddy and pepper and the wild edibles used by tribal communities. As part of the conservation of this dwindling genetic wealth, we have established conservation plots and nurseries for pepper and wild edibles (4 nos.) and 7.2 hector field gene bank for paddy with the participation of tribal communities. Nutritional and genetic analyses of paddy and tuber varieties are progressing.

The major focus of the project is, documenting the traditional knowledge, validating the knowledge scientifically, and then the refined knowledge is giving back to the community for their livelihood improvement. In this respect, we have established 8 community enterprises in the tribal colonies in Idukki, Wayanad and Thiruvananthapuram Districts. It includes Lemongrass oil extraction units, Non-Timber Forest Produces value addition units, Bamboo craft units, Paddy processing unit, tribal heritage center and nurseries for traditional varieties. Around 175 tribal families are directly benefiting from these activities. We experienced that the heritage is not just a past memory, through appropriate technology interventions it can make wonders in all aspects of modern society as well.



(A) Releasing Community Knowledge Register

(B) Wild edibles nursery established at Thiruvananthapuram

(C) Inaugural address by Prof. Chandrabhas Narayana in the Lemongrass oil unit at Wayanad

(D) Inauguration of Lemongrass oil unit at Idukki

(E) Heritage Centre established at Idukki

(F) Bamboo craft unit set up at Idukki

(G) NTFP value addition unit at Uppukunnu

(H) Traditional paddy varieties Field Gene Bank at Wayanad

Front row From left: Harikrishnan P, Mariya Mary Gigi, Aparna M, Deepthi Mohan, Dr. Archana S, Mahesh KB
Back row from left: Dr. Manoj P, Professor Chandrabhas Narayana, Dr. Anish NP

Adarsh Sen Madhu

PROJECT TEAM AT IDUKKI

From Left: Rajesh KT, Anu Theresa Antony, Hari MK, Jishnu Janardhanan

PROJECT TEAM AT WAYANAD

From Left: Abin Abraham, Roshni S, Syam Sankaren Sebastine AC

AZADI KA AMRIT MAHOSTAV

RGCB ORGANIZED A SERIES OF LECTURES AND WORKSHOPS FOR RESEARCH SCHOLARS, COLLEGE STUDENTS AND GENERAL PUBLIC AS A PART OF 75TH ANNIVERSARY OF INDIAN INDEPENDENCE. THE ACTIVITIES ARE LISTED BELOW

Sl. no	Resource Person Name and Affiliation	Title of the Event	Date
01	Dr. Sabu Thomas Scientist F, Pathogen Biology, RGCB	Water Borne Diseases- Current Scenario	28-05-2021
02	Dr.R.V. Varma Former Chairman, Kerala State Biodiversity Board Chairman, Expert Committee on Access and Benefit Sharing (ABS), National Biodiversity Authority, Chennai, Chairman, Steering Committee on ABS, Quality Council of India, New Delhi.	Participatory Approaches To Biodiversity Conservation	05-06-2021
03	Dr. Kishore Kumar. K Head of the Department of Botany Farook College (Autonomous) Kozhikode, Kerala	The End Of Living and The Beginning of Survival The Need for Ecosystem Restoration	12-06-2021
04	Dr. Suvarna Devi S Department Of Aquatic Biology & Fisheries, University Of Kerala, Thiruvananthapuram	The Future Of Oceans: Role Of Technologies And Literacy	19-06-2021
05	Mr.T.J. James Founder of Creativity Council, Thrissur Senior Fellow of Kerala Start-Up Mission	Grassroots Innovations: Prospects and Challenges	26-06-2021
06	Dr. Tessy Thomas Maliekal Scientist E-II, Cancer Research, RGCB	Cancer Prevention: The Facts To Know	02-07-2021
07	Dr.P V Mohanan Scientist- G & Head, Toxicology Division, Technical Manager, Biomedical Technology Wing, Sree chithra Tirunal Institute for Medical Sciences and Technology Poojapura, Thiruvananthapuram	Medical Device Development: Safety Concerns	09-07-2021
08	Dr.M N Balakrishnan Nair, Emeritus Professor, School of Health Science, Trans-disciplinary University, Bengaluru	Ethno-Veterinary Practices And Its Contemporary Relevance	16-07-2021
09	Dr.C.A. Jayaprakas, Principal Scientist (Entomology), Division of Crop Protection,ICAR-Central Tuber Crops Research Institute Thiruvananthapuram Emeritus Professor, School of Health Science	Need of green technologies in pest management strategies	23-07-2021
10	Dr. G. Nagendra Prabhu, Associate Professor, P. G. Dept. of Zoology & Research Centre and Principal Investigator, Centre for Research on Aquatic Resources, Sanatana Dharma College, University of Kerala	Value Addition of Aquatic Weeds - Technologies and Products	30-07-2021
11	DBT-Rajiv Gandhi Centre for Biotechnology (RGCB)	Skill and Capacity building program for tribal artisans in bamboo craft sector	04-08-2021 Duration:15 days
12	Dr K.B.Harikumar, Scientist E-I, Cancer Research, RGCB	Applications of phytopharmaceuticals in human life	06-08-2021
13	Dr. Karthika Rajeeve, Scientist E-I, Pathogen Biology, RGCB	Bacteria cancer interface: A new player in the catch	13-08-2021
14	Dr. Ajay Kumar A, Medical Officer,State Joint Secretary (KGMOA)	COVID and Post COVID Problems	28-08-2021

Sl. no	Resource Person Name and Affiliation	Title of the Event	Date
15	Soniya E.V Scientist G, Plant Biotechnology, RGCB	DNA Fingerprinting: Approaches and Applications	04-09-2021
16	Dr. N.C Anilkumar Senior Scientist Kerala State Remote Sensing and Environment Centre, Department of Planning and Economic Affairs, Government of Kerala	Geospatial technology for Sustainable development	02-10-2021
17	Dr. Pradeep Kumar. G Scientist G, Reproductive Biology, RGCB	BIOTECHNOLOGY as a career option of choice	09-10-2021
18	Dr. Ananda Mukherjee, PhD DBT-Ramalingaswami Faculty Fellow Cancer Research, RGCB	Why is cancer so hard to treat and what we can do about it	30-10-2021
19	Dr.Sabu Thomas Scientist F, Pathogen Biology, RGCB	Antimicrobial Resistance: A Silent Pandemic	24-11-2021
20	Dr. Santanu Chattopadhyay GN Ramachandran Fellow Pathogen Biology, RGCB	Antimicrobial Resistance: Helicobacter pylori	24-11-2021

LIST OF PUBLICATIONS

CANCER RESEARCH

Dr. T.R SANTHOSH KUMAR

Ravindran R, Velikkakath AKG, Narendradev ND, Chandrasekharan A, Santhoshkumar TR, Srinivasula SM. Endosomal-associated RFFL facilitates mitochondrial clearance by enhancing PRKN/parkin recruitment to mitochondria. Autophagy. 2022 ;3:1-14.

Varadarajan SN, Mathew KA, Chandrasekharan A, Lupitha SS, Lekshmi A, Mini M, Darvin P, Santhoshkumar TR. Real-time visualization and quantitation of cell death and cell cycle progression in 2D and 3D cultures utilizing genetically encoded probes. J Cell Biochem. 2022;123(4):782-797.

Lupitha SS, Darvin P, Chandrasekharan A, Varadarajan SN, Divakaran SJ, Easwaran S, Nelson-Sathi S, Umasankar PK, Jones S, Joseph I, Pillai MR, Santhoshkumar TR. A rapid bead-based assay for screening of SARS-CoV-2 neutralizing antibodies. Antib Ther. 2022;5(2):100-110.

Kulkarni S, Waugh MS, Veerabhadran B, Muralee M, Mathew AP, Krishna KM, Santhoshkumar TR, Nair CK. Immunological Effects of Laparoscopic Versus Open Rectal Cancer Surgery. Indian J Surg. 2021;83(3): 816-818.

Goyal R, Jerath G, Akhil R, Chandrasekharan A, Puppala ER, Ponneganti S, Sarma A, Naidu VGM, Santhoshkumar TR, Ramakrishnan V. Geometry encoded functional programming of tumor homing peptides for targeted drug delivery. J Control Release. 2021;333:16-27

Anandan V, Thankayyan Retnabai SK, Jaleel A, Thulaseedharan T, Mullasari A, Pillai MR, Kartha CC, Ramachandran S. Cyclophilin A induces macrophage apoptosis and enhances atherosclerotic lesions in high-fat diet-fed hyperglycemic rabbits. FASEB Bioadv. 2021;3(5):305-322.

Dr. RUBY JOHN ANTO

Shabna A, Antony J, Vijayakurup V, Saikia M, Liju VB, Retnakumari AP, Amrutha NA, Alex VV, Swetha M, Aiswarya SU, Jannet S, Unni US, Sundaram S, Sherin DR, Anto NP, Bava SV, Chittalakkottu S, Ran S, Anto RJ. Pharmacological attenuation of melanoma by tryptanthrin pertains to the suppression of MITF-M through MEK/ERK signaling axis. Cell Mol Life Sci. 2022;79(9):478.

Aiswarya SUD, Vikas G, Haritha NH, Liju VB, Shabna A, Swetha M, Rayginia TP, Keerthana CK, Nath LR, Reshma MV, Sundaram S, Anto NP, Lankalapalli RS, Anto RJ, Bava SV. Cucurbitacin B, Purified and Characterized From the Rhizome of Corallocarpus epigaeus Exhibits Anti-Melanoma Potential. Front Oncol. 2022 ;12:903832.

Swetha M, Keerthana CK, Rayginia TP, Nath LR, Haritha NH, Shabna A, Kalimuthu K, Thangarasu AK, Aiswarya SU, Jannet S, Pillai S, Harikumar KB, Sundaram S, Anto NP, Wu DH, Lankalapalli RS, Towner R, Isakov N, Deepa SS, Anto RJ. Augmented Efficacy of Uttroside B over Sorafenib in a Murine Model of Human Hepatocellular Carcinoma. Pharmaceuticals (Basel). 2022;15(5):636.

Nath LR, Swetha M, Vijayakurup V, Thangarasu AK, Haritha NH, Shabna A, Aiswarya SU, Rayginia TP, Keerthana CK, Kalimuthu K, Sundaram S, Lankalapalli RS, Pillai S, Towner R, Isakov N, Anto RJ. Blockade of Uttroside B-Induced Autophagic Pro-Survival Signals Augments Its Chemotherapeutic Efficacy Against Hepatocellular Carcinoma. Front Oncol. 2022;12:812598.

Shankar MG, Swetha M, Keerthana CK, Rayginia TP, Anto RJ. Cancer Chemoprevention: A Strategic Approach Using Phytochemicals. Front Pharmacol. 2022;12:809308.

Kalimuthu K, Keerthana CK, Mohan M, Arivalagan J, Christyraj JRSS, Firer MA, Choudry MHA, Anto RJ, Lee YJ. The emerging role of selenium metabolic pathways in cancer: New therapeutic targets for cancer. J Cell Biochem. 2022;123(3):532-542.

Haritha NH, Nawab A, Vijayakurup V, Anto NP, Liju VB, Alex VV, Amrutha AN, Aiswarya SU, Swetha M, Vinod BS, Sundaram S, Guijarro MV, Herlevich T, Krishna A, Nestory NK, Bava SV, Sadasivan C, Zajac-Kaye M, Anto RJ. Targeting Thymidylate Synthase Enhances the Chemosensitivity of Triple-Negative Breast Cancer Towards 5-FU-Based Combinatorial Therapy. Front Oncol. 2021;11:656804.

