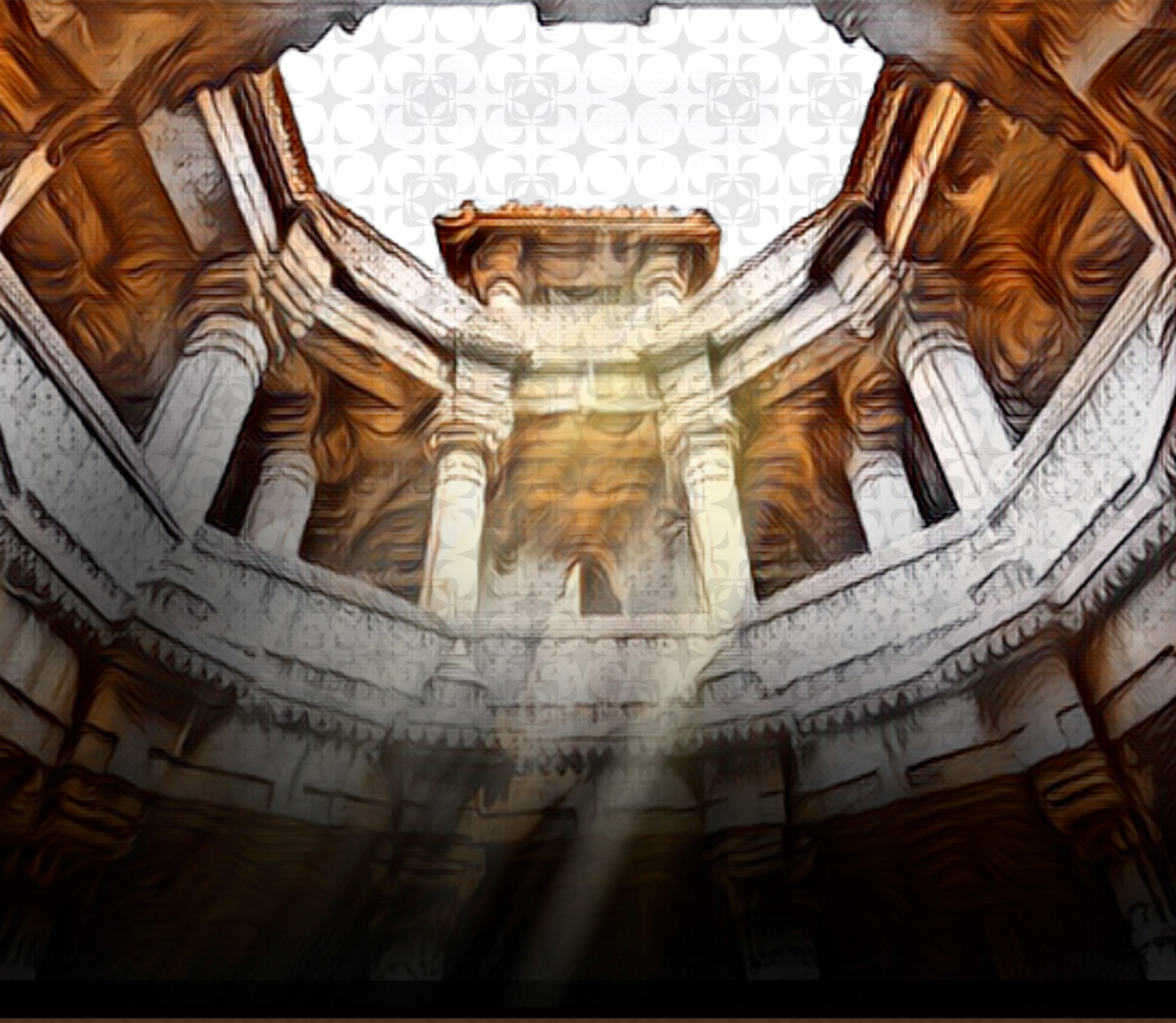

15th Young Investigators' Meeting 2023

ABSTRACT BOOK

Ahmedabad University

IndiaBioscience

Acknowledgements

IndiaBioscience and the organisers of YIM 2023 are thankful for the support they received from:

Sheela, NCBS
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Harshad Mayekar, Ahmedabad University
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Nihal Singh, IITGN
Pankaj Yadav, IITGN
Ketki Barve, IITGN
Vidya Sundaram, IITGN

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The Young Investigators' Meeting Series

Building a community of young Indian biologists.

The YIM series aims to build a vibrant community of biologists by allowing young Indian scientists from different regions and institutions to establish friendships, initiate collaborations, and learn from peer-to-peer mentoring.

The annual Young Investigators' Meeting (YIM) brings together exceptional young and senior scientists, heads of institutes, and representatives from funding agencies for 3 days of discussions and interactions focusing on science and careers in a broad range of disciplines of biology. The program features illuminating talks by renowned scientists, posters, and panel discussions that focus on a wide variety of topics, including **choosing the right research problem, collaborative research, personnel management, funding opportunities and mentorship**. Senior scientists describe their journeys, providing inspirational and amusing anecdotes about their experiences with establishing scientific careers.

Since its inception in 2009, the YIM has established its brand in the life-science fraternity. The meeting has fostered a vibrant atmosphere for exchanging ideas to improve science in India, catalyse friendships, and encourage collaborations between young Indian scientists. We also pair postdocs (PDFs) with Young Investigators (YIs) to promote new connections and facilitate a first-hand account of setting up labs in India.

YIM 2023 will provide an opportunity for the participants to get a flavour of all the different components of the traditional YIM. Eminent researchers from India and abroad have been invited as mentors and speakers; their talks would be a mixture of science and career experiences. There will be a couple of special talks on topics relevant to everyone in science. Other than these talks, there will be a series of panel discussions covering a wide range of topics: **sustainable solutions for the Indian ecosystem, mentoring, lab and grant management, funding, science outreach and communication, public health challenges**, and much more. All the participants will also present their work in the form of posters during the meeting. There will be plenty of time for informal networking during the course of three days.

At the end of the YIM, there will be a one-and-a-half-day Satellite Meeting that enables our invited PDFs to learn about jobs in India and meet Directors/ Vice-Chancellors/ Senior Scientists of institutes and universities from across India. Although YIM makes an effort to facilitate job searches for Post-Doctoral fellows (PDFs), it is not a job fair and the bulk of the meeting revolves around doing science in India and mentoring young investigators and post-doctoral fellows.

Please write to us at ***yim2023[at]indiabioscience[dot]org*** for queries.

YIM2023 Organisers

DHIRAJ DEVIDAS BHATIA
Indian Institute of Technology Gandhinagar
Email: dhiraj.bhatia@iitgn.ac.in

Dhiraj is an Assistant Professor and Ramanujan fellow in the Biological engineering discipline at IIT Gandhinagar. He completed his PhD in DNA Nanotechnology from National Centre for Biological Sciences. He then moved to Paris to join the Institute of Curie initially as a Curie fellow followed by HFSP long-term fellow to work in the areas of membrane traffic and cell biology. He returned to India in 2018 to start his own lab at IIT GN where his lab works on DNA-based nanodevices to program biological systems, generating tools for cellular engineering and regenerative therapeutics.

NISHAD MATANGE
Indian Institute of Science Education and Research (IISER) Pune
Email: nishad@iiserpune.ac.in

Nishad is an Assistant Professor and India Alliance Intermediate Fellow at the IISER in Pune. He did his PhD at IISc and moved into an independent role immediately after as an INSPIRE Faculty Fellow. His lab is trying to understand the evolutionary genetics of antimicrobial resistance in bacteria. In addition to leading an independent research group, Nishad is an enthusiastic educator and particularly enjoys teaching cross-disciplinary courses. He is also a semi-professional musician and an advocate for finding one's own path, both in science and in life!

YIM2023
Organisers

RATNA GHOSAL
Ahmedabad University, Ahmedabad
Email: ratna.ghosal@ahduni.edu.in

Ratna is trained as a field ecologist and is working as an Assistant Professor at the Biological and Life Sciences Division, Ahmedabad University, Ahmedabad. She did her PhD at the Centre for Ecological Sciences, IISc, and carried out her postdoctoral research at the Department of Fisheries, Wildlife and Conservation Biology, University of Minnesota, Twin Cities, USA. She started her journey as an independent faculty in 2018 at Ahmedabad University, where her research group works on understanding how interactions, whether at the level of species or populations or community, shape and influence different ecological processes. Her lab mainly works on freshwater fishes and mugger crocodiles using a combination of lab and field-based experimental approaches.

SHANTALA HARI DASS
IndiaBioscience, Bengaluru
Email: shantala@indiabioscience.org

Shantala completed her PhD in behavioural neuroscience from Nanyang Technological University, Singapore following which she moved to McGill University, Canada for her postdoctoral studies. Across the continents and research questions, her interest in communicating science and facilitating the evolution of the scientific community has stayed strong. At IndiaBioscience, she is keen to see their network grow, expand their activities bringing greater national and international visibility to the Indian life science community and think of creative and bilateral modes of engagement with the community.

About IndiaBioscience

IndiaBioscience is an organization that fills a unique niche in the ecosystem of the life sciences in India, by being a catalyst to promote changes that affect the culture and practice of the field, through engagement with academia, government and industry at various levels. IndiaBioscience aims to increase the visibility of science in society, by being a hub for policy discussions, science communication, and as an aggregator of information.

IndiaBioscience plays an administrative and advisory role in each year's YIM, but its engagement with the participants extends beyond the meeting. IndiaBioscience sets out to forge a long-standing bond with the YIM alumni to promote the development of their career and aid the flourishing of their research groups. Through this sustained ripple effect, it hopes to create a meaningful and lasting impact on the research ecosystem in the life sciences in India.

ADITYA PAREKH
Associate Director

ANKITA RATHORE
Program Manager- Science Communication

MANJULA HARIKRISHNA
Project Coordinator- Community Building

SHANTALA HARI DASS
Executive Director

SHWETHA C
Office Administrator

SUCHIBRATA BORAH
Program Manager- Digital Initiatives

VIJETA RAGHURAM
Program Manager- Science Education

About IndiaBioscience

Engage with us

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YIM Advisors

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Schedule of the Meeting

The schedule of the meeting is subject to change. Please visit the website for the latest schedule.

13 February

Day 1: Young Investigators' Meeting 2023

12.00 - 14.00	**Lunch**
14.00 - 14.15	**Welcome Note** by Satyajit Mayor, NCBS-TIFR, Bengaluru
14.15 - 14.45	**Keynote address**: Rajesh Gokhale, Department of Biotechnology, GoI
14.45 - 15.15	**Mentor Talk 1**: *Reconstituting membrane biology and consolidating a career in science*; Thomas Pucadyil, IISER Pune
15.15 - 15.45	**Mentor Talk 2**: *Staying in shape: Lessons from budding yeast*; Krishnaveni Mishra, University of Hyderabad
15.45 - 16.00	**Talk**: *Engaging Communities, Enabling Change*; Shantala Hari Dass, IndiaBioscience, Bengaluru
16.00 - 16.30	**Tea/Coffee**
16.30 - 16.45	**Talk**: *Support for International Research Collaborations from HFSP;* Guntram Bauer, Human Frontier Science Program, France
16.45 - 17.45	**Panel discussion 1**: Sustainable solutions for Indian ecosystem **Panelists**: Hema Somanathan, IISER Thiruvananthapuram; Krishnaveni Mishra, University of Hyderabad; Roop Mallik, IIT Bombay; Tamal Das, TIFR Hyderabad **Moderator**: Bhuvan Pathak, Ahmedabad University
17.45 - 18.45	**Special talk 1**: *Draw Your Science*; Ipsa Jain, Srishti Manipal Institute of Art, Design and Technology, Bengaluru
18:45 - 20.00	**YI Poster session** (even number)
20.00 onwards	**Dinner**

Schedule of the Meeting

The schedule of the meeting is subject to change. Please visit the website for the latest schedule.

14 February

Day 2: Young Investigators' Meeting 2023

This day YIM 2023 will take place on the Ahmedabad University campus. Transport to Ahmedabad University will be provided from IIT — Gandhinagar Guest House for all attendees.

09.00 - 10.00	Travel to Ahmedabad University
10.00 - 10.30	**Tea break** (right outside the venue)/ assembling in venue
10.30 - 11.00	**Mentor Talk 3**: *Unraveling the Mechanobiology of Collective Cell Dynamics: An Interdisciplinary Journey*; Tamal Das, Tata Institute of Fundamental Research Hyderabad,
11.00 - 12.00	**Panel Discussion 2**: Building a diverse funding portfolio **Panelists**: Guntram Bauer, HFSP; LS Shashidhara, IISER Pune & Ashoka University; Madhvi Joshi, Gujarat Biotechnology Research Centre; Sanjay Mishra, Department of Biotechnology; Vandana Gambhir, IISER Pune **Moderator:** Sharmistha Majumdar, IIT Gandhinagar
12.00 - 12.30	**EMBO Global Lecture Series**: *How did I end up where I am now? A glimpse in my scientific journey...and through the cell*; Anne Spang, Universität Basel, Switzerland
12.30 - 13.00	TBC
13.00 - 14.00	**Lunch**
14.00 - 14.30	**Special Talk 2**: *Impact of Vaccines - Public Health and Society*; Kapil Maithal, Zydus Lifesciences, Ahmedabad
14.30 - 15.00	**Mentor Talk 4**: *Guarding cytosol against intruders*; Anirban Banerjee, IIT Bombay, Mumbai
15.00 - 16.00	**Panel Discussion 3**: Engaging with public health challenges **Panelists**: Anirban Banerjee, IIT Bombay; Kapil Maithal, Zydus Lifesciences; Karishma Kaushik, SPPU; Rakesh Mishra, TIGS **Moderator**: Rashna Bhandari, CDFD

Schedule of the Meeting

The schedule of the meeting is subject to change. Please visit the website for the latest schedule.

14 February

Day 2: Young Investigators' Meeting 2023

16.00 - 17.30	**Tea/Coffee + PDF Poster**
17.30 - 18.00	**Talk**: *Funding Opportunities at India Alliance*; Debashis Mitra, DBT/ Wellcome Trust India Alliance, Hyderabad
18.00 - 19.00	**Breakout session 1** Topic: Setting and maintaining boundaries
19:00 - 20:30	**Dinner** at Ahmedabad University
20.30	Depart from Ahmedabad University

Schedule of the Meeting

The schedule of the meeting is subject to change. Please visit the website for the latest schedule.

15 February

Day 3: Young Investigators' Meeting 2023

09.00 - 09.30	**Mentor talk 5**: *Caenorhabditis elegans as a model to understand innate immunity: Lessons (un) learned*; Varsha Singh, Indian Institute of Sciences, Bengaluru
09.30 - 10.30	**Breakout session 2** Topic: Building your identity
10.30 - 11.00	**Keynote Talk**: *Life Sciences Research - Opportunities For The Near Future*; K VijayRaghavan, NCBS- TIFR, Bengaluru
11.00 - 11.30	**Tea/Coffee**
11.30 - 11.45	**Talk**: *EMBO and India: Connecting Life Scientists*; Vid Nukala, EMBO, Germany
11.45 - 12.45	**Panel Discussion 4**: Science and society **Panelists**: Carsten Janke, Institut Curie; K VijayRaghavan, NCBS; Sarah Iqbal, FAST India & SaS; Smita Jain, Cactus Communications; Suhel Quader, NCF **Moderator**: Aditya Parekh, IndiaBioscience
12.45 - 15.15	**Lunch** + Adalaj step wells
15.15 - 15.45	**EMBO Global Lecture Series:** *From brains to yeast and back again - my scientific journey*; Carsten Janke, Institut Curie, France
15.45 - 16.15	**Mentor Talk 6**: *Tales from a web and a hive*; Hema Somanathan, Indian Institute of Science Education and Research Thiruvananthapuram
16.15 - 17.30	**Poster YI** (odd numbers) + **Tea/Coffee**
17.30 - 18.30	**15 years of YIM - The Road Ahead**
18.30 - 18.45	Summary by YIM organiser
18.45 - 19.00	Closing remarks
19.00 - 20.00	YI - PDF interaction time
20.00 Onwards	Social mixer with **Dinner**

Schedule of the Meeting

The schedule of the meeting is subject to change. Please visit the website for the latest schedule.

16 February

Day 4: Young Investigators' Meeting 2023

09.00 - 09.10	Introduction to The PDF Satellite Meeting
09.10 - 10.10	**Institutional Talks Session 1** (Rajat Moona, IIT Gandhinagar; Raghu Padinjat, NCBS, Bengaluru; Maneesha Inamdar, InStem, Bengaluru; Rakesh Mishra, TIGS, Bengaluru; Suhel Quader, NCF, Mysuru)
10.10 - 11.00	**PDF Talks Session 1** (10 PDFs talk - 5 mins each)
11.00 - 11.30	**Tea/Coffee**
11.30 - 12.20	**Institutional Talks Session 2** (Subeer Majumdar, Gujarat Biotechnology University, Gandhinagar; Ullas Kolthur, TIFRH, Hyderabad; Mitali Mukerji, IIT Jodhpur; Kasturi Mitra, Ashoka University, Sonipat; Dibyendu Sarkar, CSIR-IMTECH, Chandigarh)
12.20 - 13.10	**PDF Talks Session 2** (10 PDFs talk - 5 mins each)
13.10 - 14.00	**Lunch**
14.00 - 14.50	**PDF Talks Session 3** (10 PDFs talk - 5 mins each)
14.50 - 15.40	**Institutional Talks Session 3** (Dayananda Siddavattam, Gandhi Institute of Technology and Management, Visakhapatnam; Satish Rao, Manipal Academy of Higher Education, Manipal; Sudhanshu Vrati, RCB, Faridabad; Prasun Roy, Shiv Nadar University, Delhi NCR; Usha Vijayraghavan, IISc, Bengaluru)
15.40 - 16.20	**PDF Talks Session 4** (10 PDFs talk - 5 mins each)
16.20 - 18.20	**PDF Poster Session** + **Tea/Coffee**
19.30 onwards	**Dinner** and informal discussion

Schedule of the Meeting

The schedule of the meeting is subject to change. Please visit the website for the latest schedule.

17 February

Day 5: Young Investigators' Meeting 2023

This day YIM 2023 will take place on the Ahmedabad University campus. Transport to Ahmedabad University will be provided from IIT — Gandhinagar Guest House for all attendees.

09.00	Deposit room keys
09.30 -10.30	Travel to Ahmedabad University
10.30 -11.00	Deposit luggage & Assemble at venue
11.00 - 11.50	**Institutional Talks Session 4** (Balaji Prakash, Ahmedabad University; Vinay Nandicoori, CSIR- CCMB, Hyderabad; Anuradha Vaidya, Symbiosis School of Biological Sciences, Pune; Naibedya Chattopadhyay, CSIR- CDRI, Lucknow; Pushpa Robin, MSU, Baroda)
11.50 - 12.50	**PDF Poster Session** + **Tea/Coffee**
12.50 - 13.50	**PDF-Institutional Heads Open Session**
13.50 - 14.10	Closing remarks to the PDF Satellite Meeting
14.10 onwards	Interaction with Institutional Heads, lunch and departure from Ahmedabad University
15.00	End of PDF Satellite Meeting

Supporting Organisations

DEPARTMENT OF BIOTECHNOLOGY, GOVT. OF INDIA

This Department, set up in 1986, gave a new impetus to the development of the field of modern biology and biotechnology in India. In more than a decade of its existence, the department has promoted and accelerated the pace of development of biotechnology in the country. DBT is the largest supporter of both YIM and IndiaBioscience.

DBT/ WELLCOME TRUST INDIA ALLIANCE, HYDERABAD

DBT/Wellcome Trust India Alliance (India Alliance) is an independent, dynamic public charity that funds research in health and biomedical sciences in India. India Alliance invests in transformative ideas and supportive research ecosystems to advance discovery and innovation to improve health and well-being. India Alliance stands for diversity, inclusivity, and transparency in science and works to facilitate the engagement of science with society. India Alliance is funded by the Department of Biotechnology (DBT), Government of India, and the Wellcome Trust, United Kingdom.

INDIAN INSTITUTE OF TECHNOLOGY GANDHINAGAR (IITGN)

IITGN was established in 2008 in Gujarat with the aim to foster best technical education in engineering and sciences with equal focus on basic and applied research and all the associated departments and centers. IITGN follows the Open Lab concept thereby boosting the interdisciplinary education and research across all its disciplines and research centers.

AHMEDABAD UNIVERSITY, AHMEDABAD

Ahmedabad University, a private, non-profit institution supports innovative, interdisciplinary, research-driven project-based education, and asserts the centrality of arts, sciences, engineering and management for a broad and fulfilling educational experience (https://ahduni.edu.in/). To support innovative academic programmes that enable students to grow into well-rounded leaders, the university is building a strong faculty pool - both from India and abroad - with strong communication skills, who can contribute to imaginative learning and are willing to work collaboratively as part of a community of emerging scholars.

Supporting Organisations

NATIONAL CENTRE FOR BIOLOGICAL SCIENCES, BENGALURU

NCBS is a premier research institution under the aegis of the Tata Institute of Fundamental Research, Mumbai. The mandate of NCBS is fundamental research in the frontier areas of biology. Research interests range from the study of single molecules to ecology and evolution.

SHIV NADAR UNIVERSITY

Shiv Nadar University, Delhi NCR is a multidisciplinary, research-focused, and student-centric University offering a full range of academic programs at the undergraduate, postgraduate and doctoral level. The University's goal is to become internationally recognized for the quality of its research and creative endeavors and their applicability to improving quality of life, generating new insights and expanding the boundaries of human knowledge creativity. Committed to excellence in teaching, research and service, the University aims to serve the higher education needs of India and the world beyond.

EUROPEAN MOLECULAR BIOLOGY ORGANIZATION (EMBO)

EMBO is an organization of more than 1,900 leading researchers that promotes excellence in the life sciences in Europe and beyond. The major goals of the organization are to support talented researchers at all stages of their careers, stimulate the exchange of scientific information, and help build a research environment where scientists can achieve their best work. The EMBO communities are global networks of top-level scientists at various stages of their careers. They give privileged access, in particular to young researchers, to cutting-edge science and the opportunity to build international contacts.

ROYAL SOCIETY OF CHEMISTRY (RSC)

RSC is a learned society with the goal of "advancing the chemical sciences" in our day-to-day life keeping in mind the importance of chemistry in our society. RSC provides a unique platform to connect students, teachers, researchers, scientists together for the development and recognition of professional capabilities and to publish new cutting-edge research.

Supporting Organisations

CACTUS COMMUNICATIONS PVT. LTD.

Cactus Communications is a technology company accelerating scientific advancement. CACTUS provides scientific writing services to the Top 10 global pharmaceutical, biotech, and medical device companies. The team comprises writers with advanced degrees in medicine or the life sciences. CACTUS is recognized for its expertise in providing publications and medcom services to global client teams from the US, UK, Germany, and Japan, among other geographies. CACTUS acts as a trusted advisor and works as an extension of its client teams by not only delivering high-quality work consistently, but also providing strategic guidance for their medical communications needs.

AUTHORCAFE

AuthorCafé is a technology company operating in the research management space, streamlining the processes involved. With the aim of empowering researchers, research managers, and administrators, we design and develop digital workflow solutions to a number of critical problems where manual efforts become more than rote. Our products—specifically designed for research institutions (researchers and administrators)—are the following: PhD Suite, Research Writing and Collaboration Module, and Pre-Award Suite.

IndiaAlliance
DBT wellcome

Advancing Discovery and Innovation to Improve Health

DBT/Wellcome Trust India Alliance is an independent, dynamic public charity that funds research in health and biomedical sciences in India. India Alliance invests in transformative ideas and supportive research ecosystems to advance discovery and innovation to improve health and well-being. India Alliance is funded by the Department of Biotechnology (DBT), Government of India and the Wellcome Trust, UK.

BUILDING CAPACITY IN BIOMEDICAL AND HEALTH RESEARCH

Fellowships and Grants

With a commitment to build research capacity in India and catalyse internationally competitive research, India Alliance has successfully steered three types of fellowship programmes to support researchers at different stages of their career-Early Career, Intermediate, and Senior-under the tracks of Basic Biomedical Research and Clinical and Public Health Research. The focus of our Fellowship programme is to set the funded researchers on a leadership track through a continuous system of engagement and mentoring.

To enhance India's health research ecosystem and address major health challenges for India and the world, India Alliance also offers funding for collaborative research projects and clinical research training through its Team Science Grants and Clinical/Public Health Research Centres, respectively. Team Science Grants fund interdisciplinary teams that bring together high-quality scientists from multiple institutions with complementary skills, knowledge, and resources to address an important health challenge for India. Clinical/Public Health Research Centres (CRC) are envisioned as virtual, research-oriented centres focused either on crosscutting or vertical research themes. To build clinical research capacity, integrate basic with clinical/public health research, and develop physician scientists, CRCs can have an embedded Clinical Research Training Programme (CRTP)- 3 to 4-year mentored research training fellowships for medical graduates (MBBS) and post-graduates (MD/MS).

Research Capacity Workshops

In addition to the funding programmes, India Alliance runs workshops aimed at building capacity in biomedical and health research. Developing Indian Physician Scientists (DIPS) workshops, launched in 2017, are designed to encourage young physicians to participate in research by facilitating exposure to the scientific methodology and inspirational role models. Research Methodology workshops are an attempt to enhance technical skills of researchers by providing training in epidemiology, study design, data collection, and analysis.

FOSTERING INTERDISCIPLINARY AND INTERNATIONAL COLLABORATIONS

Finding innovative and sustainable solutions to modern problems requires interdisciplinary and collaborative science, which extends beyond borders. Besides its Fellowship programmes, India Alliance funds major scientific meetings aimed at resource-sharing and forging national and international research collaborations.

INDIA | EMBO SYMPOSIA

India Alliance and EMBO co-fund up to three scientific meetings per year in India. The meetings facilitate discussions on important global challenges in the context of the life sciences and aim to promote discovery and innovation through an interdisciplinary approach.

STRENGTHENING RESEARCH ECOSYSTEMS IN INDIA

In addition to identifying and supporting the best scientific talent in India, India Alliance supports and implements enabling policies and interventions to create a robust research ecosystem in the country.

INDIA RESEARCH MANAGEMENT INITIATIVE

Institutions in India currently lack a well-developed research management system, which is important for them to navigate the high demands for funding, outreach, and governance of research. To address this lacuna, India Alliance launched the India Research Management Initiative (IRMI), a Research Management programme for India, which aims to strengthen institutional ecosystems. IRMI will also provide opportunities to Indian research managers to receive training and create a network of practitioners for serving broader career development needs.

PUBLIC ENGAGEMENT

India Alliance aims to bridge the gap between science and society through public engagement programmes that bring the scientific community and the public together to share, debate, and deliberate on important matters of science, especially those relevant to human health, which have implications for the society.

ENABLING ENGAGEMENT WITH SCIENCE

At India Alliance, we empower researchers to make their science accessible and engaging through open access publication, science communication, and public engagement. Open research ensures an unbiased, instantaneous, and unhindered flow of knowledge produced by researchers, thereby promoting innovation, communication and collaboratioos. To keep all of India Alliance-funded research openly accessible, India Alliance joined Wellcome Open Research and Europe PMC in 2017-2018. Adoption of the open research policy is bound to improve the relationships between researchers, policymakers, educators and the society at large.

SCIENCE COMMUNICATION WORKSHOPS

Effective communication of scientific facts and findings helps science to thrive and people to better appreciate its value for the society. In addition to organising various unique science communication events, the India Alliance regularly conducts Science Communication Workshops.

INDIA SCIENCE MEDIA FELLOWSHIPS

India Alliance in collaboration with Nature India launched the India Science Media Fellowship in 2019 to strengthen science journalism in the country and help establish science as a distinct genre of journalism. This fellowship will enable journalists to apply the craft of journalism to science and write nuanced science stories.

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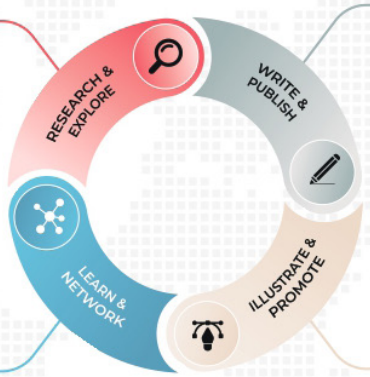

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Secretary

Department of Biotechnology, GoI

Special Talks

IPSA JAIN
Srishti Manipal Institute of Art, Design and Technology, Bengaluru
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Drawing (your) Science

Creativity and science go together, and so do arts and creativity. Opposed to popular notions, scientists engage with the arts all the time. Visual arts, in particular, makes its way to the edges of the notebooks as mindless doodles, and scrapes of napkins during conference lunches as a way to explain that burning new hypothesis. Some flex their pro-level with sketching and note taking during conference talks and lab meetings on digital apps. Besides this sketching that is part of thinking, and sense-making all scientists use images and drawings for grant proposals, publications, websites, conference posters, and numerous presentations. Drawing is an integral part of discovery as well as the presentation of discovery.

In this session, we will discuss some drawing-based science projects. Participants will also make their own sketches to share their science based on guided prompts. We will discuss the means of translating them for the 'presentation of discovery'. No experience of drawing is necessary, only a willingness to explore and extend a new dimension of their creativity.

Special Talks

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Impact of Vaccines - Public Health and Society

Over the years, vaccines have saved lives, improved life expectancy and led to economic growth more than any other medical intervention. As per World Health Organization, immunization prevents around 3.5-5 million deaths every year from diseases like diphtheria, tetanus, pertussis, influenza and measles. At the same time, health economists have also evaluated the socio-economic benefit of vaccination and one such study has shown that for each dollar invested in immunization there is a saving of 20-25 dollars over a decade in healthcare expenditure. This in fact makes a very strong case for countries to introduce vaccination from providing health security and helping socio-economic growth. However, due to inadequate equitable vaccine access, lack of funding and fragile geopolitical issues specifically in low and middle income countries, over 20 million children remain at risk from vaccine-preventable diseases (VPDs) annually and lead to over 1 million deaths. Thus, political and societal role is very critical in improving awareness, access and affordability to vaccines, which will help in eradicating VPDs.

