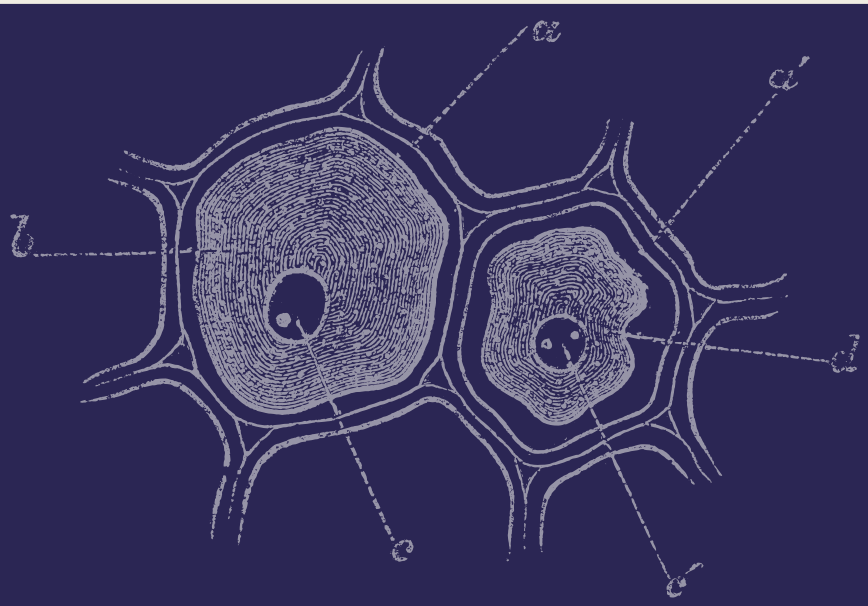
IISER
THIRUVANANTHAPURAM

FS-BIO 2023

Frontier Symposium in Biology



17 March – 19 March, 2023

School of Biology
Indian Institute of Science Education and Research
Thiruvananthapuram
(IISER TVM)

Designed by: Parth Ankam

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ABOUT FS-BIO 2023

The Frontier Symposia in Biology are annual, 2-day conferences organized by the School of Biology, IISER Thiruvananthapuram. This year the symposium will be held from 17 March – 19 March 2023 at our campus. The meetings cover a wide range of cutting-edge research topics in all fields of biology. Students and researchers from across the country come together to meet and discuss science in our picturesque campus in the foothills of the Western Ghats.

ORGANIZING COMMITTEE

Chief Patron

Prof. J. N. Moorthy, Director, IISER TVM

Convener

Prof. Hema Somananthan, Head of School of Biology, IISER TVM

Photo Credits: Tarunkishwor

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List of Speakers

Prof. Ajit Joglekar
Dr. Bhavana Muralidharan
Dr. Debasis Das
Dr. Gayathri Pananghat
Dr. Gopaljee Jha
Prof. Jagreet Kaur
Prof. Maneesha S. Inamdar
Dr. Manjari Jain
Dr. Manjula Reddy
Prof. Oishee Chakrabarti
Dr. Rajesh Chandramohanadas
Dr. Sabari Sankar Thirupathy
Prof. Saikrishanan Kayarat
Dr. Sivaram V. S. Mylavarapu
Dr. Subhash Rajpurohit
Dr. Ullasa Kodandaramaiah
Dr. Varsha Singh

FS-BIO 2023

DAY 1

(Friday, 17th March, 2023)

11:00 - 15:00	**REGISTRATION**
15:00 - 15:05	**WELCOME ADDRESS:** Prof. Hema Somanathan (Head, School of Biology, IISER TVM)
15:05- 15:15	**INAUGURAL ADDRESS**: Prof. J. N. Moorthy (Director, IISER TVM)
	SESSION 1 (Chair: Prof. S. Murty Srinivasula)
15:15 - 15:45	Prof. Maneesha Inamdar, inStem, Bangalore
15:45 - 16:15	Prof. Ajit Joglekar, University of Michigan Medical School
16:15- 16:45	Dr. Sivaram V. S. Mylavarapu, RCB, NCR Delhi
16:45- 17:15	**ANNOUNCEMENTS & REFRESHMENTS**
	SESSION 2 (Chair: Dr. Ravi Maruthachalam)
17:15 - 17:45	Prof. Jagreet Kaur, University of Delhi New Delhi
17:45 - 18:15	Dr. Gopaljee Jha, NIPGR New Delhi
18:30 -19:30	**POSTERS** (VENUE: LHC Corridor)
20:00	**Dinner for guests at Visitor's Forest Retreat**

FS-BIO 2023

DAY 2

(Saturday, 18th March, 2023)

SESSION 3 (Chair: Prof. Hema Somanathan)

09:30 - 10:00	Dr. Subhash Rajpurohit, Ahmedabad University, Ahmedabad
10:00 - 10:30	Dr. Manjari Jain, IISER Mohali
10:30 - 11:00	Dr. Ullasa Kodandaramaiah, IISER Thiruvananthapuram
11:00 - 11:30	**ANNOUNCEMENTS & REFRESHMENTS**

SESSION 4 (Chair: Prof. Nishant K. T.)