Dr. SUPARNA SENGUPTA

Sreeja JS, Jyothy A, Sengupta S. α-Fodrin in Cytoskeletal Organization and the Activity of Certain Key Microtubule Kinesins. Genes (Basel). 2021;12(5):750.

Dharmapal D, Jyothy A, Mohan A, Balagopal PG, George NA, Sebastian P, Maliekal TT and Sengupta S. β-Tubulin Isotype, TUBB4B, Regulates The Maintenance of Cancer Stem Cells. Front Oncol. 2021;11:788024.

Pammi Guru KT, Sreeja JS.; Dharmapal D, Sengupta S, Basu, PK. Novel Gold Nanoparticle-Based Quick Small-Exosome Isolation Technique from Serum Sample at a Low Centrifugal Force. Nanomaterials (Basel) 2022;12(10):1660.

Dr. S ASHA NAIR

Pradhan T, Kumar V, Surya HE, Krishna R, John S, Jissa VT, Anjana S, Chandramohan K, Nair SA. STIL Endows Oncogenic and Stem-Like Attributes to Colorectal Cancer Plausibly by Shh and Wnt Signaling. Front Oncol. 2021;11:581671.

Soman A, Asha Nair S. Unfolding the cascade of SERPINA3: Inflammation to cancer. Biochim Biophys Acta Rev Cancer. 2022; 1877(5): 188760.

Dr. PRIYA SRINIVAS

Krithiga K, Arathi R, Geetu RV, Neetha RL, Patra D, Neethu K, Warrier A, Srinivas P. Partial genome analysis of Cox1 subunit-I region in mitochondrial DNA of canine mammary tumours. J Vet Anim Sci. 2021; 52(1): 95-98.

Rajan A, Varghese GR, Yadev I, Anandan J, Latha NR, Patra D, Krishnan N, Kuppusamy K, Warrier AV, Bhushan S, Nadhan R, Ram Kumar RM, Srinivas P. Modulation of BRCA1 mediated DNA damage repair by deregulated ER-α

Dr. S. SREEJA

Vini R, Rajavelu A, Sreeharshan S. 27-Hydroxycholesterol, The Estrogen Receptor Modulator, Alters DNA Methylation in Breast Cancer. Front Endocrinol (Lausanne). 2022;13:783823.

Vini R, Azeez JM, Remadevi V, Susmi TR, Ayswarya RS, Sujatha AS, Muraleedharan P, Lathika LM, Sreeharshan S. Urolithins: The Colon Microbiota Metabolites as Endocrine Modulators: Prospects and Perspectives. Front Nutr. 2022;8:800990.

Azeez JM, Susmi TR, Remadevi V, Ravindran V, Sasikumar Sujatha A, Ayswarya RNS, Sreeja S. New insights into the functions of progesterone receptor (PR) isoforms and progesterone signaling. Am J Cancer Res. 2021;11(11):5214-5232.

LIST OF PUBLICATIONS

Vini R, Sreeja Sreekumar, Juberiya M Azeez, Sreeja S. Pomegranate Extract protects Endothelial cells from TNF-α associated damage, Advances in Biological Sciences Research (ABSR),Atlantis Proceedings (Accepted).

Dr. G.S. VINOD KUMAR

Vijayan A, C L V, Kumar GSV. Dual growth factor entrapped nanoparticle enriched alginate wafer-based delivery system for suppurating wounds. Int J Biol Macromol. 2022;208:172-181.

Nanditha CK, Kumar GSV. Bioactive peptides laden nano and micro-sized particles enriched ECM inspired dressing for skin regeneration in diabetic wounds. Mater Today Bio. 2022; 14: 100235.

Wanjale MV, Sunil Jaikumar V, Sivakumar KC, Ann Paul R, James J, Kumar GSV. Supramolecular Hydrogel Based Post-Surgical Implant System for Hydrophobic Drug Delivery Against Glioma Recurrence. Int J Nanomedicine. 2022;17: 2203–2224.

Dr. DEVASENA ANANTHARAMAN

Basu P, Malvi SG, Joshi S, Bhatla N, Muwonge R, Lucas E, Verma Y, Esmy PO, Poli URR, Shah A, Zomawia E, Pimple S, Jayant K, Hingmire S, Chiwate A, Divate U, Vashist S, Mishra G, Jadhav R, Siddiqi M, Sankaran S, Prabhu PR, Kannan TPRA, Varghese R, Shastri SS, Anantharaman D, Gheit T, Tommasino M, Sauvaget C, Pillai MR, Sankaranarayanan R. Vaccine efficacy against persistent human papillomavirus (HPV) 16/18 infection at 10 years after one, two, and three doses of quadrivalent HPV vaccine in girls in India: a multicentre, prospective, cohort study. Lancet Oncol. 2021;(11):1518-1529.

Simoens C, Gorbaslieva I, Gheit T, Holzinger D, Lucas E, Ridder R, Rehm S, Vermeulen P, Lammens M, Vanderveken OM, Kumar RV, Gangane N, Caniglia A, Maffini F, Rubio MBL, Anantharaman D, Chiocca S, Brennan P, Pillai MR, Sankaranarayanan R, Bogers J, Pawlita M, Tommasino M, Arbyn M; HPV-AHEAD study group. HPV DNA genotyping, HPV E6*I mRNA detection, and p16INK4a/Ki-67 staining in Belgian head and neck cancer patient specimens, collected within the HPV-AHEAD study. Cancer Epidemiol. 2021;72:101925.

Dr. TESSY THOMAS MALIEKAL

Senapati P, Bhattacharya A, Das S, Dey S, Sudarshan D, Vishwakarma J, Sudevan S, Ramachandran R, Maliekal TT, Kundu TK. Histone chaperone Nucleophosmin regulates transcription of key genes involved in oral tumorigenesis. Mol Cell Biol. 2022;42(2):e0066920.

Maliekal TT, Dharmapal D, Sengupta S. Tubulin Isotypes: Emerging Roles in Defining Cancer Stem Cell Niche. Front Immunol. 2022;13:876278

Mohan A, Raj Rajan R, Mohan G, Kollenchery Puthenveettil P, Maliekal TT. Markers and Reporters to Reveal the Hierarchy in Heterogeneous Cancer Stem Cells. Front Cell Dev Biol. 2021;9:668851.

Mohan A, Raj RR, Mohan G, KP P, Maliekal TT. Reporters of Cancer Stem Cells as a Tool for Drug Discovery. Front Oncol. 2021;11:669250.

Gopalakrishnan S, Uma SK, Mohan G, Mohan A, Shanmugam G, Kumar VTV, Chandrika SK, Vasudevan D, Nori SRC, Sathi SN, George S, Maliekal TT. SSTP1, a Host Defense Peptide, Exploits the Immunomodulatory IL6 Pathway to Induce Apoptosis in Cancer Cells. Front Immunol. 2021;12:740620

Dharmapal D, Jyothy A, Mohan A, Balagopal PG, George NA, Sebastian P, Maliekal TT, Sengupta S. β-Tubulin Isotype, TUBB4B, Regulates The Maintenance of Cancer Stem Cells. Fronti Oncol. 2021;11:788024

Dr. SUNIL MARTIN

Ganapathy T, Radhakrishnan R, Sakshi S, Martin S. CAR γδ T cells for cancer immunotherapy. Is the field more yellow than green? Cancer Immunol Immunother. 2022.

Muthuvel M, Srinivasan H, Louis L, Martin S. Engineering off-the-shelf universal CAR T cells: A silver lining in the cloud. Cytokine. 2022;156:155920.

Dr. K.B. HARIKUMAR

Kiran S, Parvathy J, Sukumaran T, Varghese J, Lakshmi S, Kumar SS, Babu A, Harikumar KB and Ragupathy L . Immunomodulatory properties of D-sorbitol/D-mannitol incorporated linear step-growth Co-polymers, Int J Polym Mater. 2022 (In Press)

Arndt C, Bergmann R, Striese F, Merkel K, Máthé D, Loureiro LR, Mitwasi N, Kegler A, Fasslrinner F, González Soto KE, Neuber C, Berndt N, Kovács N, Szöllősi D, Hegedűs N, Tóth G, Emmermann JP, Harikumar KB, Kovacs T, Bachmann M, Feldmann A. Development and functional characterization of a versatile radio-/immunotheranostic tool for prostate cancer management. Cancers (Basel). 2022. 14:1996.

Manu KA, Harikumar KB, Ishimoto T. Editorial: Targeting Pancreatic Cancer: Strategies and Hopes. Front Oncol. 2022. 12:873682

Prasanna R, Babu A, Balan A, Harikumar KB. The effect of caries, periodontitis and substance abuse on salivary interleukin - 6 levels. J. Indian Dent. Assoc. 2022: XV; 19-25.

Kurani H, Razavipour SF, Harikumar KB, Dunworth M, Ewald AJ, Nasir A, Pearson G, Van Booven D, Zhou Z, Azzam D, Wahlestedt C, Slingerland J. DOT1L is a novel cancer stem cell target for triple-negative breast cancer. Clin Cancer Res. 2022. 28:1948-1965.

Dr. ANI V DAS

Midhunaraj K, Mary Angelin, Ani V Das. PIWI proteins and piRNAs in cervical cancer: A propitious dart in cancer stem cell targeted therapy. Hum Cell. 2021; 34(6):1629-1641.

Dr. RADHIKA NAIR

Thankamony AP, Subbalakshmi AR, Jolly MK, Nair R. Lineage Plasticity in Cancer: The Tale of a Skin-walker. Cancers(Basel) 2021;13(14), 3602;

Dr. ANANDA MUKHERJEE

Misra S, Chowdhury SG, Ghosh G, Mukherjee A, Karmakar P. Both phosphorylation and phosphatase activity of PTEN require to prevent replication fork progression during stress by inducing heterochromatin. Mutat Res. 2022;825:111800.

Dr. RAM MOHAN RAM KUMAR

Rajan A, Varghese GR, Yadev I, Anandan J, Latha NR, Patra D, Krishnan N, Kuppusamy K, Warrier AV, Bhushan S, Nadhan R, Ram Kumar RM and Priya Srinivas. Modulation of BRCA1 mediated DNA damage repair by deregulated ER-α signaling in breast cancers. Am J Cancer Res. 2022; 12(1): 17–47.

CARDIOVASCULAR DISEASES & DIABETES BIOLOGY

Dr. ABDUL JALEEL

Anandan V, Thulaseedharan T, SureshKumar A, Karthika CL, Amjesh R, Mullasari AS, Kartha CC, Jaleel A, Ramachandran S. Cyclophilin A impairs efferocytosis and accelerates atherosclerosis by overexpressing CD 47 and down-regulating calreticulin. Cells. 2021;10(12):3598

Aneesh Kumar A, Ajith Kumar GS, Satheesh G, Surendran A, Chandran A, Kartha CC, and Jaleel A. Proteomics Analysis Reveals Diverse Molecular Characteristics between Endocardial and Aortic-Valvular Endothelium. Genes. 2021;12(7):1005

LIST OF PUBLICATIONS

Aneesh Kumar A, Anusree VR, Satheesh G, Vijayakumar G, Chandran M, Simon L, Lakshmi S, Pillai MR, Jaleel A. Hyperhomocysteinemia-related Serum Metabolome Alterations Not Normalized by Short-Term Folic Acid Treatment. Metabolomics. 2021;17(5):47

Jabeena CA, Govindaraju G, Rawat M, Gopi S, Sethumadhavan DV, Jaleel A, Sasankan D, Karmodiya K, Rajavelu A. Dynamic association of the H3K64 trimethylation mark with genes encoding exported proteins in Plasmodium falciparum. J Biol Chem. 2021;296:100614.