Mentor Talks

M01 **ANIRBAN BANERJEE**
Guarding cytosol against intruders

M02 **ANNIE SPANG**
How did I end up where I am now? A glimpse in my scientific journey...and through the cell

M03 **CARSTEN JANKE**
From brains to yeast and back again - my scientific journey

M04 **HEMA SOMANATHAN**
Tales from the web and the hive

M05 **KRISHNAVENI MISHRA**
University of Hyderabad, Hyderabad

M06 **TAMAL DAS**
Tata Institute of Fundamental Research, Hyderabad

M07 **THOMAS PUCADYIL**
Reconstituting membrane biology and consolidating a career in science

M08 **VARSHA SINGH**
Caenorhabditis elegans as a model to understand innate immunity: Lessons (un)learned

M01

ANIRBAN BANERJEE

Indian Institute of Technology Bombay, Mumbai

https://www.bio.iitb.ac.in/people/faculty/banerjee-a/

Guarding cytosol against intruders

Successful elimination of infectious microbes requires an efficient surveillance system, enabling quick pathogen sensing and clearance. We demonstrated, that apart from the classical phago-lysosomal pathways, for detection and elimination of pathogens, ubiquitin proteasomal system is pivotal. We decoded the identity of the first bacterial protein as substrate for ubiquitination and revealed a novel mechanism for killing of ubiquitinated pathogens involving a tweezer like host nanomachine. In vitro reconstitution assay showcased the necessity of the tweezer's segregase activity in rupturing bacterial surfaces, thus establishing its direct anti-bacterial property. We further demonstrated that the intracellular persistence of bacteria increased significantly by blocking, downregulating, and expressing a catalytic mutant of p97. Using a small molecule antagonist, we displayed a critical property of this tweezer-like nanomachine in protecting the mice against lethal bacterial sepsis leading to reduced morbidity. Thus, our study highlights an innovative strategy adopted by the host to tackle invading pathogens by harnessing the prowess of a tweezer like a nanomachine, whose direct activation will provide an immunity boost against severe bacterial infection

M02

ANNIE SPANG

University of Basel, Basel, Switzerland

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How did I end up where I am now? A glimpse in my scientific journey and through the cell

Cells are the basic unit of life. Understanding how they work is worth a lifelong quest. Once I decided that this quest is my quest, I tried to do everything in my power to put me on the path. I realized that I need to understand the basics of the cell and that I could not just concentrate on one issue such as the centrosome, the cell cycle or the secretory pathway. I wanted to understand everything – which is of course not possible, so you have to make concessions. The balance, I aim to strike is a holistic but still mechanistic and detailed understanding of the cell, tissues and organisms. Therefore, we work on different cellular systems and processes to elucidate the principles of intracellular communication and how they adapt to different environments and perturbations, and also during aging.

M03

CARSTEN JANKE

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From brains to yeast and back again - my scientific journey

One of the greatest headaches for young scientists is what to do for their next career step. Given the quite competitive nature of our scientific environment, this decision is often driven by the wish to work in the most fashionable type of research, using the latest fancy methods, and be in the best-ranked institutes or universities.

In my own career, I did none of this. I will present how my decisions were driven by other factors, such as by a particular idea I had in mind, sometimes by chance (yes!), but also by my personal life.

My research career started with a PhD in biochemistry at my home university, during which I explored the role of different isoforms of the microtubule-associated protein tau in Alzheimer's disease. My next steps brought me to France, where I noticed for the first time (from the literature) that microtubules are posttranslationally modified – a discovery that determined the rest of my scientific career. But before I could work on this exciting subject, I moved to the world of yeast biology. Ironically, yeast does not have tubulin modifications, but in return, it is a wonderful model system to work with. Only after this postdoc was I able to join a researcher working on tubulin modifications, and together we identified the first enzymes catalysing tubulin polyglutamylation. This discovery started my independent career. My lab has since progressed the field of tubulin modifications on many different levels – molecular, cellular, and organism – an interdisciplinary approach I was never afraid to implement. Why? Perhaps because I never followed a beaten path at any stage of my career.

M04

HEMA SOMANATHAN

Indian Institute of Science Education and Research Thiruvananthapuram

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Tales from the web and the hive

Hives of bees and the webs are marvelous examples of animal-built structures that have fascinated biologists and non-biologists alike. These extended phenotypes are the lifeline of honeybees and spiders. I will provide a brief glimpse into about we have learned about colony organisation in over a decade of studies on Asian honeybees and social spider colonies. Honeybees are celebrated examples, often considered the embodiment of animal sociality, while social spiders present a curious case in social evolution. They are only mildly successful in ecological and evolutionary terms and are in fact viewed as evolutionary 'sitting ducks' that have neither flourished worldwide or burst into speciose clades. I will present some interesting facets of behaviour and colony organisation in both these groups. I will also provide a description of my traverse through varied Indian landscapes: natural, academic, and funding landscapes.

M05

KRISHNAVENI MISHRA

University of Hyderabad, Hyderabad

http://sls.uohyd.ac.in/new/fac_details.php?fac_id=57

Staying in shape: Lessons from budding yeast

Membrane-bound organelles provide physical and functional compartmentalization of metabolic processes in eukaryotic cells. Each organelle has a defined geometry, i.e., size and shape. The size and shape of these organelles is genetically controlled but is also dynamic. The geometry of organelles are coordinated with each other and with respect to the cell geometry. The composition of lipids and proteins present in the membrane are key determinants of the shape of an organelle. In addition, organelles also measure their volume and maintain that within a defined limit and importantly, with respect to cell size. While we know that maintenance of organelle geometry involves a complex interplay of proteins and lipids, the identity of all the components is not known. Our laboratory is interested in understanding the mechanisms that regulate the shape and size of nucleus. Maintenance of the shape of nucleus, which houses the genetic material within a double membrane bilayer, is crucial for seamless spatio-temporal control over nuclear functions. The shape and size of nucleus is known to undergo remodelling during processes such as cell growth, division and certain stresses. In this talk I will share our recent insights into the molecular processes that regulate nuclear size and shape in the budding yeast, Saccharomyces cerevisiae, and discuss the implications for other organelles and systems.

M06

TAMAL DAS

Tata Institute of Fundamental Research - Hyderabad

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Unraveling the Mechanobiology of Collective Cell Dynamics: An Interdisciplinary Journey

For over a decade or longer, I have been interested in understanding how forces generated by biological cells drive collective cell movements during animal development, wound healing, and cancer. In this talk, I will present a few of our discoveries delineating a clear association between forces and the collective dynamics of cells. In that process, I will also discuss the challenges of pursuing an extremely interdisciplinary program. On the scientific aspect, I will specifically emphasize how using multiple microscopy and biophysical techniques, we have been able to show that tissue mechanics and the forces generated by biological cells together regulate the epithelial defence against cancer. On the professional aspect, I will describe my scientific journey, how we started our lab, what we have achieved so far, and where we are heading to.

M07

THOMAS PUCADYIL

Indian Institute of Science Education and Research Pune

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Reconstituting membrane biology and consolidating a career in science

The lipid bilayer is highly resilient to rupture and explains why it was selected over the course of evolution to serve a barrier function. Yet fission, or the splitting of a membrane compartment, is a central theme in biology that manifests during cell division, organelle biogenesis and vesicular transport. Fission involves the local application of forces to bend and constrict a membrane tube. Using a facile assay system of supported membrane nanotubes that can be tuned for size and lipid composition, we have carried out biochemical screens and discovered several novel proteins that catalyze fission. My talk will describe recent developments in our efforts at expanding the repertoire of fission proteins as well as elucidating their mechanism and cellular functions.

M08

VARSHA SINGH

Indian Institute of Science, Bengaluru

https://sites.google.com/view/varshalab/home?authuser=0

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

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

Personal note: Setting up a biology lab in India and running it for almost a decade has been a fun experience. Being a PI requires abilities beyond intellect, bench skills and fundable ideas. Having a good mentor (or two), being a good mentor, and being an empathetic human goes a long way. A young PI worries about how to juggle personal and professional responsibilities. The downside is everyone has to figure this out, the upside is everyone does figure it out. Along the journey, you discover your personal set of axioms to live by.

Panel Discussion

Panel Discussion 1

Sustainable solutions for Indian ecosystem

Moderator: **BHUVAN PATHAK**

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Panel Discussion

Panel Discussion 2

Building a diverse funding portfolio

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Panel Discussion

Panel Discussion 3

Engaging with public health challenges

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Panel Discussion

Panel Discussion 4

Science and society

Moderator: **Aditya Parekh**

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Institutional Heads and Representatives

Each year, representatives from various institutions across India attend the YIM, particularly the Postdoctoral Fellows' Satellite Meeting and give talks about their institutes. Listed below are the institutions and representatives at YIM 2023.

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Young Investigators' Abstracts

The abstracts have been printed exactly as submitted by the participants. The organisers of YIM 2023 are not responsible for any errors in them.

YI 01 ANAND SINGH
Rules and impacts of RNA quality control system in the regulation of global gene expression.

YI 02 ANANYA MUKHERJEE
How the CO2-concentrating mechanism improves the efficiency of photosynthesis in the green alga *Chlamydomonas reinhardtii*

YI 03 ANJAN ROY
A unifying autocatalytic network-based framework for bacterial growth laws

YI 04 ARCHANA KUMAR
To grow or defend: how crops decide their fate.

YI 05 ASHIM RAI
Structure-function mapping of Salmonella-host cytoskeleton interactions

YI 06 ASHISH KUMAR VYAS
Presence of entry receptors and viral markers suggest a low level of placental replication of hepatitis B virus in a proportion of pregnant women infected with chronic hepatitis B

YI 07 AVISHEK BANIK
Microbes mediated rhizofiltration: A possible way to reduce metal translocation in plants

YI 08 BHUVAN PATHAK
Effect of gypsum supplementation on soil microflora during peanut maturation

YI 09 CHANDANA BASU
The genes behind your fingerprints

YI 10 DILIP KUMAR
Structure guided design of novel antiviral strategies against pathogenic RNA viruses

YI 11 DIVYA NAIR
Application of DNA Barcoding, NGS & 'OMICS' Technologies for Plant Diversity Assessment, Authentication, Molecular Phylogeny and Cryptic Species Taxonomy

YI 12 GAURAV KUMAR
Ligand receptor analysis of brain cell type marker data reveals intricate neurovascular Interaction

YI 13 GREESHMA THRIVIKRAMAN
Biophysical control of 3D tissue microenvironment for health & diseases

Young Investigators' Abstracts

YI 14 GUNJAN SHARMA
Transcriptome analysis and effectome of vascular wilt pathogen *Fusarium oxysporum f. sp.* cubense tropical race 4 (TR4), causing Panama disease in banana

YI 15 ISHAAN GUPTA
Postmortem lung tissue from COVID-19 patients suggests two distinct trajectories driving mortality

YI 16 JAHNAVI JOSHI
What are the drivers of genetic diversity in soil predatory arthropods?

YI 17 JHANSI NATHAN
Effects of berberine on anti-angiogenic activity using zebrafish model

YI 18 JOGENDER SINGH
Thiol antioxidants activate the hypoxia response pathway

YI 19 KRISHNA KURTHKOTI
The error-prone polymerase DnaE2 mediates the evolution of antibiotic resistance in persister mycobacterial cells

YI 20 MOHAN TC
The intervention of phytohormone to reduce arsenic accumulation in rice grains

YI 21 MOUTUSI MANNA
Phase transition in atomistic simulations of thylakoid membrane of red algae: Lipids in temperature adaptation

YI 22 NAVEEN GOWDA
Role of FMRP in regulating the 2'O methylation in human embryonic stem cell and its differentiation

YI 23 NEETHA BALARAM
Classification of Electrical Status Epilepticus in Sleep (ESES) based on EEG patterns and spatiotemporal mapping of spikes

YI 24 NIRMALYA SEN
ETS1 is the key to acquired resistance and metastasis in Triple Negative Breast Cancer

YI 25 NISHA SINGH
Identification of novel genes/ QTLs for seed quality and nutrition traits in pigeonpea for sustainable protein source

YI 26 PAVAN AGRAWAL
Molecular mechanisms underlying social isolation stress in Drosophila

YI 27 PRASAD KASTURI
A comparative meta-analysis of membraneless organelle associated proteins with age related proteome of *C. elegans*

Young Investigators' Abstracts

YI 28 PRASOON KUMAR
Modifications in the design of paper microfluidic devices to facilitate rapid and uniform spreading of biofluids for diagnostic applications

YI 29 R SELVI BHARATHAVIKRU
Networking in Nephrogenesis; Functional characterization of Wilms Tumour 1 interactions

YI 30 RATNASEKHAR CH
Daily orchestration of metabolic pathways in Human red blood cells

YI 31 ROHAN KHADILKAR
Understanding stem cell and tissue homeostasis during developmental and disease scenarios

YI 32 SACHIN TIWARI
Cognitive protection in tauopathy environment following TBI shows correlation with delayed astrogliosis

YI 33 SHOVAMAYEE MAHARANA
Role of RNA interactions in controlling physiological properties and function of RBP condensates

YI 34 SUBRAMANIAN SANKARANARAYANAN
ROS regulation of stigma development

YI 35 SUDARSHAN GADADHAR
Tubulin code, cilia and homeostasis

YI 36 SUNIL KUMAR BODA
Biomaterials for musculoskeletal tissue engineering

YI 37 TRAYAMBAK BASAK
Collagen post-translational modifications at the interface of extracellularmatrix (ECM) remodelling, fibrosis, and regeneration

YI 38 VANIKA GUPTA
Inherent constraints on a polyfunctional tissue lead to a reproduction-immunity tradeoff

YI 39 VINOD TIWARI
Development and validation of clinically mimicable animal model of cocktail chemotherapy-induced neuropathic pain

YI 40 VIVEK DOGRA
Singlet oxygen-induced damage and signaling: clues to engineer stress-resilient photosynthetic apparatus

YI 01

ANAND SINGH

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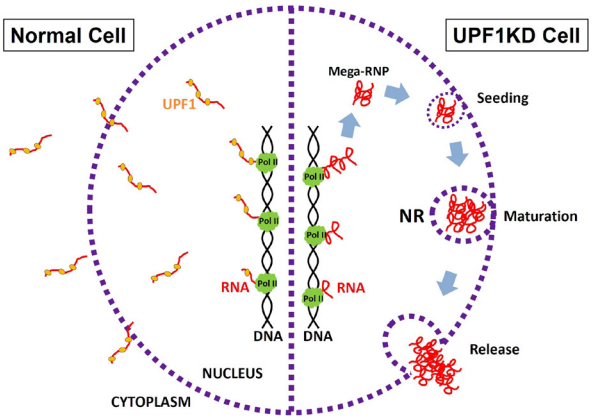
Rules and impacts of RNA quality control system in the regulation of global gene expression.

Keywords: RNA quality control, neurodegeneration, long non-coding RNA, phase separation, stress biology

Abstract:

Gene expression is a fundamental process that translates genomic information into the form of functionally active RNA and protein molecules in the cell. Faithful protein production is ensured by dedicated surveillance machinery in the cytoplasm that selectively eliminates the faulty transcripts. Nonsense-Mediated mRNA Decay (NMD) is the most effective translation-dependent cytoplasmic RNA surveillance machinery that detects and degrades the mRNA with premature termination codons (PTC). These faulty transcripts otherwise produce truncated proteins which could be potentially toxic for the cell. The molecular mechanism of NMD in RNA quality control has been well studied but recent studies have demonstrated that NMD also regulates the expression of a large fraction of transcriptome with no NMD features. Here, we provide evidence that UPF1, a core NMD component, constantly shuttles between the nucleus and cytoplasm by a mechanism that requires its RNA helicase activity. UPF1 is associated, genome-wide, with nascent mRNAs at most of the active Pol II transcription sites. Intron recognition seems to interfere with the association and translocation of UPF1 on nascent pre-mRNAs, and cells depleted of UPF1 show defects in the release of mRNAs from transcription sites and their export from the nucleus. Our data suggest that NMD factors start to act on mRNA along with their birth at the site of transcription and help in mRNP packaging and export from the nucleus to the cytoplasm. Currently, we are investigating the mode of action of NMD factors in fine-tuning of gene expression at different stages of development.



A model demonstrating functions of RNA helicase UPF1 in the nuclear RNA processing.
Credits: Anand Kumar Singh

YI 02

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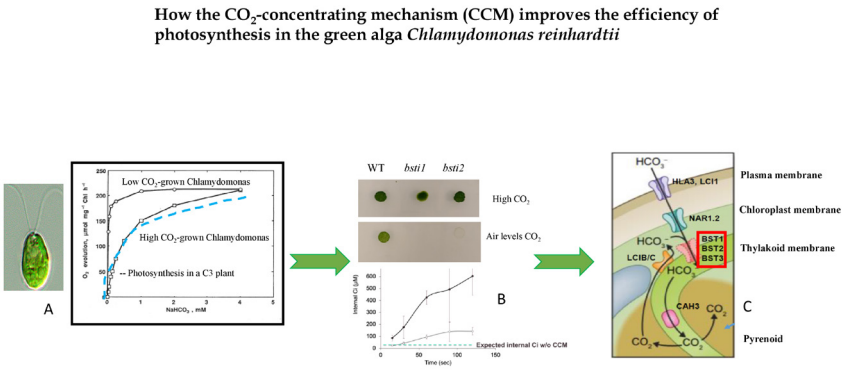
How the CO2-concentrating mechanism improves the efficiency of photosynthesis in the green alga Chlamydomonas reinhardtii

Keywords: Chlamydomonas, green algae, CRISPR, photosynthesis, carbon dioxide

Abstract:

Chlamydomonas reinhardtii is a unicellular green alga often used as a model organism. The cellular structure consists of a large chloroplast with an electron dense microcompartment called the pyrenoid. The pyrenoid is where the enzyme Ribulose bisphosphate carboxylase oxygenase (Rubisco) is localised. Unfortunately, both CO2 and the more abundant, oxygen compete for the active site of Rubisco. However, C. reinhardtii has a CO2-concentrating mechanism (CCM) that increases photosynthetic efficiency by increasing CO2 around Rubisco via a series of cellular adaptations such as bicarbonate transporters and carbonic anhydrases. Thus the higher CO2 concentration generated by the CCM increases carboxylation and lowers the rate of oxygenation. CAH3, a vital carbonic anhydrase is localised within the thylakoid lumen, meaning bicarbonate taken up by C. reinhardtii must cross three membranes (plasma membrane, chloroplast and thylakoid) to reach CAH3(Karlsson, 1998). For nearly a decade, scientists speculated over the presence of transporter proteins on the thylakoid membrane (TM). This poster will present three novel transporters on the TM and present a detailed model of the current CCM (Mukherjee, 2019). It shall also discuss what future steps can be taken, using targeted gene editing techniques like CRISPR, to characterize the algal CCM further.



Bestrophin like proteins in the thylakoid membrane of Chlamydomonas are required for maintaining a functional CCM.

References:

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2. Karlsson, J., Clarke, A.K., Chen, Z., Hugghins, S.Y., Park, Y., Husic, D.H., Moroney, J.V., & Samuelsson, G. (1998). A novel α-type carbonic anhydrase associated with the thylakoid membrane in Chlamydomonas reinhardtii is required for growth at ambient CO2. The EMBO Journal (1998)17:1208-1216

YI 03
ANJAN ROY
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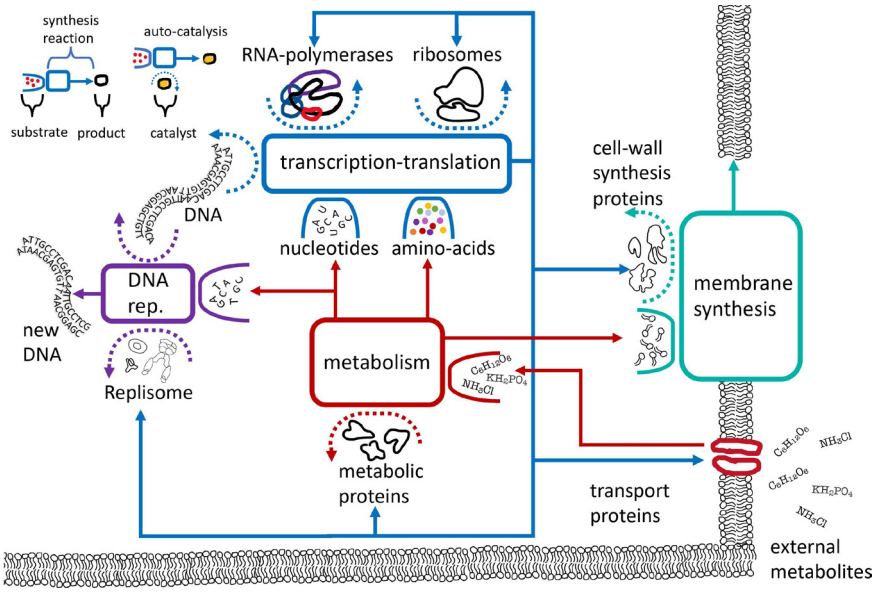
A unifying autocatalytic network-based framework for bacterial growth laws

Keywords: Theoretical biology, systems biology, bacterial physiology, autocatalysis, optimal control

Abstract:

Recently discovered simple quantitative relations, known as bacterial growth laws, hint at the existence of simple underlying principles at the heart of bacterial growth. In this work, we provide a unifying picture of how these known relations, as well as relations that we derive, stem from a universal autocatalytic network common to all bacteria, facilitating balanced exponential growth of individual cells. We show that the core of the cellular autocatalytic network is the transcription-translation machinery—in itself an autocatalytic network comprising several coupled autocatalytic cycles, including the ribosome, RNA polymerase, and transfer RNA (tRNA) charging cycles. We derive two types of growth laws per autocatalytic cycle, one relating growth rate to the relative fraction of the catalyst and its catalysis rate and the other relating growth rate to all the time scales in the cycle. The structure of the autocatalytic network generates numerous regimes in state space, determined by the limiting components, while the number of growth laws can be much smaller.



Schematic diagram of a bacterial autocatalytic network, showcasing different autocatalytic cycles coarsely grained. The top left corner shows an explanation of the graphical notation.
Credits: Roy, A., Goberman, D., Pugatch, R. (2021). A unifying autocatalytic network-based framework for bacterial growth laws. PNAS, 118(33).

YI 04
ARCHANA KUMAR
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To grow or defend: how crops decide their fate.

Keywords: Plant-insect interaction, jasmonic acid, domestication, early signaling

Abstract:

Plant and insects have co-evolved for millions of years, leading to their large numbers inhabiting earth today. Being sessile, the plant responded to the herbivores' attack through the precise perception of aggressors followed by signal transduction which leads to transcriptional reprogramming and synthesis of defense compound, whereas the lipid-derived phytohormone Jasmonic acid plays a crucial role. Early signaling components to the herbivores' attack include calcium flux, plasma membrane potential variation, reactive oxygen species production, and phosphorylation cascades. This can further lead to systemic signaling affecting parts of the plant distant from the damaged tissue. Here, systemic defense responses are one of the central mechanisms to minimize added herbivore challenges after an initial attack. Efficient plant defense imposes pressure on herbivores, which develops a way to interfere with defense mechanisms or adapt to the detrimental effect of plant toxins. In this context, relevant questions are: How do plant recognize the attacker? What defense are activated and how does this vary between population and species? How does recognition and response evolve? Can we engineer new defense capability? Here, it is also essential to know whether plants respond similarly to different types of leaf damage and feeding style. Possibly, in the process of crop domestication, we have lost some of the defense traits, which may be a precious tool for insect/ pest control. Understanding several of the above questions regulating plant and insect interaction will allow us to design future crops with enhanced defense against herbivores.

YI 05

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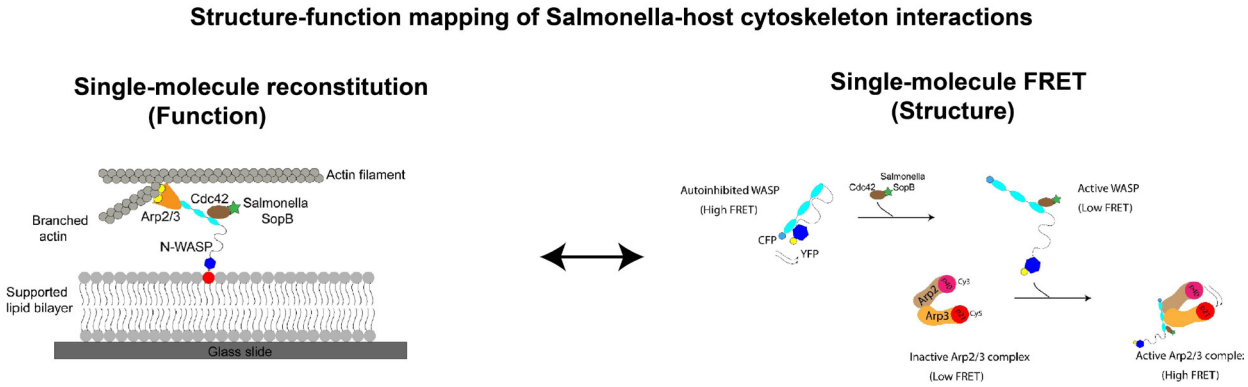
Structure-function mapping of Salmonella-host cytoskeleton interactions

Keywords: Pathogenic factors, actin remodeling, cargo transport, FRET biosensors, DNA origami

Abstract:

Salmonella hijacks the cellular cytoskeletal network by secreting pathogenic factors that mimic host cytoskeletal regulatory proteins. Although cell biological and biochemical studies have identified the key *Salmonella* pathogenic factors and their cytoskeletal targets, the structural and functional molecular mimicry mechanisms of these factors is not understood. My proposed research aims to tackle this question by implementing biophysical platforms that I have developed with the following key goals: Understanding the impact of pathogenic factors on cytoskeletal remodeling and transport through in vitro reconstitution of these processes. Dissecting the structural mechanisms of activation of cytoskeletal proteins by pathogenic factors using FRET-based conformational biosensors The fundamental hypothesis of my proposed research is that *Salmonella* pathogenic factors drive a cascade of structural activation of autoinhibited cytoskeletal proteins that in turn act on cytoskeletal filaments and motor proteins to cause filament remodeling and cargo transport respectively. The key rationale of my project is that reconstitution and protein conformational biosensors will allow us to tease apart the *Salmonella*-cytoskeleton protein interactions that are key to the hijack of cytoskeletal network. This project would impact the pathogen biology field by providing an experimental paradigm to dissect structure-function mechanisms of cytoskeletal hijack by any bacterial or viral pathogens.



Single-molecule dissection of Salmonella -cytoskeleton interaction using reconstitution and FRET biosensors. Credits: Ashim Rai

YI 06
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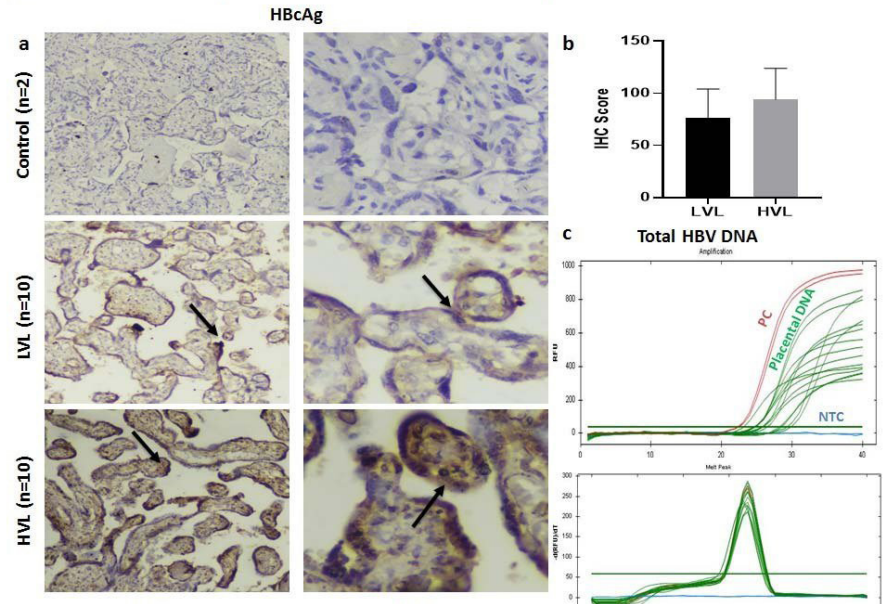
Presence of entry receptors and viral markers suggest a low level of placental replication of hepatitis B virus in a proportion of pregnant women infected with chronic hepatitis B

Keywords: Viral hepatitis, immunology, infectious disease, liver diseases

Abstract:

Background: The transplacental routes of vertical transmission of hepatitis B virus (HBV) has been known for over a decade. Here we present evidence which suggest HBV can replicate in placenta. Methods: Forty-one HBsAg positive pregnant women and 10 controls were enrolled in the study after obtaining informed consent. HBV positives were further divided in the High Viral Load (HVL) Group and Low Viral Load (LVL) Group according to INASL guidelines 2018. Presence of the HBV DNA in placenta and expression of NTCP in placenta was analyzed by qPCR/RT-qPCR and/or immunohistochemistry (IHC). Presence of cccDNA was assessed using Digital Droplet PCR while presence of pregenomic (pg) RNA was assessed through qRT-PCR and sequencing. Presence of HBeAg and HBcAg in the placenta was assessed by IHC. Results: Immunostaining of NTCP, HBeAg and HBcAg on trophoblasts along with presence of total HBV DNA, cccDNA and pgRNA indicated, that these cells are not only susceptible to HBV infection but may also support viral replication. This is further supported by the finding that trophoblasts of the several HBeAg seronegative samples harbored the HBeAg. Although, we did not find any correlation in NTCP expression and viral markers with viral load indicates placental replication may not aping hepatocytes. Conclusions: The presence of the HBV receptor, NTCP on placenta along with the presence of cccDNA, pgRNA, and HBeAg in placenta of patients without circulating HBeAg suggest that placenta act as a replication host.

Fig 1 Placenta of HBsAg positive females contains viral components



YI 07

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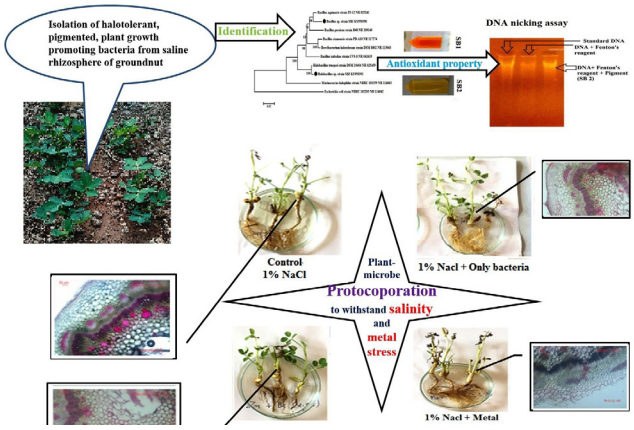
Microbes mediated rhizofiltration: A possible way to reduce metal translocation in plants

Keywords: Plant-microbe interaction, metabolomics, bioconversion, bio-imaging, bio-control

Abstract:

Contamination of heavy and transition metal in agriculturally available soil is one of the major concerns for Indian agriculture, as it interacts with cellular macromolecules resulting in losses in crop production. Plant-associated beneficial microbes produce several bioactive compounds which protect the plant from several abiotic stress. Thus exploration and methodical utilization of these microbes could augment metal stress and reduce metal translocation in plants. To evaluate bacterial rhizofiltration capability, two [Bacillus sp. and Halobacillus sp.] metal-tolerant, pigment-producing strains were characterized. The antioxidant activity of microbial pigments were assayed by DPPH and FRAP assay. GC-MS and IR spectroscopy-based identifications confirmed that SB1 produces squalene, bis-(2-ethylhexyl) phthalate and SB2 produces ethyl 2-isopropyl-2,3-ihydrofuran-3-carboxylate, methyl-undec-10-ynoate and methyl-5-oxopyrrolidine-2-carboxylate as their major pigments. In-vitro inoculation of groundnut seedlings with selected isolates under salinity (1%NaCl) and metal (Zn, Al, and Pb) stress had a positive impact on different plant physiological parameters which was correlated with PGP attributes. To evaluate microbial bioaccumulation and bioabsorption compatible algae-bacterial consortiums were developed. Scanning/Transmission electron microscopic images confirmed the biosorption and bioaccumulation of metals by algae-bacteria consortia. During the bioassay study, Sorghum seedlings were grown with bioremaidted streams showed enhanced plant growth-promoting attributes. Thus, the consortia of diverse genera of algae and bacteria can be an efficient tool for the bioremediation of various metals to reduce metal translocation in plants.