11:30 - 12:00	Dr. Manjula Reddy, Senior Scientist, CCMB Hyderabad
12:00 - 12:30	Dr. Sabari Sankar Thirupathy, IISER Thiruvananthapuram
13:00 - 14:30	**LUNCH**

SESSION 5 (Chair: Dr. Ramanathan Natesh)

14:30 - 15:00	Dr. Debasis Das, TIFR Mumbai
15:00 - 15:30	Prof. Saikrishnan Kayarat, IISER Pune
15:30 - 16:00	Dr. Gayathri Pananghat, IISER Pune
16:00 - 16:30	**ANNOUNCEMENTS & REFRESHMENTS**

DAY 2

(Saturday, 18th March, 2023)

16:30 - 17:30	**SESSION 6** (Chair: Dr. Poonam Thakur) IISER TVM STUDENT FLASH TALKS
17:30 -19:00	**POSTERS** (VENUE: LHC Corridor)
20:00	**Dinner for guests at Visitor's Forest Retreat**

FS-BIO 2023

DAY 3

(Sunday, 19th March, 2023)

SESSION 7 (Chair: Prof. Tapas K. Manna)

09:30 - 10:00	Prof. Oishee Chakrabarti, Saha Institute Kolkata
10:00 - 10:30	Dr. Rajesh Chandramohanadas, RGCB Thiruvananthapuram
10:30 - 11:00	Dr. Varsha Singh, IISc Bengaluru
11:00 - 11:30	Dr. Bhavana Muralidharan, InStem Bangalore
11:30 - 12:00	**ANNOUNCEMENTS & REFRESHMENTS**
12:00 - 12:15	**VALEDICTORY FUNCTION**

FS-BIO 2023

Speaker Abstracts

PROF. AJIT JOGLEKAR

PROF. AJIT JOGLEKAR
UNIVERSITY OF MICHIGAN

Reverse engineering kinetochore-like machines in budding yeast using *de novo* designed proteins

Over four decades of research on the centromere and the kinetochore in budding yeast has synthesized a detailed understanding of their protein composition, structure, function, and regulation. In the coming years, powerful new technologies promise to further deepen this understanding, raising the question: what comes next. We have begun efforts to reverse engineer kinetochore-like protein machines using *de novo*-designed proteins as building blocks. I will share our strategy and progress with building a two-protein complex that mimics the structure and function of the microtubule-binding Dam1 ring complex. We have two goals in mind for these efforts. In the short term, any success with our naïve strategy of replacing extant proteins with *de novo*-designed scaffolds will establish the minimum requirements for building a kinetochore-like machine; failure will deepen our understanding of the extant proteins. In the long term, our work will assemble a blueprint for building kinetochore-like machines that segregate synthetic chromosomes.

IISER THIRUVANANTHAPURAM

DR. BHAVANA MURALIDHARAN
INSTEM BANGALORE

Chromatin regulation of human neural stem cells by putative causative of intellectual disability- LSD1

The cerebral cortex is the seat of all higher order functions in the brain namely, sensory perception, decision-making, language, learning and memory. Chromatin and epigenetic regulations play a critical role in cerebral cortical development. Studying the chromatin regulatory mechanisms is important to our understanding of the fundamental process of building the brain and it is mutations in the very same networks, which lead to a range of neurodevelopmental disorders. LSD1 is a conserved histone lysine-specific demethylase which functions in the demethylation of mono- and di- methylated H3K4 and H3K9. Mutations in LSD1 have been identified to be a putative cause of a rare genetic form of intellectual disability (Pilotto *et al.*, 2016). Yet, its role in human neuronal development is unexplored. We have performed LSD1 ChIP-seq and RNA-seq upon its inhibition in human neural stem cells to ascertain its genome -wide downstream targets. Our study has revealed that the genes regulated by LSD1 are crucial for forebrain development, neuron generation, axon guidance and synapse organization. LSD1 regulates genes involved in signal transduction, cell adhesion and extracellular matrix functions. Further we found several Notch pathway genes and human enriched genes to be upregulated upon LSD1 inhibition. Overexpression of these genes in human neural stem cells mimics LSD1 inhibition and suppresses neuronal differentiation. Our study reveals key novel downstream effector functions of LSD1 in regulating human neuronal development.