Tamhane VA, Sant SS, Jadhav AR, War AR, Sharma HC, Jaleel A, and Kashikar AS. Label-free quantitative proteomics of Sorghum bicolor reveals the proteins strengthening plant defense against insect pest Chilo partellus. Proteome Sci. 2021;19(1):6

Riyas A, Kumar AA, Chandran M, Jaleel A, Biju Kumar A. The venom proteome of three common scyphozoan jellyfishes (Chrysaora caliparea, Cyanea nozakii and Lychnorhiza malayensis) (Cnidaria: Scyphozoa) from the coastal waters of India. Toxicon. 2021;195:93-103

Dr. RAKESH S. LAISHRAM

Mohanan NK, Shaji F, Koshre GR, Rakesh S Laishram. Alternative polyadenylation: an enigma of transcript length variation in health and disease. Wiley Interdiscip Rev RNA . 2022;13(1);e1692.

Francis N, Rakesh S Laishram. Transgenesis of mammalian PABP reveals new role of mRNA polyadenylation in general stress response in bacteria. iScience. 2021.24(10):103119.

Koshre GR, Shaji F, Mohanan NK, Mohan N, Ali J, Rakesh S Laishram. Star-PAP RNA Binding Landscape Reveals Novel Role of Star-PAP in mRNA Metabolism That Requires RBM10-RNA Association. Int J Mol Sci. 2021 .22(18), 9980.

Dr. SURYA RAMACHANDRAN

Anandan V, Thankayyan Retnabai, SK, Jaleel A, Thulaseedharan T, Mullasari A, Pillai MR, Kartha CC, Ramachandran S. Cyclophilin A induces macrophage apoptosis and enhances atherosclerotic lesions in high-fat diet-fed hyperglycemic rabbits. FASEB Bioadv. 2021; 3(5):305-332.

Anandan V, Thulaseedharan T, Suresh Kumar A, Chandran Latha K, Revikumar A, Mullasari A, Kartha CC, Jaleel A, Ramachandran S. Cyclophilin a impairs efferocytosis and accelerates atherosclerosis by overexpressing CD 47 and down-regulating calreticulin. Cells. 2021;10(12):3598.

Dr. S. SUMI

Chandran Latha K, Sreekumar A, Beena V, S S BR, Lakkappa RB, Kalyani R, Nair R, Kalpana SR, Kartha CC, Surendran S. Shear Stress Alterations Activate BMP4/pSMAD5 Signaling and Induce Endothelial Mesenchymal Transition in Varicose Veins. Cells. 2021;10(12):3563.

Venugopal V, Sumi S. Molecular biomarkers and drug targets in brain arteriovenous and cavernous malformations: where are we? Stroke. 2022; 53(1):279-289.

Sumi S, Kartha CC. Genetic and Epigenetic Regulation by Gut Microbe-Modulated Metabolites in Chronic Metabolic Diseases. In: Thomas, S. (eds) Human Microbiome. Springer, Singapore. 2022. 109–127.

Dr. ANANTHALAKSHMY SUNDARARAMAN

Nidhi Nair, Lariza Ramesh, Areeba Marib and Ananthalakshmy Sundararaman, Actin Cytoskeleton in Angiogenesis, Biology Open (In Press)

Andugulapati SB, Sundararaman A, Lahiry M, Rangarajan A, AMP-activated protein kinase (AMPK) promotes breast cancer stemness and drug resistance. Dis Model Mech. 2022;15(6):dmm049203.

Gurevich DB, David DT, Sundararaman A, Patel J. Endothelial Heterogeneity in Development and Wound Healing. Cells. 2021;10(9):2338.

Sudhir BJ, Keelara AG, Venkat EH, Kazumata K, Sundararaman A. The mechanobiological theory: a unifying hypothesis on the pathogenesis of moyamoya disease based on a systematic review. Neurosurg Focus. 2021;51(3):E6.

Xiangyi Gan, Lariza Ramesh, Nidhi Nair and Ananthalakshmy Sundararaman Book chapter: Fibronectin fibrillogenesis during angiogenesis Book entitled: Matrix Pathobiology and Angiogenesis; Springer Publishing (Accepted).

Victor Samuel, Thejaswitha Rajeev, Lariza Ramesh and Ananthalakshmy Sundararaman Book chapter: Integrin Trafficking in Health and Disease; Book entitled Receptor Endocytosis and Signalling in Health and Disease, Elsevier Publishing (Accepted).

NEUROBIOLOGY & REGENERATIVE BIOLOGY

Dr. OMKUMAR R .V

Remya C, Dileep KV, Koti Reddy E, Mantosh K, Lakshmi K, Sarah Jacob R, Sajith AM, Jayadevi Variyar E, Anwar S, Zhang KYJ, Sadasivan C, Omkumar RV. Neuroprotective derivatives of tacrine that target NMDA receptor and acetyl cholinesterase - Design, synthesis and biological evaluation. Comput Struct Biotechnol J. 2021;19:4517-4537.

Gunasekaran S, Jacob RS, Omkumar RV. Differential expression of miR-148b, miR-129-2 and miR-296 in animal models of schizophrenia-Relevance to NMDA receptor hypofunction. Neuropharmacology. 2022; 210: 109024

Mohanan AG, Gunasekaran S, Jacob RS, Omkumar RV. Role of Ca2+/Calmodulin-Dependent Protein Kinase Type II in Mediating Function and Dysfunction at Glutamatergic Synapses. Front Mol Neurosci. 2022;15:855752.

Dr. MOINAK BANERJEE

Banerjee M Pharmacoepigenomics a key determinant in resolving epigenomic parameters in pathogenesis, and treatment response. Pharmacogenomics, 2022; 23 (2), 81-84.

Gopinath D, Menon RK, Wie CC, Banerjee M, Panda S, Mandal D, Behera PK, Roychoudhury S, Kheur S, Botelho MG, Johnson NW. Differences in the bacteriome of swab, saliva, and tissue biopsies in oral cancer. Sci Rep 2021; 11(1):1181.

Anju Mathew, Naresh Nebhinani, Saboora Beegum M, Vijayakumar K, Moinak Banerjee. Genetics of Adolescent Suicide: A Literature review. J Indian Assoc Child Adolesc Ment Health. 2021; 17(2):135-161.

Prakash A, Banerjee M. Genomic selection signatures in Autism identifies cognitive genomic tradeoff and its relevance in paradoxical phenotypes of Autism. Sci Rep 2021;11(1):10245.

Abdul F, Sreenivas N, Kommu JVS, Banerjee M, Berk M, Maes M, Leboyer M, Debnath M. Disruption of Circadian rhythm and risk of Autism Spectrum Disorder: Role of immune-inflammatory, oxidative stress, metabolic and neurotransmitter pathways. Rev Neurosci, 2021; 33(1):93-109.

Swathy B, Banerjee M. Understanding pharmaco-epigenomic response of antipsychotic drugs using genome-wide microRNA expression profile. Front Mol Neurosci. 2022;15:786632.

Sood A, Cherian LM, Heera R, Sathyan S, Banerjee M. Association between matrix metalloproteinases- 2 and -9 gene polymorphism with basement membrane disruption in Oral Lichen Planus-case-control pilot study. J Oral Biol Craniofac Res. 2022; 12,(2),258-262.

LIST OF PUBLICATIONS

Srinivas L, Vellichirammal NN, Nair IV, Nair CM, Banerjee M. Contribution from MHC mediated risk in Schizophrenia can reflect a more ethnic specific genetic and comorbid background. Cells. 2022; 11 (17), 2695.

Alfiya F, Jose M, Chandrasekharan SV, Sundaram S, Urulangodi M, Thomas B, Radhakrishnan A, Banerjee M, Menon RN. C12orf57 pathogenic variants- a unique cause of developmental encephalopathy in a South Indian child. J Genet. 2022; 101:30

Dr. JACKSON JAMES

Wanjale MV, Sunil Jaikumar V, Sivakumar KC, Ann Paul R, James J, Kumar GSV. Supramolecular Hydrogel Based Post-Surgical Implant System for Hydrophobic Drug Delivery Against Glioma Recurrence. Int J Nanomedicine, 2022;17: 2203-2224.

Dr. DEBASREE DUTTA

Baral I, Varghese PC, Dutta D. Epigenetics as "conductor" in "orchestra" of pluripotent states. Cell Tissue Res. 2022 Jul 15.

Rajam SM, Varghese PC, Dutta D. Histone Chaperones as Cardinal Players in Development. Front Cell Dev Biol. 2022;10:767773.

Varghese PC, Rajam SM, Nandy D, Jory A, Mukherjee A, Dutta D. Histone chaperone APLF level dictates the implantation of mouse embryos. J Cell Sci. 2021; 134(1):jcs246900.

Dr. RASHMI MISHRA

John S, Krishna AP, Gayathri KG, Mishra R. Neurotherapeutic implications of sense and respond strategies generated by astrocytes and astrocytic tumours to combat pH mechanical stress. Neuropathol Appl Neurobiol. 2022;48(2) :e12774.

Krishna AP, John S, Mishra R. Proteo-Transcriptomics meta-analysis identifies SUMO2 as a promising target in glioblastoma multiforme therapeutics. Cancer Cell Int. 2021; 21(1): 575.

Dr. RAJEEVE SIVADASAN

Rajeeve K, Vollmuth N, Janaki-Raman S, Wulff TF, Baluapuri A, Dejure FR, Huber C, Fink J, Schmalhofer M, Schmitz W, Sivadasan R, Eilers M, Wolf E, Eisenreich W, Schulze A, Seibel J, Rudel T. Reprogramming of host glutamine metabolism during Chlamydia trachomatis infection and its key role in peptidoglycan synthesis. Nat Microbiol. 2021;6(4):533.

Hansen JP, Ali WM, Sivadasan R, Rajeeve K. Bacteria-Cancer Interface: Awaiting the Perfect Storm. Pathogens. 2021;10(10):1321.

Ghanawi H, Hennlein L, Zare A, Bader J, Salehi S, Hornburg D, Ji C, Sivadasan R, Drepper C, Meissner F, Mann M, Jablonka S, Briese M, Sendtner M. Loss of full-length hnRNP R isoform impairs DNA damage response in motoneurons by inhibiting Yb1 recruitment to chromatin. Nucleic Acids Res. 2021;49(21):12284-12305.

PATHOGEN BIOLOGY

Dr. AJAY KUMAR R

Muralikrishnan B, Edison LK, Dusthackeer A, Jijimole GR, Ramachandran R, Madhavan A, Kumar RA. Chrysomycin A inhibits the topoisomerase I of Mycobacterium tuberculosis. J Antibiot (Tokyo). 2022;75(4):226-235.

Pushparajan AR, Edison LK, Ajay Kumar R. Mycobacterium tuberculosis transcriptional regulator Rv1019 is upregulated in hypoxia and negatively regulates Rv3230c-Rv3229c operon encoding enzymes in the oleic acid biosynthetic pathway. FEBS J. 2022

Dr. SABU THOMAS

Betsy M, Karthika S, Amrutha ML, Alida S, Tsuyoshi K, Sabu Thomas, Jathish K. Chiral nanostructures derived from europium (iii) complexes for enhanced circularly polarised luminescence and antibacterial activity. J Mater Chem C. 2022 in press.

Divya MP, Hardip RP, Sivakumar KC, Sabu Thomas. Genomic attributes differ between Vibrio parahaemolyticus environmental and clinical isolates including pathotypes. Environ Microbiol Rep.2022;14(3):365-375.