Microbes mediated rhizofiltration
Credits: Avishek Banik

References:

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YI 08
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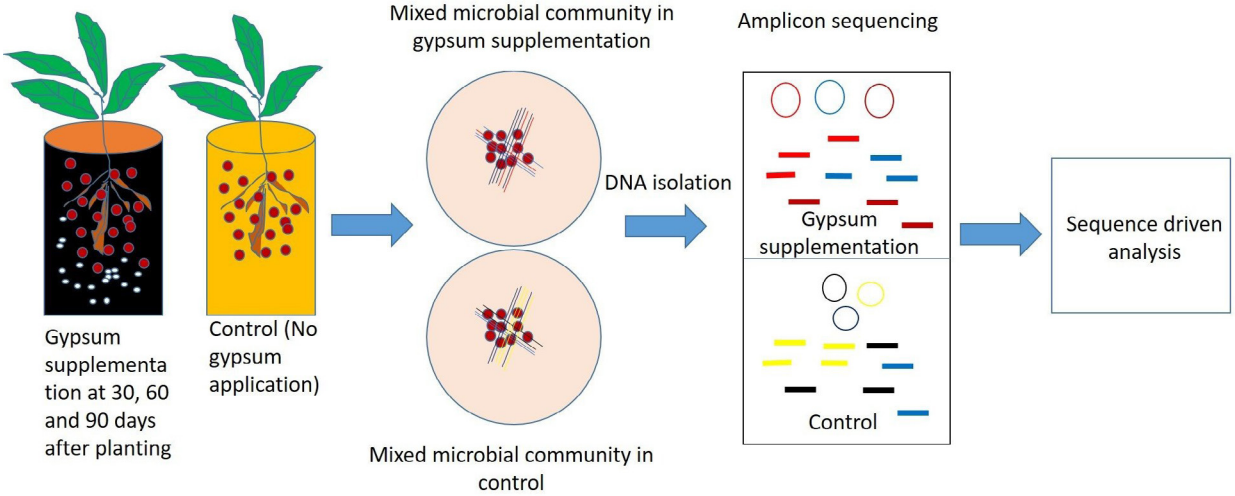
Effect of gypsum supplementation on soil microflora during peanut maturation

Keywords: Calcium signaling, abiotic stress, nutrition, developmental biology, crop improvement

Abstract:

Peanut is a unique legume owing to its geocarpic nature, i.e. the fruit develops underground. Calcium plays an important role as macronutrient in the fruit development. The geocarpic nature of peanut seed development does not allow the calcium to be supplied via roots, instead it is actively taken up by the developing fruits from the soil solution. Peanut requires a sandy loam soil, which does not hold the macronutrients properly, thus causing the nutrient deficiency very frequently. Peanut also is a nodulating legume, which relies on the nodulating bacteria for its nitrogen fixation. These factors makes it very unique for its microflora. The low levels of calcium in the soil also affects the nodulation pattern, thus affecting the soil microflora. Calcium supplementation in the form of calcium sulphate or limestone is known to ameliorate the calcium deficiency in the soil and increase the yield. The nutrient supplementation also changes the soil microflora. Studies of the microflora on such abiotic stress and its amelioration effect have been rarely addressed in peanuts. Therefore, the proposed study aims to answer, how gypsum supplementation changes the microflora composition of during peanut maturation through the metagenomics approach.



Approach for metagenomic studies on soil rhizosphere during calcium supplementation in peanuts
Credits: Bhuvan Pathak

YI 09
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The genes behind your fingerprints

Keywords: Human phenotypes, human diversity, complex traits, adaptation, selection

Abstract:

This study has been carried out by a global team of scientists where I have contributed as a co-author. Fingerprints are known to be unique to an individual and form a basis of our identification. However, these fingerprints have certain patterns that can be categorized into three types – arch, loop, and whorl. To understand the genes responsible for this fingerprint patterning, the team studied DNA from more than 23000 individuals from different ethnic groups and identified 43 genetic loci contributing to fingerprint patterning. Interestingly, they found that most of these genetic loci are from the genes involved in the limb development pathways rather than genes related to skin development. One of the topmost genes identified was EVI1, which has been known for its role in embryonic limb development. When the team further tested using mouse models of EVI1, they found that genetically modified mice with decreased expression of EVI1 developed abnormal skin patterns on their digits compared to the wild-type normal mice. Furthermore, the study also revealed the correlation of fingerprint patterns with hand proportions. For example, people with whorl-shaped fingerprints on both their little fingers tend to have longer little fingers than those who don't. This is one of the most comprehensive study on genetics of fingerprint patterns and studies like these help us to understand better the existing human phenotypes or how we vary from each other.

Human fingerprint patterns vs mouse ridge patterns
Credits: Chandana Basu

YI 10

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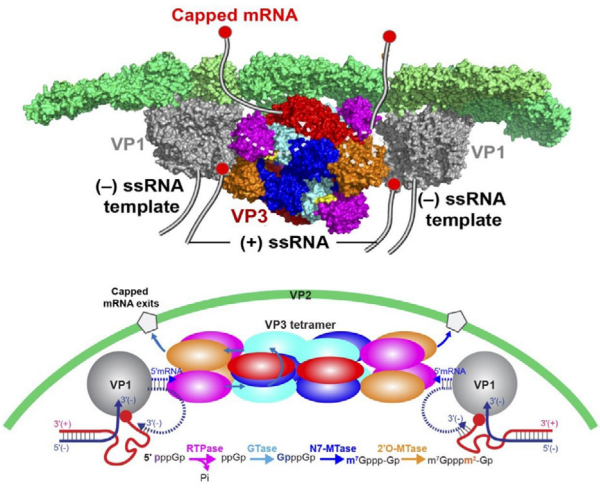
Structure guided design of novel antiviral strategies against pathogenic RNA viruses

Keywords: Structural biology, virology, RNA viruses, infectious disease, structural bioinformatics

Abstract:

RNA viruses include many human viral pathogens (~180 species). These are primarily of animal origin, and several have spilled over into human populations causing outbreaks, epidemics, and pandemics. In first two decades of the 21st century, several RNA viruses outbreaks have occurred. These include SARS-CoV (2003), Influenza (2009), MERS-CoV (2012), Ebola (2014), Zika (2015), and ongoing COVID-19 pandemic. There are no effective antivirals or vaccines available for many of these viruses. The insufficient understanding of zoonotic transmission and cumbersome process of vaccine development necessitates the demand for exploring alternate strategies to mitigate future outbreaks. The neutralizing monoclonal antibodies (mAbs) have shown their therapeutic/diagnostic potential against viral infections. Neutralizing mAbs are also critical for designing antigenic epitopes for developing next-generation vaccine candidates. The heterogeneity in viral mRNA capping is another avenue that has been largely ignored due to complexities of capping process. Advances in cryo-EM/cryo-ET methods allow us to explore the atomic details viral mRNA capping assemblies.

My group will be focusing on two broader themes: 1). Characterizing the complex structures of neutralizing monoclonal antibodies against pathogenic RNA viruses in complex with viral antigens or virus-like particles (VLPs) by using X-ray crystallography and cryo-EM. We will harness the information gathered from structures of Ag-Ab complexes to engineer potent inhibitors and test their efficacy in cell culture and animal models (collaboration with the Kumar Lab at IAV, Kerala). 2). For viral capping machineries, we will reconstitute viral transcription complexes and capture the capping process using single particle cryo-EM. We will also employ structure prediction tools to predict the structures of homologs from related species to address the heterogeneity in the viral capping assembly. My group will be using an integrated approach from structural, biophysical, and computational biology to explore antibody-based therapeutics and antiviral strategies targeting viral transcription complexes against pathogenic RNA viruses.



YI 11
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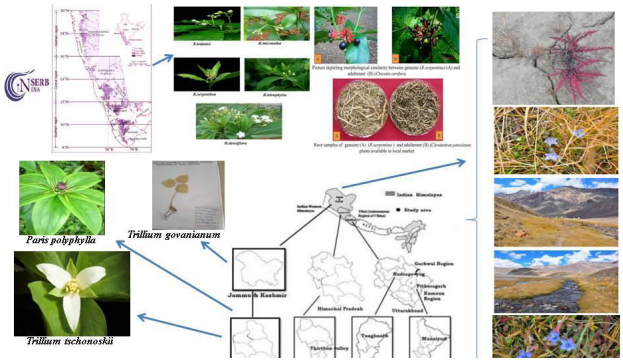
Application of DNA Barcoding, NGS & 'OMICS' Technologies for Plant Diversity Assessment, Authentication, Molecular Phylogeny and Cryptic Species Taxonomy

Keywords: Biodiversity conservation, cryptic species, metabolomics, DNA barcode, molecular authentication of medicinal plants

Abstract:

I am now concentrating on ecologically significant, medicinally, or taxonomically relevant plant species. My attempt is to explore the possibilities of technologies like DNA barcoding or sequencing or various 'omics' approaches to resolving species conservation-related issues (Wu et al., 2021; Tiwari and Rajwanshi 2022; Murua et al., 2020; Mosa et al., 2019; Nazar et al., 2022). The findings of my research were published in renowned journals like Fitoterapia, Industrial Crops and Products, and Plant Systematics (Nair et al., 2014; Nair et al., 2013a; Nair et al., 2012; Nair et al., 2013b). Currently, I am working mainly on two externally funded projects. UGC-funded project is on the "Genetic Diversity Assessment and Molecular Authentication of Endemic Himalayan Medicinal Plant Species Trillium govanianum (Wall.ex D.Don) kunth. using DNA Barcode. The second project is DST-SERB funded entitled "Molecular Authentication of Rauvolfia species from Southern Western Ghats of India Using DNA Barcoding". We found that in the market sample of Rauvolfia, samples of Chassalia curviflora or Clerodendron paniculatum were used as adulterants because of easy availability or morphological similarity (Nair et al., 2013). Molecular authentication or the development of molecular markers will help trace these adulterants even in processed samples. The ongoing work proposes to distinguish cryptic species (R.beddomei and R.micrantha) or to elucidate molecular phylogeny. My future research plan includes the documentation and metabolome profiling of flora from the high-altitudinale cold desert of the Himalayas. I also intend to develop DNA barcode details and data depository for medicinally or ecologically relevant flora from the least explored areas like high altitude cold deserts like Leh –Ladakh of the Himalayas or of the North Eastern Regions or the Andaman Nicobar Islands. My future research plans also include the application of modern sophisticated technologies of sequencing or in-silico analysis to resolve taxonomic disputes on plant species.



Application of DNA Barcoding, NGS & 'OMICS' Technologies for Plant Diversity Assessment, Authentication, Molecular Phylogeny and Cryptic Species Taxonomy
Credits: Divya Nair

YI 12

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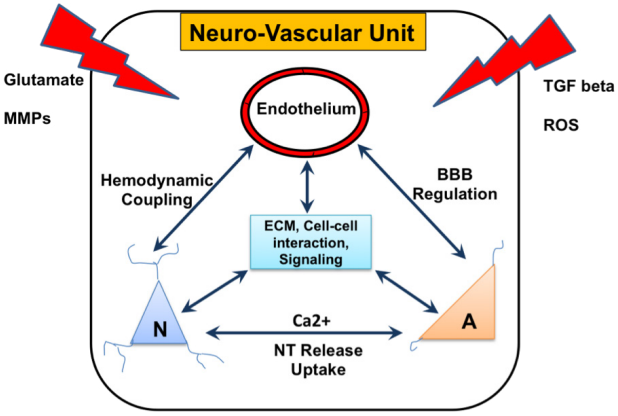
Ligand receptor analysis of brain cell type marker data reveals intricate neurovascular Interaction

Keywords: Neurobiology, neurovascular unit, hypertension, hraumatic brain injury, intracellular network

Abstract:

The brain is equipped with multiple cell types that work together to sustain its function. Notably, the interaction within the neurovascular unit, a functional unit in the brain, is critical for physiology and pathology in the brain. The neurovascular unit comprises the intercellular communication of vascular cells with neural cells, astrocytes, oligodendrocytes, and microglial cells. However, the extent of communication between these major cell populations is an ongoing area of research far from being totally mapped. Utilising expression data of ligand-receptor pairs in each brain cell type from a marker gene study, we built a cell-cell communication network within the brain neurovascular unit. The research not only replicates previously functionally established ligand-receptor pairs in intercellular communication, but it also provides novel interactions between brain cells. Besides paracrine signalling between brain cells, our analysis reveals that autocrine signalling occurs in a significant proportion in each cell type in the brain. The study also supports the multidimensional nature of neurovascular unit signalling where each cell communicates extensively in a bidirectional manner with endothelial cells in the brain and is involved in an interaction network. Together, the results of this study show how the brain's neurovascular unit talks to each other in physiological conditions and acts as a resource for the testable hypotheses in brain cell-cell communication.



Neurovascular interaction between various cells of brain including N(Neuron), A(Astrocytes),microglia and endothelium in known physiological condition. The poster shows new approach in understanding this interaction using cell specific ligand and receptor gene expression.
Credits: Gaurav kumar

YI 13
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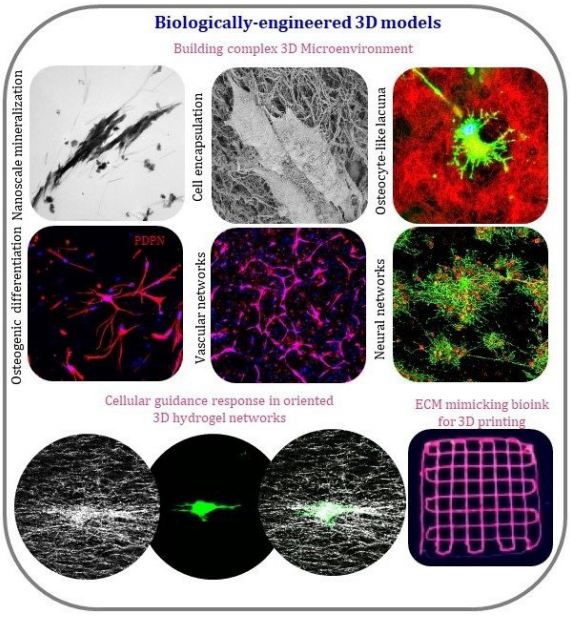
Biophysical control of 3D tissue microenvironment for health & diseases

Keywords: Regenerative medicine, microphysiological systems, bioelectronic medicine, engineered tissue/ organ equivalents, stem cells

Abstract:

From a tissue engineering perspective, recreating a culture environment that closely mimic the native tissue, which include a cellular component, matrix component and a vascular component is highly desirable to replicate the structure and intricate functions of tissues. Despite significant progress on the engineering of complex tissues and organoids in the lab, in-vitro model systems that replicate such a fundamental characteristic of tissue have remained virtually non-existent thus far. My research encompasses a multifaceted approach that integrates tools from biomaterial fabrication, stem cell biology, nanomaterial technology and physical stimulation to develop culture additives/conditions appropriate for tissue homeostasis, development and regeneration in-vitro. Part of my research focuses on the fundamental understanding of how tuning the physical properties (stiffness, conductivity, topography, orientation etc) of the underlying matrix influences the fate of healthy and diseased cells. Identifying these complex cell-matrix interaction mechanisms are critical to design tissue equivalents as well as to therapeutically target these pathways to inhibit disease progression. Overall, these findings have important implications for research on regenerative medicine, drug discovery, and as model to study tissue physiology and disease.



Schematic overview illustrating the development of functional, and predictive 3D tissue model systems for regenerative engineering
Credits: Greeshma Thrivikraman

YI 14

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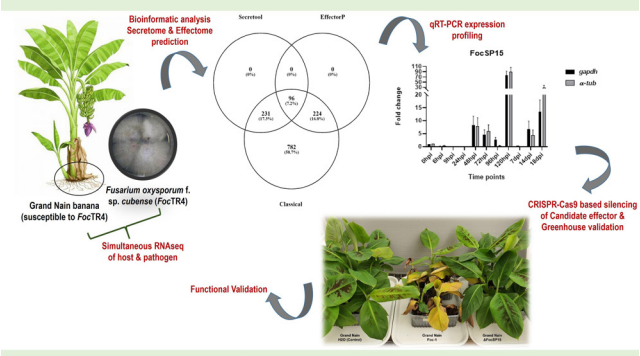
Transcriptome analysis and effectome of vascular wilt pathogen Fusarium oxysporum f. sp. cubense tropical race 4 (TR4), causing Panama disease in banana

Keywords: Plant-pathogen interaction, effectors, fungi, phylogenetics, plant pathology

Abstract:

Members of the Fusarium oxysporum species complex can cause disease in over 120 plant genera including many agriculturally important crops. Banana (Musa spp.) is one of the most popular exported fruits and serves as a staple diet for millions of people worldwide (Ploetz, 2015); with an annual approximate global production reaching 114 million tons, totalling a gross value of about US$8 billion per year (FAOSTAT, 2022). Banana production is severely affected by the Fusarium oxysporum f. sp. cubense (Foc), tropical race 4. Despite the economic importance of the panama disease, the molecular mechanisms governing the plant-pathogen interactions remains poorly understood. Secreted effector proteins are virulence factors that are encoded by fungal avirulence genes, and function by suppressing the host plant defense response. To identify the candidate effector proteins, we sequenced the transcriptome of banana roots infected with FocTR4 and bioinformatically predicted the secretome and effectome. Selected candidates were functionally validated using CSISPR-Cas9 based reverse genetics approach. This study identifies an important secreted effector involved in virulence of the FocTR4.

In future, comparative profiling of effectome of various F. oxysporum species will be initiated to reveal conserved effectors that would be significant candidates in developing resistant crops.



Schematic representation of identification and characterization of effectome of Fusarium oxysporum f. sp. cubense tropical race 4 (TR4) causing Panama disease in banana. Credits: Gunjan Sharma

References:

1. Ploetz, RC. 2015. Management of Fusarium wilt of banana: a review with special reference to tropical race 4. Crop Protection 73: 7-15.
2. FAOSTAT 2022. https://www.fao.org/faostat/en/#home.

YI 15
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Postmortem lung tissue from COVID-19 patients suggests two distinct trajectories driving mortality

Keywords: Functional genomics, single cell and spatial transcriptomics, RNA Biology, genetics, bioinformatics

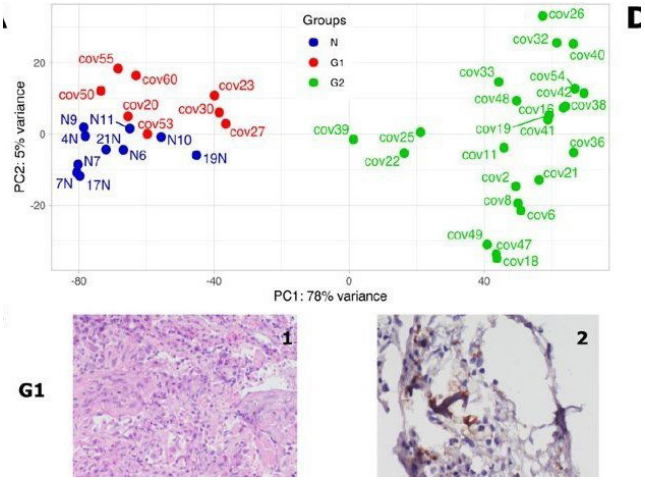
Abstract:

We have recently concluded the largest molecular study on lung tissue autopsies of patients succumbing to severe COVID-19 infection at AIIMS New Delhi. Tissues from over 30 patients from the devastating second wave and analyzed using molecular imaging and RNA-sequencing.

The study revealed three novel findings. First, COVID-19 patients were divided into 2 distinct subtypes at the level gene expression changes– about 1 in 4 patients had suppressed inflammation similar to healthy lung tissue taken from lung cancer patients while the remaining patients had a dramatic inflammation marked by upregulation of the complement system and unfolded protein response as is commonly observed in viral infection. These patients were marked by a distinct set of circulating chemokines such as CCL19 and CCL16, which may help in patient stratification by quantifying these in blood.

Second, using a novel technique called single-cell deconvolution, the researchers at IIT Delhi were also able to identify which specific cells may be responsible for differences between the two patient subtypes. This information complemented with in-silico drug screening performed by the researchers will enable the development of novel therapeutic interventions for COVID-19 infection targeted to the culprit cell-type.

Third, the two sets of patients had dramatically reduced resident lung microbiota with opportunistic pathogens such as Staphylococcus cohnii being associated with the major subtype of patients. This suggests precision intervention targeting the exact pathogen using specific antibiotics joining the chorus of investing in genomics based global health for all. Besides characterizing the change in lung resident microbiota or whole metagenome in COVID-19 patients from India for the first time, the investigators also recovered the complete genome of COVID-19 virus from the lungs of three patients . Each of these viruses were distinct but all belonged to the B.1.36 or the Delta variant lineage.



Two many ways to die of COVID-19
Credits: Anshul Budhraja

YI 16

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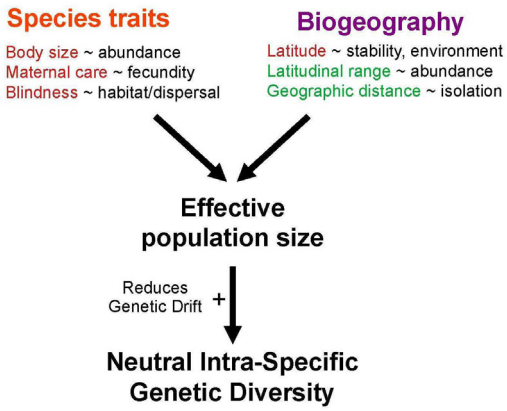
What are the drivers of genetic diversity in soil predatory arthropods?

Keywords: Ecology, evolutionary biology, biogeography, molecular phylogenetics, tropical forests

Abstract:

Intra-specific genetic diversity is an important component of biodiversity, as it informs on ecological and evolutionary processes shaping populations. We investigated its drivers in centipedes, an ancient group of soil arthropods with low dispersal ability, showing variation in species traits and biogeography. Using a collated dataset of over 1200 mitochondrial cytochrome c oxidase subunit I sequences, we found a wide variation in genetic diversity (0-0.1713) across 120 species representing all centipede orders. Over a fifth of this variation was explained by species traits and biogeography. Genetic diversity was higher in centipedes which were smaller in body size, showed maternal care, were distributed at lower latitudes and were separated by greater distances. Centipedes show relatively high genetic diversity among arthropods, which fall at the higher end of values among animals. However, the correlates of genetic diversity in centipedes, related to ecological strategy and latitude, are congruent with other well-studied taxonomic groups.



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

Credits: Jahnavi Joshi

YI 17
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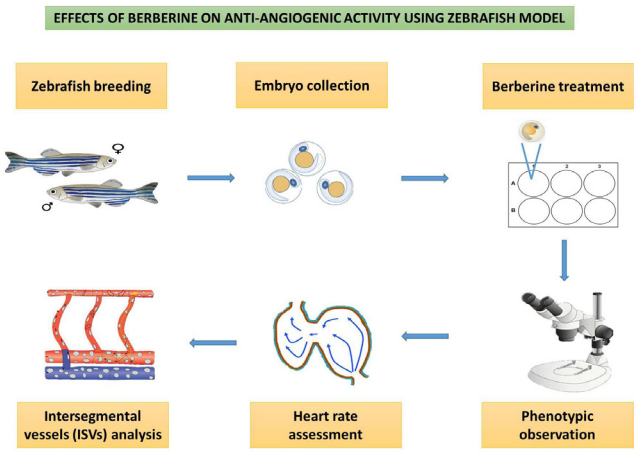
Effects of berberine on anti-angiogenic activity using zebrafish model

Keywords: Angiogenesis, hemodynamics, zebrafish, phytochemicals, berberine.

Abstract:

Angiogenesis is fundamental to several normal and pathological processes such as wound healing and tumor growth and it is therefore an important therapeutic target. Hemodynamics is the study of the effects of pulsatile blood flow on the blood vessels that carry blood and lymph. The mechanisms that regulate angiogenesis and the role of hemodynamics in vascular development are poorly understood. The present study aimed to screen the anti-angiogenic activity of berberine and also its effect on hemodynamics in the zebrafish model. The zebrafish is an established and commonly used experimental model for studying cardiovascular systems and functions. Blood vessel formation could be easily observed, and blood flow measurement is easy in zebrafish embryos. Embryos treated with various concentrations of berberine (0.01–1 mM) at 1-hour post-fertilization (hpf) generated a series of phenotypic variants with abnormal blood vessels, tail bending, edema, and hemorrhage. At higher doses, survival rates were much reduced, but hatching rates appeared to be normal. Heart rate is an important parameter that has a significant relationship with hemodynamics. Heart rate analyses were conducted in ImageJ software with prior processing of recorded videos. The obtained plot reveals a considerable drop in heart rate with increasing berberine content. There is a significant reduction in inter-segmental vessels (ISVs) in embryos treated with berberine. From these findings, we suggest that berberine may be an efficient drug for inhibiting angiogenesis in vivo and may be beneficial in the treatment of vascular diseases and cancers in future.



Effects of berberine on anti-angiogenic activity using zebrafish model
Credits: Rabiathul Shameera

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YI 18
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Thiol antioxidants activate the hypoxia response pathway

Keywords: Cellular stress responses,,Innate immunity, C. Elegans, host-microbe interactions,aging

Abstract:

The thiol antioxidants dithiothreitol (DTT) and β-mercaptoethanol cause stress in the endoplasmic reticulum (ER) by disrupting its oxidative protein folding environment, which results in the accumulation and misfolding of the newly synthesized proteins. These thiol antioxidants may potentially impact cellular physiology by ER-independent mechanisms; however, such mechanisms remain poorly characterized. Using the nematode model Caenorhabditis elegans, we show that DTT and β-mercaptoethanol modulate the methionine–homocysteine cycle by upregulating an S-adenosylmethionine (SAM)-dependent methyltransferase, rips-1 (Gokul and Singh, 2022). The upregulation of rips-1 on the thiol antioxidants was the reason for the toxicity of the thiol antioxidants. In order to understand why and how the thiol antioxidants caused the upregulation of rips-1, we carried out genetic screens to isolate mutants that had constitutive upregulation of rips-1 even in the absence of the thiol antioxidants. We discovered that rips-1 is highly upregulated in mutants that have constitutive activation of the hypoxia response pathway. On the other hand, DTT-mediated upregulation of rips-1 was fully blocked in mutants defective in hypoxia response. We demonstrate that DTT exposure results in the activation of the hypoxia response pathway, and the SAM-dependent methyltransferase rips-1 is one of the hypoxia response pathway genes. In light of our results, the physiological effects of thiol antioxidants DTT and β-mercaptoethanol, which are broadly considered ER-specific stressors, need to be reconsidered now.

References:

1. G G & Singh J. 2022. Dithiothreitol causes toxicity in C. elegans by modulating the methionine–homocysteine cycle. eLife 11: e76021.

YI 19

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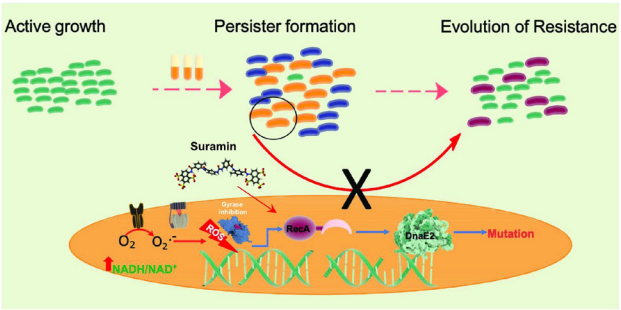
The error-prone polymerase DnaE2 mediates the evolution of antibiotic resistance in persister mycobacterial cells

Keywords: Mycobacterial reactivation, iron homeostasis, antimicrobial resistance, mycobacterial biofilm, drug repurposing

Abstract:

Application of antibiotics to susceptible bacterial culture generates a minor population of persisters that remain susceptible to antibiotics but can endure them for extended periods. Recently, antibiotic persisters (APs) of mycobacteria were reported to experience oxidative stress and develop resistance when treated with lethal doses of ciprofloxacin or rifampicin. However, the mechanisms driving the de novo emergence of resistance remained unclear. In the present study, we demonstrate that mycobacterial APs activate the SOS response causing up-regulation of the error-prone DNA polymerase DnaE2. The sustained expression of dnaE2 in APs resulted in the rapid evolution of resistance to antibiotics and negatively impacted the proliferation of APs during the recovery phase. Inhibition of RecA by suramin, an anti-Trypanosoma drug, decreases the conversion rate of persisters to resistors in a diverse group of bacteria. Our study highlights suramin's novel application as a broad-spectrum agent in combating the development of drug resistance.



Mechanism of antibiotic induced drug-resistance in Mycobacterium smegmatis
Credits: Krishna Kurthkoti

YI 20
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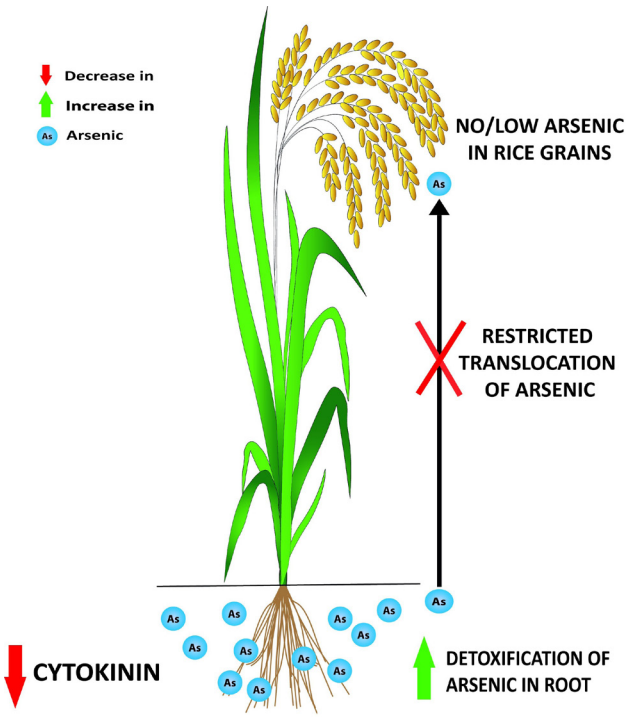
The intervention of phytohormone to reduce arsenic accumulation in rice grains

Keywords: Arsenic, phytoremediation, parthenium, tissue culture, abiotic stress

Abstract:

Arsenic (As) is an environmental and food-chain toxin. It is poisonous to all living organisms. Arsenic contamination in groundwater is a major problem in nearly 21 countries affecting more than 100 million people worldwide. Arsenic enters the food chain through the usage of arsenic-contaminated water in agriculture. In nature arsenic exists mainly in two inorganic forms; Arsenate [As(V)] and Arsenite [As(III)]. As(V) is the most abundant form of arsenic and is structurally similar to phosphate (Pi). Therefore, it is easily incorporated into plant cells through Pi transporters. The As(V) inside the cell quickly reduces to As(III) as a defence mechanism. Then, the reduced As (III) is either extruded out of the root cells or complexed with phytochelatins and sequestered into vacuoles.