DR. BHAVANA MURALIDHARAN

DR. DEBASIS DAS
TIFR, MUMBAI

Do chaperones regulate the quantal size during exocytosis?

The 'holy grail' in the study of membrane traffic is the actual fusion reaction, in which secretory vesicles fuse with the plasmalemma to form the fusion pores. These pores are the first aqueous connection between the lumen of secretory vesicles and the extracellular space. In the presynaptic nerve termini, neurotransmitters secrete through these pores in a tightly regulated manner. The process gets altered under disease conditions where too little, or, too much secretion occurs. Fusion pores are the sites of action of several regulatory factors, known to either stimulate or limit neurotransmitter secretion. We ask the question - of whether the fusion pore itself can regulate the quantal size during vesicular secretion. Our study describes that SNARE chaperones Munc13-1 and Munc18-1, differentially alter both the size and kinetic properties of individual nascent fusion pores. Hence, membrane fusion regulators can modulate the amount of chemical messengers' release, by directly modulating fusion pore conformations, which has a significant impact in cell to cell communication.

DR. DEBASIS DAS

DR. GAYATHRI PANANGHAT
IISER PUNE

Mechanistic insights into kinetic polarity of the bacterial tubulin FtsZ

FtsZ, a tubulin homolog, forms filaments that assemble laterally to form the Z-ring associated with prokaryotic cell division. FtsZ filaments exhibit treadmilling within the cell, unlike the dynamic instability seen in microtubules. The treadmilling of FtsZ filaments guides the peptidoglycan synthesis machinery for the formation of the septum during cell division. FtsZ and microtubules also differ in their kinetic polarity. Using Spiroplasma, a cell-wall-less bacterium, as model system, we aim to investigate the mechanistic aspects of cell division driven by FtsZ filaments, independent of peptidoglycan synthesis. Using structural biology and biochemical tools, we demonstrate that the ease of opening of C-terminal cleft aids the protein in transitioning between R and T states, compatible with the monomeric and filamentous states. Mutation of a residue in the interdomain cleft results in a mutant FtsZ with higher activity and improved polymerization than the wild type. Comparison between tubulin and FtsZ structures provide an explanation on how the kinetic polarity of the respective filaments formed by the two homologous proteins is opposite to each other.

DR. GAYATHRI PANANGHAT

DR. GOPALJEE JHA
NIPGR, NEW DELHI

Exploiting microbial weapons for disease tolerance in plants

We have identified a rice-associated *Burkholderia gladioli* strain NGJ1 which exhibits broad-spectrum fungal eating (mycophagous) as well as anti-bacterial activity. We demonstrated that NGJ1 deploys a prophage tail-like protein that is encoded in a cryptic bacteriophage gene cluster, as a type III secretion system effector to forage over fungi. Treatment with the purified protein or its heterologous expression in rice/tomato provides multiple fungal disease tolerance. In addition, we demonstrated that NGJ1 utilizes a type VI secretion system for antibacterial activity. Our work has exemplified that the bacterium could recruit intracellular toxins as extracellular weapons to diversify its arsenal to dominate interbacterial competitions to occupy a particular niche in the host. The ongoing efforts to utilize the leads for the effective control of bacterial as well as fungal diseases in rice/tomato will be discussed.

DR. GOPALJEE JHA

PROF. JAGREET KAUR

PROF. JAGREET KAUR
UNIVERSITY OF DELHI, NEW DELHI

Transcriptomic insights into the molecular mechanism of Arabidopsis response to *Alternaria brassicae*

Alternaria leaf blight (ALB) a serious disease of *Brassica juncea* worldwide is caused by *Alternaria brassicae*- an ascomycete fungal pathogen. Besides severe yield losses, the infection also results in poor quality of mustard oil. No known source of resistance against *A. brassicae* is available in the cultivated Brassica species. The ecotypes of Arabidopsis show a wide range of natural variation in their response to *A. brassicae* infection thus serving as a good model to dissect the cellular and molecular mechanisms underlying resistance. A comparative transcriptomics approach was undertaken to unravel the molecular responses activated at an early and late stage during infection in a resistant and susceptible accession of Arabidopsis. Differential gene expression followed by gene enrichment and pathway analysis reveal a major reprogramming of several defense related pathways and secondary metabolic processes in the infected and control plants of both susceptible and resistant accessions. Interestingly, expression profile of genes in the Phenylpropanoid biosynthesis pathway showed significant correlation with the resistance in Arabidopsis. Further dissection of this pathway provides insights into the possible role of scopoletin in host pathogen interactions in the Arabidopsis -*A. brassicae* pathosystem.