Lekshmi N, Gopinathan A, Sreekrishnan TP, Asokan A, Kumar A, Kumar G, Sabu Thomas. The bane of coastal marine environment: A fatal case of Vibrio vulnificus associated cellulitis and septicaemia. Indian J Med Microbiol. 2021;39(3):386-388.

Lekshmipriya P, Vineeth kumar TV, Joelin J, Asha RS, Thomas S, George Synergetic effect of Frog skin antimicrobial peptides in combination with antibiotics against multi host Gram negative pathogens. Int J Pept Res Ther

Dr. RADHAKRISHNAN R. NAIR

Nelson-Sathi S, Umasankar PK, Sreekumar E, Nair RR, Joseph I, Nori SRC, Philip JS, Prasad R, Navyasree KV, Ramesh S, Pillai H, Ghosh S, Santosh Kumar TR, Pillai MR. Mutational landscape and in silico structure models of SARS-CoV-2 spike receptor binding domain reveal key molecular determinants for virus-host interaction. BMC Mol Cell Biol. 2022;23(1):2.

Srinivas L, Gracious N, Nair RR. Pharmacogenetics Based Dose Prediction Model for Initial Tacrolimus Dosing in Renal Transplant Recipients. Front Pharmacol. 2021;12:726784

Seetha D, Pillai HR, Nori SRC, Kalpathodi SG, Thulasi VP, Nair RR. Molecular-genetic characterization of human parvovirus B19 prevalent in Kerala State, India. Virol J. 2021;18(1):96

MS Sasi, R Rajendran , V Meenakshy , T Suresh , R Heera Pillai , T Dilip Kumar, Athira Sugathan, K Regu. Study on Vector Dynamics of Zika Virus Outbreak in Thiruvananthapuram, Kerala, India. International Journal of Current Microbiology and Applied Science, 2021;10(12): 54-71.

Dr. HARIKRISHNAN. K

Priya P, Aneesh B, Harikrishnan K. Genomics as a potential tool to unravel the rhizosphere microbiome interactions on plant health. J Microbiol Methods. 2021;185, 106215.

Dr. RAJESH CHANDRAMOHANDAS

Reghunandanan K, Chandramohanadas R . Chemically induced phenotypes during the blood stage development of Plasmodium falciparum as indicators of the drug mode of action. Front Drug Discov. 2022: 2:920850.

Jessica JY, Jeonghun Oh, Xiang Yong Ang, Renugah Naidu, Trang TT, Chu Jae Hyoung Im, Umar Manzoor, Tuyet Kha Nguyen, Seok-Won Na, Eun-Taek Han, Christeen Davis, Won Sun Park, Wanjoo Chun, Hojong Jun, Se Jin Lee, Sunghun Na, Jerry KY Chan, Yong-Keun Park, Bruce Russell, Jin-Hee Han, Rajesh Chandramohanadas. Optical Diffraction Tomography and Image Reconstruction to measure host cell alterations caused by divergent Plasmodium species (Spectrochimica Acta Part A: Molecular and Biomolecular Spectroscopy, in Press)

Dr. JOHN BERNET JOHNSON

Kumar NA, Suma SM, Kunnakkadan U, Nag J, Mukesh RK, Lyles DS, Johnson JB. Functional dissection of the dominant role of CD55 in protecting vesicular stomatitis virus against complement-mediated neutralization. Viruses. 2021; 13(3),373.

Mukesh RK, Kalam AA, Nag J, Jaikumar VS, Kunnakkadan U, Kumar NA, Suma SM, Rajavelu A, Johnson JB. Chandipura virus induces cell

death in cancer cell lines of human origin and promotes tumor regression in vivo. Mol Ther Oncolytics. 2021; 23:254-265.

Dr. KARTHIKA RAJEEVE

Vollmuth N, Schlicker L, Guo Y, Hovhannisyan P, Janaki-Raman S, Kurmasheva N, Schmitz W, Schulze A, Stelzner K, Rajeeve K, Rudel T. c-Myc plays a key role in IFN-γ-induced persistence of Chlamydia trachomatis. Elife. 2022;11:e76721.

Dr. KARTHIK SUBRAMANIAN

Parveen S, Subramanian K. Emerging Roles of Extracellular Vesicles in Pneumococcal Infections: Immunomodulators to Potential Novel Vaccine Candidates. Front Cell Infect Microbiol. 2022;12:836070.

Dr. IYPE JOSEPH

Lupitha SS, Darvin P, Chandrasekharan A, Varadarajan SN, Divakaran SJ, Easwaran S, Nelson-Sathi S, Umasankar PK, Jones S, Joseph I, Pillai MR, Santhoshkumar TR. A rapid bead-based assay for screening of SARS-CoV-2 neutralizing antibodies. Antib Ther 2022;5(2):100-110.

Dr. KRISHNA KURTHKOTI

Salini S, Bhat SG, Natesh R, R Ajay Kumar, Kurthkoti K. The error-prone polymerase DnaE2 mediates the evolution of antibiotic resistance in persister mycobacterial cells. Antimicrob Agents Chemother. 2022;66(3):e0177321

Dr. SANTANU CHATTOPADHYAY

Retnakumar RJ, Nath AN, Nair GB, Chattopadhyay S. Gastrointestinal microbiome in the context of Helicobacter pylori infection in stomach and gastroduodenal diseases. "Human Microbiome in Health and Disease-Part B" in Progress in Molecular Biology and Translational Science. Elsevier. Ed. Das B and Singh V, Vol. 192. 2022. August 18.

Nath AN, Retnakumar RJ, Francis A, Chhetri P, Thapa N, Chattopadhyay S. Peptic ulcer and gastric cancer: is it all in the complex host-microbiome interplay that is encoded in the genomes of 'us' and 'them'? Front. Microbiol. 2022;13:835313.

Mehrotra T, Devi TB, Kumar S, Talukdar D, Karmakar SP, Kothidar A, Verma J, Kumari S, Alexander SM, Retnakumar RJ, Devadas K, Ray A, Mutreja A, Nair GB, Chattopadhyay S, Das B. Antimicrobial resistance and virulence in Helicobacter pylori: Genomic insights. Genomics. 2021;113(6);3951-3966.

Alexander SM, Retnakumar RJ, Chouhan D, Devi TB, Sanjai D, Devadas K, Thapa N, Tamang JP, Lamtha SC, Chattopadhyay S. Helicobacter pylori in human stomach: the inconsistencies in clinical outcomes and the probable causes. Front. Microbiol. 2021;12:713955.

PLANT BIOTECHNOLOGY & DISEASE BIOLOGY

Dr. SONIYA E .V

Kattupalli D, Srinivasan A, Soniya EV. A Genome-Wide Analysis of Pathogenesis-Related Protein-1 (PR-1) Genes from Piper nigrum Reveals Its Critical Role during Phytophthora capsici Infection. Genes (Basel). 2021;12(7):1007.

Santhoshkumar R, Hima Parvathy A, E. V. Soniya. Phytosynthesis of silver nanoparticles from aqueous leaf extracts of Piper colubrinum: characterisation and catalytic activity. J Exp Nanosci. 2021;16:1, 295-309.

Rani Jalajakumari Reghu, Shenu Hudson Beena1., Soniya Eppurathu Vasudevan Achuthsakar Sukumaran Nair. Virtual screening and in vitro analysis to understand the inhibitory effect of alliin on Pythium splendens- pathogen of root rot disease. Int J Curr Adv Res. 2021; 10 :24217-24222

Girija A, Vijayanathan M, Sreekumar S, Basheer J, Menon TG, Krishnankutty RE, Soniya EV. Harnessing the natural pool of polyketide and non-ribosomal peptide family: A route map towards novel drug development. Curr Mol Pharmacol. 2022;15(2):265-291.

Kattupalli D, Pinski A, Sreekumar S, Usha A, Girija A, Beckmann M, Mur LAJ, Eppurathu Vasudevan S. Non-targeted metabolite profiling reveals the interplay of phytohormones in the interaction of black pepper with Phytophthora capsici. Int J Mol Sci. 2021;22(21):11433.

Perincherry L, Stępień Ł, Vasudevan SE. Cross-Tolerance and Autoimmunity as Missing Links in Abiotic and Biotic Stress Responses in Plants: A Perspective toward Secondary Metabolic Engineering. Int J Mol Sci. 2021;22(21):11945.

Aswathy U, Viswam P, Kattupalli D, Vasudevan S. Elucidation of transfer RNAs as stress regulating agents and the experimental strategies to conceive the functional role of tRNA-derived fragments in plants. Crit Rev Biotechnol. 2022:1-18.

Santhoshkumar R, Viswam P, Akash P, Soniya EV. Imprints of PGPB association on the metabolic dynamism of Piper nigrum. Journal of Plant Interactions (Accepted).

Dr. GEORGE THOMAS

Satheesh GR, Koyyappurath S, Varghese, L, Thomas G. Genome and Transcriptome Sequence Resources and Effector Repertoire of Pythium myriotylum Drechsler. Mol Plant-Microbe Interact. 2022;35: 715–718.

Alex, T. E., Nath, V. S., Varghese, L., Geetha, K. A., Augustine, L., Ramaswamy, V. M. and Thomas, G. Transcriptome-wide identification and transcriptional profiling reveal remarkable expression modulation of redox genes in Zingiber zerumbet against Pythium myriotylum. Physiol Mol Plant Pathol. 2022; 121: 101885.

Dr. MANJULA S

Geetha RG, Krishnankutty Nair Chandrika S, Saraswathy GG, Nair Sivakumari A, Sakuntala M. ROS dependent antifungal and anticancer modulations of Piper colubrinum. Osmotin.Molecules. 2021;26(8):2239

Dr. SARASWATI NAYAR

Nayar S, Thangavel G. CsubMADS1, a lag phase transcription factor controls development of polar eukaryotic microalga Coccomyxa subellipsoidea C-169. Plant J. 2021;107(4):1228-1242.

REPRODUCTION BIOLOGY

Dr. PRADEEP KUMAR G

Sahadevan M , Kumar PG. Peptidyl Arginine Deiminase 2 (PADI2) is Expressed in Post-Meiotic Germ Cells in the Mouse Testis and is Localized Heavily on the Acrosomal Region of Spermatozoa. J. Endocrinol. Reprod. 2021;25(1), 53-65.

Subash SK, Kumar PG. Spermatogonial stem cells: A story of self-renewal and differentiation. Front Biosci (Landmark Ed). 2021;26:163-205.

Kutteyil SS, Kumar PG. Possible effects of coronavirus disease 2019 on male reproduction. J. Reprod. Healthc Med 2021;2 (Suppl_1):S77-84

Yadu N, Kumar PG. Reactive oxygen species in male reproductive cancers. In: Handbook of Oxidative Stress and Cancer (Chakraborti S, Roychoudhury S and Ray BK, eds), Springer Nature, 2021;pp. 00-00.

LIST OF PUBLICATIONS

Shabith Raj K , Kumar GP. Possible use of germline stem cells in cell-based therapeutics. ISSRF Newsletter 29, 34-37.

Dr. MALINI LALORAYA

Ghosh S, Parikh S, Nissa MU, Acharjee A, Singh A, Patwa D, Makwana P, Athalye A, Barpanda A, Laloraya M, Srivastava S, Parikh F. Semen Proteomics of COVID-19 Convalescent Men Reveals Disruption of Key Biological Pathways Relevant to Male Reproductive Function. ACS Omega. 2022;7(10):8601-8612.