Sequestration of the As(III)–thiol complexes in the root vacuoles is important in reducing the root-to-shoot translocation of As in A. thaliana. Our previous results in model plants showed that a reduction in the plant hormone cytokinin improves arsenic tolerance and accumulation in Arabidopsis and Tobacco (Mohan et al., 2016). Based on this result, towards the development of safe crops in the current project, we are developing transgenic rice to specifically reduce cytokinin in rice roots to enhance the detoxification ability of the plant and to reduce root-to-shoot translocation. With our novel strategy, we expect to significantly reduce the accumulation of arsenic in rice grains.



Strategy to reduce arsenic accumulation in rice grains
Credits: Ajay R Bhat

References:

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YI 21
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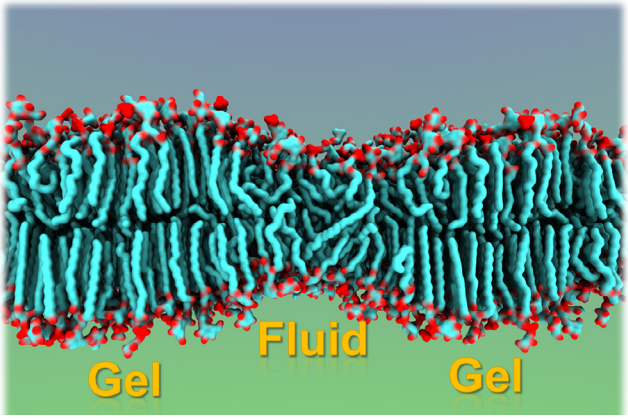
Phase transition in atomistic simulations of thylakoid membrane of red algae: Lipids in temperature adaptation

Keywords: Theoretical and computational biophysical chemistry; structure, organization, and dynamics of the cell membrane and membrane proteins; thermal adaption and the transport mechanism of marine algae, lipid modulation of receptors' conformation/function; drug-membrane interactions

Abstract:

Marine macroalgae have extensive applications in the pharmaceutical and nutraceutical industries. Temperature strongly impacts algal photosynthetic activities occurring at chloroplast thylakoid membranes. At the cellular level, the change of temperature is reflected in the oscillating algal lipid/fatty acid profile and inhibition of photosynthetic activities. The function of the thylakoid membrane system is intimately dependent on its lipid matrix, however, the molecular organization of these lipid membranes and particularly their adaptive arrangements under temperature stress remain largely unexplored. The present work employing extensive atomistic simulations provides the first atomistic view of the phase transition and domain coexistence in a model membrane composed of thylakoid lipids of a marine red alga, between 10-40 °C. The computational work demonstrates that a model algal thylakoid lipid membrane is in a gel-like state at cold (10-15 °C) and fluid-state at hot (40 °C) conditions. Within the intermediate physiological temperature range, the coexistence of gel-like and fluid-like domains is clearly evident with the preferential segregation of lipids. Incorporating cholesterol as a well-known fluidly modulator, suppress the gel-to-fluid phase transition and phase separation. The work improves our understanding of the effect of temperature on the properties and organization of the thylakoid lipid membrane, known to be important in maintaining the stability of photosynthetic apparatus and algal response to temperature stress.



Gel/fluid phase coexistance
Credits: MM

YI 22
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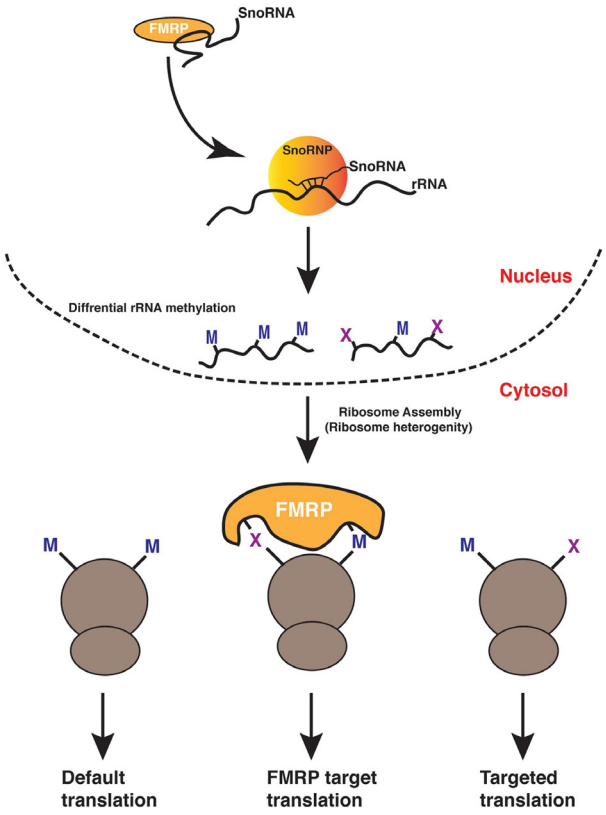
Role of FMRP in regulating the 2'O methylation in human embryonic stem cell and its differentiation

Keywords: Ribosome, RNA, translation, epitranscriptome modification

Abstract:

Ribosomes are macromolecules present in the cell and are an integral part of the translation machinery. There are many reports suggesting ribosomes are heterogeneous. Factors contributing to this may arise from rRNA and proteins. Here we are interested to understand how the absence of FMRP brings the changes in the 2'O methylation in human embryonic stem cells and their differentiation. 2'O methylation on rRNA is carried out by C/D box snoRNA and mediated by methylate transferase-fibrillarin. To understand the differential methylation of rRNA during differentiation along the neuronal lineage, we differentiated the human embryonic stem cells into neurons. Total RNA was alkaline digested and 2'O methylation positions are mapped by ribometh sequencing. Interestingly, we found more heterogeneity in the 2'O methylation in the embryonic stem cells (pluripotent state) than in the neuronal state (terminally differentiated). This data provides new insight into how rRNA 2'O methylation can contribute to defining the stemness of a cell. Mapping of 2'O methylation positions across the 80S ribosome suggests positioning around the PTC and possible translation regulation. We have also observed the major difference in methylation pattern in wildtype and Fmr1 KO in stem cell state rather than at neuronal state. We hypothesize that the presence of FMRP brings more heterogeneity in the stem cell state than in the neuronal state. Overall this study brings a new concept of ribosome heterogeneity and defines the role of FMRP in embryonic stem cells and their differentiation.



YI 23
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Classification of Electrical Status Epilepticus in Sleep (ESES) based on EEG patterns and spatiotemporal mapping of spikes

Keywords: Epileptic encephalopathy, ESES, CSWS, electrical source analysis, voltage mapping, EEG synchronisation

Abstract:

Objective:
1. Describe and classify EEG patterns in ESES
2. To sub classify EEG patterns in ESES by analysis of spikes using spatio-temporal mapping and electrical source analysis.

Methods: Overnight EEG (minimum 8hrs) of 30 children aged 2-12 years with ESES (Spike-Wave index at least 50%) selected. Average reference montage used for dipole analysis and mapping. The location and orientation of the dipoles determined by mapping positive and negative poles and applying the rules of mapping. The onset, propagation of the spikes and the latency between two hemispheres (in bi-synchronous spikes) are determined (source analysis with BESA research 7.1).

Results: 1. ESES classified in to "generalised" (80%) and focal (20%) patterns. 2. The Bi-synchronous subtype in "generalised" pattern is due to apparently synchronous bilateral activation of spikes (with lead-in of 20-60ms from one hemisphere) with a tangential/oblique dipole. Source analysis localised these spikes around peri-rolandic cortex 3. The classical description of ESES spikes as "diffuse" spikes with bi-frontal maxima is a misinterpretation in 10-20 EEG system. By using voltage mapping and source analysis, we found cortical activation in the Rolandic cortex which impart diffuse frontal negativity and parieto-occipital positivity. 4. ESES spikes have intraspike and inter-spike dipole instability and changing orientation of dipoles due to local spike propagations around the source and into depth of sulcus (authors name this "Dancing-Dipoles"). 5. Focal ESES seen as Parietal, Occipital and Tempero-occipital patterns. Frontal ESES pattern was not seen.

Significance: By detailed mapping and source analysis in ESES we successfully reinterpreted various misconceptions in literature. Classification of ESES makes the interpretation of these complicated EEG patterns simpler inorder to extract the primary and propagated sources. As the dipole is always stable in Self limited CECTS, authors believe that the phenomenon of intrinsically unstable dipole phenomenon is a reliable qualitative EEG marker of ESES.

YI 24
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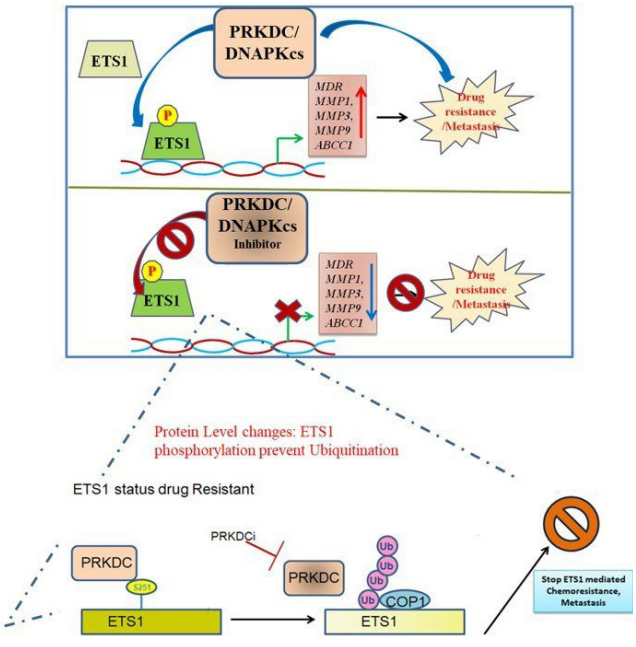
ETS1 is the key to acquired resistance and metastasis in Triple Negative Breast Cancer

Keywords: Refractory cancers, transcription factor regulation, functional genomics, posttranslational modifications, translation biology

Abstract:

Triple Negative Breast Cancer (TNBC) accounts for ~15 to 20% of all breast cancer and is often overrepresented in premenopausal and African-American women (1). Due to absence of hormone receptors, first line chemotherapy mostly results in drug resistance, metastasis and subsequent lethality (2). Although polychemotherapies and immunotherapy has shown promising aspects, the debate regarding evolution of drug resistance and metastasizing residual disease post treatment remains unresolved (1,3-4). In this regard, oncogenic transcription factor ETS1 which is specifically expressed in TNBCs (basal grade) has been implicated in metastasis and angiogenesis of TNBCs and can provide a key drug target (5).

To disseminate ETS1's role in evolution of chemoresistance and metastasis we developed drug-resistant TNBC cell lines model after prolonged exposure to clinical chemotherapeutic 5'Fluorouracil. We observed significant increase in ETS1 protein levels associated with high IC50 and migration capabilities in the resistant cells which was abrogated on silencing ETS1 expression. Gene set enrichment analysis of our resistant cells indicated significant enrichment in EMT, angiogenesis and xenobiotic metabolism pathways indicating acquired resistance and metastatic behavior. Due to heightened DNA damage, we speculate repair kinases to play a critical role in acquired resistance. We identified DNA-dependent Protein kinase, DNAPKcs(akaPRKDC) that can regulate stability and function of ETS1 protein during acquired resistance. DNAPKcs inhibition results in proteasomal degradation of ETS1 leading to decreased migration and increased apoptosis. Further, we identified DNAPKcs-dependent phosphorylation of ETS1 at residue Serine251 to be critical for its stability, function and development of resistance phenotype. Surprisingly, we were able to detect ETS1-S251 phosphorylation in chemo-refractory TNBC patient samples indicating the possibility of an evolving biomarker in context to therapy-resistant patients. Our findings suggest that chemo-resistant TNBC resulting from altered ETS1 function can be targeted using DNAPKcs inhibitor. PMID:35987766, 2) PMID:32517735, 3) PMID:32507668, 4) PMID:35181659, 5) PMID:26392377



Tug Of War: Phosphorylation of ETS1 regulates chemoresistance and metastasis in TNBC
Credits: Nirmalya Sen

YI 25
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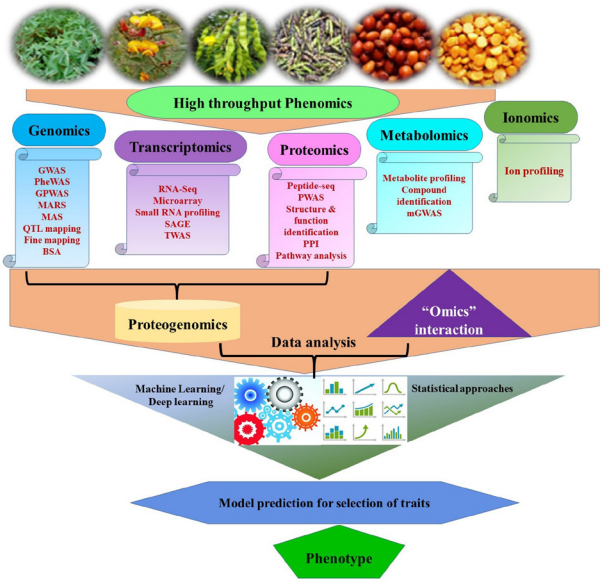
Identification of novel genes/ QTLs for seed quality and nutrition traits in pigeonpea for sustainable protein source

Keywords: Genomics, proteomics, bioinformatics, genome wide, association analysis, machine learning

Abstract:

Ever-increasing pigeonpea consumption as a major source of protein necessitates the improvement of varieties for more efficient production. The nutritional value enrichment of pigeopea is very much essential to reduce malnutrition of developing countries in the post green revolution era. To utilize its potential, a coordinated and comprehensive evaluation of germplasm is required. Identification of potential genes/alleles governing complex traits of seed quality and nutritional content such as seed weight, seed colour, total protein content (TPC), amino acid and resistance starch are essential in marker-assisted breeding for quality trait improvement of pigeonpea. The current gain in knowledge on the seed quality and nutritional value related genes and QTLs will help into develop desired genotypes for the humankind. Therefore, the present study on the profiling for the first-time to understand these complex genetic architectures of qualitative and quantitative traits in pigeonpea. For GWAS (genome-wide association study), high-throughput genotyping information of 62K SNP "CcSNPnks" genic chip genome-based SNPs discovered from 45 diverse varieties of pigeonpea utilized. The chip comprises total 62,053 SNPs from 9629 genes belonging to five different categories, including 4314 single-copy genes unique to pigeonpea, 4328 single-copy genes conserved between soybean and pigeonpea, 156 homologs of agronomically important cloned genes, 746 disease resistance and defense response genes and 85 multi-copy genes of pigeonpea. Our analysis revealed that the average protein content carrying genotypes are DG(RG)45, AKPR -324, MC-99, UP-73 and BRG-2 (16.8, 19.3, 21.5, 24.7, 30.3 gm). This led to identification of most effective genomic loci (genes) associated with seed quality and nutritional content in pigeonpea from diverse sets of wild and cultivated genetic backgrounds. The informative functionally relevant molecular tags scaled down essentially have potential to accelerate marker assisted genetic improvement by developing seed quality and nutritionally rich pigeonpea cultivars.



Systematic representation for the development of nutritional dense pigeonpea varieties through integrated Omics approaches.
Credits: Systematic representation for the development of nutritional dense pigeonpea varieties through integrated Omics approaches

YI 26

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Molecular mechanisms underlying social isolation stress in Drosophila

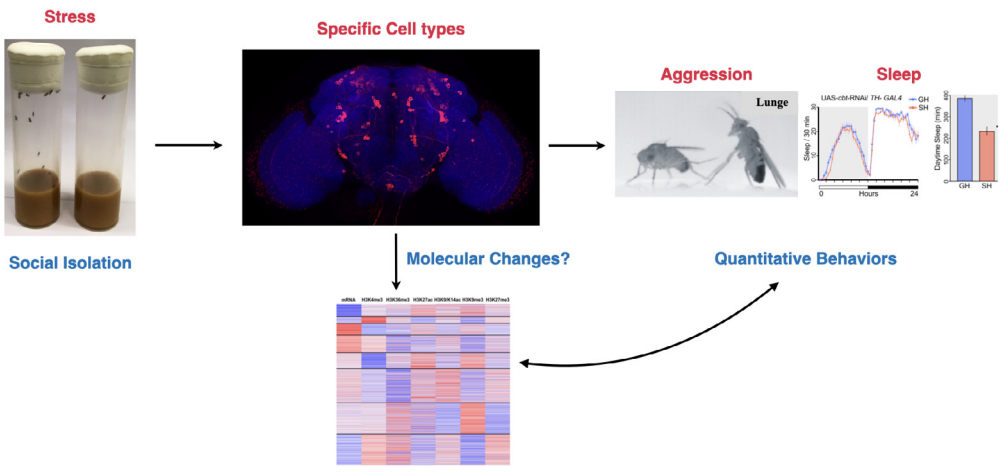
Keywords: Neuroscience, behavior, Drosophila, epigenetics, genomics

Abstract:

Social isolation is stressful and profoundly alters behaviors as observed globally during the lockdowns induced by the recent CoVID19 pandemic. Social isolation has been shown to disrupt multiple behaviors across animal kingdom including sleep, violence, feeding, mental health etc. Given the public health problem posed by social isolation it is important to understand responsible molecular mechanisms.

To approach this problem my group is using fruit fly Drosophila melanogaster as a model. Social isolation in Drosophila, similar to mammals, induces robust changes in behaviors including aggression and sleep. My earlier work has identified both whole brain and cell-type-specific transcriptional and epigenetic changes in Drosophila using cutting-edge genomic methods. Insights gained from these approaches were combined with high-throughput quantitative behavioral assays to identify causal mechanisms in the brain that shape these behaviors. RNA-seq and subsequent behavioral assays revealed a neuropeptide Dsk whose modulation alters social isolation induced aggressive behavior. To identify cell-type specific changes due to social isolation we developed 'mini-INACT' method, which helped us purify ~100 dopaminergic neurons/brain (<0.1% of total neurons). This enabled identification of epigenetic signatures in dopaminergic neurons due to social isolation vs. enrichment.

Here, I will present our latest findings from optogenetic, and machine vision based behavioral assays which reveal how neuropeptide Dsk regulates behavioral changes due to social isolation. I will also present our work on cell type specific epigenetic modulation that will help identify causal relationship between epigenetic changes and altered behaviors induced by social isolation.



YI 27
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A comparative meta-analysis of membraneless organelle associated proteins with age related proteome of C. elegans

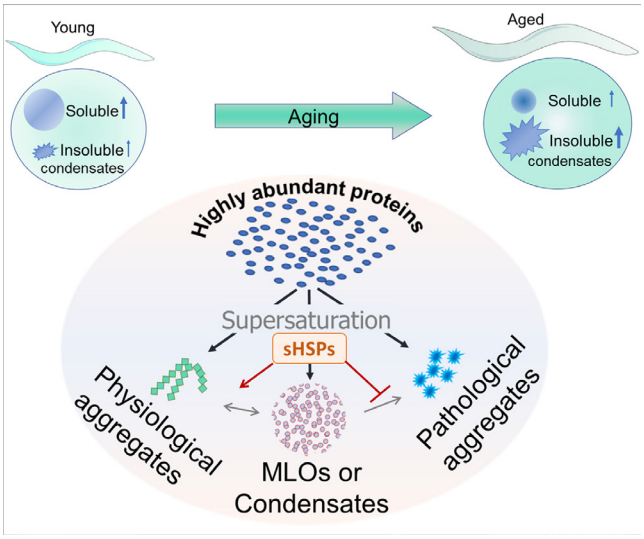
Keywords: Proteostasis, aging, liquid liquid phase separation, protein aggregation, *C.elegans*

Abstract:

Proteome imbalance can lead to protein misfolding and aggregation which is associated with pathologies. Protein aggregation can also be an active, organized process and can be exploited by cells as a survival strategy. In adverse conditions, it is beneficial to deposit the proteins in a condensate rather than degrading and resynthesizing them. Membraneless organelles (MLOs) are biological condensates formed through liquid–liquid phase separation (LLPS), involving cellular components such as nucleic acids and proteins. LLPS is a regulated process, which when perturbed, can undergo a transition from a physiological liquid condensate to pathological solid-like protein aggregates.

To understand how the MLO-associated proteins (MLO-APs) behave during aging, we performed a comparative meta-analysis with the age-related proteome of C. elegans. We found that the MLO-APs are highly abundant throughout the lifespan in wildtype and long-lived daf-2 mutant animals. Interestingly, they are aggregating more in long-lived mutant animals compared to the age-matched wildtype and short-lived daf-16 and hsf-1 mutant animals. GO term analysis revealed that the cell cycle and embryonic development are among the top enriched processes, in addition to RNP components in the aggregated proteome.

Considering the antagonistic pleotropic nature of these developmental genes and post mitotic status of C. elegans, we assume that these proteins phase transit during post development. As the organism ages, these MLO-APs either mature to become more insoluble or dissolve in uncontrolled manner. However, in the long-lived daf-2 mutant animals, the MLOs may attain protective states due to extended availability and association of molecular chaperones.



Fate of membrane less organelles (MLOs) during aging
Credits: Self

YI 28
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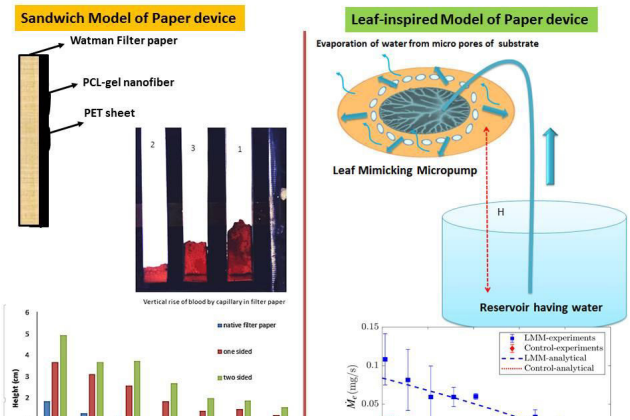
Modifications in the design of paper microfluidic devices to facilitate rapid and uniform spreading of biofluids for diagnostic applications

Keywords: Lab-on-chip devices, engineered organ models, polymeric membranes, bio-inspired design, medical devices

Abstract:

The global paper strip based diagnostic device market size was valued at USD 5.2 billion in 2018 and is anticipated to exhibit CAGR of 4.0% during the forecast period. However, one of the major challenges with these lateral flow assay devices for diagnostic application is processing the blood to obtain plasma for disease diagnosis. Hence, controlled and even spreading of complex fluids like native blood over microporous substrates in lateral flow devices is required for chemical and biological sensing applications. Owing to the non-Newtonian flow behavior, it poses a significant challenge to uniform flow in a porous substrate. Further, blood coagulation process is another barrier to flow in a microporous substrate. Herein, we describe the two strategies to overcome the challenges of fluid flow in paper devices. In the first, strategy, we have integrated a microporous paper with radially arranged bifurcating channels in PDMS to develop a leaf mimicking device. The device was able to pump water through trans-evaporation at the rate better than any other reported passive pumps. In the second strategy, a sandwich design was proposed wherein linear channel was integrated with microporous paper. The sandwich device could achieve rapid fluid pumping and even spreading of dye sample and blood overcoming the chromatography effect. We have also developed mathematical model to further assist in understanding and engineering of paper microfluidic devices proposed on above designs. This work will assist in developing diagnostic devices with using whole blood



Design strategies to enhance fluid pumping in microporous paper
Credits: Prasoon Kumar

References:

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YI 29
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Networking in Nephrogenesis; Functional characterization of Wilms Tumour 1 interactions

Keywords: Post transcriptional regulation of gene expression, stem cell biology, renal biology, epigenetics and epitranscriptomics, disease biology and molecular medicine

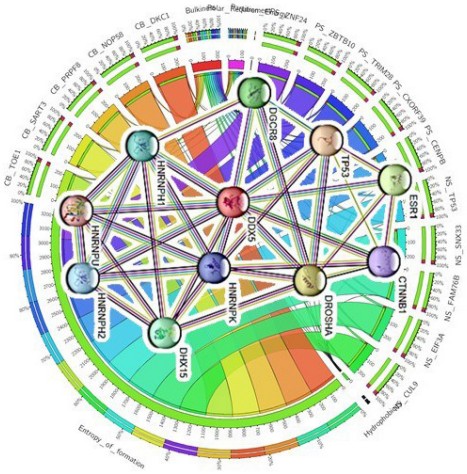
Abstract:

Developmental disorders of the kidneys and the urinary system, account for approximately 1/3 rd of antenatal defects observed during early development, which include, CAKUT (congenital anomalies of the kidneys and the urinary tract), found on an average in 1: 250 new borns and nephropathies such as Frasier Syndrome and Denys Drash Syndrome. The genetic causes of some of these disorders are known whereas in most cases, it is complex genetic and environmental factors.

Nephrogenesis has been shown to be a multistep process involving the interplay of transcription factors and signalling pathways. One such important kidney developmental protein, Wilms Tumour 1 (WT1) protein is a developmental regulator, a transcription factor and a tumour suppressor protein. WT1 has been recently shown to be a RNA Binding Protein, that regulates the stability of developmental mRNA targets. We have now identified the protein interactome of WT1, through an unbiased label free proteomic study, which shows a predominance of RNA processing pathway components. We have used a mathematical approach to analyse and predict the most important interaction nodes in the network (including splicing components), which has been validated through functional characterization. Using a genome editing methodology, we have generated cell lines expressing the Frasier Syndrome mutation and the altered protein networks in these nephropathic conditions are currently being studied. WT1 has been previously shown to interact specifically with 3'UTRs of Kidney specific developmental RNAs. We aim to elucidate the mechanism of this post-transcriptional regulation at the 3'-UTR, by investigating the role of Disordered region in regulating RNA and/or protein-protein interactions. We aim to gain insights into the mechanistic understanding of such regulatory processes from structural and functional assays which will be presented.

Networking in Nephrogenesis

Gosavi N, Dey S, Joseph I, Bharathavikru RS



The image depicts the different networks in renal cell lines
Credits: Gosavi N and Bharathavikru RS

YI 30

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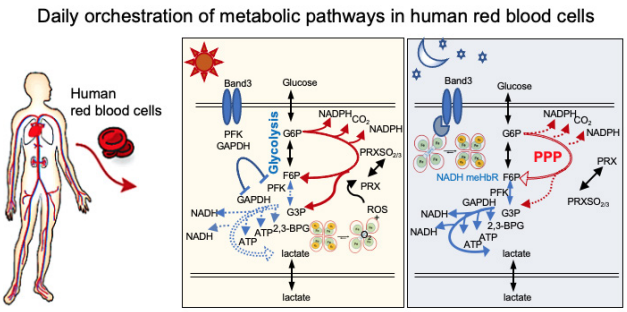
Daily orchestration of metabolic pathways in Human red blood cells

Keywords: Metabolomics, cell metabolism and disease, bio-analytical chemistry, biomarker, metabolic fingerprinting

Abstract:

Circadian clocks coordinate mammalian behavior and physiology enabling organisms to anticipate 24-hour cycles. Transcription-translation feedback loops are thought to drive these clocks in most of mammalian cells. However, red blood cells (RBCs), which do not contain a nucleus, and cannot perform transcription or translation, nonetheless exhibit circadian redox rhythms. Here we show human RBCs display circadian regulation of glucose metabolism, which is required to sustain daily redox oscillations. We found daily rhythms of metabolite levels and flux through glycolysis and the pentose phosphate pathway (PPP). We show that inhibition of critical enzymes in either pathway abolished 24-hour rhythms in metabolic flux and redox oscillations, and determined that metabolic oscillations are necessary for redox rhythmicity. Furthermore, metabolic flux rhythms also occur in nucleated cells, and persist when core transcriptional circadian clockwork is absent in Bmal1 knockouts. Thus, we propose that rhythmic glucose metabolism is an integral process in circadian rhythms



Daily orchestration of metabolic pathways in human red blood cells

YI 31

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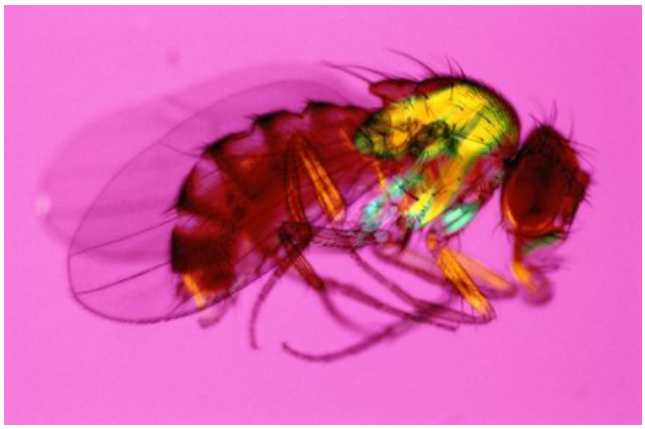
Understanding stem cell and tissue homeostasis during developmental and disease scenarios

Keywords: Stem cell - niche interactions, Drosophila model of cancer, cell signalling, tissue homeostasis, developmental biology

Abstract:

Stem cell and tissue homeostasis group at ACTREC is interested in understanding how stem cell - niche interactions are altered during disease conditions in comparison to the developmental scenario. Our lab uses Drosophila as a model system as it enables spatio-temporal gene manipulation and can be used for understanding mechanistic underpinnings of disease biology (Hales et al., 2015). One of the main advantages of using flies is the ability to perform in depth in-vivo analysis which enables investigating complex inter-organ communication. We use Drosophila hematopoietic and intestinal system to investigate how cellular signalling networks in the stem cells and the niche micro-environment get modulated in a cancer scenario (Khadilkar et al., 2014, Khadilkar et al., 2017 and Khadilkar et al., 2020). We also plan to use flies as a rapid screening platform to identify novel therapeutic candidates using fly epithelial cancer and leukemia models. We plan to use the power of genetics in Drosophila and correlate and combine it with analysis of clinical samples in order to realize and utilize the translational potential of this model.



Drosophila as a model to study human diseases

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YI 32
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Cognitive protection in tauopathy environment following TBI shows correlation with delayed astrogliosis

Keywords: Alzheimer's disease, neurodegeneration, mouse model, clinical samples and post mortem brain, glia

Abstract:

Tauopathy is a hallmark of a broad category of neurodegenerative conditions and Traumatic Brain Injury (TBI). Progression of tau pathology may lead to impaired cognitive conditions leading to dementia. However, previous studies have reported cognitively healthy patients with cortical tau pathologies. The mechanism for this cognitive protection in a tauopathy environment is being investigated by various groups. Astrocytes are essential for physiological homeostasis of brain and reactive astrogliosis is an associated pathology in neuroinflammation associated with TBI. The corelation between levels of cortical astrogliosis and dementia status of TBI patients at similar tau pathology staging is an unanswered problem. In our investigation we addressed this question by studying hippocampal and parietal cortex tissues from a subset of open access ACT study patient dataset. In our investigation, the cohort was grouped according to the tauopathy status based on Braak staging analysis and dementia status following trauma. We analysed the astrogliosis and microgliosis using GFAP and IBA1 as marker, respectively. Our work identified a significantly lower level of astrogliosis in cohort with early tauopathies and no associated dementia. This was missing in late stage tauopathies with no dementia and also with microgliosis. In summary, our analysis hints towards a possible protective role of reduced astrogliosis in dementia associated with tauopathies following TBI.