IISER THIRUVANANTHAPURAM

PROF. MANEESHA S. INAMDAR

INSTEM, BANGALORE

Mitochondrial control of stem cell fate and aging

Significant advances in *in vitro* differentiation and cellular reprogramming technologies have enabled generation of several desired cell types from pluripotent stem cells. However, a major challenge remains the diminishing efficiency of differentiation down a lineage and the ability to produce cells of desired function. The *de novo* generation of multipotent hematopoietic stem cells (HSCs) from human pluripotent stem cells (hPSCs), is a major goal of regenerative therapies. HSC transplantation assays have revealed large variability in the reconstitution kinetics of the HSC pool indicating diversity of potential. Hence, generation of appropriate adult- like HSCs with engraftable and multi-lineage reconstitution potential demands identification of additional regulators of hematopoiesis. We showed earlier that hPSC populations demonstrate a spectrum of metabolic sub-states, which can be strategically canalized to generate desired cell types. Further, the mitochondrial activity regulator Asrij/OCIAD1 affects these sub states to control early mesoderm differentiation. However, the role of mitochondrial morphology and dynamics in mammalian hematopoiesis is not well understood. Mitochondrial activity impacts fate and lineage choice of the adult HSCs, however its role during early hematopoietic development is not known. We use in vitro human pluripotent stem cell differentiation and in vivo models of mouse and Drosophila development, to understand mitochondrial regulation of hematopoiesis. Our analysis reveals previously unreported, conserved mechanisms regulating mitochondrial homeostasis actively control blood stem cells.

PROF. MANEESHA S. INAMDAR

DR. MANJARI JAIN
IISER MOHALI

Vocal complexity and linguistic laws in avian vocalizations

Vocal complexity is studied in terms of structural complexity, semantics and syntax. Two important drivers of evolution of vocal complexity are sexual selection and sociality. Sexual selection is known to drive structural complexity in display vocalizations, whereas sociality is likely to drive vocal complexity in social animals, not only in terms of structure, but also in semantics and syntax. Human language is considered as the hallmark of vocal complexity. Rudimentary form of language has been found in many non-human primates whereas similar work on birds is lacking. Using bioacoustics and behaviour as our research tools we examined, and found evidence for complexity in avian vocalizations in terms of structure, semantics, syntax and even linguistic laws. I will discuss our findings and address the issue of finding a good model system for long-term ecological research.

DR. MANJARI JAIN

DR. MANJULA REDDY

DR. MANJULA REDDY
CCMB, HYDERABAD

Dynamics of Bacterial Cell Wall

Bacteria are ubiquitous unicellular organisms and to protect themselves against harsh environmental conditions, they are surrounded by a cell wall which is made up of a unique and essential mesh-like polymer called, peptidoglycan (PG). PG sacculus is made up of glycan polymers cross-linked to each other by short peptide chains to form a net-like structure that surrounds the cytoplasmic membrane. As PG sacculus completely encases the membrane, the growth and morphogenesis of a bacterial cell are intimately coupled to enlargement of PG sacculus. Expansion of PG requires coordinated activity of PG synthases that catalyze the cross-link formation and of PG hydrolases that make space for insertion of new PG material. Using E. coli as a model organism, our lab discovered several hydrolytic enzymes that cleave the peptide cross-bridges between the glycan chains to make space for the incorporation of new PG strands. These hydrolases also facilitate PG remodeling and aid in bacterial survival under fluctuating osmotic conditions. Overall, our studies facilitate a broad understanding of bacterial cell wall synthesis which is an excellent target for development of novel antimicrobials.

PROF. OISHEE CHAKRABARTI
SAHA INSTITUTE, KOLKATA

Endoplasmic reticulum-mitochondria crosstalk maintains cellular homeostasis

It is now well established that cells have evolved rigorous surveillance systems to efficiently detect and eliminate damaged and dysfunctional cellular organelles. Multiple levels of quality control mechanisms coexist for optimal organellar functioning and to ensure cellular health. The endoplasmic reticulum-mitochondria cross-talk is crucial for intra-cellular Ca 2+ buffering as well as ensuring that mitochondrial fission-fusion dynamics continue at normal physiological levels. I will discuss how inter- and intra-organellar dynamics (with emphasis on the endoplasmic reticulum and mitochondria) regulate quality control and maintain cellular homeostasis. I will also elucidate how alterations in ER resident proteins indirectly affect mitochondrial dynamics, compartmentalization and turnover.

