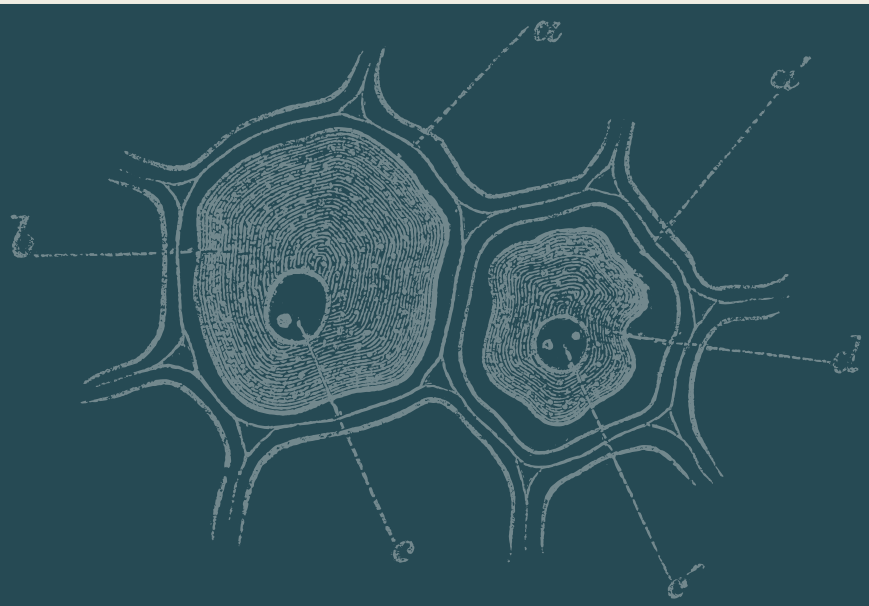
IISER
THIRUVANANTHAPURAM

FS-BIO 2022

Frontier Symposium in Biology



29 April – 01 May, 2022

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

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ABOUT FS-BIO2022

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 29 April – 01 May 2022 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

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

Convener

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

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List of Speakers

- Prof. Upinder S. Bhalla
- Prof. L. S. Shashidhara
- Dr. Jishy Varghese
- Prof. Gaiti Hasan
- Prof. S. Murty Srinivasula
- Prof. Dipshikha Chakravortty
- Prof. K. N. Balaji
- Dr. Uma Ramakrishnan
- Dr. Maria Thaker
- Dr. Kavita Isvaran
- Dr. Jyothilakshmi Vadassery
- Dr. Shantala Hari Dass
- Prof. Gautam Menon
- Dr. Soumen Basak
- Prof. Shikha Laloraya
- Dr. Sourav Datta
- Dr. P. V. Shivaprasad
- Dr. Vinita Gowda
- Dr. Amit Singh
- Dr. Bushra Ateeq
- Dr. Aravind Penmatsa
- Prof. Manidipa Banerjee
- Dr. Devendra Singh

DAY 1

(Friday, 29th April, 2022)

11:00 - 13:00	**REGISTRATION**
14:30 - 14:35	**WELCOME ADDRESS:** Prof. Hema Somanathan (Head, School of Biology, IISER TVM)
14:35 - 14:45	**INAUGURAL ADDRESS**: Prof. J. N. Moorthy (Director, IISER TVM)
	SESSION 1 (Chair: Prof. S. Murty Srinivasula)
14:45 - 15:15	Prof. Upinder S. Bhalla, NCBS, Bengaluru
15:15 - 15:45	Prof. Gaiti Hasan, NCBS, Bengaluru
15:45 - 16:15	Prof. Gautam Menon, Ashoka University, Sonepat
16:15 - 16:45	**ANNOUNCEMENTS & REFRESHMENTS**
	SESSION 2 (Chair: Dr. V. Stalin Raj)
16:45 - 17:15	Prof. K. N. Balaji, IISc, Bengaluru
17:15 - 17:45	Prof. Dipshikha Chakravortty, IISc, Bengaluru
17:45 - 18:15	Dr. Jishy Varghese, IISER TVM, Thiruvananthapuram
18:15 -20:00	**POSTERS** (VENUE: BSB Entrance Lobby & Hall)

DAY 2

(Saturday, 30th April, 2022)

SESSION 3 (Chair: Dr. Ullasa Kodandaramaiah)

09:30 - 10:00	Dr. Uma Ramakrishnan, NCBS, Bengaluru
10:00 - 10:30	Dr. Amit Singh, IISc, Bengaluru
10:30 - 11:00	Dr. Vinita Gowda, IISER Bhopal
11:00 - 11:30	**ANNOUNCEMENTS & REFRESHMENTS**

SESSION 4 (Chair: Dr. Nishant KT)

11:30 - 12:00	Prof. L. S. Shashidhara, Ashoka University, Sonepat
12:00 - 12:30	Dr. Maria Thaker, IISc, Bengaluru
12:30 - 13:00	Dr. Aravind Penmatsa, IISc, Bengaluru
13:00 - 15:00	**LUNCH** (Visitor's Forest Retreat)

SESSION 5 (Chair: Dr. Nisha N Kannan)

15:00 - 15:30	Prof. Shikha Laloraya, IISc, Bengaluru
15:30 - 16:00	Dr. Kavita Isvaran, IISc, Bengaluru
16:00 - 16:30	Dr. Soumen Basak, NII, New Delhi
16:30 - 17:00	**ANNOUNCEMENTS & REFRESHMENTS**

DAY 2

(Saturday, 30th April, 2022)

17:00 - 17:15	**GROUP PHOTO**
	SESSION 6 (Chair: Dr. Poonam Thakur)
17:15 - 17:45	Dr. Bushra Ateeq, IIT Kanpur
17:45 - 18:15	Dr. Shantala Hari Dass, IndiaBioscience
	SESSION 7 (Chair: Dr. Sabari Sankar Thirupathy)
18:15 - 19:45	**IISER TVM STUDENTS' FLASH TALKS**

DAY 3

(Sunday, 1st May, 2022)

SESSION 8 (Chair: Prof. Tapas K. Manna)

09:30 - 10:00	Prof. S. Murty Srinivasula, IISER TVM
10:00 - 10:30	Prof. Manidipa Banerjee, IIT Delhi
10:30 - 11:00	Dr. Devendra Singh, India Alliance
11:00 - 11:30	**ANNOUNCEMENTS & REFRESHMENTS**

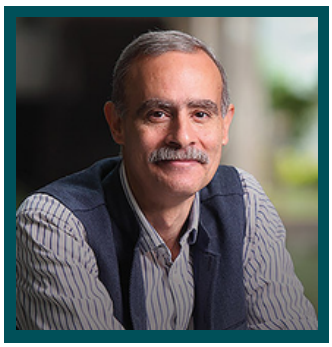
SESSION 9 (Chair: Dr. N. Sadananda Singh)

11:30 - 12:00	Dr. P. V. Shivaprasad, NCBS, Bengaluru
12:00 - 12:30	Dr. Sourav Datta, IISER Bhopal
12:30 - 13:00	Dr. Jyothilakshmi Vadassery, NIPGR, New Delhi
13:00 - 13:15	**VALEDICTORY FUNCTION**

FS-BIO 2022

Speaker Abstracts

PROF. UPINDER S. BHALLA



PROF. UPINDER S. BHALLA

NCBS, BENGALURU

Memories in Molecules, Brains, and Machines

Humans have prodigious memories. While computers can now claim larger storage capacities, and are certainly more precise, there is no comparison between searching for a particular file and the human ability to remember relevant events, in context, very rapidly. How do we do this?

I'll discuss the obvious attributes of memory - how they are formed and where they reside in the brain. Then I'll move on to more subtle questions - are memories stored in molecules, in the synapses, in the cells, or in the network? I'll also give a few glimpses of our work on modeling memory at the molecular and synaptic scale, and of our 2-photon recordings from mouse brains as they learn an association task.

I'll close with my views on how AI has taken some of these insights into memory and applied it to deep networks. I will speculate on how the brain is nevertheless able to do certain kinds of learning and computation much more efficiently than AI.

PROF. GAITI HASAN

NCBS, BENGALURU

Regulation of Neuronal Gene Expression and Function by ER Calcium Signals

Dysregulation of endoplasmic reticulum (ER) derived calcium signals, and altered calcium homeostasis occur in neurodegenerative disorders, including several Ataxias, Parkinson's, and Alzheimer's disease. The inositol 1,4,5-trisphosphate receptor (IP3R) is an integral component of ER calcium signaling in multicellular organisms. Identification of mutations in a gene encoding the inositol 1,4,5-trisphosphate receptor Type 1 (IP3R1) as the cause of Spinocerebellar Ataxia 15, 29 and Gillespie Syndrome emphasizes the importance of understanding how the IP3R impacts neuronal function and physiology.

Inositol 1,4,5-trisphosphate (IP3) is generated as a second messenger within eukaryotic cells in response to extracellular signals. In vertebrates and invertebrates, these signals include a range of neurohormones, neuromodulators such as certain neuropeptides, and neurotransmitters. This suggests multiple roles for IP3 signaling in neurophysiology. These extracellular signals bind to their cognate G-protein coupled receptors and activate membrane-bound Phospholipase C to hydrolyze phosphatidylinositol 1,4, bisphosphate (PIP2), and generate IP3 and diacylglycerol.

PROF. GAITI HASAN

PROF. GAITI HASAN

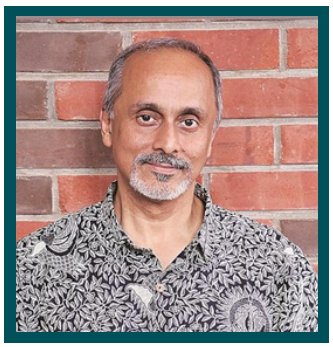
Regulation of Neuronal Gene Expression and Function by ER Calcium Signals

(Continued)

IP3, in turn, binds to ER localized IP3R leading to the release of Ca2+ from ER. Ca2+ stores followed by ER store-operated Ca2+ entry (SOCE) from the extracellular milieu through a mechanism involving the ER Ca2+ sensor STIM and the plasma membrane localized Ca2+ channel Orai.

I will discuss how cellular changes due to IP3 mediated Ca2+ release affect neuronal function and systemic physiology with the relevance of these findings to human neurological conditions.

PROF. GAUTAM MENON



PROF. GAUTAM MENON

ASHOKA UNIVERSITY, SONEPAT

Phase Separation, Activity and the Nucleolus

I will describe my recent work in which we use computational descriptions of large-scale nuclear architecture to model the biophysics of nucleolus assembly in eukaryotic cells. These models combine relatively new concepts in the description of cell-scale biological structuring - activity and phase separation - illustrating how the overlap of physics, biology, and computation can suggest fresh (and quantitative) approaches to old problems. This is a collaboration with Tejal Agarwal at Ashoka University.

PROF. K. N. BALAJI

IISc, BENGALURU

Pathogen-elicited Enhanced Host Lipids Contribute to Mycobacterial Survival: *An Intricate Role for Epigenetic Regulators*

Tuberculosis (TB) is one of the primary lung ailments that contribute significantly to the morbidity and mortality associated with infectious diseases. The etiological agent *Mycobacterium tuberculosis* (Mtb) invades the lung, wherein the bacillus is taken up by professional phagocytes such as macrophages, dendritic cells, and neutrophils. Mtb generates lipid-laden cells (foamy macrophages-FMs) as a part of its many shrewd strategies to impede the host-mounted immune onslaught. FMs are formed by the complex regulation of influx, metabolism, storage, and mobilization of lipid molecules.

Our lab provided evidence for the significance of the regulated turnover of lipids via autophagy during Mtb infection. Upon Mtb infection, induction of a histone acetylation reader was observed, pharmacological inhibition of which enhanced the autophagic flux with a concomitant reduction in lipid droplet accrual. Further investigations implicated this novel cellular node in contributing to Mtb survival and distinct pro-mycobacterial processes such as angiogenesis. Taken together, we underscore the cardinal role of Mtb-triggered epigenetic modification in manifesting key host cellular processes that aid in augmenting TB pathogenesis.

PROF. K. N. BALAJI

PROF. DIPSHIKHA CHAKRAVORTTY

IISc, BENGALURU

Salmonella's Life in a Vacuole and their Strategies to Live Happily in Studio Apartment

Salmonella typhimurium uses SPI-1 and SPI-2 encoded T3SS and virulence factors for thriving in host macrophages. Interestingly, the others genes which govern their lifestyle in vacuole remain elusive.

Morbidity and mortality by bacterial infections have been steadily increasing. The intervention strategies utilizing antibiotics and antimicrobials are becoming increasingly futile due to the emergence of multidrug and extreme drug resistance strains. The success story of bacterial vaccines are few. Owing to their small size and ability to adapt to any niche, the question is, why and how do some bacteria turn hostile? One such intelligent bacteria is Salmonella, an intracellular pathogen that lives inside a specialized vacuole called Salmonella Containing Vacuole (SCV). This vacuole is elusive, and even after a few decades of research, the composition of SCV is under continuous observation. Our lab focuses on intracellular pathogens. Being a pathogen with a diverse host range, Salmonella became one of our favorite organisms to work with. Salmonellosis or infection by Salmonella can cause typhoid fever and extra-intestinal infections like meningitis, endocarditis, and osteoarthritis. With the typhoidal and non-typhoidal serovars, the spread of Salmonella across the kingdoms, including plants, is worth discussing. The strategies employed by Salmonella to hijack the host system and cause infection will be further discussed in this talk.

PROF. DIPSHIKHA CHAKRAVORTTY

DR. JISHY VARGHESE

IISER TVM

DR. JISHY VARGHESE

Mechanisms that Help in Maintaining Nutrient Homeostasis

Living organisms are exposed to constant changes in their environment and harbor built-in mechanisms that aid in surviving such stressful fluctuations. Proper nutrient supply is crucial for normal development, growth, physiological status, lifespan, and reproduction. However, a constant supply of food cannot be guaranteed in nature. Our group is interested in understanding the genetic and molecular mechanisms that help Drosophila manage normal biological functions in response to an uneven supply of nutrients.

I will talk about two projects we are actively pursuing in the lab. In the first part, I will present data on a novel mechanism of nutrient sensing, which influences the final body size of the organism. In the second part, I will talk about how early exposure to low nutrient stress would affect the response to chronic nutrient stress in the later life stages.

DR. UMA RAMAKRISHNAN

DR. UMA RAMAKRISHNAN

NCBS, BENGALURU

Revealing Secrets about Tigers through Molecular Ecology

Tigers are charismatic. Animals like tigers excite us about biology and the wonders of nature. Yet when we start the systematic study of biology at the undergraduate and graduate level, we set aside these fascinations, this wonder, because they are too difficult to study.

Or are they?

Together with my laboratory colleagues, I have spent the last fifteen years understanding several secrets about tigers using tools like genetics. We have traversed protected areas across India to understand better mysteries about tiger movement, mating, and even unusual-looking tigers. In my talk, I will present my perspective on what we have learned and how this can help us devise a plan for the future of this charismatic animal.

DR. KAVITA ISVARAN
IISc, BENGALURU

The Emancipation of Sexual Selection

Sexual selection, the competition between individuals for sex for mates, is known to result in the evolution of bizarre, conspicuous, sometimes dangerous, often decorative traits. Our understanding of such competition derives primarily from males competing for mates. There is mounting evidence for widespread intrasexual competition in females. We are only beginning to discover the diverse range of ecological contexts in which female-female competition occurs.

I present work from our group that attempts to decipher female-female competition in diverse ecological contexts: how females compete for mates on antelope leks, how female lizards deploy multiple signals and aggression strategically during competition, and how female mosquitoes adapt unexpectedly and seemingly dangerous tactics when competing for resources for their offspring. I argue that due to key life-history differences, intrasexual competition is likely to favor traits in females that are pretty different from those historically reported in males.

DR. VINITA GOWDA

IISER BHOPAL

Using Evolutionary Features of Plant Communities to Understand Generation and Maintenance of Plant Biodiversity in India

Biodiversity refers to the biological diversity in any region, often measured using different ecological metrics such as species diversity or abundance. The measuring entity in any of these metrics is a "taxa." Therefore, these taxa's origin, maintenance, and extinction are crucial to understanding how biodiversity is generated and maintained in any region. India is known for its two megadiverse areas: the Western Ghats and Eastern Himalayas. I will present one case study from each of these regions that will highlight evolutionary and ecological mechanisms that plants may use to create and maintain taxonomic diversity. The Eastern Himalayan region is represented by taxa from the NE Indian states, which has a continuous distribution with flora from SE Asia. At the same time, the Western Ghats is different because it forms an isolated floristic region (from the NE or SE Asia), although it is historically connected to African flora. Our studies from both these regions show that most of our flora may be very young (~7-10 mya) and therefore lacks clear reproductive isolation boundaries and a high propensity for polyploidization.

The combination of hyper-diverse niches, monsoon intensification, and generalist pollinators also means that local hybridization events may be shared in both these regions, and outcrossing may be very common. While hybridization can result in taxonomically complex outcomes that seem unresolvable, it also allows us to understand how incipient speciation may look like in many of these taxa, enabling us to see how species evolve and create biodiversity in the two hyperdiverse regions of India.