TRANSDISCIPLINARY BIOLOGY

PROFESSOR CHANDRABHAS NARAYANA

Chalapathi D, Kumar A, Behera P, Sathi SN, Swaminathan R, Narayana C. Insights on aggregation of hen egg-white lysozyme from Raman Spectroscopy and MD Simulations. Molecules. 2022; 27(20):7122.

Rajaji V, Manjón FJ, Narayana C. Pressure induced topological and topological crystalline insulators. J Phys Condens Matter. 2022 23;34(42).

Kamali K, Prasad S, Sahoo MK, Behera JN, Waghmare UV, Narayana C. Unusual CO2 Adsorption in ZIF-7: Insight from Raman Spectroscopy and Computational Studies. Inorg Chem. 2022;61(30):11571-11580.

Mali, B, Sunil J, Nair HS, Narayana C, Elizabeth S. Spin reorientation to a Γ3(Cx, Fy, Az) configuration and anisotropic spin-phonon coupling in a Sm0.5Y0.5FeO3 single crystal. Phys Rev B. 2022; 105: 214417.

Kamali K, Joseph B, Narayana C. Stability of zeolitic imidazolate frameworks (ZIF-7) under high pressures and its implications on storage applications of ZIFs. J Solid State Chem. 2022; 309: 122973.

Bose D, Aggarwal S, Das D, Narayana C, Chakrabarti A. Erythroid spectrin binding modulates peroxidase and catalase activity of heme proteins. IUBMB Life. 2022;74(5):474-487.

Bonu B, Srinivas G, Kumar VP, Joseph A, Narayana C, Barshilia HC. Temperature dependent erosion and Raman analyses of arc-deposited H free thick DLC coating on Cr/CrN coated plasma nitrided steel. Surf Coat Technol. 2022; 436: 128308.

Biswas B, Chakraborty S, Joseph A, Acharya S, Pillai AI, Narayana C, Bhatia V, Garbrecht M, Saha B. Secondary phase limited metal-insulator phase transition in chromium nitride thin films. Acta Materialia. 2022; 227:117737.

Shanbhag PN, Joseph A, Orlandi F, Manuel P, Mahendiran R, Fauth F, Narayana C, Sundaresan A, Rao CNR. Effects of Ga doping on the phase transitions of V2O3. Phys Rev B. 2022; 105: 064103.

Jain P, Mazumder M, Pradeep KR, Viswanatha R, Pati SK, Narayana C. Polaronic signatures in doped and undoped cesium lead halide perovskite nanocrystals through a photoinduced Raman mode. ACS Appl Mater Interfaces. 2022; 14(4):5567-5577.

Shoker MB, Alhaddad T, Pagès O, Torres VJB, Postnikov AV, Polian A, Hajj Hussein R, Pradhan GK, Narayana C, Gardiennet C, Kervern G, Nataf L, Ravy S, Itié JP, Strzałkowski K, Marasek A, Firszt F. Exceptional phonon point versus free phonon coupling in Zn1-xBexTe under pressure: an experimental and ab initio Raman study. Sci Rep. 2022;12(1):753.

Ghosh S, Mondal S, Yadav K, Aggarwal S, Schaefer WF, Narayana C, Subramanian R. Modulation of biliverdin dynamics and spectral properties by Sandercyanin. RSC Adv. 2022;12(31):20296-20304.

Kamali K, Narayana C. Pressure dependent chemical changes of adsorbed water in MIL-47 (V) by raman spectroscopy. Mater Today: Proc. 2022; 49:1196-9.

Roy S, Bagchi D, Dheer L, Sarma SC, Rajaji V, Narayana C, Waghmare UV, Peter SC. Mechanistic insights into the promotional effect of Ni substitution in non-noble metal carbides for highly enhanced water splitting. Appl Catal B. 2021; 298:120560.

Bhadram VS, Sen A, Sunil J, Panda DP, Sundaresan A, Narayana C. Pressure-driven evolution of structural distortions in RCrO3 perovskites: The curious case of LaCrO3. Solid State Sci. 2021; 119:106708

Kamali K, Joseph B, Rajaji V, Narayana C. Pressure-Induced Loss of Long-Range Structural Order in MFM-300 (Al): An X-ray Diffraction and Raman Spectroscopic Study. J Phys Chem C. 2021;125(28):15472-8.

Das S, Radhakrishnan D, Bhadram VS, Narayana C, Bhattacharyya AJ. Brillouin light scattering study of microscopic structure and dynamics in pyrrolidinium salt based ionic liquids. Solid State Ion. 2021; 363:115603.

Dr. SANIL GEORGE

Sandeep S, Joelin J, George S, Antony MM. Ontogenetic systematic characterisation of an endemic frog Rhacophorus malabaricus Jerdon, 1870 (Anura: Rhacophoridae) from Western Ghats, Kerala, India. Zoosystema 2022;44 (6):159-176.

Joseph J, Sandeep S, George S, Antony MM. The complete mitochondrial genome of an endemic cichlid Etroplus canarensis from Western Ghats, India (Perciformes: Cichlidae) and molecular phylogenetic analysis. Mol Biol Rep. 2022;49(4):3033-3044.

Dr. MAHENDRAN K .R

Vikraman D, Satheesan R, Rajendran M, Kumar NA, Johnson JB, Krishnan RS, Mahendran KR. Selective Translocation of Cyclic Sugars Through Dynamic Bacterial Transporter. ACS Sens. 2022;7(6):1766–1776.

Krishnan RS, Jana K, Shaji A, Nair KS, Das AD, Vikraman D, Bajaj H, Kleinekathöfer U, Mahendran KR. Assembly of Transmembrane Pores from Mirror-Image Peptides. Nat Commun. 2022;13(1):5377.

Puthumadathil N, Krishnan RS, Nair GS, Mahendran KR. Assembly of alpha-helical transmembrane pores through an intermediate state. Nanoscale. 2022;14(17):6507-6517.

Neethu A, Pratibha N, Anju KA, Mahendran KR, Kumar KS. Membrane Disruptive Action of Cationic Antibacterial Peptide B1CTcu3. ChemBioChem. 2022;23(16): e202200239

Scott AJ, Niitsu A, Kratochvil HT, Lang EJM, Sengel JT, Dawson WM, Mahendran KR, Mravic M, Thomson AR, Brady L, Liu L, Mulholland AJ, Bayley H, DeGrado WF, Wallace M, Woolfson D. Constructing ion-channels from water-soluble α-helical barrels. Nat Chem. 2021;13(7):643-650.

Dr. SHIJULAL NELSON SATHI

Nelson-Sathi S, Umasankar PK, Sreekumar E, Radhakrishnan Nair R, Joseph I, Nori SRC, Philip JS, Prasad R, Navyasree KV, Ramesh S, Pillai H, Ghosh S, Santosh Kumar TR, Pillai MR. 2020. Mutational landscape and in silico structure models of SARS-CoV-2 Spike Receptor Binding Domain reveal key molecular determinants for virus-host interaction. BMC Mol Cell Biol. 2022;23(1):2.

Gopalakrishnan S, Uma SK, Mohan G, Mohan M, Shanmugam G, Kumar VTV, Chandrika SK, Vasudevan D, Nori SRC, Nelson-Sathi S, George S, Maliekal TT. SSTP1, a Host Defense Peptide, Exploits the Immunomodulatory IL6 Pathway to Induce Apoptosis in Cancer Cells. Front. Immunol 2021-740620.

Dr. LIGHTSON N.G

Ngashangva L, Hemdan BA, El-Liethy MA, Bachu V, Minteer SD, Goswami P. Emerging Bioanalytical Devices and Platforms for Rapid Detection of Pathogens in Environmental Samples. Micromachines(Basel). 2022;13(7): 1083.

LIST OF PUBLICATIONS

Das S, Ngashangva L, Mog H, Gogoi S, Goswami P. An insight into the mechanism of peroxidase-like activity of carbon dots. Optical Materials. 2021;115:111017.

Das S, Ngashangva L, Goswami P. Carbon Dots: An Emerging Smart Material for Analytical Applications. Micromachines (Basel) 2021;12(1):84.

Dr. UMASANKAR P .K

Ramesh ST, Navyasree KV, Sah S, Ashok AB, Qathoon N, Mohanty S, Swain RK, Umasankar PK. BMP2K phosphorylates AP-2 and regulates clathrin-mediated endocytosis. Traffic. 2021;22(11):377-396.

Zaccai NR, Kadlecova Z, Dickson VK, Korobchevskaya K, Kamenicky J, Kovtun O, Umasankar PK, Wrobel AG, Kaufman JGG , Gray S, Evans PR, Fritzsche M, Sroubek F, Höning S, Briggs JAG, Kelly BT, Owen DJ, Traub LM. FCHO controls AP2's initiating role in endocytosis through a PtdIns (4, 5) P2-dependent switch. Sci Adv. 2022;8(17).

Nelson-Sathi S, Umasankar PK, Sreekumar E, Nair RR, Joseph I, Nori SRC, Philip JS, Prasad R, Navyasree KV, Ramesh S, Pillai H, Ghosh S, Santosh Kumar TR, Pillai MR. Mutational landscape and in silico structure models of SARS-CoV-2 spike receptor binding domain reveal key molecular determinants for virus-host interaction. BMC Mol Cell Biol. 2022;23(1):2.

Lupitha SS, Darvin P, Chandrasekharan A, Varadarajan SN, Divakaran SJ, Easwaran S, Nelson-Sathi S, Umasankar PK, Jones S, Joseph I, Pillai MR, Santhoshkumar TR. A rapid bead-based assay for screening of SARS-CoV-2 neutralizing antibodies. Antib Ther. 2022;5(2):100-110.

Dr. DEBANJAN BHOWMIK

Gupta A, Dey S, Bhowmik D, Maiti S. Coexisting Ordered and Disordered Membrane Phases Have Distinct Modes of Interaction with Disease-Associated Oligomers. J Phys Chemi B. 2022;126 (5):1016-1023.

EXTRAMURAL PROJECTS ACTIVE BETWEEN APRIL 2021 TO MARCH 2022

CANCER RESEARCH

Dr. T.R SANTHOSH KUMAR

Sl.No	Title	Funding Agency	Year of Starting	Duration	PI/ CO-PI
01	Establishment of Fast-Lifetime imaging facility	DBT	2019	4 years	PI
02	Design and Characterization of peptide based cell targeting domains with live cell and animal imaging methods	DBT	2020	3 years	PI
03	Development of Genetically encoded fluorescent single cell sensor for cell death and ACE2-RBD-S protein binding inhibition	DBT	2022	1.5 years	PI

Dr. RUBY JOHN ANTO

Sl.No	Title	Funding Agency	Year of Starting	Duration	PI/ CO-PI
01	Evaluation of uttroside B, a furanosyl saponin from Solanum nigrum Linn as a candidate drug molecule against Aflatoxin-induced liver carcinogenesis and Non-alcoholic steatohepatitis (NASH)	SERB	2022	3 years	PI
02	Evaluation and in vivo validation of tryptanthrin analogues as potent lead molecules for malignant melanoma chemotherapy	CSIR	2021	3 years	PI
03	In vitro and in vivo validation of the efficacy of the synergistic combination of curcumin and 5-FU in exterminating breast cancer stem-cell like population using orthotopic breast xenograft model in NOD- SCID, gamma mice	The Spices Board of India	2020	3 years	PI
04	Pre-clinical evaluation of the mechanistic and immunological pharmacodynamics of a novel saponin, Uttroside-B against HCC	DBT M K Bhan Fellowship	2021	3 years	Mentor