PROF. OISHEE CHAKRABARTI

DR. RAJESH CHANDRAMOHANADAS
RGCB, THIRUVANANTHAPURAM

Dissecting Red Blood Cell Tropism Of Plasmodium Using A Multi-Omics Approach

Infection by Plasmodium parasites leading to Malaria remains a threat to the developing world, killing at least half a million people every year. These parasites infect and develop within human red blood cells (RBCs) during asexual replicative phase which is responsible for Malaria- associated clinical manifestations. Plasmodium parasites demonstrate a clear propensity towards immature red blood cells known as reticulocytes, this behavior is exclusive in the case of *P. vivax*, a parasitic form prevalent in Asia and south America. Molecular factors underpinning this host selection remains mostly elusive. To address this knowledge gap, we have embarked on understanding the chemical and physical determinants of host tropism and along the way discovered key host cell factors required for successful invasion into reticulocytes. These molecules represent important candidates for vaccine and antibody -based therapeutics and a major advancement towards the establishment of a *P. vivax* in vitro culture system to advance our knowledge in this domain.

DR. RAJESH CHANDRAMOHANADAS

DR. SABARI SANKAR THIRUPATHY

IISER TVM

Principles governing gene distribution in bacteria

Under neutral evolution, genes are expected to be distributed equally between the two strands of DNA replication. However, in many bacterial species, there is a preference for genes to be on the leading strand. The biased distribution is selected because co-directional conflicts between replication and transcription on the leading strand are less severe than head-on conflicts on the lagging strand. Thus, the impact of collisions has led to the evolution of gene-strand bias. Regardless, the bias varies extensively across bacterial species. In this study, we investigate the factors and mechanisms driving the variation and maintenance of gene-strand bias. We found an interesting relationship between inversion mutations and the maintenance of gene-strand bias and elucidated the underlying factors. In summary, we believe that selection governs genome organization by optimizing the mutations and mutagenic potential in bacteria.

DR. SABARI SANKAR THIRUPATHY

PROF. SAIKRISHNAN KAYARAT
IISER PUNE

DNA shredding: a new mode of DNA cleavage catalysed by ATP-dependent restriction enzymes

ATP-dependent restriction enzymes are one of the most common bacterial defense systems that prevent the entry of foreign DNA and protect the bacteria from phage infection. These enzymes regulate horizontal gene transfer and acquisition of genetic elements harbouring pathogenic islands and antibiotic resistance genes. Biochemical and structural studies carried out on ATP-dependent restriction enzymes SauUSI (a Type IV restriction enzyme) and LlaBIII (a Type ISP restriction enzyme) have revealed that this enzyme cleave DNA in a manner distinct from other nucleases. Double strand DNA cleavage by nucleases can be broadly classified as i) endonucleolytic resulting in hydrolysis of a pair of spatially close phosphodiester bonds on the two strands within the duplex; ii) exonucleolytic resulting in cleavage of a strand from the duplex ends. Our studies on SauUSI and LlaBIII have revealed that these enzymes, which have a nuclease coupled to an ATPase belonging to the Superfamily 2 helicases, make multiple nicks on the entire length of the DNA in between two of their DNA target sequences. Nicks at multiple locations on the DNA away from the target sequence is made possible by the translocase activity of the ATPase that propels the nuclease on the DNA. The nicks result in the DNA being shredded between the two target sequences. I will describe this unique mode of DNA cleavage and its possible physiological relevance.

PROF. SAIKRISHNAN KAYARAT

DR. SIVARAM V. S. MYLAVARAPU

RCB, NCR DELHI

Two-tiered regulation of mitotic dynein function through conserved posttranslational modification

The molecular nanomotor dynein performs several essential functions during mammalian mitosis. Dynein needs to switch efficiently between various cargoes to achieve this multifunctionality. I will discuss our work on the exquisite regulation of cargo selectivity that is imparted on dynein through conserved posttranslational modification on one of its core subunits.

DR. SIVARAM V. S. MYLAVARAPU

DR. SUBHASH RAJPUROHIT
AHMEDABAD UNIVERSITY, AHMEDABAD

Insect cuticular hydrocarbons under different environments

More than 30% of the earth's landmass consists of arid or semi-arid areas. Desertification and increase in temperature are expected results of global climate change and anthropogenic influence. There is therefore a critical need to understand how organisms will respond to these environmental changes. Insect cuticular hydrocarbons seem to be great candidates to ask questions about environmental stresses and adaptations. Cuticular hydrocarbons (CHCs) are hydrophobic compounds deposited on the arthropod cuticle that are of functional significance with respect to stress tolerance, social interactions, and mating dynamics. In this talk, I will touch base on geographical variations, thermal plasticity, and rapid secretions of cuticular hydrocarbons in *Drosophila* species populations. Following this, I will bring in some inputs from the molecular biology side where attempts have been made to find candidate genes playing important role in cuticle modifications. I will conclude by showing some results from seasonal dynamics in cuticular hydrocarbons and rapid adaptations in populations.