DR. VINITA GOWDA

DR. MARIA THAKER

IISc, BENGALURU

Agamid Adaptation to Suburban Selection

The rapid rate of urbanization worldwide and its consequences for affected species urgently warrants research and action. Whether animals effectively cope with urbanization is hotly debated, primarily since interpretations are based on different measures of animal responses. Here, I'll take a multivariate view of animal coping strategies and set up predictions for determining urban utilizers. We will use the Indian rock agama (*Psammophilus dorsalis*) as a model system. I will share results from a suite of studies examining behavior, hormones, and health that collectively suggest active physiological and behavioral coping responses. We will also take some time to think about how the use of multiple measures of animal responses enables us better to understand strategies of adaptation to the urbanization challenge.

DR. MARIA THAKER

PROF. L. S. SHASHIDHARA

PROF. L. S. SHASHIDHARA

ASHOKA UNIVERSITY, SONEPAT

Evolution of Developmental Mechanisms behind "Endless Forms, Most Beautiful"

The talk explores experimental evidence from my group and others on how micro-evolutionary changes in DNA can cause significant changes in developmental plans, ultimately resulting in morphological diversity in insects.

PROF. SHIKHA LALORAYA

PROF. SHIKHA LALORAYA
IISc, BENGALURU

The Structural Maintenance of Chromosomes Complex, Cohesin, and Its Roles beyond Cohesion

Cohesin is an SMC (Structural Maintenance of Chromosomes) protein complex that is a crucial determinant of chromosome architecture due to its DNA binding and tethering ability. Cohesin was initially identified based on its role in holding together newly replicated chromosomal DNA molecules or sister chromatids; mutants defective in cohesin subunits showed precocious dissociation of sister chromatids in mitosis, revealing its vital role in sister chromatid cohesion. Previous studies in budding yeast have revealed that in addition to sister-chromatid cohesion, cohesin is also required for mitotic chromosome condensation, DNA double-strand break repair, progression of replication forks, and barrier activity of tDNA boundary elements.

We have recently explored the role of cohesin in gene expression. Our work has revealed an unexpected role for cohesin in subtelomeric gene silencing independent of the histone-modifying silent information regulator (SIR) complex. Cohesin mutants showed preferential derepression of clusters of subtelomeric genes, and this effect extended even beyond the zone of SIR binding. Genetic interactions with known telomere silencing factors also indicated that cohesin operates independently of the SIR-mediated pathway for telomeric silencing. Cohesin dysfunction impaired tethering of telomeres to the nuclear envelope.

PROF. SHIKHA LALORAYA

The Structural Maintenance of Chromosomes Complex, Cohesin, and Its Roles beyond Cohesion

(Continued)

We propose that cohesin contributes to the repression of subtelomeric genes by chromatin compaction, which renders them inaccessible to the transcriptional machinery and localizes these genes adjacent to tethered chromosome ends within the peripheral silent compartment of the nucleus.

DR. AMIT SINGH
IISc, BENGALURU

Mycobacterium Tuberculosis Requires SufT for Fe-S Cluster Maturation, Metabolism, and Survival in vivo.

Mycobacterium tuberculosis (Mtb-causative agent) exploits Fe-S cluster containing proteins for respiration, metabolism, DNA repair, antibiotic resistance, and persistence. Therefore, the mechanisms underlying the biosynthesis of Fe-S clusters are essential to understanding the physiology of this human pathogen. Recent studies indicate that proteins containing DUF59 domains participate in Fe-S cluster assembly in few organisms. However, the function of protein-containing DFU59 domains is unknown in Mtb.

We show that Mtb expresses a DFU59 containing protein SufT that functions as an auxiliary factor utilized in Fe-S cluster maturation. SufT physically interacts with other accessory proteins (SufT and SufU), coordinating Fe-S cluster biogenesis in Mtb. We also show that SufT is required to maintain the activity of Fe-S cluster proteins during normal growth conditions and under environmental settings that enforce a high demand for Fe-S proteins.

Lastly, deficiency of SufT adversely affected Mtb's respiration, metabolism, growth inside macrophages, and ability to cause infection in mice. Altogether, our study suggests the exploration of inhibitors against Fe-S cluster biogenesis to target Mtb.

DR. AMIT SINGH

DR. SOUMEN BASAK

NII, NEW DELHI

Intestinal Inflammation Gone Awry – A Role of NF-KappaB Crosstalks

Aberrant inflammation, such as that associated with inflammatory bowel disease (IBD), is fueled by the inordinate activity of RelA/NF-κB factors. The canonical NF-κB module mediates controlled nuclear activation of RelA dimers from the latent cytoplasmic complexes. What provokes pathological RelA activity in the colitogenic gut remains unclear. A separate noncanonical NF-κB pathway is known to promote immune organogenesis involving Nfkb2 gene products. Here, I will discuss how noncanonical NF-κB signaling exacerbates inflammation in the colitogenic mouse gut or IBD patients by engaging in crosstalk with the canonical NF-κB pathway.

DR. SOUMEN BASAK

DR. BUSHRA ATEEQ

IIT KANPUR

Mechanistic Underpinnings of DLX1-Mediated Tumorigenesis and Its Potential Utility as a Drug Target in Prostate Cancer.

Signaling pathways that govern cell division, cell death, and differentiation during embryonic development are also known to play a crucial role in human malignancies. Distal-less homeobox (DLX) gene family comprising highly conserved homeobox-containing transcription factors are known for their vital role in embryogenesis. Deregulation of such genes has been associated with several cancers. For instance, Distal-less homeobox-1 (DLX1), which is involved in developing craniofacial features and GABAergic interneuron, is highly upregulated in prostate cancer. We showed that ~60% of advanced-stage prostate cancer patients display higher DLX1 levels associated with advanced-stage metastatic disease and poor survival overall. We established the oncogenic role of DLX1 in prostate cancer. We deciphered its transcriptional regulation involving ERG, a member of the ETS (erythroblast transformation-specific) family of transcription factors and androgen receptor (AR).

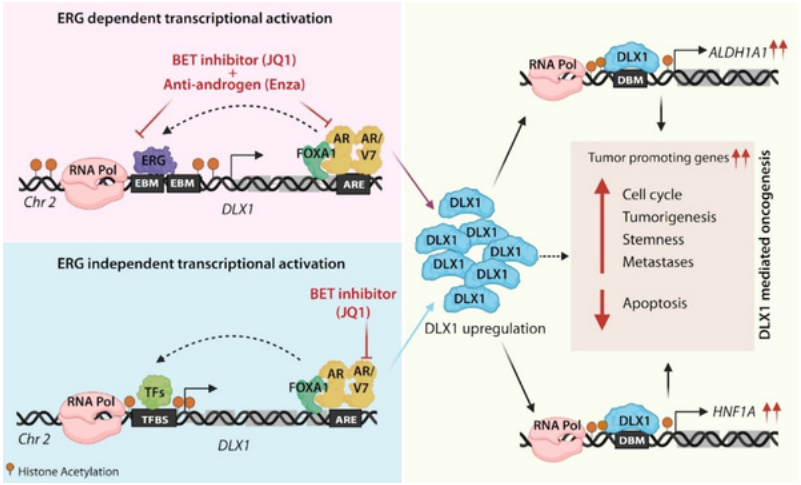
DR. BUSHRA ATEEQ

DR. BUSHRA ATEEQ

Mechanistic Underpinnings of dlx1-Mediated Tumorigenesis and Its Potential Utility as a Drug Target in Prostate Cancer.

(Continued)

Moreover, we showed that bromodomain and extra-terminal (BET) inhibitor and/or anti-androgen drug disrupts ERG/AR-mediated DLX1 transcription leading to its reduced expression and downstream oncogenic effects. Taken together, we provide strong evidence to consider BET inhibitors or/and anti-androgen drugs for the clinical management of DLX1-positive prostate cancer patients.



PROF. SRINIVASA MURTY SRINIVASULA

PROF. S. MURTY SRINIVASULA

IISER TVM

Endosomes: At Crossroads of the Golgi and Mitochondrial Homeostasis

Diverse quality-control systems ensure organelle homeostasis by facilitating isolation and elimination of damaged organelles or dysfunctional or defective proteins. Recent evidence points towards extensive inter-organelle crosstalk to enable cellular homeostasis. Endosomes are considered as intracellular sorting organelles that transport cargo between different compartments. Notwithstanding, endosomal signalling has now been implicated in the elimination of damaged mitochondria and the Golgi function. Our group recently identified an endosomal associated ubiquitin protein ligase, RFFL, primes damaged mitochondria for elimination by regulating Parkin recruitment. Moreover, we demonstrate that RFFL controls the Golgi apparatus by targeting one of the Golgi structural proteins for ubiquitination and degradation. In the talk, I present evidence to establish RFFL as a moonlighting protein that maintains organelle homeostasis.

IISER THIRUVANANTHAPURAM

DR. ARAVIND PENMATSA

DR. ARAVIND PENMATSA
IISc, BENGALURU

Ion-Coupled Antibacterial Efflux in a Superbug

Cells and organelles employ ion-coupled transporters to carry out specific transport functions in prokaryotic and eukaryotic membranes. The ionic electrochemical gradients across the bacterial membrane drive substrates' selective gating and movement against their concentration gradients. Efflux of antibacterial compounds through proton-coupled antiport is an effective mechanism for gaining antimicrobial resistance. Our recent structural and functional studies using X-ray crystallography, cryoEM, and other biochemical methods on two such efflux pumps from the superbug *Staphylococcus aureus* have allowed us to understand the role of protonation sites in promiscuous antibacterial efflux and highlight the use of single-domain camelid antibodies as chaperones to study transporter architecture and alter efflux activity.

PROF. MANIDIPA BANERJEE

IIT DELHI

Asymmetry and Quasi-Symmetry in Icosahedral Virus Capsids

Icosahedral viruses have a very stable and symmetric protein shell to protect the viral genome and transport it inside host cells. However, limited dynamic behavior of capsid components is required for conformational changes during virus entry and capsid disassembly. We are utilizing a combination of cryoelectron microscopy and whole capsid simulations to understand the dynamic behavior of a non-enveloped insect RNA virus – Flock House Virus (FHV). MD simulation of the entire capsid indicates striking differences in the flexibility of sequentially identical capsid proteins occupying different positions in the icosahedral asymmetric units of the capsid, which is consistent with previously described biological behavior. The capsid shell is permeable to the bidirectional movement of water, with the location of water tunnels within the capsid being influenced by the capsid geometry. Biochemical and structural studies of two disassembling states of FHV indicate the involvement of the 2-fold axis in genome release. One of the intermediate structures has been resolved using cryoelectron microscopy to 4.5 Å, and appears to be significantly asymmetric in nature, with icosahedral details preserved in only one half of the capsid. There are significant conformational alterations at the capsid axes of symmetry; however, the release of the genome appears to occur from the vicinity of one specific 2-fold axis of symmetry of the capsid. In conjunction with whole capsid simulation studies, the structures of these intermediates are expected to provide a molecular roadmap for disassembly. Recently, it has been shown that some degree of asymmetry is inherent in icosahedral virus capsids, which may have substantial biological implications.

PROF. MANIDIPA BANERJEE

DR. SOURAV DATTA

IISER BHOPAL

Regulation of Early Seedling Development by BBX Proteins

When a seedling emerges out of the soil, one of the critical morphological changes it undergoes is the unfolding of the embryonic leaves called cotyledons. Light promotes cotyledon opening, whereas the plant hormone Brassinosteroid (BR) inhibits cotyledon unfolding in the dark. The molecular interplay between light and BR to regulate cotyledon opening is not well understood. We identified that the B-box protein BBX32 is highly expressed in the cotyledons during de-etiolation and inhibits light-mediated cotyledon opening. Exogenous BR induces BBX32 expression in the cotyledons of seedlings grown in the dark. The BR biosynthesis inhibitor Brassinazole (BRZ) is known to cause cotyledon opening at night. We found that the BRZ-mediated cotyledon opening response in the dark is defective in BBX32 mutants. This suggests the role of BBX32 in BR-mediated suppression of cotyledon opening in darkness. BBX32 physically interacts with the transcription factors BZR1 and PIF3 and modulates the expression of shared target genes to regulate the opening and closing of cotyledons. In this talk, I will discuss the role of BBX32 in integrating light and BR signals to regulate cotyledon unfolding during early seedling development.

DR. SOURAV DATTA

DR. P. V. SHIVAPRASAD

DR. P. V. SHIVAPRASAD

NCBS, BENGALURU

Epigenetic and Small RNA mediated processes in crop plants

Small (s)RNAs are a set of key molecules resulting from RNA silencing pathways across eukaryotes. These 20-24 nt RNA molecules associate with specific protein partners called Argonautes to target nucleic acids having high base-pair complementarity. Among most eukaryotes, sRNA targeting might result in degradation of target RNAs or their translational repression. Among plants, sRNA targeting can also induce DNA methylation and histone modifications, often referred to as epigenetics through a process called RNA-directed DNA methylation (RdDM). Micro (mi) RNAs are a class of sRNA regulators typically involved degradation of target RNAs. Our lab focuses on various aspects of sRNA biogenesis and their functions, using genetic, molecular, bioinformatic and biochemical approaches using a number of model systems. I will be discussing novel sRNA-mediated pathways that played crucial roles in indica rice domestication, fruit coloration using grape as a model system, various yield-related traits and N metabolism. I will be also discussing how silencing-associated master regulators play crucial roles in chromatin architecture, induction and maintenance of histone marks and chromatin boundary formation.

DR. JYOTHILAKSHMI VADASSERY

NIPGR, NEW DELHI

Plant Perception of Insect Herbivory and Role of Ion Channels in Immune Response

Wound and herbivore perception in plants are unique as they lack a central nervous system, and hence each cell mounts a rapid defense response and transmits this information to the neighboring cells. Insect herbivores are voracious feeders and damage plants more rapidly than any other biotic stress. It is yet largely unknown how plants coordinate cellular activities to respond to herbivory. It is known that sensing herbivory by a single leaf of a plant results in the activation of different systemic signals that reach systemic tissues within seconds/minutes and trigger systemic wound responses resulting in a heightened state of stress readiness for the entire plant. Upon herbivory, plants sense elicitors in the oral secretion of insects and damaged self to activate various signals, including, Calcium (Ca2+), Reactive Oxygen Species (ROS) waves, as well as the synthesis of stress hormones like jasmonate (JAs). Jasmonate biosynthesis further leads to secondary metabolite production that is toxic to insect herbivores. Using the genetically encoded plant Ca2+ indicators (GECI), R-GECO1, and GCaMP3, we identify herbivory-specific calcium signatures, receptors, and channels in the immune signaling pathway, employing Arabidopsis thaliana and Spodoptera litura (cutworm) as a model system. We identified that the Cyclic Nucleotide Gated Channel (CNGC) family of genes and pattern recognition receptors, DORN1 and PEPR, are crucial for early plant response to insect herbivores and activation of various primary and secondary metabolites. Our data show how early signaling is critical for local and systemic defense against insect herbivores.

DR. JYOTHILAKSHMI VADASSERY

DR. DEVENDRA SINGH

INDIA ALLIANCE

DR. DEVENDRA SINGH

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DR. SHANTALA HARI DASS

DR. SHANTALA HARI DASS

INDIABIOSCIENCE

Let's talk careers in science

The scientific ecosystem in India is ever-expanding, and more opportunities than ever are present today for those who wish to build their careers in science. This multitude of choices can seem confusing and intimidating. Through this talk, I hope to bring to the stage the scope and breadth of careers in science as well as to provide requisite tools and information for navigating a career path in science. By no means will this will no be a prescriptive session. Some exercises from IndiaBioscience's Crafting Your Career workshop will be included.
So come and let's talk careers in science!

FS-BIO 2022

Poster Abstracts

RESHMA V. MENON

INDIAN INSTITUTE OF SCIENCE EDUCATION AND RESEARCH THIRUVANANTHAPURAM

How to Train Your Fly: Mechanisms Underlying Adaptive Starvation Stress Response in *Drosophila melanogaster*

Authors: **Reshma V. Menon** and **Jishy Varghese**

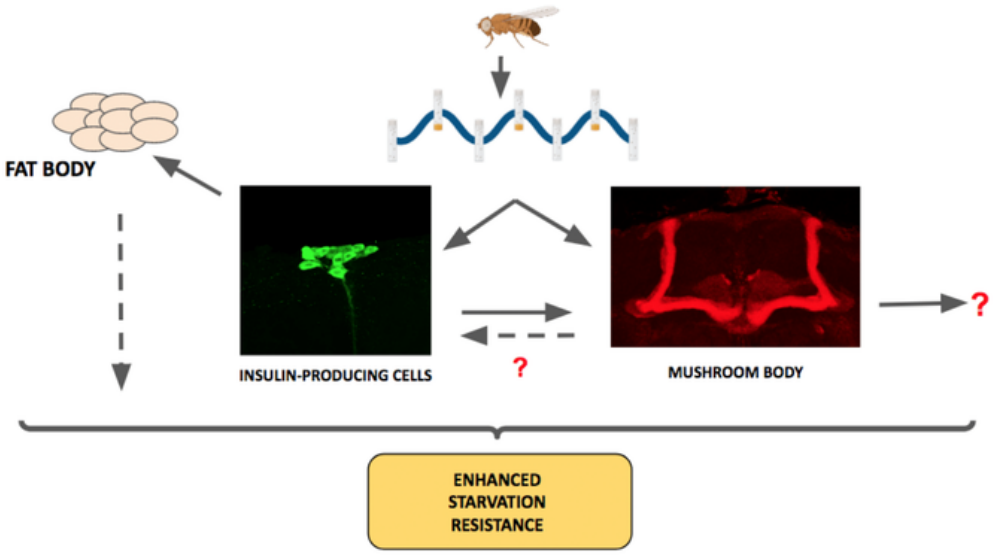
The dynamic nature of the environment causes an organism to undergo frequent exposure to environmental fluctuations that can alter its basal physiology. In brief, such fluctuations or stressors can elicit the activation of pathways that would lead to the maintenance of the basal systemic functioning - a process referred to as homeostasis. However, chronic exposure to stressors would stimulate adaptive mechanisms aimed towards coping with the recurrent threat. Such mechanisms could result in a shift from the normal baseline and establishment of a new normal physiology, a phenomenon referred to as allostasis. For animals in the wild, one of the major sources of environmental unpredictability is the availability of food. Hence, starvation-induced fine-tuning strategies arise as one of the key complexities that require thorough understanding.