Dr. SUPARNA SENGUPTA

Sl.No	Title	Funding Agency	Year of Starting	Duration	PI/ CO-PI
01	Exploration of the role of fodrin, a protein required in functional microtubule organization, in cancer and apoptosis"	ICMR	2021	3 years	PI
02	Investigating the Nanomaterial Based Exosome Sensor for Cancer Prognostic: An Approach towards Liquid Biopsy for Cancer	DBT	2017	3.5 years	PI

EXTRAMURAL PROJECTS ACTIVE BETWEEN APRIL 2021 TO MARCH 2022

Dr. ASHA S NAIR

Sl.No	Title	Funding Agency	Year of Starting	Duration	PI/ CO-PI
01	Addressing STIL as major driver of drug resistance in colorectal cancer, independent of Shh pathway.	ICMR	2022	3 years	PI

Dr. PRIYA SRINIVAS

Sl.No	Title	Funding Agency	Year of Starting	Duration	PI/ CO-PI
01	Identification of xenoestrogen induced spontaneous mutations and changes in promoter methylation status in the cancer causing genes BRCA1, BRCA2 and p53 in breast, ovarian, prostrate and pancreatic cancers.	CSIR	2020	3 years	PI
02	Targeting Cancer associated fibroblasts for Metastasis Inhibition in BRGA1 defective cancer	SERB	2018	3 years	PI

Dr. SREEJA S

Sl.No	Title	Funding Agency	Year of Starting	Duration	PI/ CO-PI
01	Elucidating the regulatory role of epigenetic players in 27 hydroxycholesterol (27 HC) mediated breast cancer proliferation.	ICMR	2021	3 years	PI
02	Study of Progesterone Receptor Foci and Progesterone Signaling in Breast Cancer Cells	DBT	2019	3 years	PI

Dr. VINOD KUMAR G . S

Sl.No	Title	Funding Agency	Year of Starting	Duration	PI/ CO-PI
01	Development of a novel three-dimensional self aggregating peptide fiber as an implant for brain tumors	SERB	2018	3 years	PI

Dr. DEVASENA ANANANTHARAMAN

Sl.No	Title	Funding Agency	Year of Starting	Duration	PI/ CO-PI
01	Human papillomavirus (HPV)-related oropharyngeal cancer burden and the natural history of oral HPV infections: an Indian perspective	DBT/ Wellcome Trust	2019	5 years	PI
02	Biomarkers of oral cancer risk prediction	DBT Glue Grant	2018	5 years	PI
03	HPV genotyping for efficacy testing of generic qHPV vaccine development: Serum Institute of India study	Serum Institute of India	2019	3 years	PI
04	Accurate and satisfactory analysis of all high risk HPV types and some of the low risks including HPV 6 and 11 antibody titers for the 2-versus 3 dose HPV vaccination clinical trial in India – Follow-up study	IARC-WHO	2020	5 years	PI

EXTRAMURAL PROJECTS ACTIVE BETWEEN APRIL 2021 TO MARCH 2022

Dr. TESSY THOMAS MALIEKAL

Sl.No	Title	Funding Agency	Year of Starting	Duration	PI/ CO-PI
01	Exploration of the role of fodrin, a protein required in functional microtubule reorganization, in cancer and apoptosis	ICMR	2021	3 years	PI

Dr. SUNIL MARTIN

Sl.No	Title	Funding Agency	Year of Starting	Duration	PI/ CO-PI
01	Engineering Natural Killer (NK) cells and γδ T cells with antiCD19 chimeric antigen receptor (CAR) for the adoptive immunotherapy	DBT-Ramalingaswamy Re-entry Fellowship	2018	5 years	Sunil Martin
02	CD19 CAR T cells to Target Refractory or Relapsed B cell Acute Lymphoblastic Leukemia (r/r B-ALL	DBT	In financial concurrence	3 years	Sunil Martin
03	Engineering of anti-CD37 CAR T cells to target B cell Non-Hodgkin's Lymphoma (B-NHL)	SERB	Technical committee Approved	2 years	Sunil Martin

Dr. HARIKUMAR K.B

Sl.No	Title	Funding Agency	Year of Starting	Duration	PI/ CO-PI
01	A mechanistic evaluation of Chiravilvadi Kashayam in colitis associated colorectal cancer	SERB	2018	3 years	PI
02	Understanding the role of sphingosine kinase isoforms in systemic lupus erythematosus (SLE)	CSIR	2018	5 years	PI
03	DOT1L regulate the metabolic and epigenetic alterations in pancreatic cancer	SERB	2021	3 years	PI
04	A lipid perspective on immune evasion mechanisms in pancreatic cancer metastasis	ICMR	2022	3 years	PI

Dr. ANI V DAS

Sl.No	Title	Funding Agency	Year of Starting	Duration	PI/ CO-PI
01	Deciphering the regulation of PiwiL1 in Cancer Stem cells	SERB	2021	3 years	PI

Dr. ANANDA MUKHERJEE

Sl.No	Title	Funding Agency	Year of Starting	Duration	PI/ CO-PI
01	Domain-specific role of tumor suppressor PTEN in genomic stability: A systematic approach.	SERB	2019	3.5 years	PI
02	Studies on noncanonical role of tumor suppressor PTEN in endometrial adenocarcinoma.	DBT-RRF	2018	7 years	PI

EXTRAMURAL PROJECTS ACTIVE BETWEEN APRIL 2021 TO MARCH 2022

Dr. RAM MOHAN RAM KUMAR

Sl.No	Title	Funding Agency	Year of Starting	Duration	PI/ CO-PI
01	Therapeutic microRNA delivery mediated by exosomes targeting cervical cancer metastases in the 3D and in vivo environments	DBT	2020	5 years	PI
02	Development of a low-cost diagnostic kit based on miRNA detection for hepatocellular carcinoma	ICMR	2022	3 years	PI

CARDIOVASCULAR DISEASES & DIABETES BIOLOGY

Dr. ABDUL JALEEL K. A

Sl.No	Title	Funding Agency	Year of Starting	Duration	PI/ CO-PI
01	Comprehensive mass spectrometry-based clinical lipidomics platforms for promoting biomedical research & advanced training for Indian researchers	DBT - SAHAJ	2021	4 years	PI

Dr. RAKESH S . LAISHRAM

Sl.No	Title	Funding Agency	Year of Starting	Duration	PI/ CO-PI
01	Alternative polyadenylation in gene expression – implications in cardiovascular diseases	DST	2020	5 years	PI
01	Star-PAP control of 3'-end processing and alternative polyadenylation in cancer progression	SERB	2020	3 years	PI

Dr. SUMI S

Sl.No	Title	Funding Agency	Year of Starting	Duration	PI/ CO-PI
01	Piezo-KLF2 axis in endothelial dysfunction and venous wall remodelling in varicose veins	SERB	2021	3 years	PI
02	Do epigenetic alterations in shear stress regulatory genes induce endothelial mesenchymal transition in patients with cerebral arteriovenous malformations?	ICMR	2019	3 years	PI
03	Molecular Pathogenesis of varicose veins	Dr N Radhakrishnan Charity fund	2018	5 years	PI
04	Role of hemodynamic shear stress in the pathogenesis of varicose veins	KSCSTE –YIPB	2018	3 years	PI

EXTRAMURAL PROJECTS ACTIVE BETWEEN APRIL 2021 TO MARCH 2022

Dr. ANANTHALAKSHMY SUNDARARARAMAN

Sl.No	Title	Funding Agency	Year of Starting	Duration	PI/ CO-PI
01	Role of RhoGTPases in the Intracellular Trafficking of Mitochondria Derived Vesicles (MDVs) and Angiogenesis	DBT-Ramalingaswami Fellowship	2020	5 years	PI
02	Characterising Mitochondria-derived Vesicle Trafficking through a Proximity Labelling Approach- A possible Novel Mito-nuclear Communication Pathway	SERB	2022	3 years	PI

NEUROBIOLOGY

Dr. OMKUMAR R . V

Sl.No	Title	Funding Agency	Year of Starting	Duration	PI/ CO-PI
01	Novel derivatives of Tacrine, a cholinesterase inhibitor, with added pharmacological actions –A preclinical experimental study	ICMR	2021	3 years	PI
02	Investigations on the role of the biochemical bistable switch in learning and memory in vivo	SERB	2019	3 years	PI

Dr. JACKSON JAMES

Sl.No	Title	Funding Agency	Year of Starting	Duration	PI/ CO-PI
01	Functional relevance of a unique subclass of Notch independent Hes-1 (NIHes-1) expressing neural stem cells in developing/adult cortex	SERB	2022	3 years	PI
02	Regulation of stemness by Pleiotropic Hes-1 expression in neuroblastoma	National Bioscience Career Award, DBT	2018	3 years	PI
03	Development of a low-cost Anosmia screening tool to mass screen asymptomatic COVID-19 carriers	SERB	2020	1 years	PI

Dr. DEBASREE DUTTA

Sl.No	Title	Funding Agency	Year of Starting	Duration	PI/ CO-PI
01	Evaluation of histone chaperone APLF as a novel biomarker in triple negative breast cancer.	DBT	2018	5 years	PI
02	Normal vs. abnormal hematopoiesis- result of a deregulated chromatin regulated by Histone chaperone HIRA?	SERB	2022	3 years	PI

EXTRAMURAL PROJECTS ACTIVE BETWEEN APRIL 2021 TO MARCH 2022

Dr. RASHMI MISHRA

Sl.No	Title	Funding Agency	Year of Starting	Duration	PI/ CO-PI
01	How Galectin-3 Drives Pressure Overload Mediated Cardiac Hypertrophy and Heart Failure	ICMR	2021	2 years	PI
02	Identification of the Role of Redox Signaling Pathways in the Mechanobiology of Glioblastoma multiforme.	DBT	2018	5 years	PI

Dr. RAJEEVE SIVADASAN

Sl.No	Title	Funding Agency	Year of Starting	Duration	PI/ CO-PI
01	Ramalingaswami Re-entry Fellowship	DBT	2021	5 years	PI

PATHOGEN BIOLOGY

Dr. SABU THOMAS

Sl.No	Title	Funding Agency	Year of Starting	Duration	PI/ CO-PI
01	Development of probiotic therapy for enhancing urolithin production by using bacterial flora of human origin	SERB	2018	4 years	PI
02	Adaptive Molecular Diagnostics	Wellcome Trust, UK	2021	1 years	PI

Dr. RADHAKRISHNAN R NAIR

Sl.No	Title	Funding Agency	Year of Starting	Duration	PI/ CO-PI
01	Association of gene encoding APRIL and BAFF with IgA Nephropathy , A case control study	ICMR	2020	3 years	PI
02	Development of a point of care device for measuring N-terminal fragment of BNP precursor (NT-ProBNP) from blood samples	ICMR CARE	2019	3 years	CO-PI
02	Development of a point of care Lateral Flow Diagnostic Platform for detection of viral antigens and antibodies, IgG & IgM, of Corona Virus SARS-CoV-2 enabling efficient and swift diagnosis and mass screening	BIRAC	2020	1 years	CO-PI

Dr. KARTHIKA RAJEEVE

Sl.No	Title	Funding Agency	Year of Starting	Duration	PI/ CO-PI
01	Unravelling the role of Chlamydial deubiquitinase in evading the host innate immune system.	SERB SRG	2022	2 years	PI
02	Deciphering the novel role of immune cells in the spread and dissemination of Chlamydia trachomatis.	DST SERB POWER fellowship	2021	3 years	PI
03	Creation of patient derived endometrial organoids for understanding the underlying causes of RIF	DBT	2022	3 years	CO-PI