DR. SUBHASH RAJPUROHIT

DR. ULLASA KODANDARAMAIAH
IISER TVM

How background features influence animal camouflage

One of the most ubiquitous strategies against predation is a type of camouflage referred to as background matching, wherein prey animals avoid predation by adopting body colour patterning similar to that of their backgrounds. It is intuitive that the extent of background matching – i.e., how well an animal's colour pattern matches that of its background – influences the effectiveness of camouflage. However, background properties can also influence camouflage. In the first project, we manipulate background complexity in multiple ways and show that predators take longer to detect prey on backgrounds with high colour diversity. Surprisingly, the diversity of brightness levels among elements comprising the background did not affect detection times. In the second project, we explore how background complexity influences the optimal camouflage strategy when the prey has a choice between two distinct backgrounds. Prey can either be specialists, where they match one of the backgrounds at the cost of being less cryptic on the other, or generalists, where they adopt a colour pattern intermediate to that of multiple backgrounds. We explore a range of conditions involving variation in distinctness (i.e, dissimilarity) between backgrounds and background complexity. Our results show that complex backgrounds favour the evolution of a generalist strategy, but only when the difference between the backgrounds is small. I discuss the implications of our results for our understanding of evolution animal colour patterns, especially in relation to background choice behaviour.

DR. ULLASA KODANDARAMAIAH

IISER THIRUVANANTHAPURAM

DR. VARSHA SINGH
IISC BANGALORE

Caenorhabditis elegans as a model to understand innate immunity: Lessons (un)learned

Recognition of pathogens in a timely manner is the keystone for protective immune response in eukaryotes. In larger animals, innate immune system utilizes a number of sensors called pattern recognition receptors (PRRs) to sense pathogen associated molecular patterns (PAMPs) or endogenous damage associated molecular patterns (DAMPs). The PRRs could be membrane bound such as toll like receptors or cytosolic such as nod like receptors. Several small invertebrates such as *Caenorhabditis elegans* lack many classical PRRs. However, they have very effective and directed immune response to various pathogens. We hypothesize that such animals likely have non canonical PRRs. We utilized C. elegans, a bacterivore, to understand if the worm utilizes nonimmune cells for pattern recognition during infection. We find that sensory neurons regulate survival to broad classes of pathogens- Gram negative bacteria, Gram positive bacteria and pathogenic yeast. Olfactory neurons of worms show specific defect in sensing pathogenic bacterium Pseudomonas aeruginosa. We show that a volatile, 1-undecene, produced by the bacterium induces immune response in *C. elegans* via olfactory neurons. Do other pathogens produce molecular PAMPs? Do vertebrates sense volatile PAMPs via non canonical PRRs? Work from several multicellular organisms suggest this to hold true.

DR. VARSHA SINGH

FS-BIO 2023

Poster Presentations

1

ALLEN MARIA JACOB

To understand the regulation of microtubule cytoskeleton by few genes obtained by genome wide CRISPR-Cas9 screening

GeDiT Lab

2

ANUSHREE BHATNAGAR

Structural and Functional Characterization Of Aggresome-Like Induced Structures (ALIS) In Response To Infection

Laboratory of Immune Cell Biology

3

ASHVITHA B.

Understanding the molecular basis of circadian clock precision in Drosophila melanogaster populations selected for a narrow gate of adult Emergence

Chronobiology lab

4

ASMI JEZEERA

Spatial vision in Indian stingless bee, *Tetragonula iridipennis*

BEE Lab

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BHAGYA LAKSHMI R.

ch-TOG regulates kinetochore-microtubule end-on attachments by stabilizing CENP-E at the kinetochore

Cytoskeleton & Cell Division Laboratory

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FATHIMA RUMAISA

Anti-inflammatory potential of *Pterospermum rubiginosum* bark extract in LPS stimulated RAW 264.7 Macrophages

University of Kerala

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JERVIS FERNANDES

Sexually dimorphic microRNA regulates lifespan in male *Drosophila*

DREAM lab

8

KRISHANU DEY DAS

CARP1 : A novel regulator of Golgi dynamics

Laboratory of Immune Cell Biology

9

MALHAR ATRE

Selection modulates gene inversions to maintain gene-strand bias in bacteria

Mutations Lab

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NAVYASREE K. V.