The fundamental pathway involved in responding to the nutritional cues and the resultant metabolic calibration is the well-conserved insulin signaling pathway. Drosophila possesses 8 insulin-like peptides (DILPs) - DILP1-8 - that bear homology to mammalian insulin. Of these, DILP2, DILP3, and DILP5 which are produced and secreted by 14 medial neurons of the brain, are of prime importance for the maintenance of energy homeostasis in adult flies and their release is contingent on nutrition. However, the response of insulin signaling with respect to adaptive stress response remains elusive.

How to Train Your Fly: Mechanisms Underlying Adaptive Starvation Stress Response in *Drosophila melanogaster*

(continued)

Using *Drosophila melanogaster*, we have developed a 12-day time-restricted feeding regime that aims to effectively mimic a state of prolonged starvation. We report that the flies experiencing the bouts of starvation under this "training" process register a degree of "metabolic memory" by showcasing enhanced starvation resistance in comparison to their fed counterparts. In addition, we delve into the mechanistic basis of the adaptive starvation stress response by exploring the central and systemic role of insulin signaling pathway and the possible inter-organ communication in conferring metabolic leverage to the trained flies.



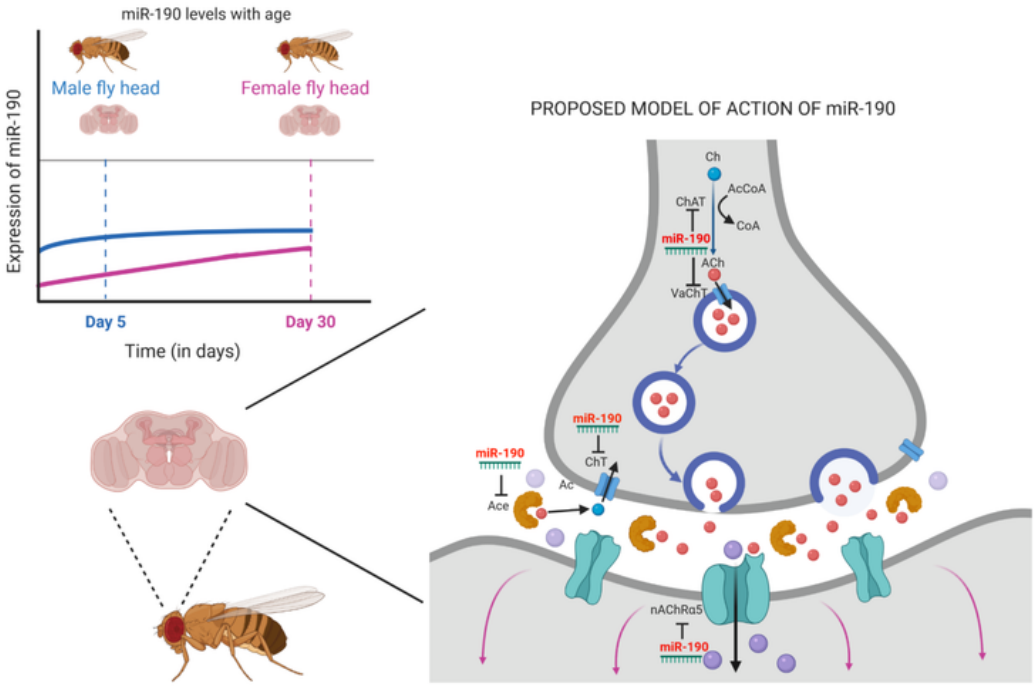
JERVIS FERNANDES

INDIAN INSTITUTE OF SCIENCE EDUCATION AND RESEARCH THIRUVANANTHAPURAM

Sexually Dimorphic microRNA miR-190 Regulates Lifespan in Males Drosophila

Authors: **Jervis Fernandes** and **Jishy Varghese**

MicroRNAs are short noncoding RNAs that buffer against fluctuations in gene expression in a myriad of physiological conditions. Here, we carried out a screen to identify the role of microRNAs in the maintenance of age-dependent neuronal functions in adult *Drosophila*. We report that miR-190 acts in the neurons to regulate lifespan, feeding and age-related locomotor activity specifically in male flies. miR-190, a highly conserved microRNA, shows higher expression levels in male flies and acts by regulating target genes that are responsible for maintaining neuronal activity and lifespan.



DREAM LAB

IISER THIRUVANANTHAPURAM

SOHELA SARKAR

INDIAN INSTITUTE OF SCIENCE EDUCATION AND RESEARCH THIRUVANANTHAPURAM

Role of Tracheal Cell-Specific Nutrient-Sensing Pathways during Growth and Development.

Authors: **Sohela Sarkar**, Sruthy S. P. and **Jishy Varghese**

Insulin and insulin-like growth factors are crucial for regulating growth and adult body size of a multicellular organism. Changes in oxygen and nutrient supply can alter insulin signalling. This in turn influences development, growth, metabolism and adult physiology. Pathways involved in sensing and responding to oxygen deprivation (hypoxia) and nutrient restriction, such as the canonical HIF1-alpha signalling pathway and TOR signalling pathway respectively, are conserved within every cell of an organism. Molecular cross-talks between these key signalling pathways aid in maintaining physiological homeostasis in response to oxygen and nutrient levels in the environment. Using *Drosophila melanogaster* as our model organism, we aim to study the importance of such molecular cross-talks within specific tissues in coordinating the systemic growth and development of an organism.

Here we show, for the first time, that the insect tracheal cells, primarily involved in oxygen sensing and delivery to various tissues, also act as local nutrient sensors. Recent proof shows that tracheal branching is dependent on the nutrient status. We show that the tracheal system influences systemic growth of the organism, in response to the nutrient availability. Our preliminary results suggest that tracheal cells can directly sense nutrient levels, and regulate adult body size and metabolism of the fly. This is most likely as a result of altered mTOR signalling in tracheal epithelial cells in conjunction with the remote control of insulin signalling from the insulin producing cells (IPCs) within the fly brain.

DREAM LAB

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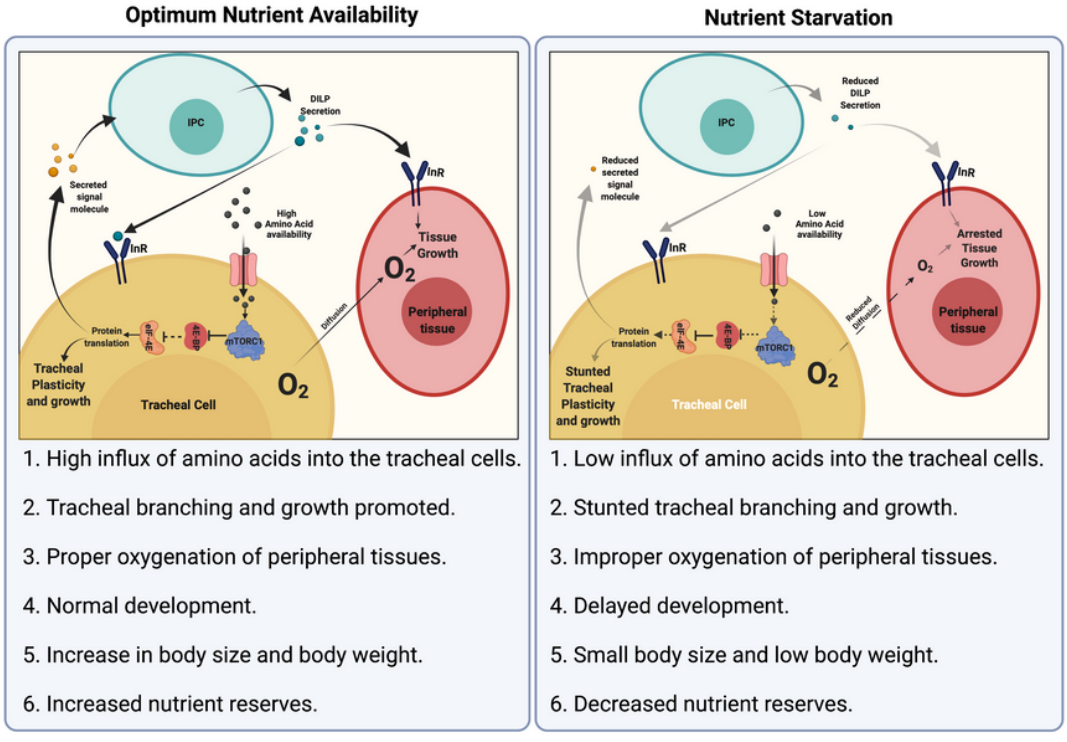
Role of Tracheal Cell-Specific Nutrient-Sensing Pathways during Growth and Development.

(Continued)

Further, our studies aim to identify novel molecules that mediate the inter-organ communication between the tracheal cells, IPCs and other peripheral tissues such as the fat body (FB) that ultimately help in coordinating steady growth, despite fluctuating levels of nutrients and oxygen.



TARUNKISHWOR YUMNAM

INDIAN INSTITUTE OF SCIENCE EDUCATION AND RESEARCH THIRUVANANTHAPURAM

Pupal Colour Plasticity in Tropical Pierid Butterflies

Authors: **Tarunkishwor Yumnam**, Birupakssa Banerjee and **Ullasa Kodandaramaiah**

Pupal Colour Plasticity (PCP) in many lepidopteran species has an adaptive significance by helping pupae match their background colours. Studies on PCP have largely used human assessment of colour to categorize pupae as green or brown. This subjective binary categorization limits the understanding of finer pupal colour variations and their function. Treating pupal colour as a continuous variable, we conducted studies on PCP in two pierid butterflies, *Catopsilia pomona* and *Eurema blanda*, which share the same host plant. In both lab and wild populations, we show that a large proportion of *C. pomona* pupae match the colours of their substrates, with leaf-borne pupae tending to be greener and off-leaf pupae browner. Pupal colour also responded to finer colour variations of leaf substrate, highlighting the importance of treating pupal colour as a continuous variable. In leaf-borne wild pupae, the leaf's length, the thickness of the midrib where pupation occurred, and pupation position on the leaf influenced the pupal colour. Similarly, PCP in *E. blanda* is significantly affected by substrate colour; with green pupae being formed on green substrates and brown ones on brown substrates. *E. blanda* has a gregarious larval phase, and we tested the effect of larval density on PCP. We found that larvae from high-density treatment were darker on average, and also included a higher frequency of brown pupae. Visual inspection of adult *E. blanda* shows variation in wing melanization. Our findings, thus, present *E. blanda* as a potential model to test trade-offs among melanin-based traits viz. pupal melanization, wing melanization and melanin-based immunity in adults. Overall, our results underscore the need for further research on PCP as a background-matching strategy in light of predation.

VANASIRI LAB

IISER THIRUVANANTHAPURAM

SNEHA SADANAND JOSHI

INDIAN INSTITUTE OF SCIENCE EDUCATION AND RESEARCH THIRUVANANTHAPURAM

Understanding the Ecology of Hybrid Zone Formation in Impatiens

Authors: **Sneha Sadanand Joshi** and **Ullasa Kodandaramaiah**

Hybridization between diverging lineages of closely related taxa is a common phenomenon and plays a vital role in shaping diversification patterns. When populations of two diverging lineages come in contact with each other, a narrow hybrid zone is formed. Hybrid zones in which hybrids are restricted to a narrow stretch while parental populations exist in allopatric distribution, forming a clinal pattern of traits across the zone of contact, are termed tension zones. Such tension zones are maintained by the balance between gene flow and a combination of exogenous and endogenous selection pressures.

Here we report the structure and ecology of natural hybrid zones formed by two closely related species, *Impatiens rosea* and *Impatiens balsamina*, in the Northern Western Ghats and adjoining coastal areas. The two species exhibit strictly allopatric distributions separated by narrow stretches of hybrid zones. We accessed the effect of various exogenous and endogenous factors such as environmental niche, local adaptation, hybrid fitness, and reproductive niche on maintaining the structure of hybrid zones. The extent of hybridization was mapped by generating geographic clines of various floral traits of parental and hybrid populations across two hybrid zones.

VANASIRI LAB

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VANASIRI LAB

Understanding the Ecology of Hybrid Zone Formation in Impatiens

(Continued)

The results suggest moderate overlap in the environmental niche with undifferentiated niche identities of both parental and hybrid populations. The effect of local adaptation on maintaining non-overlapping distribution is observed only at one site where the elevation gradient coincides with the hybrid zone. High overlap in the reproductive niche (flowering phenology and pollinator visitation) and the absence of selection against hybrids are the factors responsible for forming hybrid zones but do not have any effect on restricting the population boundaries in the current study region. Cline modeling indicated discordant clinal patterns across floral traits and hybrid zones, suggesting asymmetric introgression patterns and the differential action of selection pressure across multiple traits and different hybrid zones.

ASMI JEZEERA M.

INDIAN INSTITUTE OF SCIENCE EDUCATION AND RESEARCH THIRUVANANTHAPURAM

Spatial Resolution and Contrast Sensitivity of Flight Control of the Stingless Bee, *Tetragonula iridipennis*

Authors: **Asmi Jezeera M.**, Suvarna K., Bhargav R. M., Emily Baird, Almut Kelber, **Hema Somanathan**

Information from the visual system is crucial for navigation in flying insects, including bees. Though their eyes have a low spatial resolution, honey bees extract information based on the image motion in the retina (optic flow).

Optimization of spatial resolution may be required for different behavioral tasks and may differ from the spatial resolution estimated using anatomical methods (theoretical upper limit). For example, the spatial resolution of *Apis cerana* estimated using different behavioral methods (Zhang et al., 2014; Chakravarthi et al., 2018) and using anatomical methods (Somanathan et al., 2009) was different. Though the spatial resolution of *Bombus terrestris* was estimated to be very similar in two different behavioral contexts, the contrast sensitivity was observed to be different in these contexts (Chakravarthi et al., 2016; 2017).

Spatial Resolution and Contrast Sensitivity of Flight Control of the Stingless Bee, Tetragonula iridipennis

(Continued)

The constraints of the visual system limit the behaviors dependent on vision, and miniaturization adds further restrictions on the visual system. In stingless bees, there is only limited information about the ability to use visual motion patterns. In this study, the spatial resolution and contrast sensitivity of the *Tetragonula. iridipennis* for flight control was estimated. Our results suggest that *T. iridipennis* has a spatial resolution of at least 0.04 cycles per degree and 0.025 cycles per degree for lateral and ventral optic flow, respectively. The contrast sensitivity of *T. iridipennis* is at least 1.56 for 0.2 cycles/cm. Though the lateral position and speed of flight of T. iridipennis depended on the lateral optic flow, the height of flight from the ground was influenced by the ventral optic flow. The spatial resolution of *T. iridipennis* for flight control is lesser than the theoretically estimated limit. These results also suggest that *T. iridipennis* has a poor spatial resolution and contrast sensitivity compared to *A. cerana, A. mellifera,* and *B. terrestris*.

SUDEEP R.

INDIAN INSTITUTE OF SCIENCE EDUCATION AND RESEARCH THIRUVANANTHAPURAM

Foraging Behaviour in *Apis dorsata*

Authors: **Sudeep R.** and **Hema Somanathan**

Pollinators, while foraging, encounter several potential sources of floral resources. The choices made during foraging trips can help identify the foraging strategies being executed by the pollinators in question. Bees are among the most well-studied pollinators, and honeybees are among the most abundant pollinators in several habitats. Several studies in the field and lab have shown that individual bees tend to show fidelity towards a species or a morph in their visitation pattern. This type of floral fidelity, exhibited by certain pollinating animals, where they keep visiting the same type of flower species or morph while bypassing several other rewarding flowers, has been termed as floral constancy.

Floral constancy can be affected by several factors such as flower colour, odour, shape, reward parameters, foraging experience, social cues, handling difficulty, abundance and distribution of flowers etc. Experiments using artificial setups can answer specific questions with respect to the effect of these factors on the foraging patterns.

Foraging Behaviour in *Apis dorsata*

(Continued)

In the present study, we addressed the following using experiments with *Apis dorsata* foragers and arrays containing yellow and blue artificial stimuli: 1) spontaneous constancy, 2) effect of reward variability on constancy and 3) effect of training colour on constancy. The results indicate a strong bias towards blue colour after training on neutral colours (spontaneous constancy), which does not seem to be affected by the reward status on the blue stimuli, indicating a strong sensory bias towards blue colour. However, this bias can change with training on the less preferred colour. Extensive training on both test colours in alternating sequence seems to eliminate bias toward any of the test colours in their total choices. These results suggest that constancy in *Apis dorsata* is influenced by sensory biases and easily overwritten by recent foraging experience, indicating flexibility to adapt to changing floral resources.