EXTRAMURAL PROJECTS ACTIVE BETWEEN APRIL 2021 TO MARCH 2022

Dr. KARTHIK SUBRAMANIAN

Sl.No	Title	Funding Agency	Year of Starting	Duration	PI/ CO-PI
01	Disarming bacterial pathogens using novel peptides that target pore-forming toxins: from in silico to in vivo	DST-INSPIRE	2020	5 years	PI
02	Investigating pneumococcal adaptation to intracellular survival within the host and characterization of macrophage extracellular vesicles for novel vaccine development.	DBT-Ramalingaswami grant	2021	5 years	PI
03	Unravelling bacterial immunoevasion and host immune reprogramming strategies in invasive pneumococcal diseases.	SERB-SRG grant	2021	5 years	PI

Dr. SARA JONES

Sl.No	Title	Funding Agency	Year of Starting	Duration	PI/ CO-PI
01	Elucidating the functional relevance of novel NS1 mutations in Influenza A H1N1 2009 pandemic virus	SERB	2022	3 years	PI

Dr. KRISHNA KURTHKOTI

Sl.No	Title	Funding Agency	Year of Starting	Duration	PI/ CO-PI
01	Characterization of iron starvation induced dormancy in mycobacteria and its application in drug discovery	DBT	2017	6 years	PI
02	Deciphering the role of mycobacterial error-prone polymerase DnaE2 in antibiotic persistence and conferring adaptation to stress during biofilm formation	SERB	2019	3.5 years	PI

Dr. SANTANU CHATTOPADHYAY

Sl.No	Title	Funding Agency	Year of Starting	Duration	PI/ CO-PI
01	Helicobacter pylori infection in Sikkim and possible use of probiotics isolated from ethnic fermented foods of Sikkim against H. pylori	DBT	2018	4 years	PI

EXTRAMURAL PROJECTS ACTIVE BETWEEN APRIL 2021 TO MARCH 2022

PLANT BIOTECHNOLOGY & DISEASE BIOLOGY

Dr. GEORGE THOMAS

Sl.No	Title	Funding Agency	Year of Starting	Duration	PI/ CO-PI
01	Delineation and characterization of defense signaling pathways and genetic regulation of induced systemic resistance in Zingiber¬-Pythium pathosystems.	DBT	2018	3.5 years	PI

Dr. SARASWATI NAYAR

Sl.No	Title	Funding Agency	Year of Starting	Duration	PI/ CO-PI
01	A comprehensive study of MADS-box transcription factors in Chlamydomonas and Volvox to uncover their role in unicellular and multicellular flagellated motile green algae	SERB Power Grant	Approved	3 years	PI

REPRODUCTION BIOLOGY

Dr. PRADEEP KUMAR G

Sl.No	Title	Funding Agency	Year of Starting	Duration	PI/ CO-PI
01	Evaluation of the role of AIRE in germ cell development and differentiation	CSIR	2018	3 years	PI
02	Mapping of CNNM1 expression during gonocyte development in mouse	SERB	2020	2 years	PI
03	Prospective study on the screening of the expression of an array of sperm proteins and its correlation with assisted reproductive technology outcome	ICMR	2020	3 years	PI

Dr. MALINI LALORAYA

Sl.No	Title	Funding Agency	Year of Starting	Duration	PI/ CO-PI
01	Investigating the role of superoxide in regulating the major events during embryo implantation.	SERB	2020	3 years	PI
02	Molecular Analysis of Circadian Rhythm in Polycystic Ovarian Syndrome Patients.	DBT	2020	3 years	PI
03	Ascertaining the causes of low tregs in polycystic ovarian syndrome patients.	ICMR	2021	3 years	PI
04	Creation of patient derived endometrial organoids for understanding the underlying causes of RIF.	DBT	2022	3 years	PI

EXTRAMURAL PROJECTS ACTIVE BETWEEN APRIL 2021 TO MARCH 2022

TRANSDISCIPLINARY BIOLOGY

PROFESSOR CHANDRABHAS NARAYANA

Sl.No	Title	Funding Agency	Year of Starting	Duration	PI/ CO-PI
01	Development of Portable Raman Spectrometer for Identifying the Amyloid in the Peripheral Region of the Body	DST	2021	3 years	PI
02	Scientific reinvention of Ethnic Food and Medicine from Kerala for Functional Food and Drug Development	DST	2021	3 years	PI

Dr. MAHENDRAN K .R

Sl.No	Title	Funding Agency	Year of Starting	Duration	PI/ CO-PI
01	Structure determination and targeting of ubiquitously expressed membrane integrated form of chloride intracellular channels (CLICs) for discovery of small molecular anti-cancer therapeutics	DBT	2019	3 years	PI
02	Structural Assembly of Functional Transmembrane peptide nanopores: From Synthesis to Single-Molecule Sensing"	DBT	2021	3 years	PI
03	Engineered alpha-helical pores for single-molecule sensing of amyloid structures	SERB	2022	3 years	PI
04	The porin passport control for antibiotic translocation: From single-molecule detection to biological relevance	DBT	2022	3 years	PI

Dr. SHIJULAL NELSON SATHI

Sl.No	Title	Funding Agency	Year of Starting	Duration	PI/ CO-PI
01	Major Gene Influxes in Microbial Genome Evolution	DST- INSPIRE	2016	5 years	PI
02	The Structure and Evolution of Environmental Resistomes	DST	2018	3 years	PI
03	Epidemiological Monitoring of SARS CoV-2, and its variants in wastewater systems in the major cities of Kerela, India	SERB	2022	1 years	PI

EXTRAMURAL PROJECTS ACTIVE BETWEEN APRIL 2021 TO MARCH 2022

Dr. LIGHTSON N.G

Sl.No	Title	Funding Agency	Year of Starting	Duration	PI/ CO-PI
01	Studies of Non-enzymatic paper-based bioanalytical devices for point-of-care diagnostic applications	SERB	2022	3 years	PI
02	Paper-based Kits for On-site Detection of Methanol and Formaldehyde	BIRAC	2021	2 years	PI

Dr. UMASANKAR P . K

Sl.No	Title	Funding Agency	Year of Starting	Duration	PI/ CO-PI
01	Endocytic modulation of BMP signaling: deciphering mechanistic insights into health and disease	DBT	2016	6 years	PI

Dr. DEBANJAN BHOWMIK

Sl.No	Title	Funding Agency	Year of Starting	Duration	PI/ CO-PI
01	Ramanujan Fellowship	SERB	2021	5 years	PI

Ph.D AWARDED

CANCER RESEARCH

Dr. RUBY JOHN ANTO

Sl.No	Name of the Students	Title of Thesis	University	Awarded/ Submitted	Year
01	Swetha M	Evaluation of Uttroside B as a candidate drug against Hepatocellular carcinoma and comparison of its therapeutic potential with that of Solanum nigrum Linn leaf extract	University of Kerala	Submitted	2022

Dr. PRIYA SRINIVAS

Sl.No	Name of the Students	Title of Thesis	University	Awarded/ Submitted	Year
01	Krithiga. K	Cancer stem cell types and its link with prognosis in canine mammary carcinomas	University of Kerala	Awarded	2021
02	Arathi Rajan	Role of ER signaling on BRCA1 mediated DNA damage repair, in estrogen responsive breast cancer cells	University of Kerala	Awarded	2022
03	Geetu Rose Varghese	hCG, the pregnancy hormone mediated immune modulation in BRCA1 defective breast cancer	University of Kerala	Submitted	2021

Dr. SREEJA S

Sl.No	Name of the Students	Title of Thesis	University	Awarded/ Submitted	Year
01	Lakshmi M L	Estrogen mediated regulatory role of ezrin in Follicular thyroid cancer	University of Kerala	Awarded	2021

Dr. VINOD KUMAR G.S

Sl.No	Name of the Students	Title of Thesis	University	Awarded/ Submitted	Year
01	Amritha Vijayan	Design and synthesis of biodegradable polymer systems for wound healing	University of Kerala	Awarded	2021

Dr. RADHIKA NAIR

Sl.No	Name of the Students	Title of Thesis	University	Awarded/ Submitted	Year
01	Archana PT	Understanding the role of phenotypic heterogeneity in breast cancer	MAHE, Manipal	Submitted	2022

Ph.D AWARDED

CARDIOVASCULAR DISEASES & DIABETES BIOLOGY

Dr. RAKESH S. LAISHRAM

Sl.No	Name of the Students	Title of Thesis	University	Awarded/ Submitted	Year
01	Nimmy Francis	Linking the two A tails: role of polyA binding protein in mRNA stability	MAHE, Manipal	Awarded	2022
02	Ganesh Koshre	Mechanism of polyadenylation and its regulation by signalling pathways and phosphorylation	MAHE, Manipal	Awarded	2022

NEUROLOGY & REGENERATIVE BIOLOGY

Dr. JACKSON JAMES

Sl.No	Name of the Students	Title of Thesis	University	Awarded/ Submitted	Year
01	Dr. Lalitha S	Functional implication of Pax6 in eye development: Retinogenesis to intra-retinal axon guidance	University of Kerala	Awarded	2021

Dr. RASHMI MISHRA

Sl.No	Name of the Students	Title of Thesis	University	Awarded/ Submitted	Year
01	Sebastian John	Targeting tumour cell biomechanical homeostasis for novel anti-GBM (Glioblastoma multiforme) therapeutics.	MAHE, Manipal	Awarded	2022

PATHOGEN BIOLOGY

Dr. R.AJAY KUMAR

Sl.No	Name of the Students	Title of Thesis	University	Awarded/ Submitted	Year
01	Akhil Raj P	Functional characterization of Rv1019, a putative transcriptional regulator of Mycobacterium tuberculosis H37Rv, and delineation of its role in gene regulation.	University of Kerala	Awarded	2022

Ph.D AWARDED

Dr. JOHN BERNET JOHNSON

Sl.No	Name of the Students	Title of Thesis	University	Awarded/ Submitted	Year
01	Nisha Asok Kumar	Molecular dissection and functional elucidation of the interaction of rhabdoviral signatures with complement proteins.	MAHE, Manipal	Submitted	2022
02	Reshma K.M.	Development and characterization of oncolytic rhabdoviral vectors.	MAHE, Manipal	Submitted	2022

PLANT BIOTECHNOLOGY & DISEASE BIOLOGY

Dr. E.V.SONIYA

Sl.No	Name of the Students	Title of Thesis	University	Awarded/ Submitted	Year
01	Divya Kattupalli	A transcriptomic and metabolomic approach to decipher the defence mechanisms and crosstalk between phytohormone signalling pathways in black pepper (Piper nigrum L.)	University of Kerala	Awarded	2021
02	Sweda Sreekumar	Exploration of key regulatory factors controlling the synthesis of Bioactive compounds in Black pepper	University of Kerala	Awarded	2021
02	Aswathi U	Elucidating the role of transfer RNAs and their derivatives as stress regulating agents during Phytophthora capsici infection in Black pepper (Piper nigrum L.)	University of Kerala	Awarded	2021

REPRODUCTION BIOLOGY

Dr. G.PRADEEP KUMAR

Sl.No	Name of the Students	Title of Thesis	University	Awarded/ Submitted	Year
01	Mahitha Sahadevan	MicroRNA mediated regulation of gene expression in the division and differentiation of spermatogonial cells in mouse testis	University of Kerala	Awarded	2022
02	Irfan Khan P	Role of CyclinM1 in Male Germ Cell Development and Differentiation	University of Kerala	Submitted	2022

Ph.D AWARDED

TRANSDISCIPLINARY BIOLOGY

Dr. SANIL GEORGE

Sl.No	Name of the Students	Title of Thesis	University	Awarded/ Submitted	Year
01	Anoop V S	A molecular taxonomic reappraisal and fine scale population genetic structure of Euphlyctis karaavali, an edible frog species of Kerala	University of Kerala	Awarded	2022

Dr. MAHENDRAN K.R

Sl.No	Name of the Students	Title of Thesis	University	Awarded/ Submitted	Year
01	Neethu Puthumadathil	Structural and functional characterization of synthetic transmembrane peptide pores	MAHE, Manipal	Awarded	2021

FACULTY AWARDS /HONORS/ RECOGNITIONS

CANCER RESEARCH

DR. RUBY JOHN ANTO

2022: Selected for the TRIALECT-sponsored Fellowship for attending the 'Clinical Trials Traineeship Program' being conducted at INSERM, Paris, France in August, 2022.