Cholesterol regulate insulin- induced mTORC1 axis in mammalian cells

Rajiv Gandhi Center for Biotechnology

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PREMA MONDAL

CARPs in Stress Response

Laboratory of Immune Cell Biology

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RETNAKUMAR R. J.

Deciphering the molecular evolution of Helicobacter pylori virulence using whole genome analysis

Rajiv Gandhi Centre for Biotechnology

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RITOBRATO CHATTERJEE

Modulation of the Golgi architecture by TRIM32 and its muscular dystrophy mutant

Laboratory of Immune Cell Biology

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SAJESH VIJAYAN

Forage, forage against the dying of the light - nocturnal colour vision in the giant honey bee *Apis dorsata*

BEE lab

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SANTHOSH KUMAR S.

Modeling PD pathology by injection of α-synuclein fibrils in the mouse brain

Thakur Neurodegeneration Lab

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SNEHA SADANAND JOSHI

The effect of habitat specialisation on genetic divergence in two Impatiens species

Vanasiri Lab

IISER THIRUVANANTHAPURAM

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SOHELA SARKAR

To Breathe is to Grow: Amino acid sensing by the trachea controls systemic growth and fat metabolism in *Drosophila melanogaster*

DREAM lab

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SUMAN DASH

Heterozygosity alters Msh5 binding to meiotic chromosomes in the baker's yeast

Genome Stability

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SWATHI BALAKRISHNAN

Genomics and transcriptomics for conservation and management of forest genetic resources

Kerala Forest Reasearch Institute

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SWETHA GOPAL

A role for the circadian photoreceptor cryptochrome in regulating triglyceride metabolism in *Drosophila melanogaster*

Chronobiology Lab

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USHMA ANAND

E3 ubiquitin ligase, FBXW7 regulates levels of centriole duplication protein, STIL

Cytoskeleton & Cell Division Laboratory

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VARSHA R.

Association of autophagy in isoproterenol stimulated cardiomyoblast hypertrophy: An insight into the use of autophagy targeted drugs

Amrita School of Biotechnology, Amrita Vishwa Vidyapeetham

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MOHIT PRADIP RAJABHOJ

Use of haploid genetics to reveal the role of gametophytic lethal genes MEDEA and DEMETER in early shoot development in *Arabidopsis thaliana*

Plant Centromere Biology lab

FS-BIO 2023

Flash Talks

1

ANNA GEO

miR-277 regulates the phase of circadian activity-rest rhythm in *Drosophila melanogaster*

Chronobiology Lab

2

INDUKALA K.

Adaptive phenotypic plasticity of mandibles in relation to host plants

Vanasiri lab

3

KAVYA MOHAN N.

Plant-visitor interactions in a tropical dry deciduous community

BEE Lab

4

MALHAR ATRE

Why do lagging strand genes exist?

Mutations Lab

5

MOHIT PRADIP RAJABHOJ

Use of haploid genetics to reveal the role of gametophytic lethal genes MEDEA and DEMETER in early shoot development in *Arabidopsis thaliana*

Plant Centromere Biology lab

6

POORVISHAA V. M.

Maternal GWAS and antiseizure medicine induced foetal Malformations

GeDit Lab

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RAHUL SHARMA

CARPs regulate STUB1 and it's pathogenic mutants aggregation kinetics by mono-ubiquitination.
Authors: Rahul Sharma, Prema Mondal & S.Murty Srinivasula

Laboratory of Immune Cell Biology

8

RESHMA V. MENON

How to train your fly: mechanisms underlying adaptive starvation stress response in *Drosophila melanogaster*

DREAM Lab

9

SHUBHAM H. MEHATRE

Elucidating the influence of hematopoietic niche components on splenic hematopoiesis