SAJESH VIJAYAN

INDIAN INSTITUTE OF SCIENCE EDUCATION AND RESEARCH THIRUVANANTHAPURAM

Defensive Shimmering Responses in *Apis dorsata* are Triggered by Dark Stimuli Moving against a Bright Background

Authors: **Sajesh Vijayan** and **Hema Somanathan**

Due to the absence of physical barriers, the open-nesting giant honeybee *Apis dorsata* has evolved a spectacular collective defence behaviour – known as "shimmering" – against predators, which is characterised by travelling waves generated by individual bees flipping their abdomens in a coordinated and sequential manner across the bee curtain. We examined if shimmering is visually-mediated by presenting moving stimuli of varying sizes and contrasts to the background (dark or light) in bright and dim ambient light conditions. Shimmering was strongest under bright ambient light, and its strength declined in dim light. *A. dorsata* shimmered only when presented with the darkest stimulus against a light background but not when this condition was reversed (light stimulus against da ark background). We suggest that this is an effective anti-predatory strategy in open-nesting *A. dorsata* colonies, exposed to high ambient light, as flying predators are more easily detected when they appear as dark moving objects against a bright sky. Moreover, the stimulus detection threshold (smallest visual angular size) is much smaller in this anti-predatory context (1.6o - 3.4o) than in the context of foraging (5.7o), indicating that ecological context affects the visual detection threshold.

BEE LAB

IISER THIRUVANANTHAPURAM

ADITYA GHOSHAL

INDIAN INSTITUTE OF SCIENCE EDUCATION AND RESEARCH THIRUVANANTHAPURAM

Weight Asymmetry and Competitive Effects in Indian Social Spider *S sarasinorum*

Authors: **Aditya Ghoshal,** Anumit D Saralkar, **Hema Somanathan**

Intraspecific competition is a major factor that affects the stability and persistence of a population thus shaping population dynamics. Nicholson (1954) proposed two types of intraspecific competition, scramble, wherein resources are shared among all individuals. This type is prevalent when resources are too large for single individuals to monopolize. Contest competition is defined as the phenomenon where successful individuals monopolize resources at the expense of unsuccessful ones. In cases where the resource is small enough to be hoarded, fitter individuals benefit from it while zealously defending it from other individuals. Social spiders are an excellent model system to study competition. There is an asynchronous growth rate between colony members leading to a substructuring of the female population based on developmental stages. We investigated the prey capture and feeding behavior of juvenile social spiders where a weight asynchrony existed between the spiders. We found that mean weight differences of bigger and smaller spiders strongly correlate with the asynchrony within the group as well as the amount of prey consumed in a bout. However, we did not find any difference in the proportion of weight change between bigger and smaller spiders. Furthermore, the spiders exhibited a scramble mode of competition with nearly even food sharing between individuals. Further experiments will shed light on the temporal development on the competitive patterns in older sub-adults and adult colony members.

RESHMA BASAK

INDIAN INSTITUTE OF SCIENCE EDUCATION AND RESEARCH THIRUVANANTHAPURAM

Comparative Brain Morphology among Castes of Stingless Bee, *Tetragonula iridipennis*

Authors: **Reshma Basak,** Goutami Priyadarshini Nayak, **Hema Somanathan**

Stingless bee *Tetragonula iridipennis* are small Old World eusocial bees that build colonies in stone walls, barks of trees, etc. Previous work from our lab (Jazeera et al., 2021) showed that these bees have poor visual acuity compared to honeybees. Due to their extremely small size compared to the honeybees, these bees might use olfactory cues for navigation and nest recognition. The main objective of my work was to investigate the trade-off in investment between olfactory and optic brain regions (neuropils). Furthermore, I intend to study the differences in brain morphology between various castes across their life history. To this end, I dissected the brains of one-day-old bees, nurse bees, waste collecting bees, and guard bees, along with extranidal pollen and nectar foragers. These brains were optically sectioned using autofluorescence. We calculated the sizes of the olfactory and optic lobes to delineate the various castes and also further compared them with other bee species.

BEE LAB

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GENOME STABILITY LAB

SAMEER JOSHI

INDIAN INSTITUTE OF SCIENCE EDUCATION AND RESEARCH THIRUVANANTHAPURAM

Regulation of LOH tract Length by IRC20

Authors: **Sameer Joshi,** Suman Dash, Nikilesh Vijayan, **Nishant K. T.**

Loss of Heterozygosity (LOH) due to mitotic recombination is frequently associated with the development of various cancers (e.g., retinoblastoma). LOH is also an important source of genetic diversity, especially in organisms where meiosis is infrequent/absent. A previous study from our lab suggested that the evolutionarily conserved IRC20 (Increased Recombination Centre) gene might be responsible for enhanced LOH in *Saccharomyces cerevisiae*. IRC20 is a putative helicase and E3 ubiquitin ligase involved in the homologous recombination pathway. We analysed genome-wide LOH events, gross chromosomal changes, and single nucleotide mutations in ten *S. cerevisiae* mutation accumulation lines of irc20, which underwent 50 mitotic bottlenecks. LOH was enhanced significantly in irc20 as compared to wild type.

Further, we observed that LOH tracts in irc20 were shorter than the wild type. Gross chromosomal changes and single nucleotide mutations were not enhanced in irc20 mutants. Although meiotic crossover frequencies were similar, we also observed increased meiotic gene conversion events in irc20 compared with wild type. Overall, our results suggest that the IRC20 gene is important for regulating LOH tract length. These results are significant because factors regulating LOH tract size are poorly understood.

IISER THIRUVANANTHAPURAM

GENOME STABILITY LAB

AMAMAH FARZLIN FARNAZ

INDIAN INSTITUTE OF SCIENCE EDUCATION AND RESEARCH THIRUVANANTHAPURAM

Distinct Binding of Msh5 and other Pro-Crossover Factors Regulated by Meiotic Double Strand Break Repair Outcomes

Authors: **Amamah Farnaz**, Suman Dash, Ajith V. P., Sagar Salim, Ghanim Fajish, Akira Shinohara, **Nishant K. T.**

In the baker's yeast *Saccharomyces cerevisiae* and mammals, meiotic recombination is fundamental to sexual reproduction as it facilitates accurate segregation of homologous chromosomes at Meiosis I. The failure to segregate homologs leads to aneuploidy and is the cause of multiple pathologies like Down's syndrome, miscarriages and infertility. Two distinct crossover pathways exist. Msh4-Msh5 and Mlh1-Mlh3, act through the Class I pathway, which is part of the ZMM proteins, to generate the majority of crossovers. 'ZMM' encompasses the proteins Zip1, Zip2, Zip3, Zip4, Msh4, Msh5, Mer3, and Spo16, which work collectively to stabilise joint molecule intermediates and promote crossovers during meiosis. A smaller set of crossovers are generated using the Mms4-Mus81 endonuclease as part of the Class II pathway. Earlier studies from the lab showed that the Msh4-Msh5 complex binds in vivo to a subset of DSB hotspots, chromosome axis and centromeres. These in vivo binding sites of Msh5 are similar to that of other ZMM proteins like Zip3.

IISER THIRUVANANTHAPURAM

GENOME STABILITY LAB

Distinct Binding of Msh5 and other Pro-Crossover Factors Regulated by Meiotic Double Strand Break Repair Outcomes

(Continued)

Although binding sites of Msh5 and other pro-crossover factors like Zip3 have extensive overlap, Msh5 associates with centromeres independent of Zip3. Additionally, in earlier studies, we observed that Msh5 shows enhanced enrichment on smaller chromosomes with enhanced DSB densities compared to Zip3. We investigated if the regulation of Msh5 binding is distinct from other ZMM proteins. We analyzed the genome-wide in-vivo binding sites of the Class I crossover protein Msh5 during meiosis using the ChIP-Seq method in the strains sgs1△, pch2△ , and tel1△ where DSB repair outcomes are affected. Specifically, these mutants show enhanced use of the class II crossover pathway. We observe that Msh5 binding to DSB hotspots is reduced in these mutants. However, the binding of other ZMM proteins like Zip3 (others Zip2) is maintained in these mutants. Our results suggest that Msh5 binding to its in vivo sites may be regulated distinctly from other ZMM proteins.

CHRONOBIOLOGY LAB

AISHWARYA SEGU

INDIAN INSTITUTE OF SCIENCE EDUCATION AND RESEARCH THIRUVANANTHAPURAM

Why Does Caffeine Reduce Sleep?

Authors: **Segu Aishwarya** and **Nisha N. Kannan**

Caffeine is one of the widely consumed psycho-stimulants in the world. It has been widely understood that caffeine fragments sleep and promotes wakefulness. However, the exact molecular mechanism behind the action of caffeine on sleep is yet to be understood. Also, humans consume caffeine on a day to day basis, which accounts for prolonged intake of caffeine. The impact of prolonged exposure to caffeine is shown to cause a circadian impairment and decrease life span. In the present study, we examined the differential effect of short and prolonged exposure to caffeine on homeostatic sleep and circadian rhythm in young and mature *Drosophila*. The results of our study showed for the first time that short exposure to caffeine treatment, although it reduces sleep in young and mature flies, does not affect the homeostatic sleep circuit. But, this reduction in sleep was mostly due to reduced feeding.

On the other hand, prolonged caffeine treatment did not exert any significant effect on the duration of sleep in flies, similar to caffeine tolerance already reported in human beings. Nevertheless, prolonged caffeine ingestion delayed the timing of sleep in flies and decreased the morning and evening anticipatory activity, indicating that it affects circadian rhythm. These flies also exhibited reduced amplitude of clock gene transcript oscillation and altered the behavioural rhythm with either a longer free-running period or arrhythmicity under constant darkness. The shift of caffeine consumption from reducing sleep to not affecting sleep is dependent on the time duration of caffeine treatment.

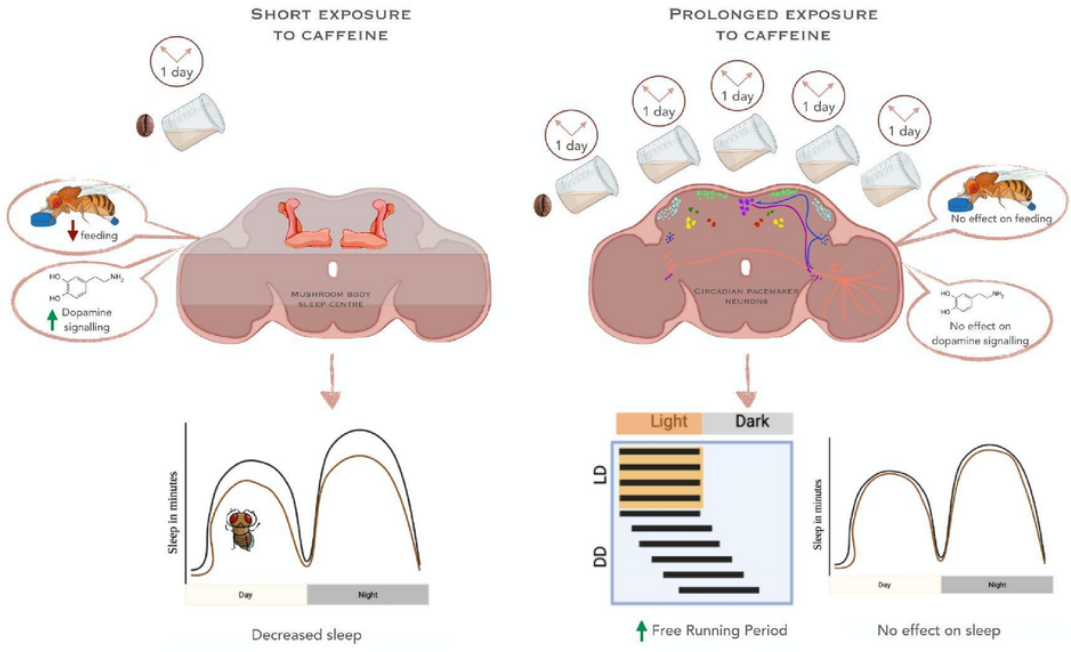
IISER THIRUVANANTHAPURAM

CHRONOBIOLOGY LAB

Why Does Caffeine Reduce Sleep?

(Continued)

The change in the dopamine signalling of the PAM neurons is shown to cause the effect of caffeine on sleep. Apart from this, prolonged caffeine treatment delayed the pre-adult development and also reduced the life span. In summary, the results of our studies showed that short exposure to caffeine decreased sleep, whereas prolonged caffeine treatment disrupts the circadian clock and affects myriad physiological processes.



CHRONOBIOLOGY LAB

SWETHA GOPAL

INDIAN INSTITUTE OF SCIENCE EDUCATION AND RESEARCH THIRUVANANTHAPURAM

Understanding the Interplay between Circadian Clock and Metabolism in *Drosophila melanogaster* – A Role for the Photoreceptor Cryptochrome

Authors: **Swetha Gopalakrishnan** and **Nisha N. Kannan**

The biological rhythms generated by the endogenous circadian clocks across the tree of life regulate a myriad of behavioral, metabolic and physiological processes. Although evidence from various studies indicates the importance of the circadian timing system in regulating metabolism, the impact of the external light-dark cycle in clock-mediated metabolic regulation remains unexplored. Constant light disrupts circadian rhythms and the circadian photoreceptor cryptochrome (cry) is essential for resetting the clock in response to light which has been studied in detail. In this study, we observed that the adult cryptochrome mutant (cry01) flies exhibited increased starvation resistance and triglyceride levels under both 12h:12h light/dark cycle (LD) and constant light (LL) compared to the control w1118 flies. The rate of triglyceride utilization was also markedly different in cry01 flies at 12, 15 and 18 hours post starvation. A growing body of evidence show that the peripheral clocks residing at various tissues are well-coordinated with the central clock in the brain to achieve metabolic homeostasis. When cry was tissue-specifically downregulated in the central pacemaker neurons, we observed that the flies showed enhanced starvation resistance under LD and a decrease in triglyceride levels under LL compared to the flies reared under LD. Under LD, we observed that the adult flies with cry down-regulated in fat bodies showed a decrease in both the starvation resistance and triglyceride levels.

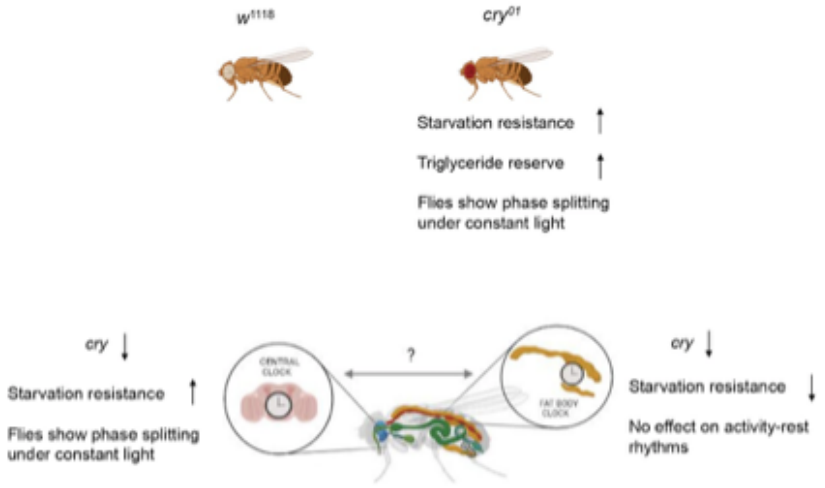
IISER THIRUVANANTHAPURAM

CHRONOBIOLOGY LAB

Understanding the Interplay between Circadian Clock and Metabolism in Drosophila melanogaster – A Role for the Photoreceptor Cryptochrome

(Continued)

However, under LL, there was not any significant difference. These results suggest that photoreceptor cryptochrome could affect metabolism in ways not fully understood yet. Our further studies will focus on understanding if downregulation and overexpression of cryptochrome affect the rhythmic expression of genes involved in metabolism and its impact on the utilisation of energy reserves in flies.



IISER THIRUVANANTHAPURAM

CHRONOBIOLOGY LAB

ANNA GEO

INDIAN INSTITUTE OF SCIENCE EDUCATION AND RESEARCH THIRUVANANTHAPURAM

miRNA Mediated Regulation of Activity-Rest Rhythm in *Drosophila melanogaster*

Authors: **Anna Geo**, Maria John, Rasajna M. and **Nisha N. Kannan**

Circadian clocks temporally organise the behaviour and physiology of an organism with rhythmicity of about 24 hours. Circadian clocks have evolved in diverse organisms ranging from cyanobacteria to mammals to ensure the coordination of the internal biological processes with the daily changes in the external environment due to the rotation of the earth on its axis. The clock is endogenous and self-sustaining, capable of persisting even in the absence of external environmental cues. The clock is also capable of resetting or entraining itself with respect to environmental conditions such as light and temperature, thus ensuring the synchrony of the individual organism's behaviour and physiological processes with the time of the day. In *Drosophila*, the master clock consists of ~150 clock neurons scattered across the fly brain. The clock neurons are characterised by the robust 24-hour feedback oscillations of the four major clock genes viz, period, timeless, clock and cycle, which constitutes the Transcription-Translation Feedback Loop (TTFL). The master clock is further regulated via post-transcriptional and post-translational mechanisms, and one of the most important post-transcriptional regulatory mechanisms is regulation via microRNAs (miRNAs). miRNAs are small 22 nucleotide sequences capable of binding to the 3'-untranslated region (3'UTR) of mRNAs, leading to either translational repression or mRNA degradation.