YI 33

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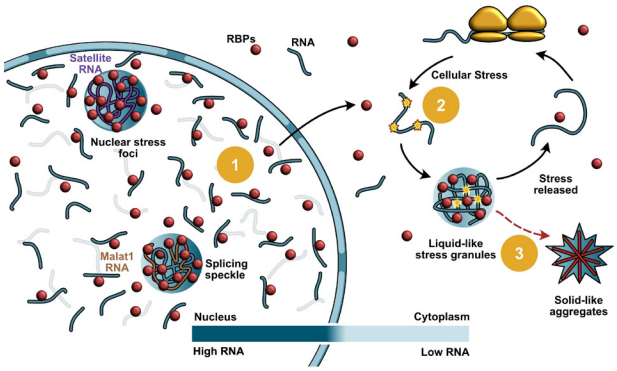
Role of RNA interactions in controlling physiological properties and function of RBP condensates.

Keywords: Cell biology, neurodegeneration, phase separation, RNA binding proteins, RNA interactions

Abstract:

A large fraction of the human proteome consists of RBPs. These proteins perform diverse functions in cells. Many of these RBPs like FUS, EWSR1, TAF15, TDP43 and hnRNAP1, which are present at high concentrations in the nucleus of the mammalian cells, contain low complexity domains making them prone to undergo liquid-liquid phase separation, a physicochemical process to make micron scale condensates in both the cellular environment and in vitro. In cells, these RBPs are present at concentrations where they can readily phase separate into condensates. We are currently studying how cells control the formation of RBP condensates at specific times and locations. Additionally, these phase separation-prone proteins tend to aggregate and form solid-like assemblies in the cytoplasm in neurodegenerative diseases- Amyotrophic Lateral Sclerosis and Frontotemporal Lobar Degeneration, the underlying mechanism for which is unclear. I will present evidence to elucidate the mechanisms which inhibit the spontaneous formation of RBP condensates and solid-like transitions in cells. Further, I will also present evidence for the role of RBP condensates in controlling inflammation, which may explain the neuroinflammation seen in many neurodegenerative conditions.



This image shows that the nucleus has a higher concentration of RNA and RBPs, and during stress conditions, the RBPs released from the nucleus and RNA released from ribosome form stress granules together which in disease conditions can form aggregates.
Credits: Shovamayee Maharana

YI 34

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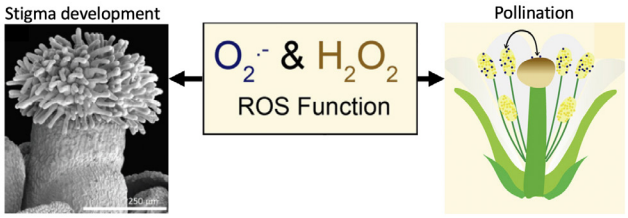
ROS regulation of stigma development

Keywords: Plant reproduction, self-incompatibility signalling, cell-cell communication, plant development, plant biotechnology

Abstract:

In angiosperms, the stigma is the first point of contact between the pollen and pistil during pollination. The stigma facilitates pollen capture and adhesion, pollen germination and pollen-tube guidance through the transmitting tract. In Arabidopsis thaliana, the stigma is composed of numerous single cells called stigma papillae. Despite their critical function in plant reproduction, little is known about the molecular mechanisms of stigma papillae growth and maturation. Here, we show that reactive oxygen species (ROS) plays an important role in stigma papillae development. Manipulating the ROS species in the stigma thorough pharmacological treatments or thorough genetic approaches revealed a critical role of ROS homeostasis in papillae growth and differentiation for optimal poillination.



ROS regulation of stigma development
Credits: Subramanian Sankaranarayanan

YI 35

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Tubulin code, cilia and homeostasis

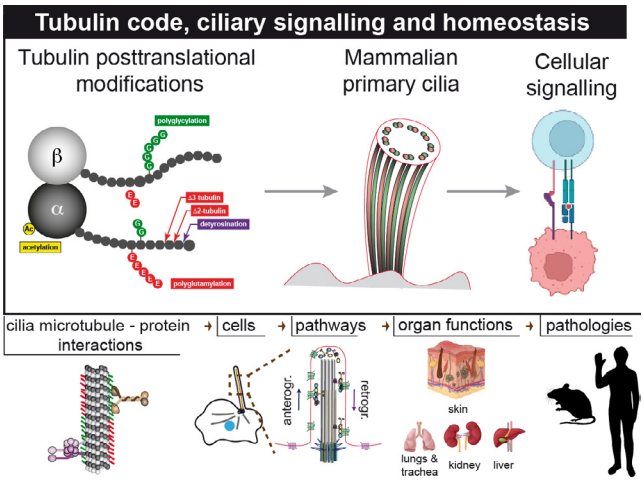
Keywords: Cilia and flagella, microtubules, tubulin posttranslational modifications, ciliopathies, signalling

Abstract:

Axonemes, the core microtubule-based structures of cilia and flagella, are a hub of various tubulin posttranslational modifications (PTMs) – a key component of the 'tubulin code' that emerges as a regulator of microtubule properties and functions. Cilia are enriched in two key tubulin PTMs, glutamylation and glycylation. My work has established the presence of glycylation on primary cilia and that it stabilizes them like motile cilia. In a mouse model totally lacking glycylation, I also established that male mice are sub-fertile with sperm cells defective in flagellar beat and overall motility. Most sperm swim in a circular pattern leading to a loss in progressive swimming, thus providing the first molecular evidence for the role of glycylation in mammalian cilia and flagella.

Understanding the role of tubulin PTMs in cilia has predominantly come from studies on motile cilia with little or no understanding of regulating primary cilia functions. Primary cilia are a hub of signalling pathways, which are regulated by trafficking the signalling molecules through cilia via intraflagellar transport (IFT). Disrupting primary cilia and/or its function leads to several clinical disorders, collectively termed ciliopathies. Recent studies show that primary cilia are also key for regulating tissue homeostasis, regeneration and repair, which requires an intricate network of signalling pathways within primary cilia. However, the underlying molecular mechanisms and the involvement of microtubules and their PTMs are barely understood.

My lab will study the crosstalk between primary cilia on different cells that regulate tissue homeostasis, repair post injury/infections. A major focus will be to understand how tubulin PTMs modulate ciliary trafficking and primary cilia function in regulating organ functions. We will also study the underlying molecular mechanisms of clinical ciliopathies due to defects in tubulin PTMs, thus establishing tubulin PTMs as a key regulator of organ function and tissue homeostasis.



Tubulin code, ciliary signalling and tissue homeostasis
Credits: Sudarshan Gadadhar

YI 36
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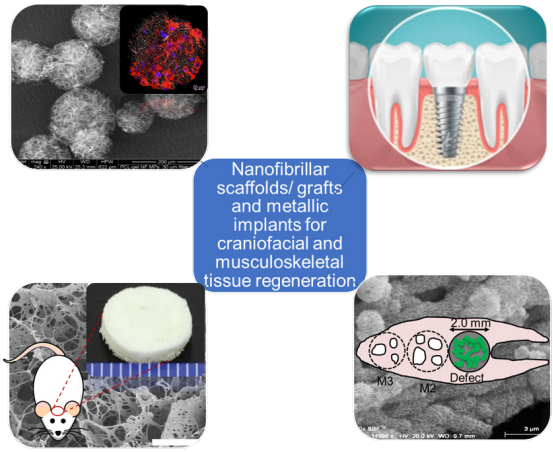
Biomaterials for musculoskeletal tissue engineering

Keywords: Biomaterials and tissue engineering, biomimetic peptides, bioadhesives, biofabrication and organ-on-a-dish models, antimicrobials

Abstract:

With longevity and aging, musculoskeletal injuries are on the rise and so is the need for biomedical implants/ grafts. Bone disorders including osteoporosis in post-menopausal women and large segmental bone defects arising from tumor removal, injury in warfare/ accidents are pertinent healthcare problems. Autologous bone grafts suffer from donor site morbidity, while allogenic and xenogenic grafts pose risk of disease transmission, immune rejection and poor osseointegration. Synthetic bone grafts such as Medtronic's Infuse graft and Geistlich Bio-Oss are suitable alternatives. Inspired by above synthetic grafts, we fabricated 3D nanofiber aerogel sponges and incorporated BMP-2 derived peptides for augmenting craniofacial bone defects [1, 2]. On similar lines, we developed 3D nanofiber microspheres as cell microcarriers for potent stem cell delivery [3]. As against resorbable bone grafts, non-degradable titanium implants have been in use in orthopedics for over 5 decades. Despite remarkable osseointegration of titanium, soft tissue integration around similar percutaneous osseointegrated devices is a pertinent problem. Lack of soft tissue sealing around metallic fixtures such as in the case of limb amputees paves the way for microbial infection and inflammation. To this end, skin extracellular matrix derived peptide and anti-inflammatory coatings were explored to encourage transmucosal soft tissue sealing around dental implants [4].



Biomaterials for Musculoskeletal Tissue Engineering
Credits: Sunil Kumar Boda

References:

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YI 37

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Collagen post-translational modifications at the interface of extracellularmatrix (ECM) remodelling, fibrosis, and regeneration

Keywords: Cardiac fibrosis, collagen post-translational modifications, mass-spectrometry, heart failure, extracellular-matrix

Abstract:

Cardiac fibrosis-mediated heart failure (HF) is one of the major forms of end-stagecardiovascular diseases (CVDs). Cardiac fibrosis is an adaptive response of the myocardium upon any insult/injury. Excessive deposition of collagen molecules in the extracellular matrix (ECM) is the hallmark of fibrosis. This fibrotic response initially protects the myocardium from ventricular rupture. Although in mammals this fibrotic response progresses towards scar-tissue formation leading to HF, some fishes and urodeles have mastered the art of cardiac regeneration following injury-mediated fibrotic response. Zebrafish have a unique capability to regenerate the myocardium after post-amputation injury. Following post-amputation, the ECM of the zebrafish heart undergoes extensive remodelling and deposition of collagen. Being the most abundant protein of ECM, collagen plays important role in the assembly and cell-matrix interactions. However, the mechanism of ECM remodelling is not well understood. Collagen molecules undergo heavy post-translational modifications (PTMs) mainly hydroxylation of proline, lysine, and glycosylation of lysine during biosynthesis. The critical roles of these PTMs are emerging in several diseases, embryonic development, cell behaviour regulation, and cell-matrix interactions. The site-specific identification of these collagen PTMs in zebrafish heart ECM is not known. As these highly modified peptides are not amenable to mass spectrometry (MS), the sitespecific identification of these collagen PTMs is challenging. Here, we have implemented our in-house proteomics analytical pipeline to analyse two ECM proteomics datasets (PXD011627, PXD010092) of the zebrafish heart during regeneration (post-amputation). We report the first comprehensive site-specific collagen PTM map of zebrafish heart ECM. We have identified a total of 36 collagen chains (19 are reported for the first time here) harbouring a total of 95 prolyl-3-hydroxylation, 108 hydroxylysine, 29 galactosyl-hydroxylysine, and 128glucosylgalactosyl-hydroxylysine sites. Furthermore, we comprehensively map the three chains (COL1A1a, COL1A1b, and COL1A2) of collagen I, the most abundant protein in zebrafish heart ECM. We achieved more than 95% sequence coverage for all three chains of collagen I. Our analysis also revealed the dynamics of prolyl-3-hydroxylation occupancy oscillations during heart regeneration at these sites. Moreover, quantitative site-specific analysis of lysine-O-glycosylation microheterogeneity during heart regeneration revealed a significant ($p < 0.05$) elevation of site-specific (K1017) glucosylgalactosyl-hydroxylysine on the col1a1a chain. Taken together, these site-specific PTM maps and the dynamic changes of sitespecific collagen PTMs in ECM during heart regeneration will open up new avenues to decode ECM remodelling and may lay the foundation to tinker with the cardiac regeneration process with new approaches.

YI 38
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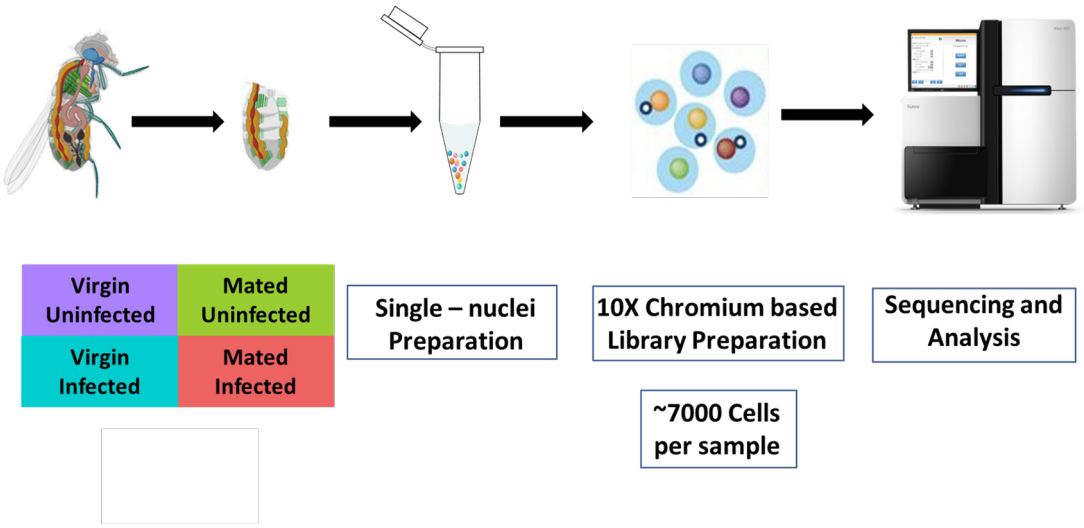
Inherent constraints on a polyfunctional tissue lead to a reproduction-immunity tradeoff.

Keywords: Evolution, host-pathogen interactions, life-history, Drosophila

Abstract:

The insect fat body performs remarkably diverse functions including metabolic control, reproductive provisioning, and systemic immune responses. How polyfunctional tissues simultaneously execute multiple distinct physiological functions is generally unknown. Immunity and reproduction are observed to trade off in many organisms but the mechanistic basis for this tradeoff is also typically not known. Using single-nucleus sequencing, we determined that the Drosophila melanogaster fat body executes diverse basal functions with heterogenous cellular subpopulations. However, as an emergency function, the immune response engages the entire tissue. When challenged with bacteria, we found that reproductively active females exhibited ER stress signatures and impaired capacity to synthesize new protein in response to infection, including the decreased capacity to produce antimicrobial peptides. Transient provision of a reversible translation inhibitor to mated females prior to infection rescued general protein synthesis, specific production of antimicrobial peptides, and survival of infection. The commonly observed tradeoff between reproduction and immunity appears to be driven, in D. melanogaster, by a failure of the fat body to simultaneously handle protein translation demands of reproduction and immunity. We suggest that inherent cellular limitations in tissues that perform multiple functions may provide a general explanation for the wide prevalence of physiological and evolutionary tradeoffs.



How does insect fat body control reproductiona nd immunity?
Credits: Vanika Gupta

YI 39

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Development and validation of clinically mimicable animal model of cocktail chemotherapy-induced neuropathic pain

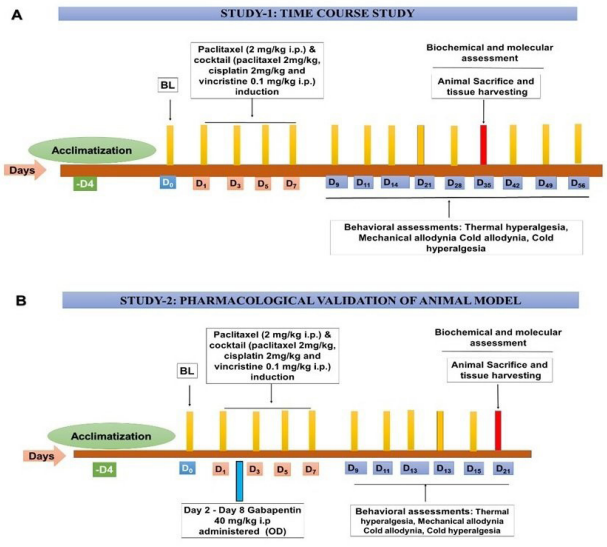
Keywords: Neuroscience, pain research, chronic neuropathic pain, nociception, chemotherapy-induced neuropathic pain

Abstract:

Intro: Chemotherapy-induced neuropathic pain (CINP) is among the most common adverse effects with the use of anti-cancer agents but till date no US-FDA approved effective treatment is available for the management of the same. One of the reasons for this could be the unavailability of preclinical animal models which can best represent the clinical situation.

Methods: Antitumor agents are prescribed in the combination of 2/3 drugs, based on this observation, in this study we used cocktail of chemotherapy (paclitaxel, cisplatin & vincristine) for the development of novel CINP model & compared with a conventional paclitaxel model in rats.

Results: Our finding s that rats administered with cocktail of chemotherapy significantly increased the pain sensitivity which persisted upto the 8th week but, the paclitaxel treated rats showed pain up to 5th week. Next, we found an upregulation of mRNA expression of different receptors such as TRPA1, TRPV1, TRPM8, NR2B, & neuro-peptides including substance P and CGRP in the DRG & spinal cord of the CINP rats as compared to both PTX & vehicle-treated rats on day 35. The levels of neuro-inflammatory markers such as TNF-α, IL-1β & nitrosative stress was also increased in cocktail-treated rats compared to both PTX & vehicle treated group. Further, on 14th day both cocktail & PTX treated rats showed significant pain sensitivity which was significantly attenuated by gabapentin 40 mg/kg i.p. The treatment with gabapentin also reversed the molecular & biochemical alterations in the DRG, spinal cord & sciatic nerve of both cocktail & PTX treated rats as compared to vehicle treated group. Conclusion: The novel cocktail treated CINP animal model successfully demonstrated the face, predictive and constructive validity & therefore it could be utilized as an additional resource for unravelling the mechanism responsible for the development of pain & screening of pharmacological agents against CINP.



The study framework of a novel animal model for CINP
Credits: Vinod Tiwari

YI 40
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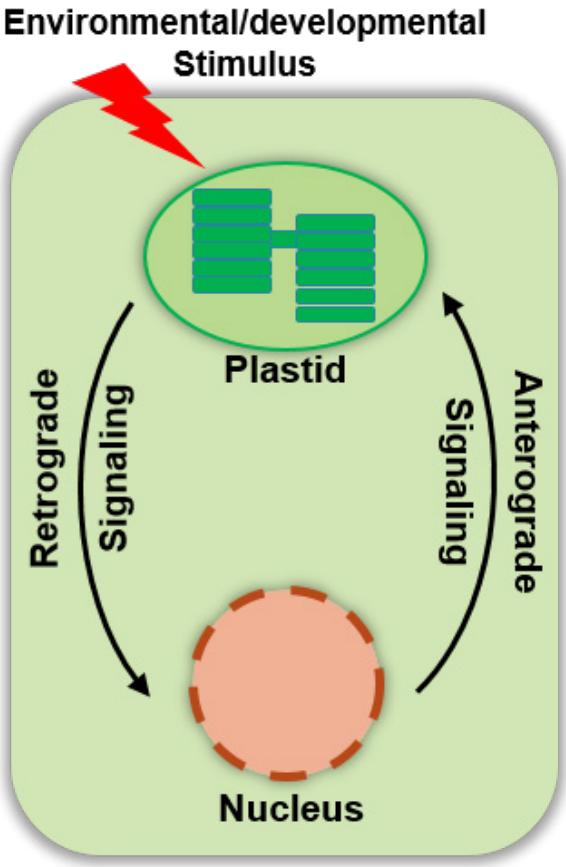
Singlet oxygen-induced damage and signaling: clues to engineer stress-resilient photosynthetic apparatus

Keywords: Molecular plant biology, stress and adaptation, chloroplast biology, chloroplast-to-nucleus retrograde signaling, photosynthetic engineering

Abstract:

Plants being sessile face a series of environmental perturbations together with internal developmental events. An emerging body of evidence shows that cellular organelles, especially chloroplast, play a vital role in sensing those stimuli and priming the cognate response, including acclimation, growth inhibition, and programmed cell death. Chloroplast is an essential organelle that not only provides site for photosynthesis, but several essential biomolecules, including fatty acids, phytohormones, and several vital metabolites, are synthesized here. The environmental and developmental cues primarily target these vital processes in the chloroplast, especially the photosynthetic machinery, leading to the generation of reactive oxygen species (ROS), including singlet oxygen ($^1O_2$), superoxide anion, hydrogen peroxide, and hydroxyl anion. Among these ROS, $^1O_2$ is peculiar as it is generated when molecular oxygen gains energy released from excited chlorophyll or tetrapyrroles, whereas others involve the gain of an electron. Exposure to fluctuations in light and temperature and other stresses such as drought and pathogens results in an increased accumulation of $^1O_2$ exceeding the scavenging capacity of antioxidant system. Accumulated $^1O_2$ damages various biomolecules in the photosynthetic apparatus especially, two photosystems. Increased damage of photosystems leads to photoinhibition and a decline in photosynthetic efficiency. In response, the damaged products of these biomolecules can trigger retrograde signaling that underline the plant's response. Understanding how ROS ($^1O_2$) targets various biomolecules and activates retrograde signaling cascades is essential for engineering stress-resilience in chloroplasts and plants. Towards this, we revealed distinct signaling pathways instigated upon the oxidation of carotenoids, lipids, and proteins. In addition, we have recently mapped a set of photosynthetic proteins undergoing oxidative modifications. Based on this basic information, we intend to engineer stress/ROS-resilient photosynthetic components using modern biotechnological tools.



PDF
Abstracts

The abstracts have been printed exactly as submitted by the participants. The organisers of YIM 2023 are not responsible for any errors in them.

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AA amyloid fibrils from diseased tissue are structurally different from in vitro formed SAA fibrils

PDF 02 ANANT JAIN
Fluorescent lifetime imaging of CAMKII during behavioral time scale plasticity at CA1 synapses

PDF 03 ANAS SHAMSI
MARK4 inhibited by AChE-inhibitors, Donepezil and Rivastigmine tartrate: Insights into Alzheimer's disease therapy

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ACC deaminase producing Enterobacter sp. as plant growth enhancer and a promising salinity stress mitigator and modulator of rhizospheric microbiome in Cajanus cajan: Mitigating salinity stress the eco-friendly way

PDF 05 ANUSHA SHANKAR
Hot and cold animals: integrating organismal physiology, ecology, and -omics in the tropics

PDF 06 ANWESHA GHOSH
Putting things into perspective: a story of the changing face of the Indian Sundarbans

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A supergene underlies social polymorphism in the desert ant

PDF 08 ARUN PRAKASH
Immune regulation and epidemiological consequences of specific immune priming in Drosophila melanogaster

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Mitochondrial Complex I (MCI) controls NMJ function and plasticity through distinct pre- and post-synaptic mechanisms

PDF 10 BUVANESWARI G
Development of gut microbiota-derived bacterial probiotics for glycemic control during endocrine-disrupting chemical-induced diabetes

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PDF 12 DIVYA JHA
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Functional regulation of RNA-protein condensates in the Drosophila female germline

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Autophagy protein Atg11 and spindle pole body component Spc72 help maintain astral microtubule integrity essential for high-fidelity chromosome segregation

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Biodiversity bigdata lab

PDF 25 PRATIK KUMAR
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PDF 26 RAGHAVAN THIAGARAJAN
Distinct organisations of actin regulate the ascent, distribution and patterning of basal bodies

PDF 27 RAHUL MAHESHWARI
Laser activatable nanographene colloids for combined therapy of triple-negative breast cancer

PDF Abstracts

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High-through screening of natural compounds as the potential autophagy modulators in regulation of Alzheimer's disease using developed stable iso-genic tagged cells

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The stem cell model of dorsal spinal cord development paves a way to investigate complex sensory disorders *in vitro*.

PDF 30 SHANAYA PATEL
Identification of potential salivary exosomal miRNA signature that predicts early risk prediction and poor prognosis in oral cancer patients: A liquid biopsy approach

PDF 31 SHEIKH MANSOOR
The significant role of interleukin-11 and downstream signalling molecules in the pathogenesis and treatment of esophageal cancer

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A systems approach to discover mechanisms of mitochondrial genome maintenance

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NGS quantification of viral clonal architecture identifies HTLV-1 asymptomatic carriers at high risk of progression to aggressive leukemia

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Deciphering a novel pathway of sulfide metabolism in budding yeast

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Rhythmic expression of lncRNAs and its function in floral development and the circadian clock

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Predation risk regulates assortative mating in a desert isopod

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Lights, Colors, and Resilience: integration of environmental cues with adaptive responses in plants under abiotic stress conditions

PDF 01
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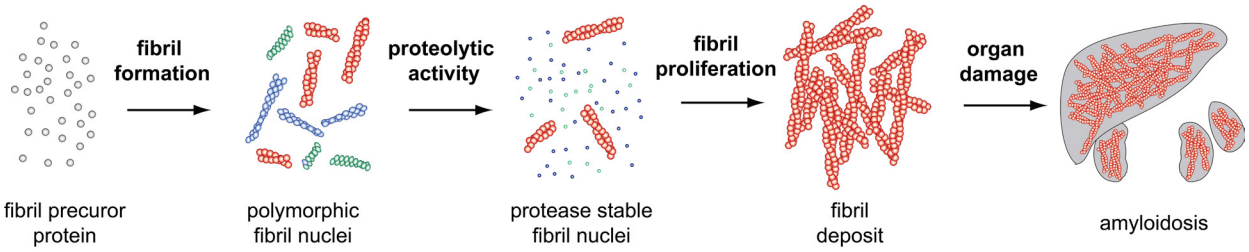
AA amyloid fibrils from diseased tissue are structurally different from in vitro formed SAA fibrils

Keywords: Structural biology, X-ray crystallography, cryo-electron microscopy, protein folding, ribosome biogenesis.

Abstract:

The systemic Amyloid A amyloidosis is a potentially fatal disease which affects human and animal species. It arises from misfolding of the blood protein serum amyloid A (SAA) and accompanies chronic inflammatory conditions, such as rheumatoid arthritis, leprosy or tuberculosis (Ref 1). Physico-mechanical properties of deposited fibrils are proven to be causal for pathogenicity of AA amyloidosis. A further disturbing feature of AA amyloidosis is its prion-like characteristics (Ref 2). Despite their known pathological effects structural information regarding AA amyloid fibrils is sparse. As part of this work, structural comparison was carried out for the fibril morphologies adopted by murine SAA 1.1 protein in AA amyloidotic mice and in vitro. Using cryo electron microscopy derived structures we here show that amyloid fibrils which were purified from AA amyloidotic mice are structurally different from fibrils formed from recombinant SAA protein in vitro. ex vivo amyloid fibrils consist of fibril proteins that contain more residues within their ordered parts and possess a higher β-sheet content than in vitro fibril proteins. They are also more resistant to proteolysis than their in vitro formed counterparts. These data suggest that pathogenic amyloid fibrils may originate from proteolytic selection, allowing specific fibril morphologies to proliferate and to cause damage to the surrounding tissue.



The proteolytic selection mechanism for formation of pathogenically relevant amyloid fibril morphology.
Credits: Marcus Faendrich, Akanksha Bansal

References:

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PDF 02
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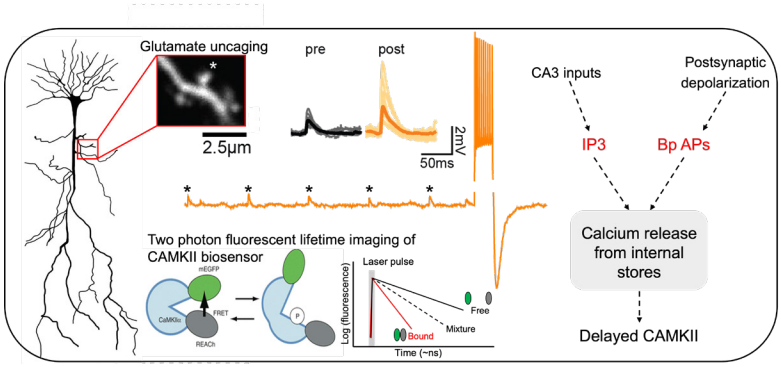
Fluorescent lifetime imaging of CAMKII during behavioral time scale plasticity at CA1 synapses

Keywords: Neurophysiology, synaptic biology, sex difference, two-photon imaging, neuropathology.

Abstract:

Hippocampal place cells, once formed, are stable for a given environment and can last for many days suggesting that an activity dependent synaptic plasticity underlies the induction/modulation of place cells. A recent study by Bittner et al., 2017 showed that a novel non-hebbian form of plasticity induces CA1 place cell formation, where calcium plateau integrates with CA1 inputs over seconds to induce place cells. In our study, we characterized this behavioral time scale plasticity (BTSP) at single synapses in CA1 neurons. Using glutamate uncaging in hippocampal slices, we found that potentiation can be induced in a synapse specific manner regardless of whether uncaging pulses were given before or after depolarization. Furthermore, as CA1 synapses receive inputs from different brain regions, we induced BTSP at different types of CA1 synapses using the same protocol and found that BTSP occurred specifically in the proximal apical dendrites and not in basal or distal dendrites. Next, we sought to determine what biochemical pathway is activated for seconds to pair depolarization with synaptic inputs. Previous two-photon fluorescent life time imaging (2pFLIM) of CAMKII sensor showed stimulus locked CAMKII activity during long-term potentiation that lasts for 1-3 seconds, making it an ideal candidate to integrate the two inputs during BTSP. We first confirmed the requirement of CAMKII in BTSP by doing experiments in slices made from T286A transgenic mice, where we failed to induce BTSP. However, surprisingly, 2pFLIM of CAMKII sensor during BTSP at single synapses showed no activation of CAMKII at single synapses and found a delayed CAMKII activity almost 30-40 second following BTSP induction. Lastly, pharmacological experiments revealed that calcium release from internal stores are important for this delayed CAMKII activity during single synapse BTSP. Understanding activation profiles of kinases in behaviorally relevant plasticity mechanisms will provide insights into their specific functions during behavior.