CARDIOVASCULAR DISEASES & DIABETES BIOLOGY

Dr. RAKESH S. LAISHRAM

Elected Member, Guha Research Conference 2022

PATHOGEN BIOLOGY

Dr. SABU THOMAS

DBT Nominee - Institutional Biosafety Committee, Mahatma Gandhi University, Kottayam

Best Scientist Award-2022 by UTOCA

Chairman, Working Committee Group, Centre of Excellence in Microbiome, K- DISC, Govt. of Kerala

Dr. KARTHIKA RAJEEVE

SERB POWER fellowship

Dr. KARTHIK SUBRAMANIAN

DBT-Ramalingaswami Re-entry faculty fellowship

SERB-SRG award

PLANT BIOTECHNOLOGY & DISEASE BIOLOGY

Dr. SARASWATI NAYAR

Attendance Award for Plant Biology 2021 by Early Career Plant Scientists, American Society for Plant Biology (ECPS, ASPB)

TRANSDISCIPLINARY BIOLOGY

PROFESSOR CHANDRABHAS NARAYANA

The honorary fellowship of the Indian Society of Analytical Scientists, March 2022.

Dr. DEBANJAN BHOWMIK

Ramanujan Fellowship.

AWARDS RECEIVED BY PH.D STUDENTS/ RESEARCH FELLOWS/POST-DOCTORAL FELLOWS

CANCER RESEARCH

Dr. T.R.SANTHOSH KUMAR

Aswathy S. Best Oral presentation for Hormone receptor heterogeneity in breast cancer: understanding the non-genetic regulation of receptor dynamics at 3rd Indo Oncology Summit 2021 Bhuvaneshwar on 25-09-2021

Aswathy S. Best Oral presentation for Hormone receptor heterogeneity in breast cancer: understanding the non-genetic regulation of receptor dynamics at International Conference on environmental, agricultural, chemical and biological sciences (ICEACBS) Virtual, 22-01-2022

Tiffee P J. Best Oral presentation for Understanding the dynamics of lysosomal cell death pathway in drug resistant cancer cells at International Conference on environmental, agricultural, chemical and biological sciences (ICEACBS) Virtual, 22-01-2022

Aparna GJ. Best Oral presentation for Telomere independent nuclear and mitochondrial functions of telomerase (hTERT) in the regulation of cell cycle and cell death. At International Conference on Advances in Biosciences and Biotechnology (ICABB-2022) Department of Biotechnology, Jaypee Institute of Information Technology, Noida, Uttar Pradesh, India ,20-01-2022

Dr. S.SREEJA

Vini Ravindran. Best Oral presentation, 27-hydroxycholesterol, the endogenous Selective Estrogen Receptor Modulator (SERM) induces abberrant DNA methylation in breast cancer.International conference 5th BioSangam,'BioSangam 2022: Emerging trends in Biotechnology', MNNIT, Allahabad.

NEUROBIOLOGY & REGENERATIVE BIOLOGY

Dr. OMKUMAR RV

Sowmya Gunasekaran. AJAL full stipend to attend CAJAL Advanced Neuroscience Training Programme Course in Ageing and Cognition, September 2021, Bordeaux School of Neuroscience, Bordeaux, France

Dr. MOINAK BANERJEE

Neethu Mohan. First prize for Epilepsy poster competition in the 16th World Congress on Controversies in Neurology, Virtual- March 2022

Neethu Mohan. Best poster presentation award in the 34th Kerala Science Congress organized by KSCSTE, India- February 2022

Dr. JACKSON JAMES

Parvathy Surendran. Best Oral Presentation, Tlx3 is a crucial determinant for early cerebellar patterning, Kerala Science Congress, 2022, Thiruvananthapuram

Meera V. Best Oral Presentation, Is non-canonical Hes-1 expresson responsible for the maintenance of adult neural stem cells of embryonic origin in the SVZ?, RGCB-Merit Award Presentation, 15/11/2021, Thiruvananthapuram

Dr. DEBASREE DUTTA

Pallavi Chinnu Varghese. Best talk presentation award', 'Ph.D Conclave -2022' held at Manipal Academy of Higher Education (MAHE), Manipal on 27- 28th May 2022.

Pallavi Chinnu Varghese and Ishita Baral. Received ASBMB Graduate Travel Award to attend annual meeting at Philadelphia, USA, 2022

Pallavi Chinnu Varghese. For poster presentation, Role of Histone Chaperone APLF in Mammalian Embryo Development, received travel award to present her work at International Society for Stem Cell Research to be held at California, USA, 2022

Pallavi Chinnu Varghese. Received DBT travel award to attend ASBMB annual meeting at Philadelphia, USA, 2022

Pallavi Chinnu Varghese. Role of Histone Chaperone APLF in Mammalian Embryo Development, received Student Merit Award for best work presentation at RGCB, November 18th 2021.

PLANT BIOTECHNOLOGY & DISEASE BIOLOGY

Dr. E.V.SONIYA

Sora S. Best poster award, Genome wide analysis for deciphering the N6-methyladenosine epitranscriptome machinery of black pepper, Online poster competition – Genomics in plants, animals and microbes, Inter- University Centre for Genomics and Gene technology, Department of Biotechnology, University of Kerala, Kaariavattom, September 27, 2021.

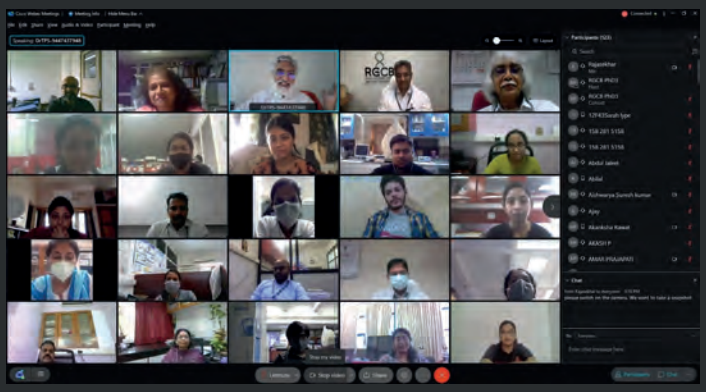
TRANSDISCIPLINARY BIOLOGY

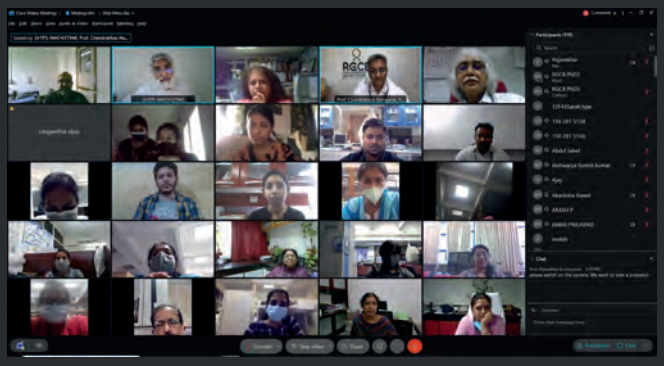
Dr. K.R.MAHENDRAN

Smrithi Krishnan R. Best oral presentation at 3rd Students Indian Peptide Society (SIPS) symposium, March 31st to April 1st 2022, IIT Bombay, India.

Devika Vikraman. Selected for the prestigious IGSTC fellowship to work at Nanion Technologies funded by Indo-German Science & Technology Centre (IGSTC) Fellowship established by the Department of Science and Technology (DST) and the Federal Ministry of Education and Research (BMBF).

JUNE 2021





International Yoga Day celebrated and Dr. T.P Sasikumar delivered the invited lecture on 21st June

AUGUST 2021

Professor Chandrabhas Narayana hoisted the National Flag on the occasion of 75th Independence day of our nation

AUGUST 2021

The SadbhavanaDiwas was observed on 20th August

EVENTS@RGCB 2021-22

SEPTEMBER 2021

Celebrated 14th September as Hindi Divas

NOVEMBER 2021

CV Raman lecture series: The invited talks was delivered by Shri. Jayant Sahashrabuddhe, National Organising Secretary at VijnanaBharati on 7th November

NOVEMBER 2021

RGCB foundation day lecture was given by Prof.M.R.S.Rao, JNCASR, Bengaluru on 18th November

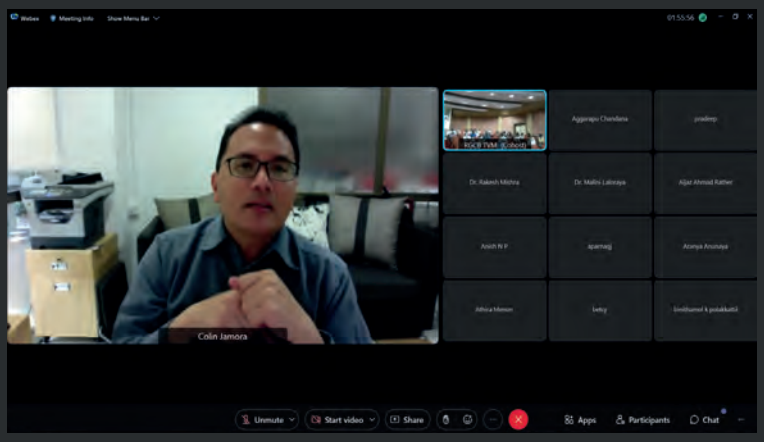
DECEMBER 2021

RGCB Pavilion at India International Science Festival (IISF) from 10-13th December at Goa

JANUARY 2022

Professor Chandrabhas Narayana unfurled the National Flag on the occasion of 73rdRepublic day of our nation

FEBRUARY 2022



Dr. Colin Jamora, InStem, Bengaluru given the Science day special lecture on 28th February

FEBRUARY 2022

RGCB stall at the VigyanSarvatraPujyate held between 22nd to 28th February at New Delhi

JANUARY 2022

International Women's day celebration and felicitation of the longest-serving women staffs of RGCB on 8th March

ANNUAL REPORT COMPILATION COMMITTEE 2021-2022

Dr. T.R Santhosh Kumar, Scientist G and Dean
Mr. R. Jayachandran Nair, Senior General Manager
Mr. R. Kumar, Senior Manager
Dr. Rajesh Chandramohandas, Scientist E-II
Dr. K.B. Harikumar, Scientist E-II
Dr. Kathiresan Natarajan, Scientist C
Ms. R. Lekshmi, Manager (Technical Services)
Ms. Ramya Rajan, Engineer (IT)

PC: Mr. Ganesh Babu B

RGCB

DISCOVERIES FOR A
BETTER TOMORROW

Rajiv Gandhi Centre For Biotechnology (RGCB)
An Autonomous Institute of the Department of Biotechnology, Ministry of Science & Technology, Government of India
Thycaud Post, Poojappura, Thiruvananthapuram 695 014, Kerala, India.
Ph: +91-471-2529400, 2347975, 2348753, Fax: +91 471 2348096
webmaster@rgcb.res.in, www.rgcb.res.in