IISER THIRUVANANTHAPURAM

CHRONOBIOLOGY LAB

miRNA Mediated Regulation of Activity-Rest Rhythm in *Drosophila melanogaster*

(Continued)

In the current project, to study the role of miRNAs in post-transcriptional regulation of circadian rhythms, a genetic screen was initiated in which a large transgenic library of microRNA-mutants and sponge lines were used to perform knockout/ knockdown studies and we assessed its impact on the clock controlled activity-rest rhythms in *Drosophila*.

Results suggest that miRNAs are involved in the regulation of locomotor activity-rest rhythm, free running period and rhythmicity in flies. We started with the miRNAs that have high expression in the clock neurons and checked for the behavioural phenotypes of miRNA mutants followed by tissue specific downregulation and overexpression of the miRNAs using different GAL4 drivers. In this presentation, I will be discussing the preliminary findings from three miRNAs : miR-277, miR-8 and miR-285. Downregulation of miR-277 in the neurons expressing circadian neuropeptide pigment dispersing factor (pdf) affected the morning activity in the flies with an advancement in the phase of the morning peak under Light Dark cycle and reduced free running period under constant darkness. The effect is more prominent under lower light intensities as is evident by the formation of a distinct morning peak of activity prior to lights on. Presence of miR-8 in the clock neurons was found to be crucial for maintaining the 24hr periodicity of the activity-rest rhythm. miR-285 expression in the glial cells isn't important for the control of night time sleep in flies. Our further studies are focused on identifying the physiologically relevant potential targets of these miRNAs.

MONICA PURUSHOTHAMAN

INDIAN INSTITUTE OF SCIENCE EDUCATION AND RESEARCH THIRUVANANTHAPURAM

Role of Unique Loops in Oligomerization and ATPase Function of Plasmodium falciparum Gyrase B

Authors: **Monica Purushothaman,** Suman Kumar Dhar, **Ramanathan Natesh**.

DNA Gyrase is a type II-A ATP dependent topoisomerase that introduces negative supercoiling in the DNA. The importance of DNA Gyrase for the survival of pathogens and its unequivocal absence in humans makes it an ideal drug target. DNA Gyrase is also found in the apicoplast of apicomplexan parasites, which has an irrefutable role in the survival of the pathogen. Gyrase B (GyrB) from *Plasmodium falciparum* (PfGyrB), an apicomplexan parasite, has unique biochemical characteristics that are different from its bacterial counterparts. In this work, we identified two unique regions, termed L1 and L2 regions in the Pf GyrB N-terminal domain (PfGyrBN) and studied them. Towards this aim, we cloned, expressed, and purified PfGyrBN, PfGyrBNΔL1 and PfGyrBNΔL1ΔL2 to demonstrate the effect of the unique stretches of amino acid residues that are present in *Plasmodium falciparum* Gyrase B but are absent in other bacterial species. Through a series of biophysical and biochemical experiments, we have characterized the importance of the L1 and L2 region in the role of ATP hydrolysis and the dimeric state of the protein. We found that PfGyrBNΔL1 and PfGyrBNΔL1ΔL2 show reduced ATPase activity in comparison with PfGyrBN, indicating that the L1 region of PfGyrB is essential for ATP hydrolysis.

NSMB LAB

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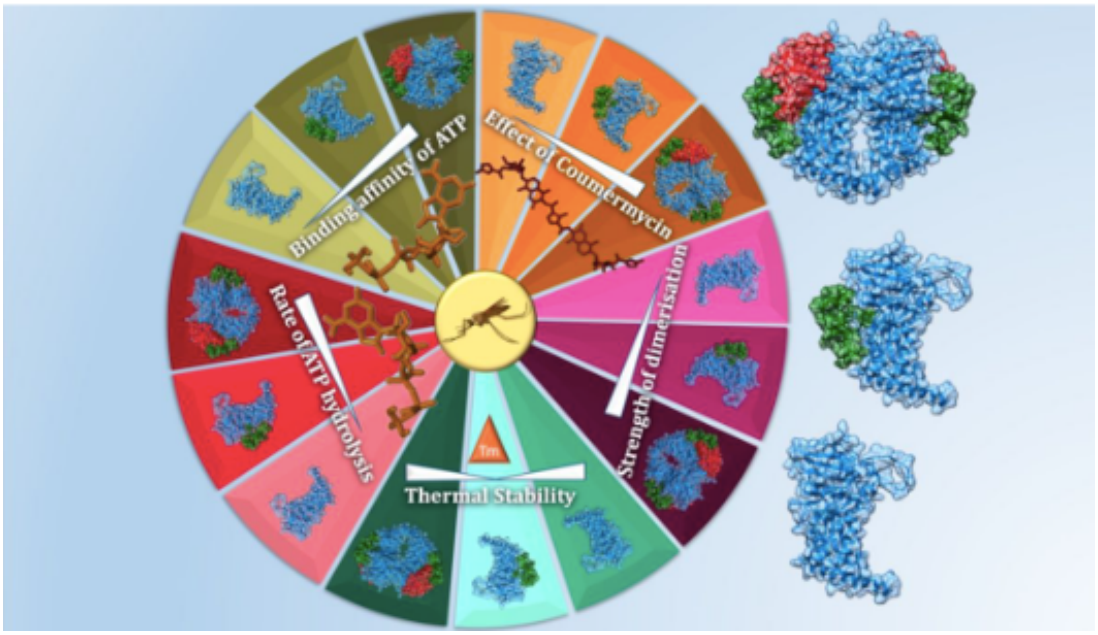
Role of Unique Loops in Oligomerization and ATPase Function of Plasmodium falciparum Gyrase B

(Continued)

We demonstrate that the binding affinity of ATP is decreased in the absence of the L1 and L2 regions. We also found that the L1 region plays a role in the dimerisation of PfGyrBN and may provide a unique dimer interface than the GyrB from other bacterial species. Hence, the L1 region has an indispensable role in the function of the protein and is unique to PfGyrB. Based on our results, we propose that this region provides a unique drug target to design a drug-specific to *Plasmodium falciparum* Gyrase B (Purushothaman et al., 2021).



VIROLOGY SCIENTIFIC RESEARCH LAB

JESWIN JOSEPH

INDIAN INSTITUTE OF SCIENCE EDUCATION AND RESEARCH THIRUVANANTHAPURAM

Emergence of SARS-COV-2 Spike Variants Raises the Chances of Neutralizing Antibody Escape Phenotype and Requires the Development of Broadly Reactive Vaccines

Authors: **Jeswin Joseph**, Sukhada Darpe, Grishma Kulkarni, **V. Stalin Raj**

The emergence of numerous severe acute respiratory syndrome coronavirus-2 (SARS-CoV-2) variants of concerns (VOCs), including the Alpha, Beta, Gamma, Delta, and Omicron lineages, has worsened the global pandemic scenario posed by SARS-CoV-2 with several mild to critical disease conditions. The rapidly emerging mutants have diverse variations in their spike glycoprotein, which is the key target for most of the neutralizing antibodies (nAbs) and may affect the potential of different vaccine candidates and therapeutic mAbs. Understanding the diverse spike mutations and predicting the chances of emergence of potent neutralizing antibody escape variants is critical to preventing current or future threats caused by SARS-CoV-2 variants. First, we analyzed the frequency of spike mutations from 10000 spike sequences using a custom-made Python script and annotated the amino acid changes in the spike glycoprotein. We found that D614G mutation is most frequent among SARS-CoV-2 variants, followed by T478K, L452R, and P681R. In order to predict the functional effect of these mutations in evading nAbs, we retrieved the epitopes of 74 experimentally validated SARS-CoV-2 neutralizing mAb epitopes and mapped them against the VOCs.

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VIROLOGY SCIENTIFIC RESEARCH LAB

Emergence of SARS-COV-2 Spike Variants Raises the Chances of Neutralizing Antibody Escape Phenotype and Requires the Development of Broadly Reactive Vaccines

(Continued)

Most of the mAb epitopes (87.84%) were localised to the receptor-binding domain (RBD) and overlap with each other, whereas limited (12.16%) are found in the N-terminal domain (NTD). Surprisingly, 69 out of 74 mAb targets have at least one mutation at the epitope sites, and among the VOCs, the Omicron showed the highest changes (20aa) at epitope sites. Moreover, highly nAb epitopes found in the RBD show higher mutations (4-10aa changes) when compared to lower or modest nAbs suggesting that these epitopes might co-evolve with the immune pressure. In summary, the current study delineates the need to determine the spike mutations at the epitope sites, leading to the development of broadly reactive immunogens targeting multiple SARS-CoV-2 variants.

ALLEN MARIA JACOB

INDIAN INSTITUTE OF SCIENCE EDUCATION AND RESEARCH THIRUVANANTHAPURAM

To Understand the Role of E3 Ubiquitin Ligases in Regulating Cytoskeleton

Authors: **Allen Maria Jacob**, Manpreet Kaur and **N. Sadananda Singh**

Post-translational modifications are biochemical (covalent) modification in a protein after a protein is translated, and it has functional roles like protein degradation, translocation etc. Varying number of post-translational modifications have been reported. Examples include acetylation, methylation, ubiquitination, tyrosination, phosphorylation etc. Timely degradation of proteins prevents unwanted effects. Once a protein achieves its mission, it is degraded within the cell through two distinct degradation machineries, namely: Lysosome degradation system and Ubiquitin-Proteasome Pathway. The cytoskeleton is a network of filaments of varying diameters spread throughout the cell and performs various functions like cell division and specific delivery of cargoes. They are a filamentous network which maintains cell shape, cell movement, cell integrity etc. It is a contractile skeleton of cells, therefore, named aptly cytoskeleton. CRISPR screens are used to identify genes which are relevant to a particular phenotype. It results in the discovery of a few genes or genetic sequences which elicit a specific function or phenotype. In our project, we are performing a positive screening, which is an approach through which one selects cells that have a growth advantage due to some mutations. A previous positive screening identified PHGDH as the gene encoding resistance to HCC upon Sorafenib treatment.

To Understand the Role of E3 Ubiquitin Ligases in Regulating Cytoskeleton

(Continued)

For our studies we have used Bassik human CRISPR knockout sublibrary Proteostasis, and screening was conducted using HEK293-T cell line which had stable gRNA expression for genes present in proteostasis sublibrary. Screening using paclitaxel (tubulin stabilizer) and nocodazole (tubulin de-stabilizer), gave us few genes observed to be deleted in the surviving cells which concludes that deletion of these genes enhances cell survival upon paclitaxel and nocodazole treatment. An E3 ligase, RNF5 has been observed in the screening. Further studies need to be performed to validate the effects of RNF5 deletion on cell cytoskeleton and tubulin morphology.

MANPREET KAUR

INDIAN INSTITUTE OF SCIENCE EDUCATION AND RESEARCH THIRUVANANTHAPURAM

Study of molecular regulators for the cytotoxic effect of Doxorubicin

Authors: **Manpreet Kaur,** Sidharth T, and **N. Sadananda Singh**

Doxorubicin (DOX) is the first-line drug choice to treat various solid and hematologic malignancies in adult and pediatric patients. It acts as a topoII poison by blocking topoisomerase II DNA re-ligation activity during biological DNA replication and transcription processes. It also increases the oxidative stress in the cells, leading to their death by apoptosis. Despite its significant anti-tumor effects, DOX can cause irreversible cardiac complications in a dose-dependent manner, limiting its clinical use. The molecular investigation of doxorubicin-induced cytotoxicity is an ongoing study. Identifying the genes that modulate Doxorubicin response has clear benefits for identifying individuals at risk for toxicity and modulate response and would also assist the pharmacogenomics of the drug.

Study of molecular regulators for the cytotoxic effect of Doxorubicin

(continued)

To identify the genes involved in Doxorubicin response, we used the existing CRISPR-Cas9 screening technology. A positive CRISPR knockout screen identifies enriched genes that potentially increase susceptibility to the treatment condition. Using a genome-wide CRISPR deletion library, we knocked out all the human protein-coding genes in HEK293T Cas9 expressing cell line and, upon a selection with DOX, gave us enriched genes based on gRNA count. After cross-referring with another CRISPR deletion DOX screening, we selected 14 genes that could be the potential regulators of DOX response. Their respective knockout shows better survival upon treatment with DOX in cell viability assays. NUP153, ARPC5, and ROBO1 showed possible involvement in a novel pathway related to topoII or DNA break repair during the treatment of knockout cells with a topoII inhibitor. Further, we aim to study the role of these genes in DOX response.

ANU P. V.

INDIAN INSTITUTE OF SCIENCE EDUCATION AND RESEARCH THIRUVANANTHAPURAM

Unravelling the Role of Energy Producing Metabolic Pathways in Murine Hematopoietic Emergence

Authors: **Anu P. V.** and **Satish Khurana**

In vertebrates, a lifelong supply of all the blood cell types in suitable numbers are maintained by the hematopoietic stem cells (HSCs). During development, these HSCs emerge in the aorta-gonad-mesonephros (AGM) from specialized embryonic vascular cells called hemogenic endothelium through a transdifferentiation process called endothelial-to-hematopoietic transition (EHT). During this process, selected endothelial cells switch to a hematopoietic transcriptional program, undergo morphological changes and become hemogenic. A complex interplay of key transcription factors and signalling pathways coordinates the whole process. Specific metabolic signatures of a cell can precisely define its phenotype. Evidence shows that cellular phenotype and function can be driven according to the changes in cellular metabolism. Metabolic programs, which are stage specific, allow stem cells to adapt their function in different microenvironments. In adults, it is believed that the hypoxic bone marrow microenvironment regulates HSC function and protects them from oxidative stress. It is not clear whether hypoxic response and change in metabolic status regulate the generation and expansion of HSCs from the vasculature of midgestation embryos. Studies with endothelial deletion of HIF-1α revealed a decrease in phenotypic aortic hematopoietic cluster cells.

STEM CELLS AND DEVELOPMENT LAB

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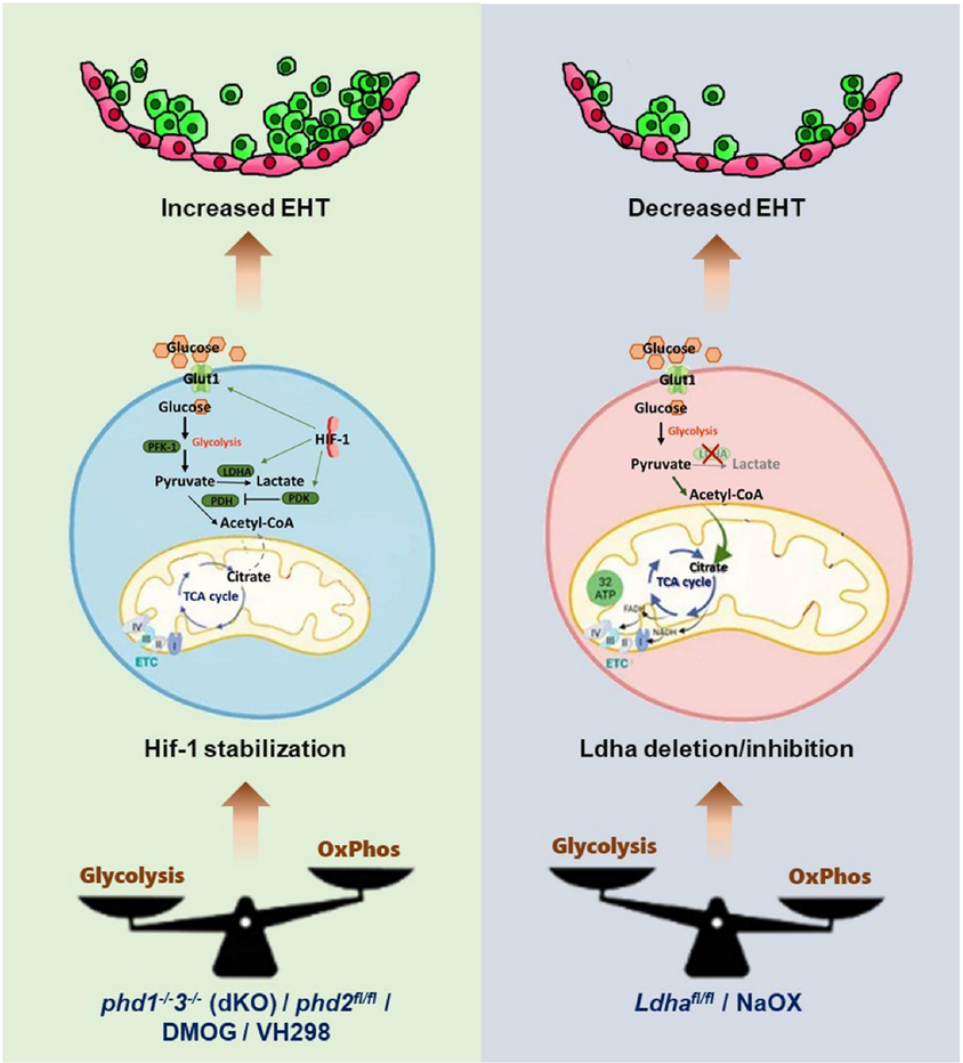
Unravelling the Role of Energy Producing Metabolic Pathways in Murine Hematopoietic Emergence

(Continued)

We tried to understand the basal metabolic status of the hemato-endothelial system along with the analysis of mitochondrial and ROS content. Using pharmacologic and genetic mouse models, we targeted metabolic or oxygen-sensing enzymes in order to modulate the metabolic status of the hemato-endothelial system. The results suggest that the endothelial cells maintain a steady state of glycolysis and oxidative phosphorylation and blocking the former results in reduced levels of EHT.