Understanding CAMKII activity in behaviorally relevant plasticity mechanisms
Credits: Krithika Ramachandran

PDF 03
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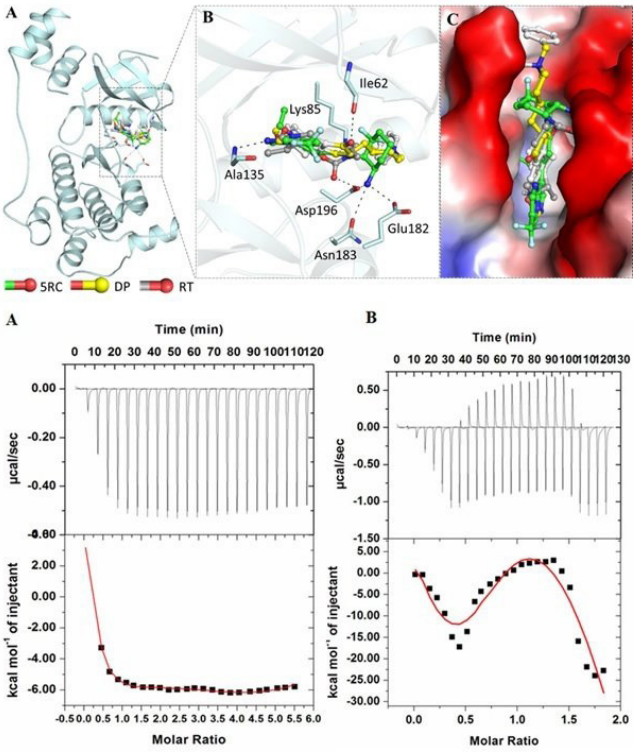
MARK4 inhibited by AChE-inhibitors, Donepezil and Rivastigmine tartrate: Insights into Alzheimer's disease therapy

Keywords: Cancer therapeutics, protein biochemistry, neurodegenerative disorders, structure based drug design, protein aggregation and glycation.

Abstract:

Microtubule affinity regulating kinase (MARK4) plays a key role in Alzheimer's disease (AD) development as its overexpression is directly linked to increased tau phosphorylation. MARK4 is a potential drug target for AD thus being targeted for the development of new therapeutic molecules. Both Donepezil (DP) and Rivastigmine tartrate (RT) are acetylcholinesterase inhibitors (AChE inhibitors) and are in use to treat symptomatic patients of mild to moderate AD. Keeping the therapeutic implication of DP and RT in AD, we performed binding studies of these drugs with the MARK4. Both DP and RT show an excellent binding affinity to the MARK4 with a higher binding constant (K) of 107 M-1. The temperature dependency of binding parameters revealed the MARK-DP complex to be guided by static mode while the MARK-RT complex to be guided by both static and dynamic quenching. Both drugs inhibit MARK4 with IC50 values are 5.3 µM and 6.74 µM for DP and RT, respectively. The evaluation of associated enthalpy change (ΔH) and entropy change (ΔS) implied the complex formation to be driven by hydrogen bonding making it seemingly strong and specific. Isothermal titration calorimetry (ITC) further advocated spontaneous binding. In vitro observations were further complemented by a molecular docking study suggesting appreciable affinity and interaction to the functionally active residues of the MARK4 active site pocket. This study signifies the implications of AChE inhibitors, RT, and DP Alzheimer's therapy targeting MARK4 too.



Binding mode of donepezil and rivastigmine tartrate with MARK4
Credits: Anas Shamsi

PDF 04
ANNAPURNA BHATTACHARJEE
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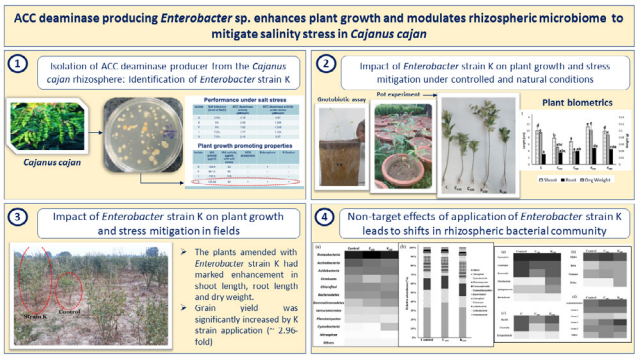
ACC deaminase producing Enterobacter sp. as plant growth enhancer and a promising salinity stress mitigator and modulator of rhizospheric microbiome in Cajanus cajan: Mitigating salinity stress the eco-friendly way

Keywords: Plant microbe interactions, abiotic stress biology, plant molecular biology, environmental sustenance, sustainable agriculture.

Abstract:

Stress factors negatively impact crop productivity, threatening global food security. Thus, sustainable agriculture using eco-friendly approaches is key to agronomic improvement. Despite the tremendous potential of ACC deaminase producing microbes as stress busters, few studies report their application in combating stresses in fields. Thus, this study first intended to obtain an efficient indigenous multifaceted ACC deaminase producer from rhizospheric soil of C. cajan for enhance survival and increment in crop productivity enhancement under salt stress. Further, the impact of such a dual-purpose, sustainable amendment was evaluated on plant growth, and stress mitigation. ACC deaminase positive bacteria from the rhizospheric soil of C. cajan were isolated, enumerated and screened, based on gnotobiotic root elongation assay and other plant growth promoting properties. Selected bacterial strains were used for plant growth experiments, first in controlled growth chamber followed by experiments in pots, to examine their performance under salinity stress. Plant growth attributes were enhanced in plants amended with Enterobacter strain K under salinity stress condition as compared to control plants. Further, stress marker levels (proline and malondialdehyde) were found to be altered in Enterobacter strain K amended plants under salinity stress in contrast to control plants. Alterations in rhizospheric bacterial community, assessed by 16S rRNA amplicon sequencing analysis, revealed distinct shifts in soil microbiome upon amendment with Enterobacter strain, leading to salinity stress mitigation, plant growth promotion and positive non-target impacts on soil microbiome. Thus, ACC deaminase producer Enterobacter strain K played dual role of stress mitigator and plant growth promoter, while causing shifts in rhizospheric bacterial community. Notably, this strain exhibited salinity stress mitigation in C. cajan in a naturally saline agricultural field too. Overall, this study demonstrated successful application of an ACC deaminase producer in stress mitigation, transitioning from field to laboratory, and application back to fields.



ACC deaminase producing Enterobacter sp. enhances plant growth and modulates rhizospheric microbiome to mitigate salinity stress in Cajanus cajan
Credits: Microsoft powerpoint

PDF 05
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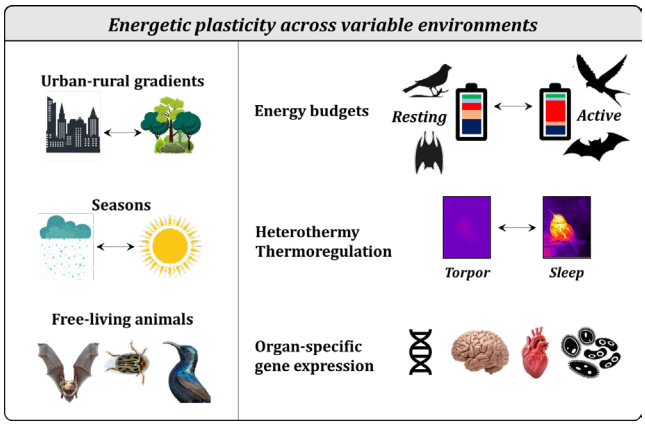
Hot and cold animals: integrating organismal physiology, ecology, and -omics in the tropics

Keywords: Physiology, energetics, molecular biology, ecology, conservation.

Abstract:

I use an integrative and multi-disciplinary approach to study how animals adapt and respond to challenging environmental conditions, while deriving lessons for wildlife conservation and human health. I am especially interested in the physiology and evolution of heterothermy (variable body temperatures) in vertebrates as a strategy to deal with variable environmental conditions. Animals from insects to birds and mammals use varying degrees of heterothermy to save energy by lowering their body temperatures, and correspondingly decreasing their energy expenditure. Heterothermy usually occurs under conditions where either the energetic demands are high (e.g., cold conditions), or energy supply is low (e.g., limited food availability). Insects such as beetles and caterpillars use diapause or aestivation to enter a suspended metabolic state for weeks or months. Some bird and mammal species, including hummingbirds, nightjars, and bats, use 'torpor' to lower their body temperatures and metabolic needs at night. Over 200 bird and mammal species so far are known to use some form of torpor, but much remains to be uncovered about the mechanisms underlying torpor. I will assess how animals respond to variable environments across three axes. 1. Basic science: animal physiology, -omics, and evolution. My primary questions are: How prevalent is heterothermy among Indian endotherms (birds and mammals)? What genetic pathways underlie heterothermy in birds vs. mammals? And what evolutionary pathways for heterothermy converge/diverge in Indian species vs. New World species? 2. Applications in human health. At its most applied, this work on heterothermy could inform medical research on induced hypothermia for surgeries in stroke and cardiac patients. 3. Applications in conservation science. I will aim to answer this question: How does behaviour, physiology, and genetics change across human land use gradients, in free-living endotherms? And then to work with conservation practitioners to implement the results of these research in conservation action.



Overview of my proposed research plan. I study energetic plasticity (e.g., energy budgets and heterothermy) from ecological, physiological, and molecular perspectives in free-living animals.
Credits: Anusha Shankar

PDF 06

ANWESHA GHOSH

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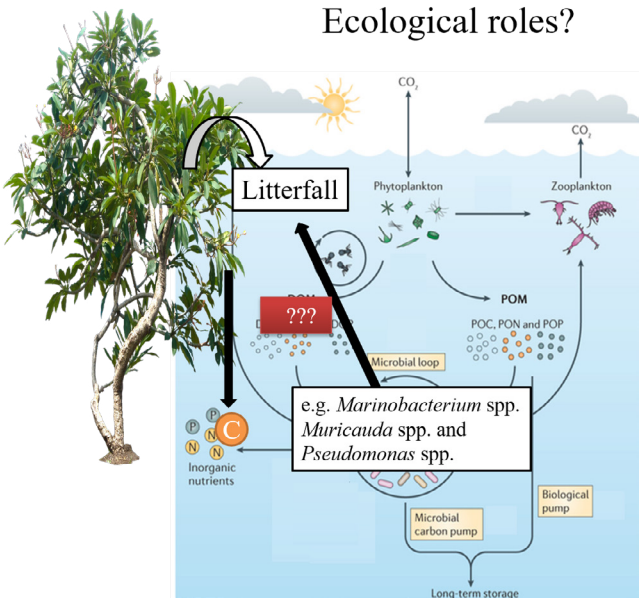
Putting things into perspective: a story of the changing face of the Indian Sundarbans

Keywords: Microbial ecology, bacterioplankton, ecosystem responses, ecosystem health, blue economy

Abstract:

Litterfall constitutes a major source of allochthonous matter for bacterioplankton communities in estuarine mangroves. Tannic acid, an abundant component of mangrove litterfall, leaches out and contributes substantially to DOM pools in estuaries. Estuarine conditions of Sundarbans were mimicked in a laboratory mesocosm set-up using barrels to understand the influence of tannic acid on bacterioplankton communities. Estuarine water from a station, Stn3 of Sundarbans Biological Observatory Time Series (SBOTS) was enriched with tannic acid and the change in functional bacterioplankton community structure was analysed on the start (Day 0), intermediate (Day 7) and end (Day 15) of the experiment. Tannic acid was shown to significantly affect the concentration of dissolved nitrate and trace elements in the barrels. Proteobacteria was the most dominant bacterial phylum in Control and tannic acid enriched barrels (Barrel 1 and 2) on Day 0. With the progression of experiment, Proteobacteria decreased significantly in the Control barrel indicating the dependence of this phylum on steady flux of nutrients. Proteobacteria in the tannic acid enriched barrels remained high indicating that it may be capable of using tannic acid as a source of carbon and nitrogen. Tannic acid inhibited Actinobacteria, Acidobacteria and Verrucomicrobia that existed in large abundance in the Control barrel on Day 15 but were absent in the tannic acid enriched barrels. This experiment indicated that bacterioplankton communities of Sundarbans could harbour genes necessary for breakdown of complex components of litterfall and recycle them into the marine microbial loop. Breakdown of tannic acid could influence the marine nitrogen and carbon cycling by releasing DON and DOC respectively into the adjacent estuaries. An understanding of the breakdown of tannic acid and other components of mangrove litterfall and its influence on the resident biological communities of estuarine mangroves could be essential for our understanding of carbon cycling in coastal ecosystems.



Ecological role of bacterioplankton in mangrove ecosystems
Credits: Anwesha Ghosh

PDF 07

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A supergene underlies social polymorphism in the desert ant

Keywords: Evolutionary biology, ecology, speciation, genomics, phylogenetics.

Abstract:

Social insects show great variation in social organisation. The desert ant Cataglyphis niger displays polymorphism in colony structure, where most colonies are monogyne (having a single queen) while others are polygyne (having multiple egg-laying queens) and form large supercolonies that may consist of hundreds of nests. We investigated the genomic and evolutionary basis of this polymorphism. We sampled 30 nests from a single population where both the social forms are represented. We used dyadic aggression assays to distinguish the social forms. We then used reduced-representation genomic sequencing (RAD-seq) to genotype 20– 24 individuals per nest. Kinship analyses was carried out to confirm social structures. When Fst values were compared between monogyne and polygyne samples, hundreds of high Fst loci were detected, all of which were located in an ~8Mbp region on one chromosome, suggesting the presence of a supergene— a group of tightly linked genes in a region of suppressed recombination. We also observe high linkage disequilibrium in this region of the chromosome, further supporting this hypothesis. This chromosome is analogous to so-called "social chromosomes" described in other ant species. I will present our work so far and discuss ecological and evolutionary hypotheses on how this genomic architecture is maintained in this species.

PDF 08

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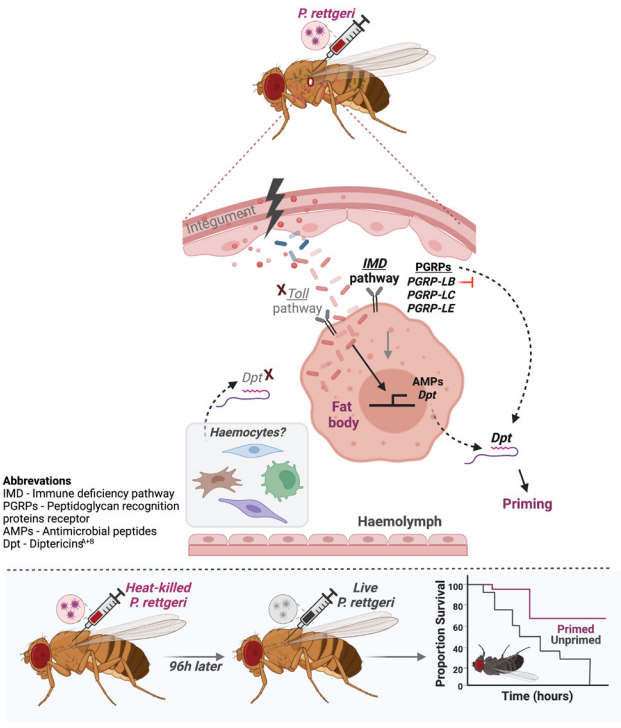
Immune regulation and epidemiological consequences of specific immune priming in Drosophila melanogaster

Keywords: Evolutionary biology, immunology, host-pathogen interactions, disease tolerance, immune priming

Abstract:

Insects lack the specialized immune-memory cells responsible for vertebrate-like acquired immunity. However, there is increasing evidence that past infection experience by the same pathogen can 'prime' the insect immune response, resulting in improved survival upon reinfection. The mechanisms underlying these phenomenological accounts of priming are diverse, and often not completely clear. Here, we investigated the generality, specificity and mechanistic basis of immune priming in Drosophila melanogaster when infected with the gram-negative bacterial pathogen Providencia rettgeri. By using a combination CRISPR/Cas knockout, loss-of-function and UAS-RNAi knockdown fly lines, we find that priming in Drosophila is a long-lasting response, occurring in several genetic backgrounds and is particularly stronger in male flies. We further explore the epidemiological consequences of immune priming and find it has the potential to reduce pathogen transmission by affecting pathogen shedding.

Mechanistically, we find that flies lacking major components of the IMD immune signalling pathway are no longer able to improve survival following initial heat-killed exposure with P. rettgeri. We show that the enhanced survival of individuals primed with an initial non-lethal bacterial inoculum coincides with a transient decrease in bacterial loads, and that this is likely driven by the IMD-responsive antimicrobial-peptide Diptericin-B in the fat body. Further, we show that while Diptericin is required as the effector of bacterial clearance, it is not sufficient for immune priming, which requires regulation by peptidoglycan recognition proteins PGRP-LB, PGRP-LC and PGRP-LE. We discuss potential explanations for the observed sex differences in priming, and further show that priming has the potential to reduce disease spread and pathogen transmission by affecting pathogen shedding.



Features of immune priming response to subsequent systemic bacterial infections in fruit flies.
Credits: biorender.com

PDF 09
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Mitochondrial Complex I (MCI) controls NMJ function and plasticity through distinct pre- and post-synaptic mechanisms

Keywords: Drosophila, neurodegeneative diseases, electrophysiology, synaptic, homeostasis, genetics

Abstract:

Neurons are polarized cells with immense energy demands. Healthy pools of mitochondria mainly fulfill those demands. In response to altered energy states of the neuron, mitochondria can adapt to maintain energy homeostasis and nervous system function. This adaptation, also called mitochondrial plasticity, can be observed as changes in morphology, function, or localization of mitochondria at synapses. Through an RNAi-mediated genetic screen in Drosophila melanogaster (300 RNAi lines), we examined homologs of genes associated with human neurodegenerative diseases, including mitochondrial diseases. We found that Mitochondrial Complex I (MCI) subunits were essential for maintaining mitochondrial morphology and neuromuscular junction (NMJ) function.

For our screen, we observed weakened NMJ function by electrophysiology after genetic loss or RNAi-mediated depletion of 13/14 of the MCI subunit genes we tested. For follow-up work, we conducted a detailed characterization of MCI deficiency caused by loss of the nuclear-encoded NADH dehydrogenase subunit 20 (ND-20L) gene, a homolog of human NDUFS7. The ND-20L-depleted larvae exhibited phenotypes resembling symptoms of mitochondrial disease, including progressive muscle degeneration and presynaptic cytoskeleton, enhanced mitochondrial reactive oxygen species (ROS) formation, loss of mitochondria, and finally, mitochondrial fragmentation and trafficking defects. Subsequent analyses revealed diverse phenotypes in different tissues. MCI deficiency in neurons induced profound cytological phenotypes, but there appeared to be a compensatory response: namely, accumulation of more active zone material at the synapse. Our genetic and electrophysiological analyses suggest that the active zone enhancement, ER-mediated calcium release and import to mitochondria contribute to maintaining evoked neurotransmission when MCI is lost in neurons.

PDF 10
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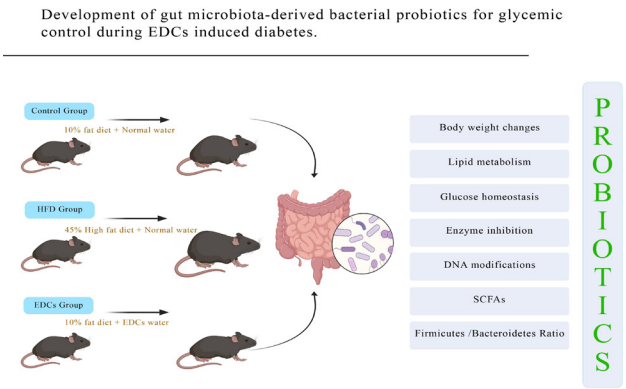
Development of gut microbiota-derived bacterial probiotics for glycemic control during endocrine-disrupting chemical-induced diabetes.

Keywords: Gut microbiota and human health, endocrine-disrupting chemicals, environmental microbiology, microbial technologies, chemomicrobiomics

Abstract:

Diabetes is becoming one of the biggest health problems worldwide. There are epidemiologic links between EDCs and diabetes. Recently, interest has been drawn towards the potential role of endocrine disrupting chemicals (EDCs) in diabetes due to world wide spread prevalence. Our KMCH-Non-communicable disease (NCD) epidemiological studies revealed the non-association of traditional risk factors with prevalence of diabetes in rural communities. Subsequently, we have revealed the synergistic role of gut microbiota and endocrine-disrupting chemicals in development of glucose intolerance. Here, we have developed two different mice models of diabetes: i) treated with 45% high fat diet (HFD) ii) treated with a mixture of EDCs. After 120 days of treatment, both the mice models developed hyperglyemia and exhibited glucose intolerance. There is a significant increase in body weight of mice treated with HFD but not in mice treated with EDCs. This reflects the scenario of diabetes in developing and underdeveloped nations. Metagenomic DNA was isolated from the mice fecal samples and 16S rDNA sequencing was performed and analysis revealed the differential microbial profile between the two diabetes mice models of different etiology. The expression profile of key bacterial species were validated in the human diabetes fecal samples by qPCR. Currently, we are in the process of isolation and characterization of differentially expressed bacterial species and assessment of their therapeutic potential (probiotic) to alleviate hyperglycemia in mice treated with EDCs.



Differential gut microbiota profile of high fat diet and endo-crine-disrupting chemicals-induced glucose intolerance. Credits: BioRender.com

PDF 11
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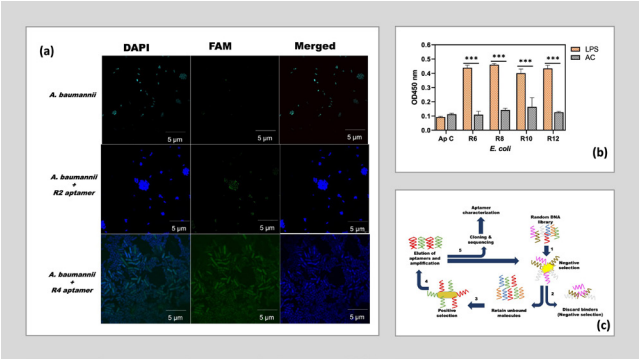
Website: thsti.res.in

Aptamer based Point-of-care assay for detection of neonatal sepsis causing pathogens

Keywords: Diagnostic platforms/electrodes, microbes and anti-microbial resistance, electrochemical sensors, nanomaterials, aptamers/biorecognition elements

Abstract:

Neonatal sepsis (NS) occurring just after the birth of the child and till 28 days is the third leading cause of morbidity and mortality in neonates worldwide. The conventional methods of detection of sepsis consumes lot of time, are costly and have compromised sensitivity. Thus, development of a rapid, accurate, sensitive, specific test for detection of NS causing pathogens is of prime importance. To address this unmet need; we have developed an electrochemical sensor mediated by aptamers for early detection of lipopolysaccharide (LPS) of E. coli and Whole cell of Acinetobacter baumannii. Aptamers are biomimetic synthetic receptors that are selected in vitro by SELEX procedure (Figure 1). Thus, here we have synthesized aptamers against lipopolysaccharide (LPS) of E. coli and Whole cell of Acinetobacter baumannii. For a highly effective and precise aptamer selection, two strategies (i) a microtiter plate (MTP) based SELEX strategy for E. coli LPS and (ii) Microcentrifuge tube (MCT) based whole-cell SELEX strategy for Acinetobacter baumannii was followed. We herein successfully develop a panel of highly affine aptamers that specifically recognised (a) E. coli and (b) Acinetobacter baumannii. These aptamers were able to discriminate the targeted bacteria from P. aeruginosa, S. aureus and K. pneumoniae. The techniques used for validating the specificity were ALISA, confocal microscopy and flow cytometry. The best performing aptamer candidates were used as a molecular recognition element on a screen-printed electrode and were able to detect as low as as ~102 CFU/mL of Acinetobacter baumannii bacterial cells and 2 fM LPS in human serum background. The developed aptamer-based device can be used for potential point-of-care pathogen detection applications due to its simplicity and affordability.



(a) Confocal Microscopic images of A. baumannii binding, (b) ALISA results of round populations of Aptamers giants E. coli LPS (c) SELEX strategy
Credits: Chaitali Singhal

References:

1. Singhal C, Khanuja M, Chaudhary N, Pundir CS, Narang J. 2018. Detection of chikungunya virus DNA using two-di-mensional MoS2 nanosheets based disposable biosensor. Scientific Reports 8 (1): 1-11.

PDF 12
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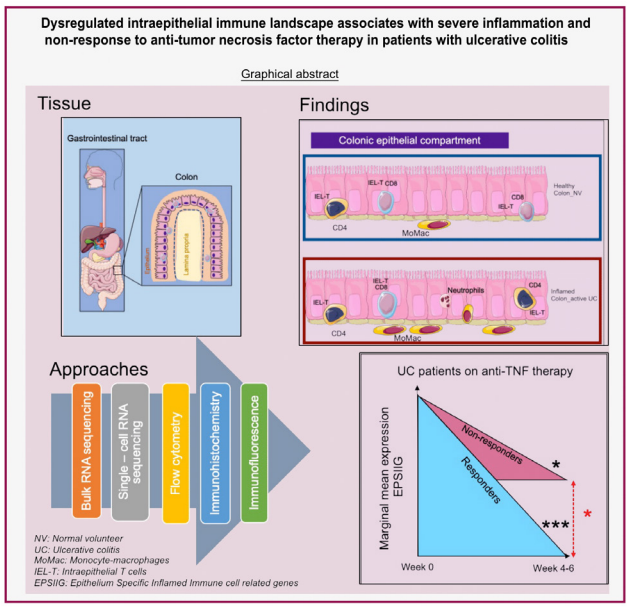
Dysregulated intraepithelial immune landscape associates with severe inflammation and non-response to anti-tumor necrosis factor therapy in patients with ulcerative colitis

Keywords: Intestine, immunology, inflammation, IBD, COVID-19

Abstract:

A subset of patients with ulcerative colitis (UC) do not response to anti-TNF inhibitors, underscoring the need for a deeper understanding of the cellular and molecular alterations in UC. While most of the studies on UC focus on the whole intestinal tissues or lamina propria, the intraepithelial immune cells (IIC) remain understudied. Using total RNA sequencing, single-cell RNA sequencing, quantitative histopathology, quantitative immunofluorescence staining and multiparametric flow cytometry across a primary clinical cohort of patients with UC (n=103) and normal volunteers (NV) (n=116), we identified an inflammation-associated altered cellular landscape within the colonic epithelial compartment (EC). We used an external cohort (VC-1, MSCCR) to correlate our inflammation-associated IIC gene signature (IICinf, differentially expressed genes upregulated in the inflamed samples compared to controls) with disease severity of UC patients. We found that the IICinf gene signature positively correlated with increasing clinical, endoscopic, and histological disease severity of IBD patients in the VC-1 and corresponded to myeloid cells, T cells and plasma cells. Diving deeper into the pathotype profiles, we saw an enrichment of neutrophils, inflammatory monocytes-macrophages, regulatory T cells and Th17 cells with a concomitant depletion of steady state populations of epithelial cells and gd-T cells near the inflamed epithelia. Finally, we projected our IICinf gene signature onto the treatment response in two independent clinical cohorts VC-2 and VC-3 consisting of UC patients on anti-TNF therapy and showed that epithelium enriched pathotypes from our single cell sequencing dataset associated with treatment response. Here, we have identified, previously unreported, immune cell dysregulation within the inflamed colonic epithelium of active UC patients and have deciphered the association of these pathotypes with treatment response. In conclusion, our study details altered intraepithelial immune cell dynamics in patients with UC and identifies epithelium-associated pathotypes as the primary drivers of anti-TNF response.



Myeloid cells drive inflammation and impact treatment response!
Credits: BioRender, Illustrator

PDF 13

GRACE LHAINEIKIM

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Floral transition: A bi-modal switch or a protracted process?

Keywords: Flowering, developmental plasticity, plant developmental genetics, apical dominance, lateral organ initiation

Abstract:

The compound shoot and the compound inflorescence of tomato are comprised of sequentially formed axillary branch systems. These distinct branch types, vegetative and floral respectively, are triggered to grow out with the onset of floral transition and reflect the lack of apical dominance imposed by apical floral meristems. We show here that the initial growth of vegetative sympodial meristem is evident at a time window after meristem doming is initiated but before floral organ primordia are visible. During that time, the apical meristem transcriptome is highly dynamic and comprised of several short-lived transient programs. Of these, sequential activation of PUCHI and LOB30 is found in the apical domain destined to become sympodial flower, and in the axil of the last leaf which is destined to become a vegetative sympodial shoot meristem. Targeted inactivation of both genes significantly delayed the initiation of both meristem types. Elimination of practically all short-lived floral transition programs by inactivation of vegetative expressed MADS-box genes resulted in similar, albeit stronger effects, culminating in the formation of a solitary flower instead of a compound inflorescence. As short-lived floral transition programs include both promoters and inhibitors of axillary branch systems initiation, a wide range of inflorescence architectures can form in tomato. This capacity may facilitate the rapid evolution and diverse forms of inflorescence shoots.

A gradual progression to flowering
Credits: Grace Lhaineikim

PDF 14
HARINATH DOODHI
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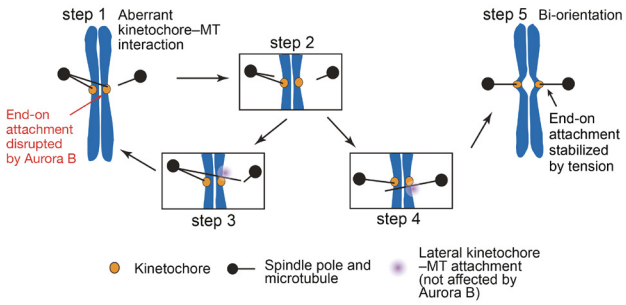
Reconstitution of sister kinetochores interaction with microtubules to study error correction during mitosis

Keywords: Mitosis, microtubule, kinetochore, error correction, motor proteins

Abstract:

For proper chromosome segregation, sister kinetochores must interact with microtubules from opposite spindle poles; this is called bi-orientation. To establish bi-orientation prior to chromosome segregation, any aberrant kinetochore–microtubule interaction must be resolved (error correction) by Aurora B kinase that phosphorylates outer kinetochore components. Aurora B differentially regulates kinetochore attachment to the microtubule plus end and its lateral side (end-on and lateral attachment). However, due to the dense microtubule network within the spindle in cells, the exchange of kinetochore-microtubule attachments could not be studied further. Recently, I reconstituted the kinetochore–microtubule interface in vitro by attaching Ndc80 protein complexes (Ndc80Cs) to a nanobead. The Ndc80C–nanobeads enabled the direct comparison of lateral and end-on MT attachment strengths and showed that Dam1 phosphorylation by Aurora B specifically weakens end-on attachments in comparison with lateral attachments (Doodhi et al., JCB 2021). Dam1 phosphorylation weakens its interaction with the Ndc80 complex and disrupts end-on attachment and promotes new lateral attachment leading to error correction. Though this study revealed a fundamental mechanism of error correction for the establishment of bi-orientation, similar reconstitutions with purified kinetochore particles showed different behaviour from Ndc80C-nanobeads. I will discuss how reconstituting interactions of a sister kinetochore pair with microtubules in vitro will address the mechanism of error correction by Aurora B kinase.