Stem Cells and Development Lab

10

SUMAN DASH

Heterozygosity alters Msh5 binding to meiotic chromosomes in the baker's yeast

Genome stability Lab

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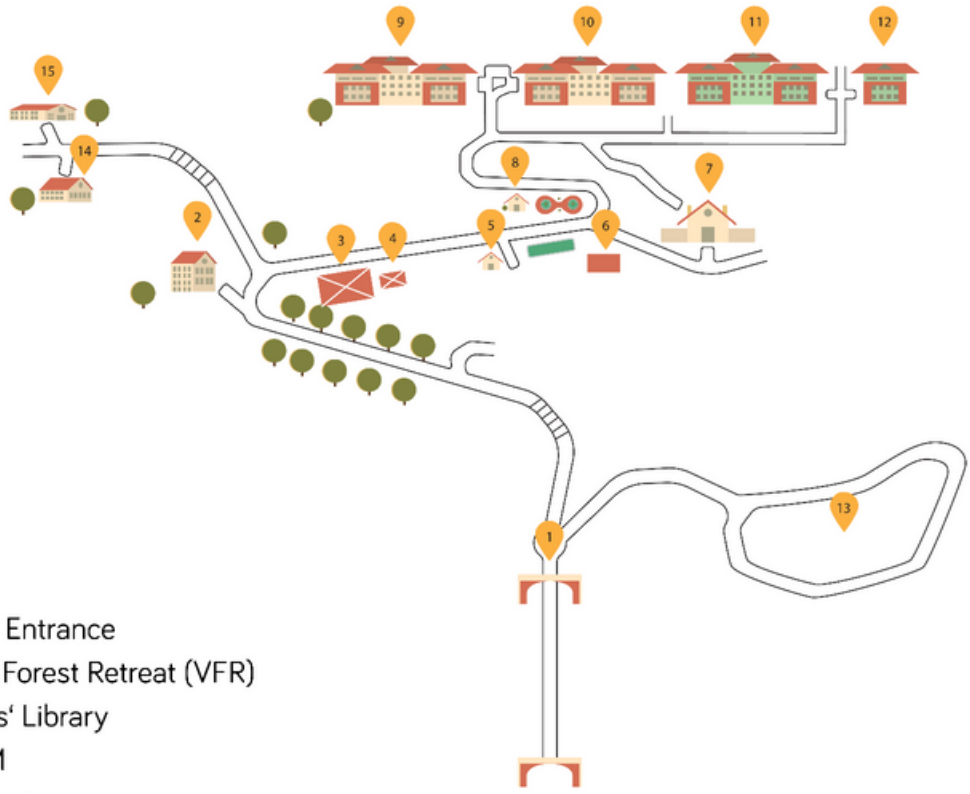
VISHNU M. NAIR

E3-Ubiquitin ligase, FBXW7 regulates mitotic checkpoint protein in human cell

Cytoskeleton & Cell Division Laboratory

Campus Map



1. Campus Entrance
2. Visitors' Forest Retreat (VFR)
3. Students' Library
4. SBI ATM
5. Restaurant
6. Bus Stop
7. Central Dining Hall
8. Student Lounge and Cafe
9. Physical and Mathematical Sciences Block
10. Chemical Sciences Block
11. Biological Sciences Block
12. Animal House
13. Students' Hostel area
14. Medical Center
15. Central Dining Hall 3

Design and illustration: @shyam_m_sm

Internal Shuttle Servie (Mini Bus) (Monday to Sunday)

Main Gate	BSB /CSB/ PSB	CDH1	Residence C3/B1	Anamudi Block Hostels	Residence C3/B1	Anamudi Block Hostels	CDH1	PSB/CSB/BSB	Main Gate
7.40am			**7:50**						
		7:55		**8:00**					
				8:00			**8:05**		
		8:05		**8:10**					
				8:10			**8:15**		
		8:15		**8:20**					
				8:20			**8:25**		
		8:25		**8:30**					
				8:30			**8:35**		
					8:40			**8:45 (CSB)**	
	8:45			**8:50**					
				8:50			**8:55**		
		8:55		**9:00**					
				9:00			**9:05**		
		9:05		**9:10**					
				9:10			**9:15**		
		9:15		**9:20**					
				9:20			**9:25**	**9:30**	
Monday to Saturday only	**10.10**		**10.20**		**10.30**			**10.40**	

Main Gate	BSB /CSB/ PSB	CDH1	Residence C3/B1	Anamudi Block Hostels	Residence C3/B1	Anamudi Block Hostels	CDH1	PSB/CSB/BSB	Main Gate
	12:30pm			**12.40 (via CDH1)**					
				12:40			**12:45**		
		12:45		**12:50**					
				12:50			**12:55**	**1:00**	
Monday to Saturday only	**1:00**		**1:10**				**1:15**		
		1:15		**1:20**					
				1:20			**1:25**		
		1:25		**1:30**					
				1:30			**1:35**		
		1:35		**1:40**					
				1:40			**1:45**		
		1:45			**1:50**			**2:00**	
						2:15		**2:20**	
	04.30pm		**04.40pm**		**4.50pm**				**5.00PM**
Monday to Saturday only	**05.30pm**		**05.40pm**	**-**	**-**	**-**		**05.50pm**	
	06.00pm		**-**	**06.10pm**	**-**	**06.15pm**		**06.25pm**	
		07:25pm		**07:30pm**		**07:35pm**	**07:40pm**		

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