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IRENE MARIAM ROY

INDIAN INSTITUTE OF SCIENCE EDUCATION AND RESEARCH THIRUVANANTHAPURAM

Understanding the Role of Integrin Signaling in Hematopoietic Stem Cell Niche Modulation

Authors: **Irene Mariam Roy**, Samantha Zaunz, Srinu Reddi, Anu P. V., Catherine M. Verfaillie, **Satish Khurana**

Hematopoietic Stem Cells (HSCs) generate adult blood cells in required proportion all through the lifetime of an individual. Their survival and proper functioning requires a robust niche, which provides physical support and molecular signals for physiological demands. The chemokine, stromal cell derived factor (SDF)-1α, plays an important role in maintenance of HSCs in their niche and their homing upon transplantation. The regulation of Sdf-1α at its transcriptional level is still under investigation, and which factors affect its expression are still uncharted. Here, we report a hitherto unknown role of integrin signaling in transcriptional regulation of Sdf-1α. Transgenic mouse with deletion of Integrin-αv ligand, Periostin (Postn), led to an increase in the expression of Sdf-1α in the bone marrow (BM) niche cells. We noted an increase in Sdf-1α expression in BM stroma post-inhibition of Src phosphorylation. In addition, CRISPR-Cas9 based genetic deletion of Postn and c-Src kinase corroborated the impact of the signaling pathway involved in the regulation of Sdf-1α expression.

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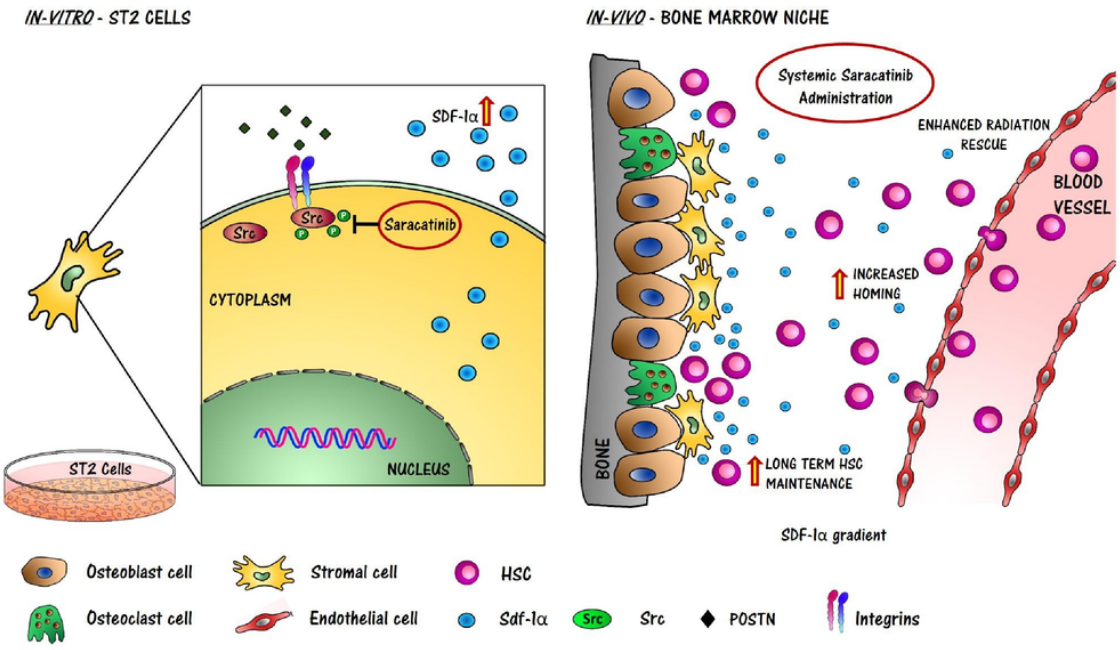
Understanding the Role of Integrin Signaling in Hematopoietic Stem Cell Niche Modulation

(Continued)

Importantly, mice administered with Saracatinib (SRB), a potent Src inhibitor, led to an increase in the chemokine expression and secretion into the BM plasma. It also induced self-renewal proliferation of HSCs leading to expansion in their numbers. The functional improvement of the BM HSC population was reflected in faster recovery from radiation induced hematopoietic injury. Increase in the level of Sdf-1α also resulted in more efficient homing of HSCs, transplanted into the SRB treated animals. Overall, we report Src-mediated integrin signaling as an important transcriptional regulator of Sdf-1α. In addition to providing evidence of a consistent transcriptional regulation via integrin signaling, this study provides a possible strategy to improve BM transplantation outcomes in regenerative clinical treatments.



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SHUBHAM HARIBHAU MEHATRE

INDIAN INSTITUTE OF SCIENCE EDUCATION AND RESEARCH THIRUVANANTHAPURAM

Outside-in Integrin Signaling in Splenic HSC Function

Authors: **Shubham Haribhau Mehatre**, Akhila S. Kumar, Amulya V. Hejjaji and **Satish Khurana**

A secondary lymphoid organ, Spleen hosts highly dormant hematopoietic stem cells. Molecular pathways essential for splenic HSC maintenance, and regulating their function in the spleen at a steady state, remain elusive. Our earlier published work demonstrated that lack of Periostin (Postn) and integrin-αv (Itgav) interaction induces faster proliferation in HSCs with developmental stage-dependent functional effects (Khurana S. et al. in Nat. Comm. 2016, Biswas A et al. in Stem Cell Reports 2020). In this study, we examined the role of the Postn-Itgav axis in lymphohematopoietic activity in the spleen that hosts a rare population of HSCs. Histological examination of the spleen revealed that myofibroblasts of the trabecular and capsular areas expressed high levels of Postn within the spleen tissue. In addition, vascular smooth muscle cells also expressed Postn. Vav-iCre mediated deletion of the Postn receptor, Itgav in hematopoietic system, increased the splenic HSC pool with higher proliferation rates. However, in vitro hematopoietic assays demonstrated a poorer differentiation potential. Itgav deletion also altered the splenic architecture by reducing the white pulp and declining in B-cell numbers. Histological examination of Postn deficient spleen also showed an increase in the spleen trabecular areas. Through CFU-S12 assays, we showed that hematopoietic support potential of stroma in the Postn-deficient splenic hematopoietic niche was defective. We demonstrate that Postn-Itgav interaction plays a vital role in spleen lymphohematopoiesis (Mehatre S et al. in J. Immunol. 2021).

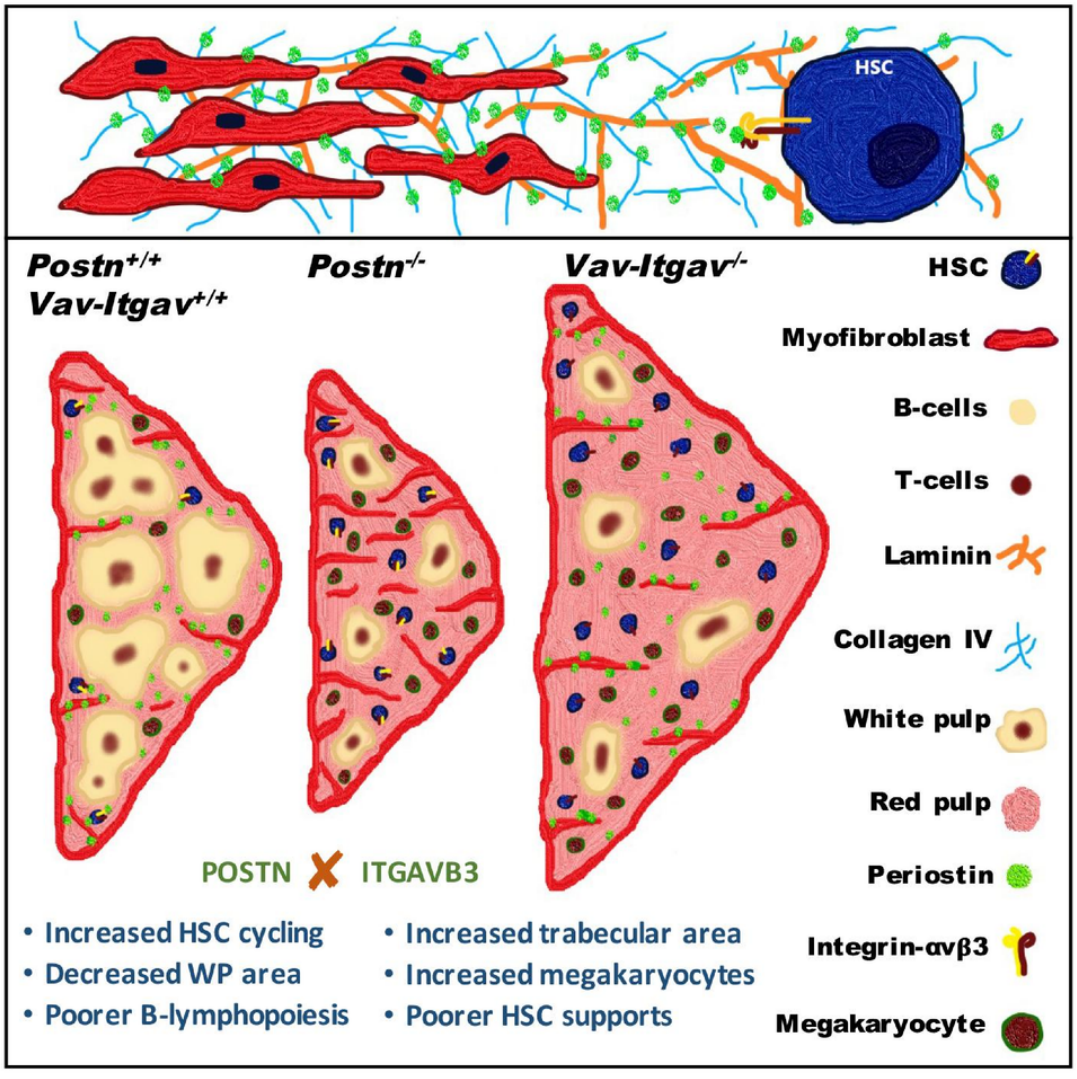
IISER THIRUVANANTHAPURAM

STEM CELLS AND DEVELOPMENT LAB

Outside-in Integrin Signaling in Splenic HSC Function

(Continued)

We demonstrate that Postn-Itgav interaction plays a vital role in spleen lymphohematopoiesis (Mehatre S et al. in J. Immunol. 2021). We demonstrated myofibroblasts of splenic capsule produces Periostin and Sdf-1α, a key regulator of HSC maintenance. Interestingly, HSCs are localized adjacent to SMCs in the vicinity of 30µm to 60µm distance. In our ongoing experiments, we address the spatial details of HSCs in the spleen niche. Hitherto unknown regulatory mechanisms for splenic HSC function may lead to aid in an improved hematopoietic recovery following several of the clinical regimens.



STEM CELLS AND DEVELOPMENT LAB

SHAILENDRA KUMAR SINGH

INDIAN INSTITUTE OF SCIENCE EDUCATION AND RESEARCH THIRUVANANTHAPURAM

Oxygen sensing pathway in the maintenance of adult neural stem cell pool

Authors: **Shailendra Kumar Singh**, Sreeparvathy Vayankara Edachola, Dhanagovind PT, Geert Carmeliet, Peter Carmeliet, Catherine Verfaillie, **Satish Khurana**

Neurogenesis is a well-orchestrated process by which the cells of the central nervous system are generated. Postnatally, there are two major neurogenic niches in the mammalian brain – the Subgranular Zone (SGZ) and the Subventricular Zone (SVZ), both considered to be hypoxic. Disruption of the hypoxia pathway through loss-of-function studies have previously been shown to result in defective neural stem cell (NSC) pool maintenance and also defective neurogenesis. We sought to examine the effect of stabilization of HIF-1α by disrupting the oxygen sensing pathway. Deletion of the prolyl hydroxylase domain (PHD) proteins 1 and 3 (Phd1 -/- ,3 -/- ; dKO) led to enhanced activation of hypoxic signaling. In the dKO mouse brain, we observed a significant decrease in the overall proliferative activity of cells in the SGZ. The NSC population displayed dramatic changes whereby the total pool size was reduced. The morphology of the Sox2 + GFAP + adult NSCs was also substantially altered with decrease in the length of the radially-oriented fibers. Concomitantly, we observed a marked decrease in the proliferative neural progenitors, which was reflected in a decrease in the number of DCX + newborn neurons. Contrarily, there was a significant increase in the number of astrocytes, indicating predisposition of the NSC population towards astroglial differentiation at the expense of neurogenesis. Overall, we report the involvement of hypoxia pathway in the stem cell fate decisions of the adult NSC population.

IISER THIRUVANANTHAPURAM

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Oxygen sensing pathway in the maintenance of adult neural stem cell pool

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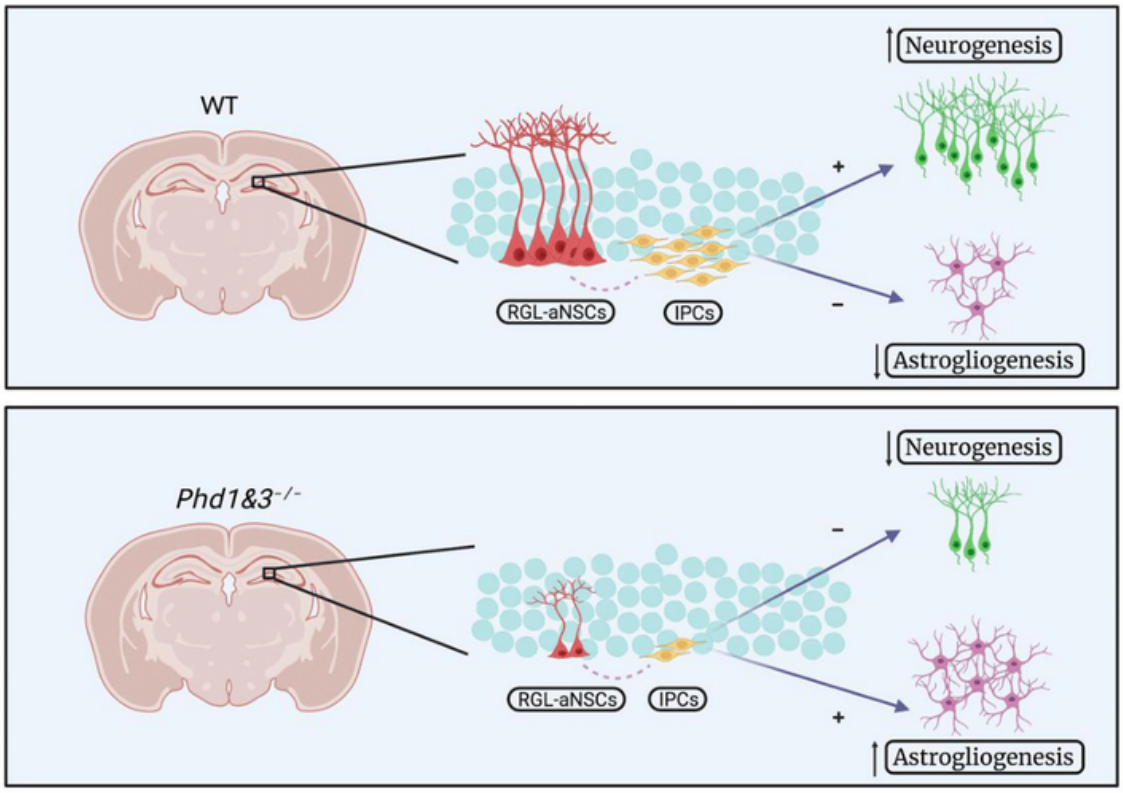

VARUN SUNDER

INDIAN INSTITUTE OF SCIENCE EDUCATION AND RESEARCH THIRUVANANTHAPURAM

Do Replication-Transcription Collisions Promote Gene Expression Noise?

Authors: **Varun Sunder** and **Sabari Sankar Thirupathy**

Phenotypic heterogeneity is where cells display phenotypic variation in a homogenous environment despite being isogenic. A critical cause of such heterogeneity is gene expression noise, the cell-to-cell variation in gene expression levels that arises due to inherent stochasticity in each molecular process that drives gene expression. It is ubiquitous to all living systems and influences genetic control over metabolism, cell-fate decisions, development, and stress response pathways, ultimately affecting cellular fitness. Here, we aim to study the effect of replication-transcription collisions on gene expression noise and its phenotypic consequences.

Replication-transcription collisions are physical collisions between the replication and transcription machinery as they traverse the same DNA template in the same direction (co-directional) or opposite directions (head-on). Both types of collisions are known to interfere with the movement of the replication fork and cause fork stalling, dsDNA breaks, mutagenesis, and premature transcription termination. As collisions directly interrupt transcription, we hypothesize they could generate fluctuations in mRNA and consequently protein levels in isogenic cells, thus promoting gene expression noise.

MUTATIONS LAB

Do Replication-Transcription Collisions Promote Gene Expression Noise?

(Continued)

To study the effects of collisions on gene expression noise, we have developed a single-cell gfp reporter chromosomally inserted either in co-directional or head-on orientation in B. subtilis We observed that gene orientation affects gene expression levels and noise. This effect depends on transcription and translational capacity, with higher gene expression leading to higher noise. Together, our results suggest that replication-transcription collisions may contribute to gene expression noise.