Swap and stop – Kinetochores play error correction with microtubules
Credits: Harinath Doodhi, Tomoyuki U Tanaka

PDF 15
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Structural investigations into the tubular invasion apparatus of parasitic microsporidia

Keywords: Cryo-electron microscopy, cryo-electron tomography, infection biology, microsporidia, evolutionary biology

Abstract:

Microsporidia are a group of obligate intracellular parasites that infect hosts ranging from arthropods to nematodes to chordates. Microsporidia also exemplify extreme reductive evolution, wherein deletion of numerous biochemical pathways otherwise considered essential has produced the smallest known eukaryotic genomes, reduced mitochondria called mitosomes, and a highly miniaturized cytoplasmic ribosome. Despite these drastic omissions, microsporidia have also evolved specialized mechanisms for invading and hijacking host cell systems. Among these, a microsporidia-specific organelle, the polar tube, is particularly noteworthy. During the extracellular spore stage, the polar tube is tightly packed in a spring-like fashion. Upon exposure to the right environmental stimuli, the spores germinate in an explosive tube firing to deliver the sporoplasm into the host cell. This unique infection apparatus comprises polar tube proteins (PTP1-6) and possesses surprising mechanical properties. However, the exact structural composition and organization of the tube and mechanism of sporoplasm delivery all remain unknown, partly due to the recalcitrant biochemical challenges in purifying and characterizing components of the polar tube. We structurally characterize germinated polar tubes in situ using cryo-electron tomography. During germination, which takes just about 1 second, the coiled polar tube rapidly everts to around 30 times the length of the spore and delivers the sporoplasm from otherwise inactive spores. Our work also uncovers real-time structural snapshots of sporoplasm delivery wherein hibernating ribosomes and other cellular complexes could be resolved unambiguously. Further, unseen structural details in the makeup of the polar tube and novel structural heterogeneity were observed.

PDF 16
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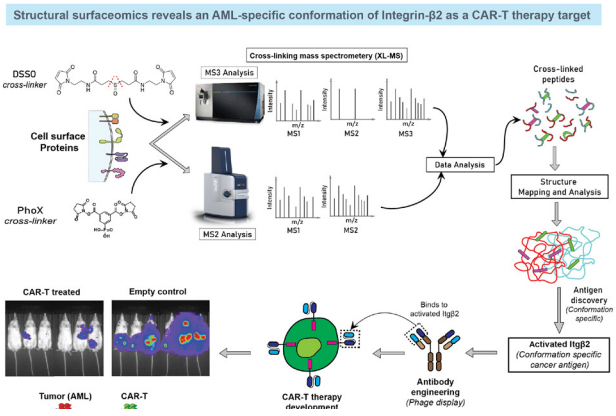
Structural surfaceomics reveals an AML-specific conformation of integrin-β2 as a CAR-T therapy target

Keywords: Proteomics, CAR-T therapy, Immunotherapy, Cancer and Antibody Engineering

Abstract:

Cellular therapies, particularly CAR-T therapies have led to immense excitement in cancer care. However, its clinical reach is still limited due to dearth of cancer specific markers. To this end, we developed a proteomics technology platform called "Structural Surfaceomics" by integrating Cell-Surface Proteomics (CSP) with Cross-linking Mass Spectrometry (XL-MS). This technology for the first time allows unbiased mining of protein-conformation specific cancer cell surface antigens, which are otherwise invisible to the canonical approaches such as RNA-seq or quantitative proteomics. This not only expands the toolkit of cancer target discovery but is also readily available for its applications to address therapeutic development for other diseases. For proof of concept, we successfully implemented this technology and identified active conformation of integrin-β2 as a novel therapeutic target for Acute Myeloid Leukemia (AML), a disease with poor prognosis, dismal outcome and unmet therapeutic need. Using phage display selection approach, we also engineered an antibody which binds specifically to this active conformation of integrin-β2 and not to its inactive form. This antibody was then reconstructed into single-chain variable fragment (scFV) to develop a novel CAR-T therapy for AML. The toxicity evaluations of this CAR-T were performed in human immune system (HIS) mice and were found to have very good safety profile compared to CD33-CAR-T (AML CAR-T with known severe toxicity, used as a technical control here), which led to massive depletion of human cells causing severe toxicity and myeloablation, substantiating our toxicity assessment approach. Notably, integrin-β2 is exclusively expressed in hematopoietic system, alleviating toxicity concerns elsewhere in the body. Our CAR-T was found to be very efficacious in vivo using patient derived xenograft (PDX) mice models. We have already been granted provisional US patent for this novel CAR-T therapy and is being currently pushed for clinical trials. (Manuscript under minor revision in Nature Cancer NATCANCER-A07532).



Structural surfaceomics reveals an AML-specific conformation of Integrin-β2 as a CAR-T therapy target
Credits: Kamal Mandal

PDF 17
KAMALESH KUMARI
Weizmann Institute of Science, Israel
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Website: https://www.weizmann.ac.il/Biomolecular_Sciences/Avinoam/group-members

Exocytosis by actomyosin-mediated vesicle membrane crumpling and sequestration

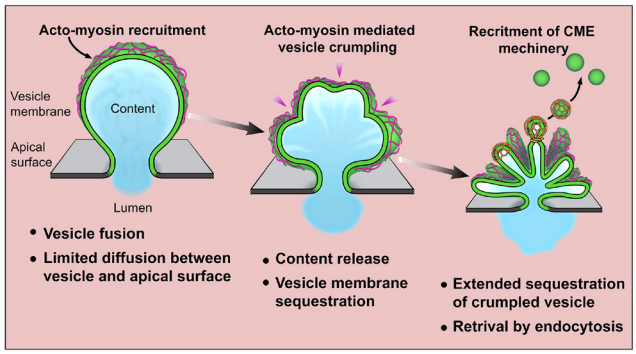
Keywords: Membrane trafficking in health and diseases, mechanisms of membrane remodeling, membrane homeostasis in health and diseases, exocrine secretion and its implications, correlative-light and electron microscopy (CLEM)

Abstract:

Exocrine secretion is involved in a plethora of functions ranging from cell signaling, metabolism to acting as protective barriers. Secretion by exocrine cells relies on large micron-scale vesicles, several of which fuse to a limiting apical surface at once. This will add large amounts of the membrane to the cell surface thus, maintaining the apical cell surface in terms of size, shape, and composition becomes challenging. Despite the prevalence and physiological significance of secretory organs, the mechanism involved in maintaining membrane hemostasis during large vesicle secretion was unknown.

We delved into this fundamental question, using a combination of live-cell super-resolution microscopy, and correlative-light and electron microscopy (CLEM) methodologies, on the Drosophila larval salivary glands and mouse acinar pancreas. We uncovered a novel pathway of exocytosis by vesicle membrane folding and sequestration mediated by actomyosin assembly on the vesicle, that prevents addition of membrane into apical surface. This highly folded vesicle membrane then undergoes targeted endocytosis that caters to apical membrane homeostasis (1,2).

Furthermore, we investigated the spatiotemporal organization of the actomyosin that is necessary to orchestrate exocytosis. We observed that myosin-II undergoes anisotropic clustering into a mesh-like organization on a relatively uniform F-actin coat, to generate the forces needed to crumple the vesicle. We next explored the signaling aspects that set up this myosin meshwork. We identified a new GEF on the vesicular membrane- RhoGEF2, the pattern of which governs the mechanistic framework for myosin organization. Thus, we identify key molecular elements involved in regulating membrane folding and homeostasis that has wide implications for secretory tissue functions.



Exocytosis by actomyosin-mediated vesicle membrane crumpling and sequestration
Credits: Kamalesh Kumari

References:

1. Exocytosis by vesicle crumpling maintains apical membrane homeostasis during exocrine secretion. K. Kamalesh, N. Scher, T. Biton, E. D. Schejter, B. Z. Shilo, O. Avinoam, Dev. Cell.56,1603-1616(2021).
2. A mechanochemical mechanism couples exocrine secretion to endocytic membrane retrieval. V. Haucke, Dev. Cell.56,1557-1559(2021).

PDF 18
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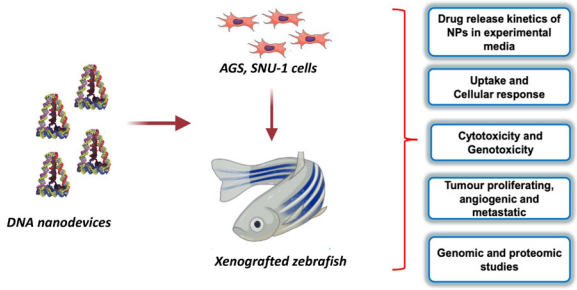
Development and validation of DNA-nanoparticles for early screening of cancer in zebrafish model

Keywords: DNA nanodevices, biosensing, bioimaging, zebrafish, therapeutics

Abstract:

DNA offers excellent control of matter at the nanoscale and biological activities imparted to it by complimentary biomolecules. More importantly, their use in nano theranostics, a field that combines diagnostics with therapy via drug or gene delivery in an all-in-one platform, has been applied extensively in recent years to provide personalized cancer treatments. Gastric cancer is the 4th leading malignancy and the 2nd leading cancer death worldwide [1-3]. Asian countries are most affected by GC with the least survival rate in the last five years, which indicates the aggressive potential of GC. Docetaxel is FDA approved chemotherapeutic for GC and in the present study, we will use docetaxel as a drug molecule for the GC. However, docetaxel leads to severe systemic toxicity such as alopecia, mucositis, fatigue, sensory neuropathy, fluid retention, and rash and hypersensitivity reactions. The current systemic administration of docetaxel is highly inefficient with poor tumour accumulation. Therefore, it is prudent to develop a highly efficient delivery system of the docetaxel conjugated with DNA functionalized nanoparticles (DNA-NPs), which can act on the localised tissue and reduce their systemic toxicity. Zebrafish have attracted researchers from around the globe to develop cancer models due to the visualisation of tumour growth. It has gained attention as it can be used for larger chemical molecule screening at reasonable costs compared to rodent models.



Schematic showing the proposed work plan
Credits: Microsoft power point

References:

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PDF 19

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Novel proteomic strategies for uncovering high-quality interactome networks on a proteome-scale

Keywords: Proteomics, systems biology, protein-protein interactions, cross-linking mass spectrometry, structural Biology

Abstract:

Motivation

Studying protein-protein interactions at systems-level provides a complete view of the synergy between different functional pathways. It also offers a holistic picture of rewiring of the interaction networks in different biological conditions such as disease phenotypes. Cross-linking mass spectrometry is a revolutionary proteomic technology that can uncover novel protein-protein interactions along with their structural dynamics at the whole proteome level. However, being a rapidly evolving high-throughput technology, it suffers from an alarmingly high false positive rates due to the lack of reliable data processing and quality-control tools.

Results

In this work we first identified and demonstrated the limitation of an established validation approach in filtering out potential false positives and addressed the problem by proposing a robust alternative validation framework1. Further, we discovered the issue of high false positive rates using the already published datasets in the literature. Additionally, we designed and developed a new cross-link search engine named 'MaXLinker' using a novel data processing approach (US patent issued, 2022). Our algorithm thoroughly outperformed the existing software in terms of both specificity and sensitivity of the cross-link identifications2. We further carried out a proteome-scale cross-linking mass spectrometry study on human cell lysates and reported the more than 9,300 cross-links at 1% false discovery rate, representing 585 unambiguous protein-protein interactions. Finally, we performed a systematic orthogonal experimental validation, confirming the robust quality of the novel interactions identified in our study.

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1. Yugandhar K, Wang Ting-Yi, Wierbowski SD, Shayhidin EE & Yu H. 2020. Structure-based validation can drastically underestimate error rate in proteome-wide cross-linking mass spectrometry studies. Nature Methods, 17:985-988.

2. Yugandhar K, Wang Ting-Yi, Leung AKY, Lanz MC, Motorykin I, Liang J, Shayhidin EE, Smolka MB, Zhang S & Yu H. 2020. MaXLinker: proteome-wide cross-link identifications with high specificity and sensitivity. Molecular & Cellular Proteomics 19: 554-568.

PDF 20
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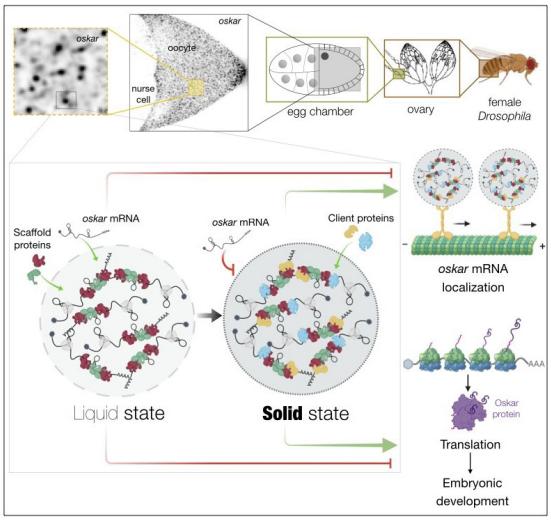
Functional regulation of RNA-protein condensates in the Drosophila female germline

Keywords: Bimolecular condensates, material properties, RNA-binding proteins, RNA localization, Germline.

Abstract:

Asymmetric localization of oskar RNA in the oocyte is crucial for embryonic patterning and germline formation in Drosophila. oskar mRNAs are transported as ribonucleoprotein (RNP) granules, wherein the mRNA is translationally repressed until localized. By using super-resolution microscopy, we show that oskar granules are spherical in shape, suggesting their initial assembly through liquid-liquid phase separation. However, tracking oskar granules in live oocytes reveal that they have solid-like physical properties, contrary to the typical liquid-like behavior of many phase-separated biomolecular condensates. Using purified oskar RNA and the scaffold granule proteins Bruno and Hrp48, we confirmed in vitro that oskar granules undergo a liquid-to-solid phase transition. Whereas the liquid phase allows RNA incorporation, the solid phase precludes incorporation of additional RNA while permitting RNA-dependent partitioning of client proteins. Therefore, fundamental questions arise as to the significance of the material properties of oskar RNPs during their assembly, transport and translation. By physically tethering the intrinsically disordered region of human Fused in Sarcoma (FUS) to oskar mRNA, we modulated the granule material properties in vivo and show that the resulting liquid-like properties impaired oskar localization and translation with severe consequences on embryonic development (1). Thus, combining biochemistry, cell biology and genetics, we address how physiological phase transitions shape RNA-protein condensates to regulate localization and expression of a maternal RNA that instructs germline formation.



Liquid-to-solid phase transition of oskar RNA granules is crucial for Drosophila embryonic development
Credits: Mainak Bose; Biorender

References:

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PDF 21
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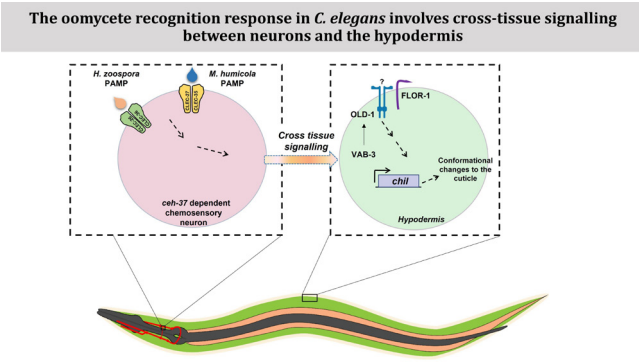
Identification of neuronal and epidermal determinants of immune signaling underlying oomycete recognition in C. elegans

Keywords: Innate Immunity, cell signaling, C. elegans, host-pathogen interaction, ageing

Abstract:

Innate immune responses can be triggered by the detection of pathogen-associated molecular patterns or damage-related host biomolecules, by specific host receptors present in specialized immune cells, such as macrophages and dendritic cells. In the absence of such cells in C. elegans, neuronal and epithelial cells play a role in recognition and defense in a pathogen-specific manner, however the exact machinery underlying these processes often remains elusive. We recently identified oomycetes as natural pathogens of C. elegans and described a protective transcriptional program that is likely activated by neuronal recognition of the pathogen leading to induction of multiple chitinase-like (chil) genes in the epidermis. CHIL proteins enable worms to modify their cuticle and thereby antagonize infection by reducing oomycete attachment. We performed a forward genetic screen to identify the molecular determinants of this neuron-to-epidermis signaling underlying oomycete recognition. We report that the response is initiated by activation of the C-type lectin receptors CLEC-27/CLEC-35 in chemosensory neurons, which are encoded by adjacent and co-transcribed genes in the genome. While the CLEC-27/CLEC-35 pair is required for recognition of the oomycete Myzocytiopsis humicola, another CLEC pair CLEC-26/CLEC-36 is required to detect the phylogenetically divergent oomycete Haptoglossa zoospora. Neuronal recognition is followed by activation of a kinase-pseudokinase pair in the epidermal membrane formed by OLD-1 and FLOR-1 respectively leading to the induction of chil genes in the epidermis. We also identify the PAX6 homolog VAB-3, commonly studied for its conserved role in animal development, as the transcription factor regulating old-1 gene expression, and consequently the response to oomycete recognition. Overall, our findings shed light on how neuron-to-epidermis communication shapes nematode's defense against oomycete pathogens.



The oomycete recognition response in C. elegans involves cross-tissue signalling between neurons and the hypodermis Credits: MS PowerPoint

PDF 22
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Autophagy protein Atg11 and spindle pole body component Spc72 help maintain astral microtubule integrity essential for high-fidelity chromosome segregation

Keywords: Spindle positioning, asymmetric cell division, ageing, astral microtubules, moonlighting function

Abstract:

By combining in silico analysis of known protein-protein interactions of autophagy (Atg)-related proteins with chromosome segregation machinery, and cellular fitness of autophagy mutants in the presence of thiabendazole, we identified Atg11 as a potential regulator of chromosome transmission in budding yeast. Cells lacking Atg11 exhibited a high rate of chromosome loss that is enhanced at an elevated temperature. Further analyses indicate a delayed anaphase onset and an inverted SPB inheritance in atg11Δ cells, having the old SPB in the mother and the newly formed one in the daughter. Time-lapse microscopy indicates Atg11 transiently localizing proximal to the old SPB. To probe whether Atg11 interacts with an SPB component, we explored possible interactions between Spc72 and Atg11 by bimolecular fluorescence complementation (BiFC) and yeast two-hybrid (Y2H) assays. These assays confirm the direct interaction between Atg11 and Spc72. Consistent with this, a subset of atg11Δ cells displayed the atypical localization of Spc72 and Kar9, a protein required for metaphase spindle positioning. Having established a possible interaction between Atg11 and proteins known to play roles in spindle positioning, we probed how Atg11 may contribute to this process. We demonstrate that loss of Atg11 led to shorter astral microtubules resulting in metaphase spindle positioning and alignment defects which further increased with the loss of Atg11 in spc72Δ cells. Taken together, our study implicates the role of Atg11 together with Spc72 in preserving astral microtubule integrity in *Saccharomyces cerevisiae*.

References:

1. Reza MH, Aggarwal R, Verma J, Chowdhury R, Manjithaya R, Sanyal K*. 2022. A moonlighting function of Atg11 in spindle positioning. bioRxiv (doi: https://doi.org/10.1101/2021.12.15.472744).
2. Reza MH*, Patkar R*, Sanyal K*. 2021. Vacuolar transporter Mnr2 safeguards organellar integrity in aged cells. Molecular Microbiology. doi: https://doi.org/10.1111/mmi.14776. (*Corresponding author)
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4. Yadav V, Yang F, Reza MH et al. 2019. Cellular dynamics and genomic identity of centromeres in cereal blast fungus. mBio10(4): e01581-19.

PDF 23
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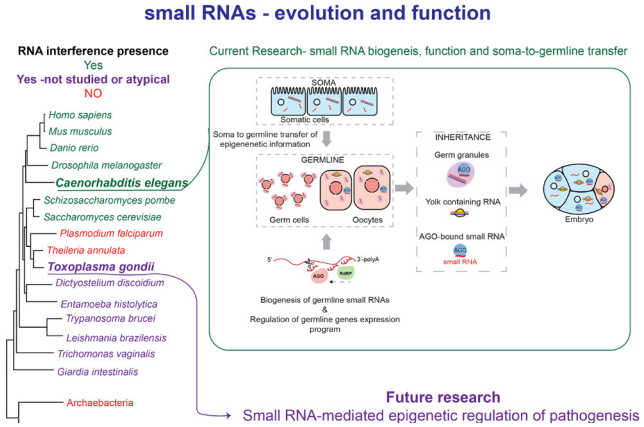
Argonaute navigating the balance between protein translation and small RNA synthesis.

Keywords: Argonaute, epigenetics, small RNAs, host-parasite interaction, infection

Abstract:

In *C. elegans* germline, thousands of mRNAs are concomitantly expressed with antisense sRNAs, which are loaded into the Argonaute CSR-1. Despite their essential functions for animal fertility and embryonic development, how CSR-1 sRNAs are produced remains unknown. I show that CSR-1 slicer activity is primarily involved in triggering the synthesis of sRNAs on the coding sequences of germline mRNAs. CSR-1-cleaved mRNAs prime the RNA-dependent RNA polymerase, EGO-1, to synthesize small RNAs in phase with ribosome translation. Moreover, codon optimality and efficient translation antagonize CSR-1 slicing and small RNA biogenesis. I propose that codon usage differences encoded into mRNA sequences might be a conserved strategy in eukaryotes to regulate small RNA biogenesis and Argonaute targeting. I further investigated the role of yolk delivery from the intestine to oocytes as a means for soma-to-germline transfer of small RNAs produced in response to pathogen exposure and their delivery to the embryo.

More recently, I used my experience in small RNA biology to initiate a new project to study the role of small RNAs in Covid-19 infection. We identified a SARS-CoV-2-derived microRNA, which is processed by host DICER and loaded by human argonaute protein. Finally, I showed that this viral microRNA can suppress the activation of interferon-stimulated genes to help evade the host immune response.



small RNAs - biogenesis, functions and soma-to-germline transfer to mediate epigenetic inheritance
Credits: Meetali Singh

References:

1. Singh, M., Cornes, E., Li, B., Quarato, P., Bourdon, L., Dingli, F., Loew, D., Proccacia, S. & Cecere, G. 2021. Translation and codon usage regulate Argonaute slicer activity to trigger small RNA biogenesis. Nat Commun 12, 3492.

PDF 24

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Biodiversity bigdata lab

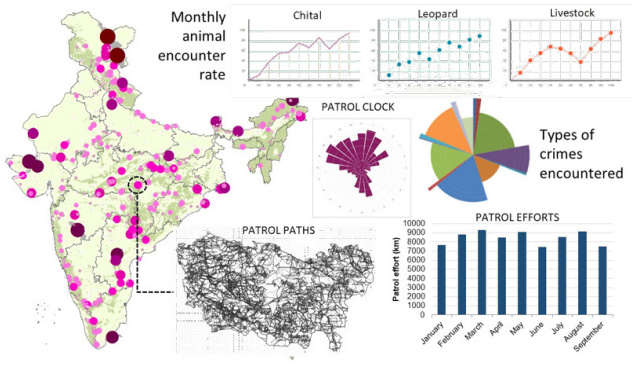
Keywords: Macroecology, conservation science, invasion ecology, nature-based solutions, ecoinformatics

Abstract:

Our enormously complex and diverse biosphere is rapidly losing its signature diversity and functions due to climate change and biodiversity loss. This compounded loss has cascading impacts on human welfare. While climate change is explicitly monitored providing evidence-based solutions to mitigate its impacts, the same is not true for biodiversity. Absence of systematic information impedes development of evidence-based solutions and actionable policies. One crucial hindrance is the absence of reliable assessment on changing ecosystems. Unlike climate change which can be effectively monitored using remote sensing, biodiversity necessitates continuous large-scale on ground assessments which is mostly resource intensive. My research shows outcomes of ingeniously planned continuous large-scale biodiversity assessments in India, smart technologies for these assessments and their global relevance.

Since 2006, around 380,000 km2 natural areas are sampled quadrennially, using systematic searches (522,996 km), camera traps (121,337 km2) and inventory plots (~150,000 plots). This information helped us model national-scale biodiversity patterns, notably megafauna recovery, spread of plant invasions, restoration priorities, potential for nature-recovery, and ecoinformatics tools for assisting ground actions. Subsequently, through our global networking we developed projections of rapidly changing tropics and potential for restoring key ecological mechanism to steward biodiversity amidst the rapid changes. We are highlighting these outcomes in the upcoming IPBES assessment for restoration of native biodiversity.

Using this experience, I wish to establish ecoinformatics research center to accommodate biodiversity Bigdata, remote sensing derivatives and citizen science initiatives to assist conservation decisions, prioritization for restoration investments and nature-based solutions. I present the idea to develop cutting-edge infrastructure to provision biodiversity evidence to scientific institutions, managers and policymakers; teach PhD and masters courses on ecoinformatics; and train conservation practitioners on evidence-based management. Catering the scientific curiosity and conservation decisions, we see this lab revolutionize biodiversity conservation.



Information on biodiversity, remote sensing, and management interventions will be integrated into computational servers from across the areas in India, to provide near real-time information on biodiversity changes. Biodiversity Bigdata lab can then help assess the effect of conservation actions like habitat management, patrolling, protection measures, etc. on recovery of megafauna or decline of human pressure in the area. It will provide interface to managers to assist evidence-based decisions.
Credits: Ninad Avinash Mungi

PDF 25

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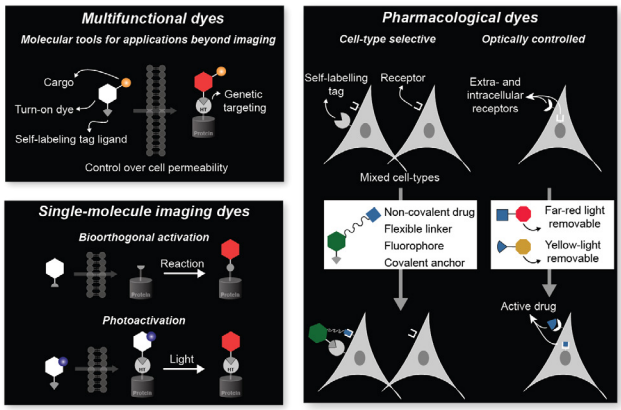
Next-generation fluorescent tools to visualize, measure, and manipulate biology

Keywords: Single-molecule imaging, multifunctional dyes, cell-type pharmacology, fluorescent dyes, cellular imaging

Abstract:

Advances in our understanding of cellular processes are often limited by our ability to visualize and manipulate biomolecules. Innovations in fluorescence microscopy have led to imaging and tracking individual fluorophore-tagged proteins with "superresolution". The demand for more photons is driving a renaissance in small-molecule fluorophores, which show superior properties to fluorescent proteins and can be deployed with genetic specificity. However, organic fluorophores that also allow manipulation of labeled proteins is still in its infancy. I have developed three sets of tools to fill this gap.

1. Multifunctional dyes leverage the brightness and tunable cell permeability of far-red Janelia Fluor (JF) dyes to push their utility from solely imaging labeled proteins to also manipulating them via the dye-linked cargo. We have demonstrated the potential of these genetically targetable dyes for live-cell imaging and affinity purification of intracellular proteins, recruiting proteins from heterochromatin to euchromatin, and recruiting transcription machinery to specific DNA sequences. These dyes are enabling superior reagents for cell biology and pharmacology; thereby, representing a new avenue in the development of dyes.
2. Single-molecule imaging dyes: I have developed two strategies to obtain fluorogenic (nonfluorescent to fluorescent) dyes to overcome the current limitations of activatable labels for localization microscopy of proteins. The first type becomes fluorescent upon photoactivation whereas the second type becomes fluorescent upon bioorthogonal click reaction with a genetically encoded non-canonical amino acid.
3. Cell-type and optical pharmacology: Most pharmacophores are studied in a population of mixed cell-types due to a lack of tools to unravel their activity on their protein targets in defined cell-types. I have combined dyes with pharmacologics for exerting optical control over their targeting to genetically defined cell-types, and for photopharmacological manipulation of endogenous receptors without any genetic manipulation.



A toolbox of dyes for genetic targeting, imaging, and manipulation of biomolecules
Credits: Pratik Kumar

PDF 26
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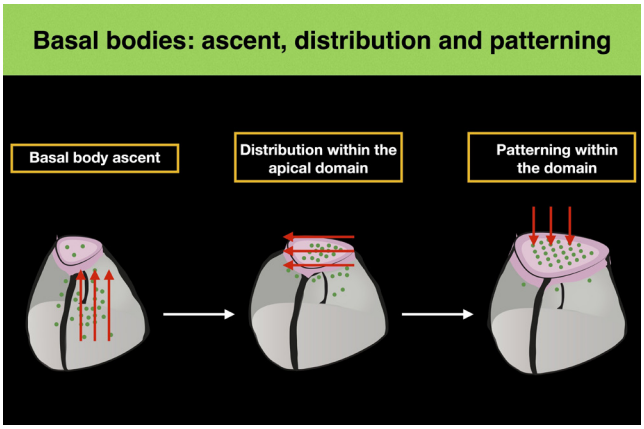
Distinct organisations of actin regulate the ascent, distribution and patterning of basal bodies

Keywords: Mechanics and dynamics of development, morphogenesis in embryos, self-organization phenomena, physics of active gels, quantitative imaging.

Abstract:

Motile cilia play a crucial role in properly distributing mucus and other cell secretions in the respiratory tract. Nucleation and anchoring of these motile cilia are carried out by centriole-like structures called basal bodies at the cell cortex on the apical side. These basal bodies are brought to the apical surface, distributed, and patterned, while the apical domain of the cell is expanding. But how these complex processes are executed simultaneously is not understood. Here, using a combination of imaging techniques and Xenopus embryonic epithelia as a model, we find actin to be the major driver of these processes. We show that actin reorganizes into cables and meshwork to perform such diverse tasks. Cables transport basal bodies from the basal to the apical side, and meshwork distributes the basal bodies across the apical domain of the cell while simultaneously expanding the apical domain. Results from high-resolution and high-speed imaging show a correlation between basal body dynamics and actin meshwork reorganization. While the basal bodies undergo diffusive behavior locally, they exhibit directional motion at the scale of the apical domain. We hypothesize that this complicated behavior could result from actin polymerization and cross-linking that generate pushing force for the apical domain expansion. We are currently developing a theoretical model to test this hypothesis and to understand the physical aspects of simultaneous force generation and patterning.