MUTATIONS LAB

ANJALI VARIYAR

INDIAN INSTITUTE OF SCIENCE EDUCATION AND RESEARCH THIRUVANANTHAPURAM

Mechanisms of Mutations Induced by Replication-Transcription Collisions

Authors: **Anjali Variyar**, Sowmya Murugan and **Sabari Sankar Thirupathy**

Insertion and deletion (indels) mutations are implicated in many human anomalies like cancer and neurodegeneration. Hence, it is imperative to study the origin and mechanisms of indels. Studies have identified various mechanisms that contribute to indels, almost all of which are initiated by DNA replication stress or the ensuing DNA repair. However, the cellular phenomena that trigger replication stress and generate indels remain elusive. One of the important mutational processes involves the clashes between the machinery of life, the replisome, and the transcription complex while simultaneously using the DNA template. Such collisions can be either co-directional or head-on, threaten genome stability and cause mutations, particularly the most lethal indels.

Here, we investigated the role of genetic factors that avert or resolve replication-transcription conflicts in modulating collision-induced mutations. To this end, we probed the roles of error-prone DNA polymerases, transcription, and DNA repair factors. We used mutation assays to measure the spontaneous mutation rate in the gram-positive bacterium *Bacillus subtilis* and analyzed the mutation spectra. Our results suggest a coordinated role for a DNA polymerase and transcription factor in modulating the collision-induced mutations. Further, the mutation signatures of collisions seem to depend on the DNA recombinational repair pathway. Together, we believe these mechanisms are likely conserved in higher organisms, including humans, and be potential targets for therapeutic prevention.

IISER THIRUVANANTHAPURAM

MALHAR ATRE

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Selection Modulates Gene Inversion Rates to Maintain Gene-Strand Bias

Authors: **Malhar Atre**, Shabduli Sawant, Bharat Joshi, Shreya Sharma and **Sabari Sankar Thirupathy**

MUTATIONS LAB

In rapidly dividing bacterial cells, replisomes traverse the DNA template preoccupied by RNA Polymerases leading to collisions between the two machinery. Such collisions can be either in co-directional (same) or head-on (opposite) orientation depending on the relative direction of transcription. Replication-transcription conflicts cause double strand breaks, mutagenesis, genomic instability and cell death, with head-on conflicts being more severe.

Bacterial genomes preferentially have a majority of their genes located in a co-directional orientation, giving rise to the phenomenon - gene-strand bias. Such a biased distribution of genes is believed to have evolved to minimize the harmful effects of head-on conflicts. However, the gene distribution bias displays a large variation across bacterial kingdom. The underlying mechanism generating gene-strand bias, its variation and maintenance, remains unexplored.

IISER THIRUVANANTHAPURAM

MUTATIONS LAB

Selection Modulates Gene Inversion Rates to Maintain Gene-Strand Bias

(Continued)

Here, we investigated the impact of gene inversions that specifically flip gene orientation, on the gene-strand bias, across bacterial phyla. Inversions were determined in core genomes of diverse bacterial species using gene orientations and phylogeny. We observed a strong variation in gene inversion rates as a function of gene-strand bias. The rate of inversions, surprisingly showed a strong negative correlation with increasing gene-strand bias. We found various factors that mediate gene inversions like recombination, sequence repetitiveness and mobile genetic elements are independently insufficient to explain the negative correlation, suggesting a role for natural selection to maintain the biased gene distribution. Concordantly, we found that larger inversions, potentially disturbing the bias, are avoided in highly biased genomes. We noticed that the negative trend is associated with species that lack the DNA polymerase PolC, while those that have PolC, show no trend. Further, the rate of inversions are 10-times more in bacteria lacking PolC. In conclusion, we propose that selection optimizes the rates of inversion to maintain the gene-strand bias, which is constrained by the nature of replication.

CYTOSKELETON AND CELL DIVISION LAB

RENJITH M. R.

INDIAN INSTITUTE OF SCIENCE EDUCATION AND RESEARCH THIRUVANANTHAPURAM

EB1-Binding Microtubule Tip Localization Motif of Ska1 Regulates Chromosome Alignment in Human Cells

Authors: **Renjith M. R.** and **Tapas K. Manna**

Segregation of genetic material compressed in the form of chromosomes from mother to daughter cells needs to be maintained accurately during mitosis. The key to this process is the correct coupling of the kinetochore of the chromosome to the dynamic plus ends of microtubules. The mechanisms by which kinetochore couples to microtubule plus ends and the architecture of functional protein complexes at the microtubule-kinetochore interface are poorly understood. In budding yeast, ring structures formed by Dam1 complex proteins on the microtubules are implicated to couple kinetochores to the depolymerizing microtubule by dynamically moving/sliding along the microtubule lattice following microtubule depolymerization. The mechanisms of kinetochore coupling and the organization of the molecular factors involved in the process in metazoans have not been completely identified. The absence of Dam1 complex components in higher eukaryotes necessitates the importance of identifyingto identify the regulators in higher eukaryotes for this function. Vertebrate Spindle and kinetochore associated (Ska) proteins have been proposed to have an analogous role to Dam1. Microtubule plus end-binding protein, EB1 plays a critical role in coupling microtubule plus ends to the kinetochore by mediating interaction with the Ska in human cells. However, the mechanism underlying EB1 interaction with Ska is not incompletely understood.

IISER THIRUVANANTHAPURAM

CYTOSKELETON AND CELL DIVISION LAB

EB1-Binding Microtubule Tip Localization Motif of Ska1 Regulates Chromosome Alignment in Human Cells

(Continued)

We found that a flexible loop region connecting the N- and the C-terminus of Ska1 mediates interaction with EB1 and is required for metaphase chromosome alignment. Deletion of the loop perturbs the kinetochore localization of Ska complex proteins and induces chromosome congression defects. It was observed that Ska1 consists of a motif, SHLP, which is similar to the SXIP motif, known to be critical for the interaction of several microtubule plus-end proteins with EB1. Deletion or mutation of Ska1 SHLP motif leads to loss of Ska1 localization at the kinetochore and further, the mutation disrupts the Ska1-EB1 interaction. High-resolution time lapse High-speed atomic force microscopy imaging has revealed interesting insights into the dynamics of EB1 and Ska1 and their oligomeric structures. Ska1 anchored to the coiled-coil region of EB1 dimer through its loop forming a linearly extended structure. NMR data revealed that like several other SxIP motif-containing proteins, Ska1 interacts with the conserved residues in the EB Homology domain of EB1. Based on cellular, biochemical and structural data we have identified that the Ska1 unstructured region containing motif plays a crucial role in the regulation of EB1- Ska1 interaction and stable kinetochore-microtubule attachment during chromosome segregation. The results identify a general mechanism in conferring the microtubule plus end binding specificity of kinetochore.

IISER THIRUVANANTHAPURAM

CYTOSKELETON AND CELL DIVISION LAB

USHMA ANAND

INDIAN INSTITUTE OF SCIENCE EDUCATION AND RESEARCH THIRUVANANTHAPURAM

E3 ubiquitin ligase, FBXW7 regulates centriole duplication protein, STIL

Authors: **Ushma Anand**, Binshad B, Arunima Muliyil, Mirsana P, Anjana A, Reshma Khurup, **Tapas K. Manna**

Centrosomes are the main microtubule organizing centers in animal cells. During the cell cycle, centrosomes duplicate only once during S phase to ensure that at mitotic onset, a cell carries two centrosomes that will form the poles of the mitotic spindle. Initiation of new centriole biogenesis involves recruitment of a ring-like oligomeric structure consisting of CEP152 and its associated proteins onto the proximal end of the mother centriole, which follows recruitment and activation of polo-like kinase 4 (Plk4). Plk4 kinase seeds the new centriole by phosphorylating pro-centriole protein STIL (SCL/TAL1 interrupting locus) and facilitating formation of the cartwheel-like template by recruiting SAS-6. Elevated expression of several of these factors, notably STIL, SAS-6 Plk4 induces centriole over-duplication and multipolar defects. Mechanisms on how the levels of centriole duplication factors are optimally controlled are poorly understood.

Here we find that E3-ubiquitin ligase. SCF-FBXW7 with its substrate targeting subunit FBXW7 regulates levels of STIL in cultured human cells. siRNA-mediated depletion of FBXW7, increased the level of STIL, more prominently during the G1/S phase, the time when new centriole formation is initiated. Conversely, FBXW7 over-expression results in down-regulation of STIL level and further, it is rescued, when the substrate-binding WD40 of FBXW7 was deleted. Concordant with these findings, we also found that localization STIL at the centrioles is reduced, when the ligase is overexpressed.

IISER THIRUVANANTHAPURAM

CYTOSKELETON AND CELL DIVISION LAB

E3 ubiquitin ligase, FBXW7 regulates centriole duplication protein, STIL

(Continued)

Biochemical results showed that FBXW7 interacts with and ubiquitinates STIL. Pharmacological inhibition of PLK4, which phosphorylates STIL, suppressed FBXW7-mediated STIL degradation suggesting its role in this process. However, analysies with STIL deletion constructs also indicated that FBXW7 primarily targets the STAN domain for degradation, which is the binding region for SAS-6. Experiments are underway to elucidate the molecular details of Plk4-mediated STIL phosphorylation and STIL degradation and further, understand the effects of primary microcephaly (MCPH)-specific STIL mutations on its stability.

CYTOSKELETON AND CELL DIVISION LAB

VISHNU M. NAIR

INDIAN INSTITUTE OF SCIENCE EDUCATION AND RESEARCH THIRUVANANTHAPURAM

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

Authors: **Vishnu M. Nair**, Amit Santhu Sabu, **Tapas K. Manna**

Faithful chromosome segregation requires correct attachment of the chromosomal kinetochore with the spindle microtubules. Cells utilize a dedicated surveillance machinery, known as the spindle assembly checkpoint (SAC), to sense spindle-attachment errors, and relay the signals for correction. Subsequently, the SAC proteins need to be degraded in order to allow chromosome segregation to proceed. Molecular mechanisms of how the levels of the SAC proteins are temporally controlled during mitosis are incompletely understood. Here, we have identified involvement of an E3-ubiquitin ligase, FBXW7, a conserved member of the Fbox-type ubiquitin ligase family, in regulation of mitotic checkpoint in human cells. FBXW7 depletion leads to increased levels of the SAC protein, BubR1 and also its associated binding partners localized at the outer kinetochore, such as CENP-E and CENP-F. Conversely, over-expression of FBXW7 results in significant reduction of the levels of these proteins. FBXW7 deleted cells exhibit distinct chromosome alignment defects in mitotic cells and induces prolonged mitotic delay. Biochemical results reveal that FBXW7 binds to and ubiquitinates BubR1. Pharmacological inhibition of cyclin dependent kinase 1 (Cdk1) rescues FBXW7-mediated BubR1 degradation and further, phospho-deficient mutation of the Cdk1-targeting site of BubR1 mimics such effect, whereas the phospho-mimetic mutation stimulates BubR1 degradation. The results so far suggest that FBXW7-mediated BubR1 degradation plays a critical role mitotic checkpoint activation/silencing and further, Cdk1-mediated BubR1 phosphorylation is required for BubR1 targeting by the ligase.

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Unraveling the Genome Instability Triggered during CenH3 Mediated Uniparental Genome Elimination: Characterization of a Bushy Mutant

Authors: **Vaishak K. P.**, Ramesh Bondada, Mohammed Afsal Badarudeen, Niranjana S. Manoj, Pavithra C. K., **Ravi Maruthachalam**

Distant hybridization between two unrelated species, results in a genomic conflict in the hybrid zygote during early embryonic cell divisions leading to the production of aneuploids, uniparental haploids apart from hybrid interspecies hybrids. Despite its documentation 10 decades ago, the mechanistic insights behind this genome conflict is poorly understood mainly due to lack of genetic and genomic tools in the experimental species studied. Of late, the dicot plant *Arabidopsis thaliana* has emerged as a model to unravel the mechanistic basis of uniparental genome elimination (UGE) giving rise to haploid progeny, as it is now possible to mimic the consequences of distant hybridization in an intraspecific cross by simple manipulation of centromeres by altering the centromere specific histone H3 variant CenH3. In one such interploidy UGE cross aimed to reduce the ploidy of a natural tetraploid Arabidopsis accession Wa-1, we obtained a diploid Wa-1 progeny harboring a minichromosome resulting from an incomplete genome elimination process.

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Unraveling the Genome Instability Triggered during CenH3 Mediated Uniparental Genome Elimination: Characterization of a Bushy Mutant

(Continued)

When this minichromosome-containing line is propagated over generations, we observed a sudden origin of a mutant phenotype in the F3 generation, named bushy because of its diagnostic bushy growth of vegetative meristems. Phenotypic characterisation of bushy mutation suggests the precocious activation of axillary meristem along with enhanced vegetative growth providing perennial-like life features to the bushy mutant. Genetic analysis reveals the monogenic recessive inheritance of the causative mutation. This mutation is mapped near to a previously known resistance(R) gene; At1g61180, UNI of Chromosome 1 of A. thaliana; of which a semi-dominant mutant, uni1-D, shows similar bushy-like phenotypes. However, knockout alleles of UNI have no visible phenotype, likely attributed to the functional redundancy with highly similar paralogous R genes including a gene in its adjacent locus, At1g61190. Further, our preliminary results suggest that the intricate balance between cytokinin-mediated growth and salicylic acid-mediated defense responses maintained through the efficient allocation of metabolites through the phenylpropanoid pathway are affected in the mutant.

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T. M. TEJAS

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An in-planta approach to build an army of haploids for efficient crop improvement

Authors: **Tejas T. M.**, Ramesh Bondada, Guru Vigknesh, Hemanth Kethavath, **Ravi Maruthachalam.**

Uniparental genome elimination (UGE) is a phenomenon wherein after successful fertilisation, one of the parental chromosomes is selectively eliminated during embryonic mitosis resulting in a haploid embryo. This in vivo process of haploid induction has been brought into action by epigenetically manipulating the centromeres. The centromere-specific histone 3 called CENH3 (centromeric histone H3) when replaced by a chimeric version, the GFP- tailswap (N-terminal of CENH3 swapped with the N-terminal of H3.3 histone tagged with GFP), it complemented the null CENH3 mutant (cenh3 -/-) and yielded up to 40% haploid progeny upon crossing to the wild type *A. thaliana* accessions. Different accessions of *A. thaliana* yielded haploids with varying frequencies, hinting at the genetic control of haploid induction.

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An in-planta approach to build an army of haploids for efficient crop improvement

(Continued)

Therefore, to dissect the genetic basis of UGE, we exploited the natural genetic diversity of wild type *A. thaliana* to screen for accessions yielding high haploid induction rates in a haploid induction cross. The screen revealed two accessions HKT 2.4 and Bor-4, and among them, Bor-4 which yielded ~70% haploids, possesses a mutation in the gene Vim-1 that causes hypomethylation of the centromeres, now hinting at the epigenetic control of UGE. Therefore, to achieve a hyper haploid inducer, we introduced an additional level of epigenetic modifications to the centromeres of GFP-TS using pharmacological treatments by Azacitidine and by introgressing mutant alleles essential in the maintenance of methylation.

Consequently, we observed improved haploid induction frequencies upon crossing to the wild type *A. thaliana* accession. Therefore, we believe this study will serve as a tool to improve the translational ability of in plant haploid induction onto commercially valuable crop species.

Thus, understanding the key genetic and epigenetic factors influencing the haploid induction process and unravelling the molecular process of UGE is the scheme of the project.

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RISHITH RAVINDRAN

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Endosomal-Associated RFFL Facilitates Mitochondrial Clearance by Enhancing PRKN/Parkin Recruitment to Mitochondria

Authors: **Rishith Ravindran,** Anoop Kumar, G. Velikkakath, Nikhil Dev Narendradev, Aneesh Chandrasekharan, T. R. Santhoshkumar and **Srinivasa M. Srinivasula**.

Mutations in the ubiquitin ligase PRKN (parkin RBR E3 ubiquitin-protein ligase) are associated with Parkinson disease and defective mitophagy. Conceptually, PRKN-dependent mitophagy is classified into two phases: 1. PRKN recruits to and ubiquitinates mitochondrial proteins; 2. formation of phagophore membrane, sequestering mitochondria for degradation. Recently, endosomal machineries are reported to contribute to the later stage of the membrane assembly. We reported a role for endosomes in the events upstream of phase 1. We demonstrate that the endosomal ubiquitin ligase RFFL (ring finger and FYVE- like domain containing E3 ubiquitin-protein ligase) is associated with damaged mitochondria, and this association preceded that of PRKN. RFFL interacted with PRKN, and stable recruitment of PRKN to damaged mitochondria was substantially reduced in RFFL KO cells. Our study unraveled a novel role of endosomes in modulating upstream pathways of PRKN-dependent mitophagy initiation.

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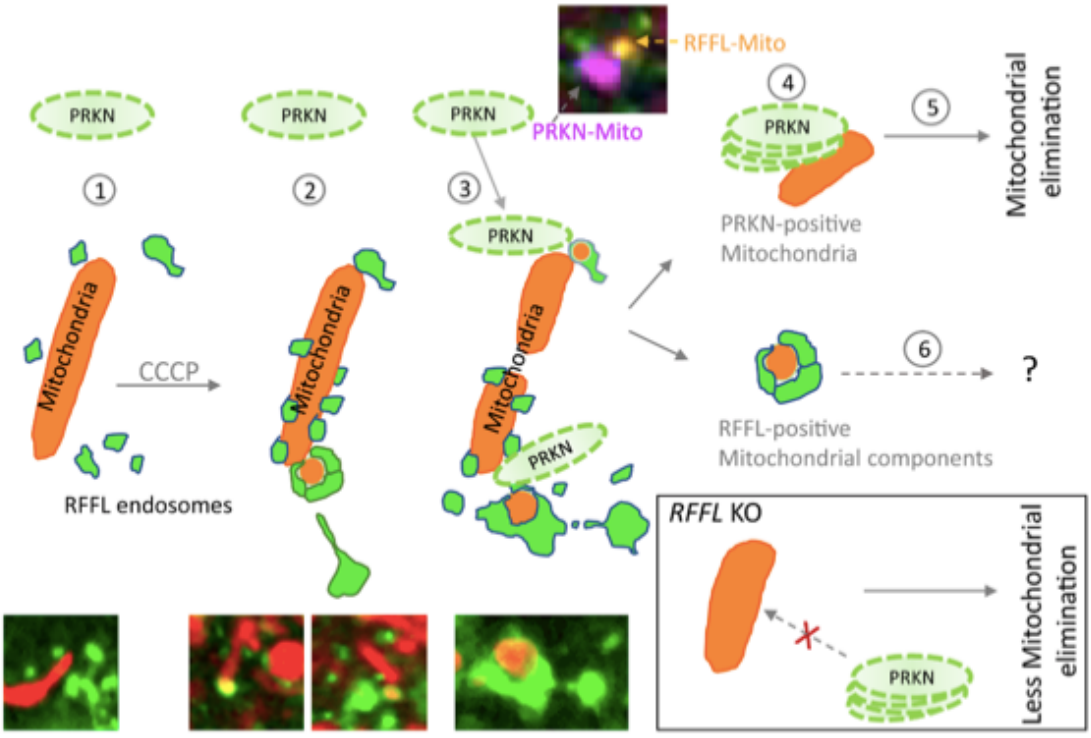
Endosomal-Associated RFFL Facilitates Mitochondrial Clearance by Enhancing PRKN/Parkin Recruitment to Mitochondria

(Continued)



(1) RFFL-positive endosomal vesicles transiently localized with mitochondria. (2) Mitochondrial content during the earlier stage of damage is surrounded by RFFL vesicles. (3) PRKN localized with the fragmented mitochondria in close proximity with RFFL-positive mitochondria. (4) PRKN stably localized with damaged mitochondria. (5) PRKN localized mitochondria undergo mitophagy. (6) The mechanism that cells employ to eliminate RFFL-mitochondrial content preferentially either through autophagic machinery or other pathways yet to be elucidated.

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PLANT CELL AND DEVELOPMENTAL BIOLOGY LAB

ARPAN MUKHERJEE

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B-Box Domain Proteins Regulate Thermomorphogenesis In *Arabidopsis*

Authors: **Arpan Mukherjee,** Shubhi Dwivedi**, Sourav Datta**

Temperature can modulate plant morphology as well as affect plant survival. Large variations in temperature can have a significant impact on plant survival. However, slight increase in ambient temperature, that generally ranges from 26-30°C for *Arabidopsis*, modulates its morphological and developmental changes (e.g., elongated hypocotyl, hyponasty, increased root system architecture and early flowering). These morphological changes help plants to mitigate the harms caused by higher temperature and the phenomena is known as thermomorphogenesis. B-Box proteins are light responsive transcription factors that regulate several physiological responses including photomorphogenesis, flowering and shade avoidance. Here, we found that the expression of two BBX genes, BBX-A and BBX-B are regulated in a temperature dependent manner. We also observed that the loss-of-function mutants bbx-a and bbx-b exhibit hyposensitivity towards higher ambient temperature. Additionally, our yeast two hybrid data also suggests that these BBXs interact with some known thermomorphogenetic factors like BBX-B with HY5 (ELONGATED HYPOCOTY 5) and BBX-A with both HY5 and ELF3 (EARLY FLOWERING 3). Thus, these data suggest the possible role of BBX-A and BBX-B in promoting thermomorphogenesis.

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Profiling the epitranscriptomic arm of immunity mediated by N6-methyladenosine in *Phytophthora* foot rot of black pepper

Authors: **Sora S** and **E V Soniya**

Piper nigrum L. is popularly called black pepper or the "king of spices" due to its heavy global demand. It is a perennial woody climbing vine that can grow up to 50-60cm and prefers hot and moist conditions for optimum growth. An oomycete pathogen, *Phytophthora capsici*, the causative agent of footrot disease, poses the major production constraint in black pepper cultivation. *P.capsici* is primarily soil-borne, and all parts of the plant are susceptible to infection. The sessile nature of the plant necessitates the requirement of global changes in epigenetic and epitranscriptomic changes to ward off environmental challenges. RNA is a critical biomolecule that can perform the informational carrier roles and be involved in gene expression regulation. The functional diversity of RNA is further contributed by the prevalence of covalent chemical modifications, which constitute the epitranscriptome. In plants, the best studied and the most prevalent internal RNA modification that is known to present in both coding and non-coding RNAs with established functions in plant development and stress responses is N6-methyladenosine (m6A). m6A controls all aspects of RNA metabolism, including splicing, stability, translation and nuclear to cytoplasmic export.

An arsenal of proteins controls the reversible nature of m6A modification, including m6A writers/methylases that deposit the mark, m6A erasers/demethylases that remove the mark, and finally, these marks are decoded by the m6A readers/RNA binding proteins.

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Profiling the epitranscriptomic arm of immunity mediated by N6-methyladenosine in *Phytophthora* foot rot of black pepper

(continued)

This is a highly conserved mark in both plants and animals, and it occurs in the conserved consensus motif ' RRACH' (R = A/G; H = U/A/C); recently, many plant-specific motifs have been discovered. It is seen enriched towards the 5'UTR, 3'UTR and adjacent to the stop codons and this varies depending on the cell type and the stress conditions of the cell. The gene function studies have revealed the dynamicity of this modification as exemplified through changes in the expression pattern of writers, readers and erasers under biotic and abiotic stress conditions in plants. However, detailed studies are still not present regarding the molecular levels of regulation mediated by the m6A mark, especially in the context of biotic stress.

Here, the dot blot analysis was carried out to profile the variation in m 6 A, which revealed a slight increase in m 6 A in the *P.capsici* treated black pepper plant compared to the uninfected control plant. Therefore, methylation RNA immunoprecipitation analysis was performed to obtain a transcriptome-wide map of m 6 A methylation. The sequencing results confirmed the differential enrichment of m 6 A peaks in the infected plant, and specific unique motifs were obtained enriched with m 6 A in black pepper. The GO and KEGG enrichment analysis of the genes enriched with m 6 A facilitated biotic stress response by regulating chloroplast related pathways, protein processing and plant-pathogen interaction pathways. This study highlights the importance of the epitranscriptomic arm of immunity mediated by m 6 A in a crop like black pepper in response to an oomycete pathogen, P.capsici. It is one of the first studies to be conducted so far. The relevance of the m 6 A mediated regulation of plant immune responses helps develop crops with improved tolerance in the future.

Profiling the epitranscriptomic arm of immunity mediated by N6-methyladenosine in *Phytophthora* foot rot of black pepper

(continued)

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The Endophyte *Piriformospora indica* in Shortening the Juvenile Phase of *Piper nigrum* L. by Fine-Tuning the Floral Response Pathways

Author: **Lekshmi R. S.**

Piriformospora indica, the mutualistic biotrophic root colonizing endosymbiotic fungus belonging to the order Sebacinales, offers host plants various benefits and enhances its growth and performance. The effect of colonization of *P. indica* in *Piper nigrum* L. cv. Panniyur1 on growth advantages, floral induction and evocation was investigated. Growth and yield benefits are credited to the alteration in the phytohormone levels fine-tuned by plants in response to the fungal colonization and perpetuation. Phytohormones were estimated using LC- MS/MS and quantified by qRT-PCR, and the results indicated the remarkable contribution of the endophyte colonization. qRT-PCR results revealed a significant shift in the expression of putative flowering regulatory genes in the photoperiod induction pathway *(FLOWERING LOCUS T, LEAFY, APETALA1, AGAMOUS, SUPPRESSOR OF CONSTANS 1, GIGANTEA, PHYA, and CRY1)* gibberellin biosynthetic pathway genes *(Gibberellin 20-Oxidase2, GA2ox, DELLA protein REPRESSOR OF ga1-3)* autonomous *(FVE, FCA)*, and age pathway *(SQUAMOSA PROMOTER LIKE9, APETALA2)*. The endophytic colonization had no effect on vernalization *(FLOWERING LOCUS C)* or biotic stress pathways *(SALICYLIC ACID INDUCTION DEFICIENT 2, WRKY family transcription factor 22)*. The data suggest that P. nigrum responds positively to P. indica colonization, affecting preponement in floral induction as well as evocation, and thereby shortening the juvenile phase of the crop

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PLANT CELL AND DEVELOPMENTAL BIOLOGY LAB

AJAR ANUPAM PRADHAN

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Characterization of a light regulated MATE transporter modulating root development

Authors: **Ajar Anupam Pradhan** and **Sourav Datta**

MATE (Multidrug And Toxic compound extrusion) transporters are the group of transporters that contain a MatE domain. In *Arabidopsis* 58 MATE transporters have been identified till date. These play very versatile roles in plants such as toxic compound extrusion, secondary metabolite transport and phytohormone transport. Members of the MATE transporters are also reported to be responsive to light. Here we identified a loss of function mutant of an *Arabidopsis* MATE transporter matex which has a reduced Root system architecture (RSA) compared to the wild type. The role of light signaling regulating the development of aerial parts of the plants is quite well characterized, however its function in modulating root development is less explored. The mRNA levels of MATEx is elevated upon exposure to continuous white light (cWL). matex seedlings grown under cWL contain smaller primary root and shorter root hairs whereas seedlings overexpressing MATEx exhibit well-developed RSA. The expression levels of other root hair specific genes are also reduced in the matex mutants but higher in the overexpressors. The expression of MATEx is reduced under continuous Red light (cRL) and results in less developed RSA, indicating a red light specific modulation. MATEx thus represents a potential regulator of light mediated root development.

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A BBX protein integrates light and ethylene signalling pathways to optimize seedling emergence in soil

Authors: **Kavuri Venkateswara Rao** and **Sourav Dutta**

Seeds under the soil cover experience dark and mechanical stress. In order to successfully come out of the soil seedlings undergo skotomorphogenic development that involves formation of long hypocotyl, unopened cotyledons, and a transient apical hook. Apical hook plays a significant role in the soil emergence of a seedling as it protects the apical meristem from mechanical damage while emerging out from the soil. Seedlings sense the dark environment and mechanical pressure through light signaling factors like B-Box proteins and ethylene signaling factors like EIN2/EIN3/EIL1 respectively, to drive the asymmetric distribution of the auxin in the apical hook. Mechanical stress induces the ethylene production that stabilizes the EIN3/EIL1 transcription factors. These transcription factors promote the expression of HLS1(HOOKLESS1), a key gene regulating apical hook formation. HLS1 promotes the apical hook formation acting upstream of the auxin signaling pathway. We identified a B-box transcription factor that delays apical hook opening in the presence of ethylene. Here, we try to elucidate the molecular mechanism by which the B-box transcription factor connects light and ethylene signaling and modulates auxin distribution to optimize apical hook release and soil emergence.

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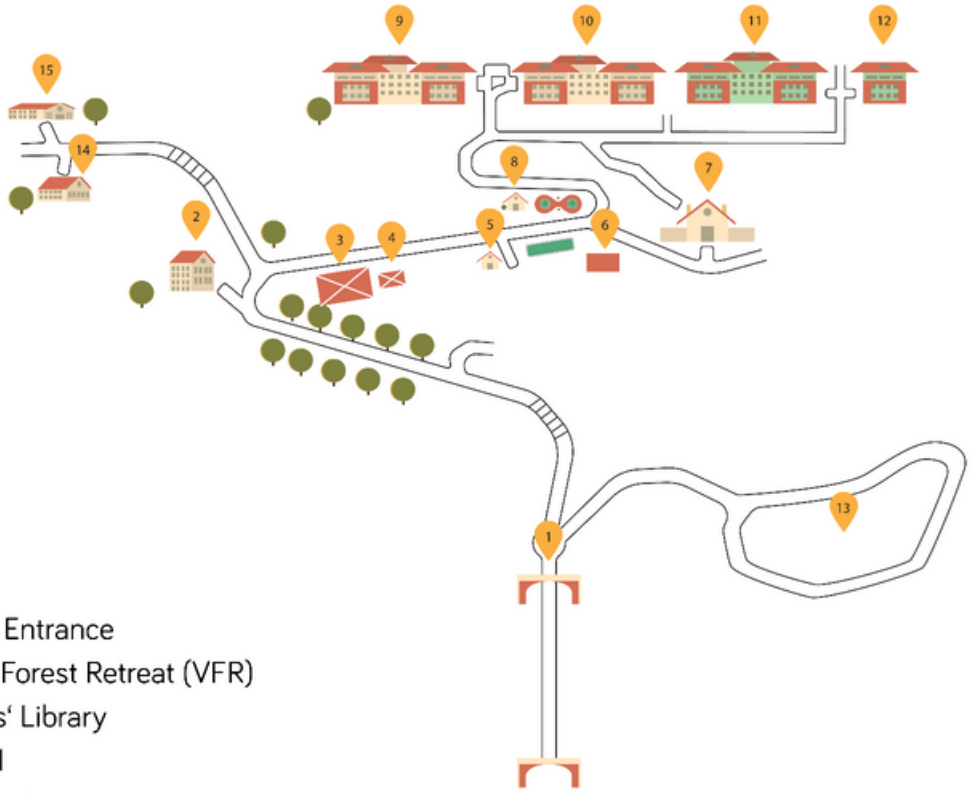
Campus Map



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		7:55		8:00					
				8:00			8:05		
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				8:10			8:15		
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		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	

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	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	
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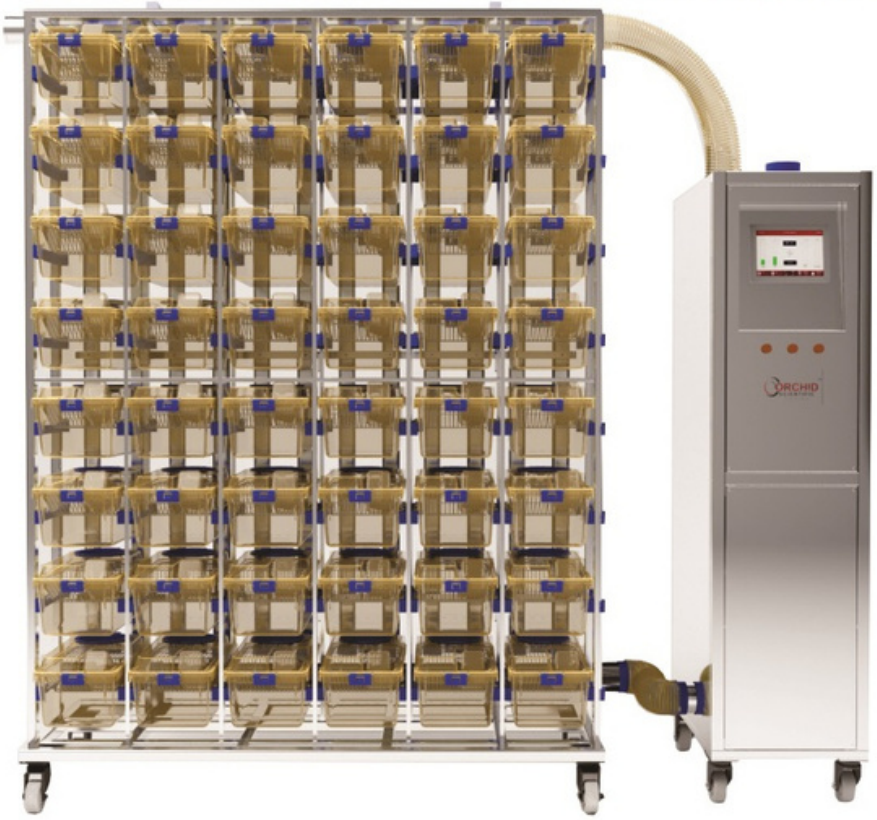

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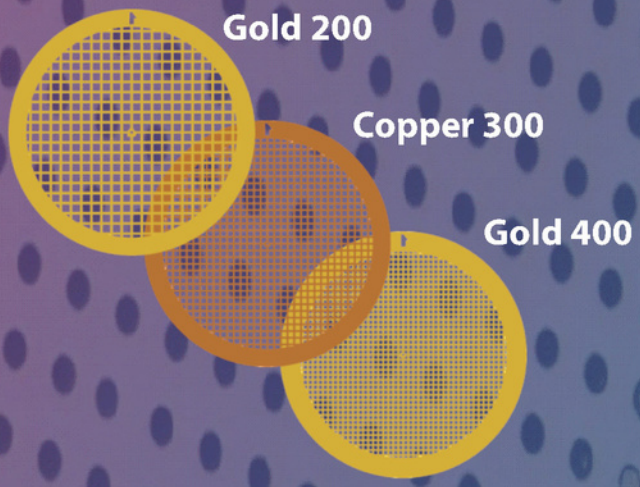

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