Basal bodies: ascent, distribution and patterning
Credits: Raghavan Thiagarajan

PDF 27
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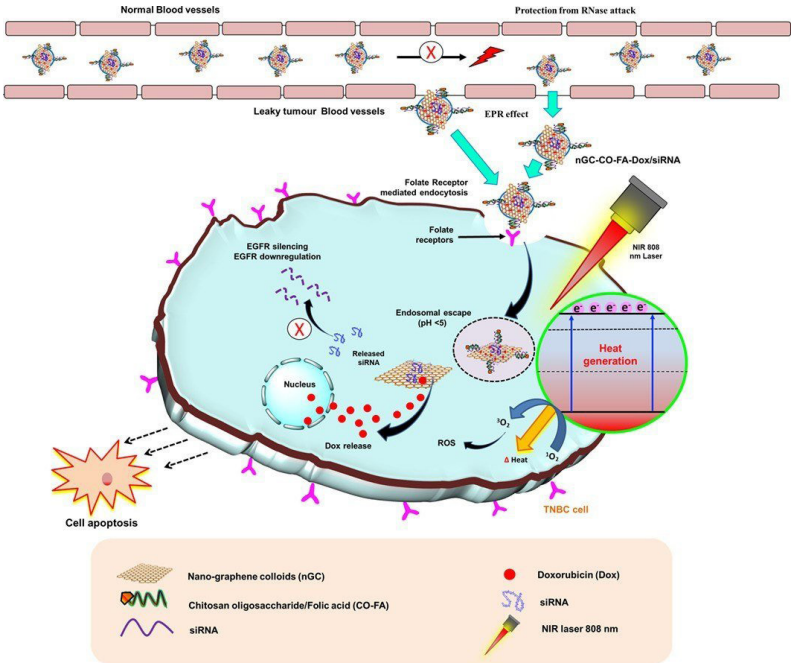
Laser activatable nanographene colloids for combined therapy of triple-negative breast cancer

Keywords: Oligonucleotide technology, gene delivery, drug delivery, combined cancer treatment, phototherapy

Abstract:

This investigation reports the green approach for developing laser activatable nanoscale-graphene colloids (nGC-CO-FA) for chemo-photothermal combined gene therapy of triple-negative breast cancer (TNBC). The nano colloid was found to be nanometric as characterized by SEM, AFM, and zeta sizer (68.2 ± 2.1 nm; 13.8 ± 1.2 mV). The doxorubicin (Dox) loaded employing hydrophobic interaction/π-π stacking showed >80% entrapment efficiency with a sustained pH-dependent drug release profile. It can efficiently incorporate siRNA and Dox and successfully co-localize them inside TNBC cells to obtain significant anticancer activity as evaluated using CCK-8 assay, apoptosis assay, cell cycle analysis, cellular uptake, fluorescence assay, endosomal escape study, DNA content analysis, and gene silencing efficacy studies. nGC-CO-FA/Dox/siRNA released the Dox in temperature-and a pH-responsive manner following NIR-808 laser irradiation. The synergistic photo-chemo-gene therapy using near infrared-808 nm laser (NIR-808) irradiation was found to be more effective as compared to without NIR-808 laser-treated counterparts (ΔT: 37 ± 1.1 ◦C → to 49.2 ± 3.1 ◦C; 10 min; 0.5 W/cm2), suggesting the pivotal role of photothermal combined gene-therapy in the treatment of TNBC.



Delivery of gene, drug and heat inside cancer cell
Credits: Maheshwari R

PDF 28
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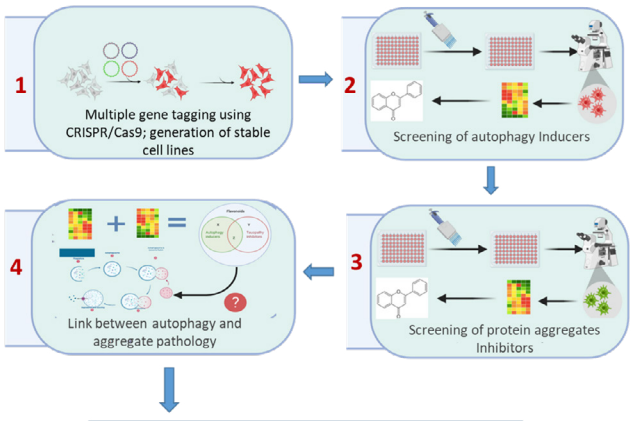
High-through screening of natural compounds as the potential autophagy modulators in regulation of Alzheimer's disease using developed stable iso-genic tagged cells

Keywords: Animal cell biology, autophagy, isogenic stable cell lines, neurodegeneration, phytochemicals

Abstract:

In this study, we used CRISPaint Technology, a CRISPR/Cas9 gene-editing tool, to make tagged cells. It allowed us to tag proteins at their C-terminal. Using this method, we tagged several genes at a time that are involved in autophagy (LC3B, SQSTM, ATGs and LAMP1 etc.) and other associated pathways linking both (AMPK, mTOR, and PI3K, etc.). We used four plasmids carrying the Cas9 gene, target gene gRNA, donor gRNA, and donor (mCherry/ GFP). The Cas9 is an endonuclease, which cuts the target gene and donor molecule at a specific site recognized by target gene gRNA and donor gRNA, respectively. To generate tagged cells, we co-transfected all four plasmids. The tagged cells were selected by treating cells with the drug (e.g., puromycin). Since donor plasmid carries a selection marker (e.g., puromycin resistance gene), only tagged cells were live after drug selection. These are the only cells expressing the physiological level of the tagged proteins. To tag many proteins, we used different target genes' gRNA for the gene supposed to be tagged. Further, for the generation of monoclonal cell lines, single cell cloning was performed for each tagged cell lines. "A single cell clone is essentially generated from an original 'multiclonal' population, but has been separated from the rest in order to create a pure, clonal population that is genetically identical." We picked up some clones of HEK293T tagged at various genes and allowed them to grow separately for generation of monoclonal cell lines. These monoclonal cell lines will be useful for high throughput screening of different type of molecules, compounds, phytochemicals.



Schematic workflow of the study
Credits: Ritu Varshney

PDF 29
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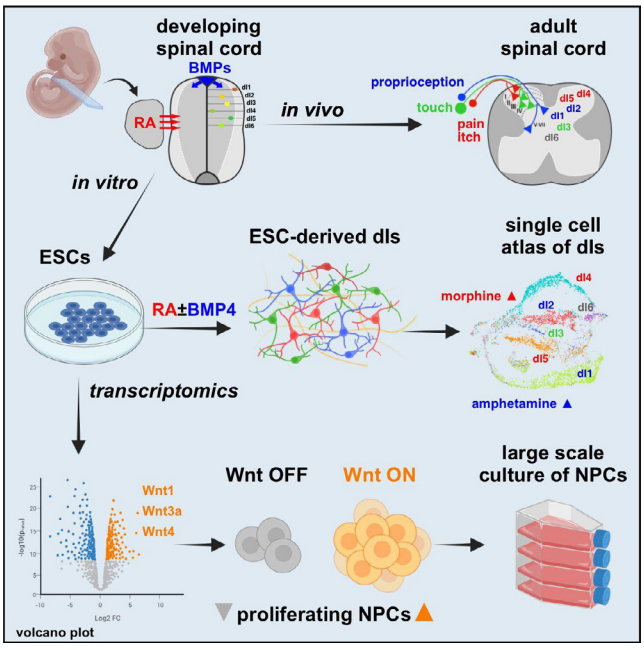
The stem cell model of dorsal spinal cord development paves a way to investigate complex sensory disorders in vitro.

Keywords: Embryonic stem cells, neural development and disease modeling, induced pluripotent stem cells, somatosensory circuits, embryonic development

Abstract:

Somatosensory circuits in the spinal cord allow us to sense the world around us through touch and pain and the ability to move coordinately. These circuits emerge during early spinal cord development when the growth factors like retinoic acid (RA) and bone morphogenetic proteins (BMPs) specify six classes of dorsal sensory interneurons (dI1-6). Damage to these interneuron circuits, either from spinal cord injuries or neurodegeneration, leads to paralysis and loss of sensation. While no treatments are available to regain sensation after injury or diseases, stem cell-based regenerative therapies offer hope by providing specific cell types to rebuild the lost sensory circuits. I reproduced the logic of dorsal spinal cord development in vitro using two growth factors, retinoic acid (RA) and bone morphogenetic protein 4 (BMP4), and obtained the entire complement of dorsal interneurons (dI1-dI6) from both mouse and human embryonic stem cells (ESCs). Through bioinformatic approaches to compare in vivo and in vitro datasets, I have revealed that these ESC-derived dIs are strikingly similar to their endogenous counterparts and contain maturation signatures that include the neuropeptides that regulate the sensory processing of pain, itch, and temperature. Novel signatures were also identified, including distinct psychoactive and analgesic drug-related signaling pathways in different dI populations, opening new horizons for drug testing platforms to identify new analgesic compounds. The in vitro modeling of spinal cord development further allowed us to identify the mechanisms that regulate progenitor proliferation and subtype identity, enabling the mass production of dIs for regenerative and disease-modeling applications. Using these methods, we are now utilizing stem cell-derived dIs to model complex neurogenetic disorders affecting human sensation, such as autism and chronic pain.



Stem cell modeling of spinal cord development for regenerative and in vitro modeling of sensory disorders.
Credits: Sandeep Gupta

PDF 30
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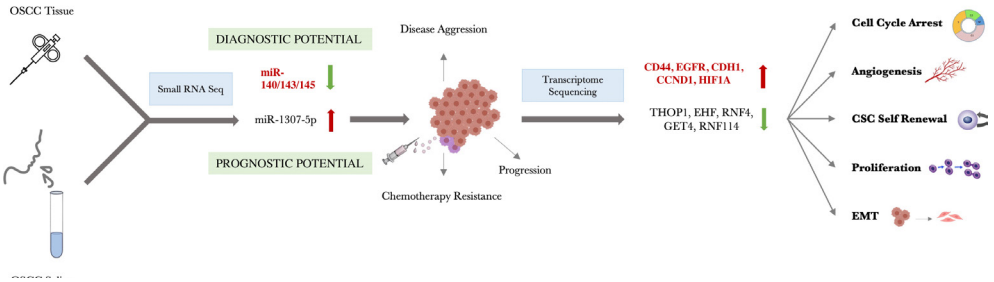
Identification of potential salivary exosomal miRNA signature that predicts early risk prediction and poor prognosis in oral cancer patients: A liquid biopsy approach

Keywords: Head and neck cancers, early detection, liquid biopsies, cell free DNA , exosomal miRNAs

Abstract:

Overall survival rates of oral cancer patients have been dismal. This is largely attributed to late-stage diagnosis and absence of disease-specific biomarkers. Hence, it is imperative to identify biomarkers that can be used for early diagnosis. Salivary exosomal miRNAs as biomarkers enable repeated sampling, real-time disease monitoring and assessment of therapeutic response compared to conventional tissue biopsies. In this study, we identified miRNAs from salivary exosomes of oral cancer patients as biomarkers that will aid in improved patient outcomes using a liquid biopsy approach. Additionally, we explored miRNA-mRNA regulatory networks using transcriptome and miRnome sequencing and evaluated the functional role of these networks in oral carcinomas.
Three miRNAs (miR-140, miR-143, and miR-145) were downregulated in salivary exosomes of oral cancer patients compared to normal controls. Additionally, miR-1307-5p was exclusively expressed in tumours and salivary exosomes of oral cancer patients and not in their non-cancerous counterparts. These miRNAs showed a significant clinical correlation with disease progression, aggressiveness, and chemo-resistance in oral squamous cell carcinoma patients. Network analysis of target genes of the three miRNA signature identified hub genes HIF1a, CDH1, CD44, EGFR, and CCND1 known to be responsible for oral cancer progression. However, miRNA-1307-5p was responsible for suppressing expression of THOP1, EHF, RNF4, GET4, and RNF114 which have not been previously reported in oral cancers. In-vitro studies using anti-miRs for these 3 miRNAs suggest a role of these miRNAs in modulating proliferation, cell cycle regulation, induction of apoptosis, migration, invasive potential, epithelial mesenchymal transition and dysregulating various signalling pathways in oral cancers.
Our findings reveal the diagnostic potential of salivary exosomal miR-140/143/145 and the potential of miRNA-1307-5p for predicting tumour progression and poor patient survival in oral cancers. This study uncovers putative mechanisms by which dysregulation of these miRNAs could effectively convert a normal epithelial phenotype into an oral carcinoma.



Schematic representation of the potential clinical and functional role of identified salivary exosomal miRNAs in early risk prediction and poor prognosis of oral cancer patients
Credits: N/A

PDF 31
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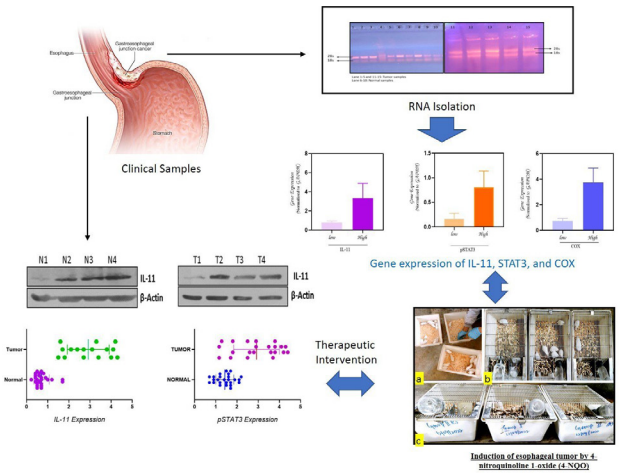
The significant role of interleukin-11 and downstream signalling molecules in the pathogenesis and treatment of esophageal cancer

Keywords: Cancer, signaling, transcriptomics, metagenomics, therapeutics

Abstract:

Interleukin IL-11 drives many of cancer 'hallmarks' through downstream constitutive activation of a STAT3 signaling pathway in epithelial cancers like Esophageal cancer (EC) cells and prevents cell apoptosis and stimulates cell proliferation in tumor progression. An effort to develop drugs targeting STAT3-activating cytokines for the treatment of EC is very promising and the IL-11 antagonist seems the best target in this regard. In the current study Twenty-five samples (Tumor and Adjacent) were collected from SKIMS tertiary care hospital. Patient history, consent, and clinical parameters were recorded/noted. Among 25 patients 18 are males and 7 were females, 13 (52%) patients were smokers and 12 (48%) were Non-smokers, 12 (48%) had adenocarcinoma and 13 (52%) had squamous cell carcinomas. Among IL-11, 3 patients had below 1-fold (low) mRNA expression and 22 had higher gene expression with 4-fold (average) mRNA expression and the difference was significant ($p<0.05$). IL-11, pSTAT3, and COX mRNA expression in 25 individual human esophageal cancer samples were found significantly higher than in adjacent normal tissues ($p<0.05$). The protein expression of IL-11 was upregulated in tumor samples than in adjacent normal tissues, there was a 2-4-fold higher protein expression of 1L-11 in tumor samples than in normal. The same pattern of higher protein expression was seen in pSTAT3, where in tumor samples there was a 2-5-fold higher expression than adjacent normal. The incidence of cancer and expression of signaling molecules was higher in smokers and salt tea consumers. Men had a higher rate of esophageal cancer than women, with significant differences in nutritional status, socioeconomic position, and cigarette/tobacco usage. Targeting IL-11 and/or its receptor in conjunction with other effective anticancer medicines appears to be a promising therapeutic target for esophageal cancer treatment.



IL-11, pSTAT3, and COX mRNA and protein expression in human esophageal cancer samples
Credits: Sheikh Mansoor

PDF 32
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Discovering novel host-virus interactions using functional proteomics

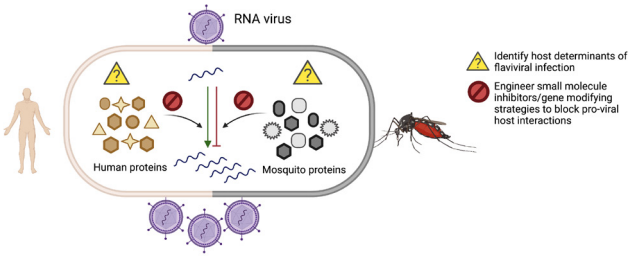
Keywords: Virology, RNA biology, mosquito, molecular biology

Abstract:

Mosquito borne flaviviruses, such as Dengue virus (DENV) and Zika virus are a growing threat to human health. They are able to subvert biochemical machineries from both human and mosquito hosts for efficient propagation. Identifying the host factors co-opted by these viruses and understanding the underlying mechanisms is critical to developing antiviral interventions.

We used a biotinylation based approach (RaPID) to identify proteins that interact with DENV 3' untranslated region (3'UTR) in mosquito cells and tested the impact of selected proteins on DENV infection after dsRNA-mediated gene depletion. Among the tested proteins, partial knockdown of Sec61A1 (a known proviral factor for DENV) and Loquacious (Loqs) proteins resulted in a significant decrease in DENV viral titers. We validated the interaction of Loqs with DENV RNA through RNA immunoprecipitation and in-situ hybridization experiments. Subcellular fractionation experiments demonstrated Loqs to be localized to the endoplasmic reticulum which is the primary site of viral translation and replication. While depletion of Loqs did not affect association of DENV RNA with the polysomes, it resulted in a decrease in the amount of newly synthesized viral RNA in metabolic labeling experiments, suggesting a greater role for Loqs in viral RNA replication than translation.

In addition to DENV, depletion of Loqs also inhibited replication of other flaviviruses including Zika virus and Yellow fever virus but didn't affect Chikungunya virus (alphavirus) suggesting that Loqs is an important host factor for general flaviviral replication.



Discovery of novel host factors that determine viral infection and disease phenotypes across species
Credits: BioRender.com

PDF 33

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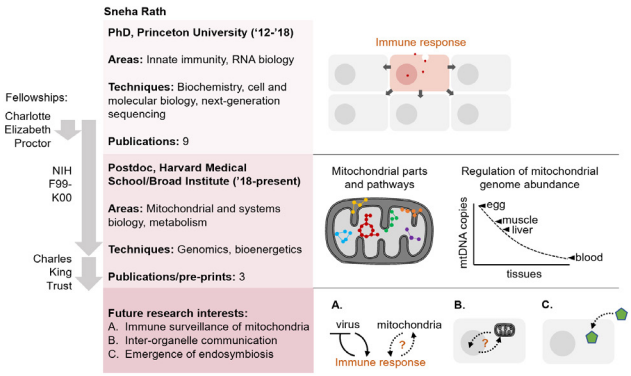
A systems approach to discover mechanisms of mitochondrial genome maintenance

Keywords: Genomics, mitochondrial biology, inter-organelle communication, endosymbiosis, innate immunity

Abstract:

Mitochondria evolved from a bacterial endosymbiont to become multi-functional hubs of respiration, metabolism, and signaling. Over this ~1.5-billion-year endosymbiotic relationship, most ancestral genes were transferred to the nucleus or lost altogether. However, few genes still remain in the mitochondrion, separate from nuclear DNA, in almost all eukaryotes. The human mitochondrial genome (mtDNA) encodes 13 core proteins in the respiratory chain and varies up to 10,000-fold in copy number from ~100 in blood to ~half a million in the unfertilized egg. Each cell maintains an intrinsic, optimal mtDNA setpoint via yet unknown mechanisms. A decline in this setpoint causes rare but severe disorders with no proven therapies and underlies the common age-related mitochondrial dysfunction with relevance to Parkinson's and Alzheimer's Disease. My postdoctoral work focuses on how cells sense and regulate mtDNA copy number and explores mechanisms to cope with mtDNA loss. I study the natural phenomenon where cells depleted of their mtDNA tend to recover and re-establish their initial mtDNA copy number. First, I have leveraged this system to dissect the minimal bioenergetic requirements of mtDNA replication. Second, I have profiled this trajectory of reversible mtDNA loss at fine timescales in multi-omic dimensions. This work has revealed distinct, staged responses that start locally and escalate to impairment of several extra-mitochondrial processes. Third, I have analyzed the genome-wide map of perturbations that aggravate or buffer mtDNA loss – my follow-up work now dissects the underlying mechanisms and interdependence of these genetic interactions. Collectively, my molecular insight into how cells sense and cope with mtDNA loss can inform treatment of mtDNA depletion syndrome and elucidates a general cellular logic for the maintenance of extra-nuclear genomes.



My scientific trajectory

PDF 34

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NGS quantification of viral clonal architecture identifies HTLV-1 asymptomatic carriers at high risk of progression to aggressive leukemia

Keywords: Bioinformatics, genomics, annotation, biodiversity, viral oncogenesis, evolution.

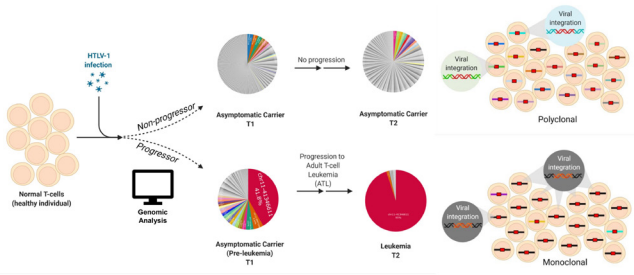
Abstract:

Background:
Human T-cell Leukemia Virus-1-infected asymptomatic carriers are characterized by the presence of multiple T-cell clones, each characterized by a unique proviral integration site (IS) in the host genome. Only ~20% of "high-risk carriers" (identified as having a high PVL, ⩾ 4 HTLV-1 copies per 100 PBMCs) will progress to Adult T-cell Leukemia (ATL), a treatment-refractory aggressive disease. There is an urgent need for a molecular tool that can better risk-stratify these patients, thereby avoiding unwarranted fear.
Our group has developed a method for quantifying the clonal distribution of IS ("clonality") using linker-mediated PCR followed by next generation sequencing (NGS), making it clinically applicable for diagnosis of leukemic patients with monoclonal architecture. We hypothesized that clonality sequencing can be used to identify the premalignant stage of ATL in carriers by detecting the presence of the dominant ATL precursor clone prior to the onset of symptoms.

Methods:
We studied a unique cohort of HTLV-1-infected individuals enrolled in the JSPFAD survey initiated in Japan in 2002. We report the analysis of longitudinal samples obtained from high PVL asymptomatic carriers who subsequently developed ATL and compare these with high and low PVL carrier groups followed over an equivalent period and who did not develop malignancy. We explored the potential association between clonality and the patients' clinical outcome many years later.

Results:
i) NGS clonality outperforms PVL as a predictive biomarker of progression towards an aggressive disease, ii) clonality better discriminates asymptomatic carriers from patients with indolent ATL, iii) >30% of progressors harbour multiple integrations within a single predominant T-cell clone as determined by TCR NGS. Clonality is also powerful in identification of potential progressors with multiple insertions or those with low PVL.

Conclusion:
Monitoring clonality signatures in HTLV-1 asymptomatic carriers will allow individuals with increased risk of ATL to be better managed presumptively.



Viral integration site clonality aids HTLV-1 linked leukemia risk assessment
Credits: Created with BioRender.com

PDF 35
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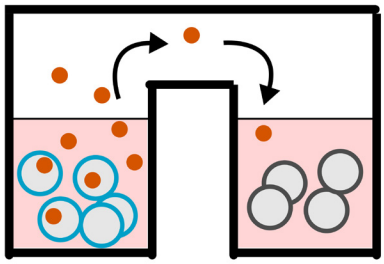
Deciphering a novel pathway of sulfide metabolism in budding yeast

Keywords: Redox biology, metabolic interactions, microbial communities, cellular metabolism, budding yeast

Abstract:

Cells often interact via secreted metabolites. If the metabolites are gaseous, they could mediate interactions between seemingly unconnected cell populations. Hydrogen sulfide is one such volatile metabolite that nearly all cell types generate by degrading sulfur-containing amino acids. The gas can cross membranes unassisted and lead to varied effects: High doses of sulfide can poison eukaryotic cells, while lower doses can promote longevity in yeast, antibiotic resistance in bacteria and epithelial integrity in the human gut. Here, I will discuss how sulfide can mediate cell-cell interactions in Saccharomyces cerevisiae by triggering a hitherto unknown pathway of sulfur assimilation. The current understanding of yeast sulfur metabolism asserts that the enzyme Met17 is necessary for yeast to assimilate inorganic sulfate. However, we found that Met17-deficient yeast can in fact grow on sulfate, albeit only at high initial cell densities. I will show that this density-dependent growth is driven by a sulfide-sensitive pathway, and discuss how we seek to understand the mechanisms of this pathway via quantitative experiments and modelling. We hope that this work will not only reveal novel aspects of yeast sulfur metabolism, but will also help us develop quantitative tools to study other gas-mediated microbial interactions.



Gaseous metabolites can mediate interactions between seemingly unconnected microbial populations

PDF 36

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A novel microneedle-based device for painless diabetes management

Keywords: Microneedles, painless drug delivery, transdermal/intradermal drug delivery, insulin injections, effective diabetes control

Abstract:

Pain and repeated injection-associated dermal changes are major concern for diabetic patients. Tissue damage in dermal layers of skin due to repeated injections with conventional syringes causes skin fibrosis or scar tissue formation. If left untreated, dermal fibrosis can lead to abnormal insulin/drug absorption and other associated problems. Rotating the injection sites and use of fresh needles are the clinical recommendations to prevent dermal fibrosis. We have developed an innovative hollow-microneedle (MN)-based device that can fit into any standard luer slip syringe for generic drug delivery. The importance of specialized needle profile and skin gripping has been taken into consideration for developing this successful hollow MN-based device. For the injections to remain painless, the device is designed to achieve intradermal delivery of drugs with injection depths in the sub-millimeter range (600 to 800 µm). The painless nature and efficient drug delivery have been demonstrated in our preclinical studies of SD rats. The safety and long-term usage of our device have been compared with conventional insulin syringes confirming its clinical suitability. Moreover, the design features in the device cause minimal disruption in the existing injection techniques, hence minimizing the training requirements for healthcare professionals for reliable intradermal delivery of various drugs.

PDF 37
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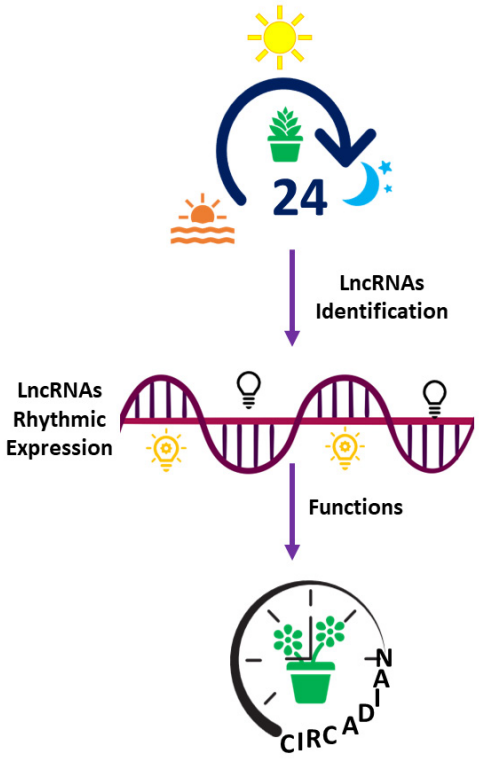
Rhythmic expression of lncRNAs and its function in floral development and the circadian clock.

Keywords: Plant molecular biology, epigenetics & Chromatin biology, gene regulation, chromatin interactome, long non-coding RNA

Abstract:

The circadian clock is regulated by signaling networks that enhance a plant's ability to coordinate internal events with the external environment. In this study, we examine the rhythmic expression of long non-coding RNAs (lncRNAs) using multiple transcriptomes of Arabidopsis thaliana in the diel light cycle and integrated this information to have a better understanding of the functions of lncRNAs in regulating the circadian clock. We identified 968, 1050, and 998 lncRNAs at 8h light, 16h light and 8h dark conditions, respectively. Among these, 423, 486, and 417 lncRNAs were uniquely present at 8h light, 16h light, and 8h dark, respectively, whereas 334 lncRNAs were common under the three conditions. The specificity of identified lncRNAs under different light conditions was verified using qRT-PCR. The identified lncRNAs were less GC-rich and expressed at a significantly lower level than the mRNAs of protein-coding genes. In addition, we identified enriched motifs in lncRNA transcribing regions that were associated with light-responsive genes (SORLREP and SORLIP), flower development (AGAMOUS), and circadian clock (CCA1) under all three light conditions. We identified 10 and 12 different lncRNAs targeting different miRNAs with perfect and interrupted complementarity (endogenous target mimic). These predicted lncRNA-interacting miRNAs govern the function of a set of genes involved in the developmental process, reproductive structure development, gene silencing and transcription regulation. We demonstrated that the lncRNA transcribing regions were enriched for epigenetic marks such as H3.3, H3K4me2, H3K4me3, H4K16ac, H3K36ac, H3K56ac and depleted for heterochromatic (H3K9me2 and H3K27me1) and repressive (H3K27me3) histone modifications. Further, we found that hypermethylated genomic regions negatively correlated with lncRNA transcribing regions. Overall, our study showed that lncRNAs expressed corresponding to the diel light cycle are implicated in regulating the circadian rhythm and governing the developmental stage-specific growth.



Rhythmic expression of lncRNAs and its function in floral development and the circadian clock.
Credits: Vikash Kumar Yadav

PDF 38
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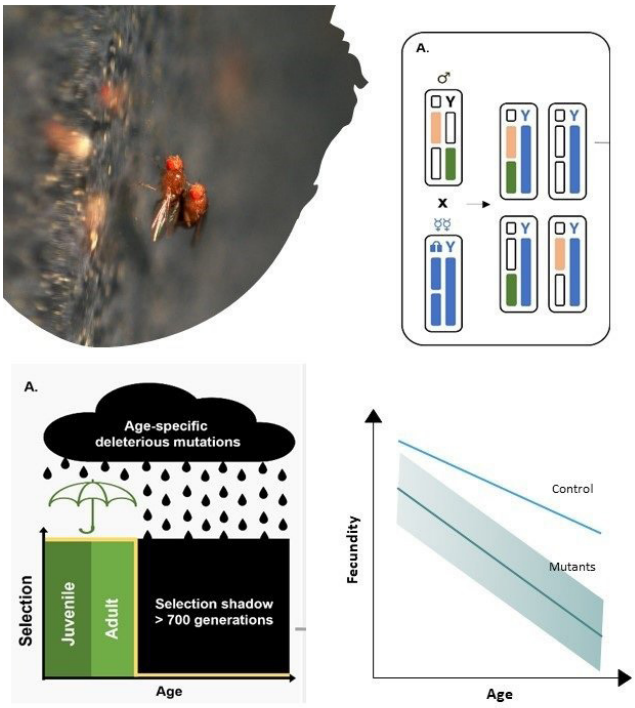
Age-specific effects of spontaneous deleterious mutations in Drosophila melanogaster

Keywords: Life-history evolution, behaviour, cognitive ageing, climate change, local adaptation

Abstract:

Ageing is a progressive decline of organismal performance with age and is a near to universal feature in multicellular organisms. Evolution of ageing is explained by the fact that natural selection cannot act beyond the reproductive age of organisms. Hence selection is blind to most mutations that accumulate with age; over many generations such mutations may have a deleterious late-life effect. This insight led to the formulation of two evolutionary theories of ageing in the 1950s viz. Mutation Accumulation (MA) and Antagonistic Pleiotropy (AP). The MA and AP are not mutually exclusive, and agree that ageing is caused by deleterious mutations that are restricted to late-life; support has been found for both of them. However, a recurrent finding in many ageing studies is a positive genetic correlation between early and late life performance, termed 'positive pleiotropy' (PP). Recently developed models conclude that ageing is caused by deleterious mutations that have a small early-life negative effect, which then gradually becomes more negative with age – a possible explanation for PP. I simultaneously tested PP, MA and AP ageing theories, using a versatile fruit-fly genetic system. I hypothesized that spontaneous deleterious mutations, in general, cause ageing through negative early-life effects that increase with age. I tested this hypothesis using a large, outbred, lab-adapted population and a novel protocol that allows spontaneous mutation accumulation (SMA) in their heterozygous state across entire haploid genomes. I show that after 27 generations, deleterious mutations indeed accumulated in 31 different SMA lines. Early-life mutations have constant effect regardless of age, unlike the original assumption. The pattern seen can be explained by MA and AP groups of deleterious mutations cancelling out later in life, leading to stabilization of ageing rates. The overall trend in my study suggests that deleterious mutations do not increase its negative effects with age



The evolution of ageing through mutations with age-specific effects
Credits: Vinesh N Shenoi and Urban Friberg

PDF 39
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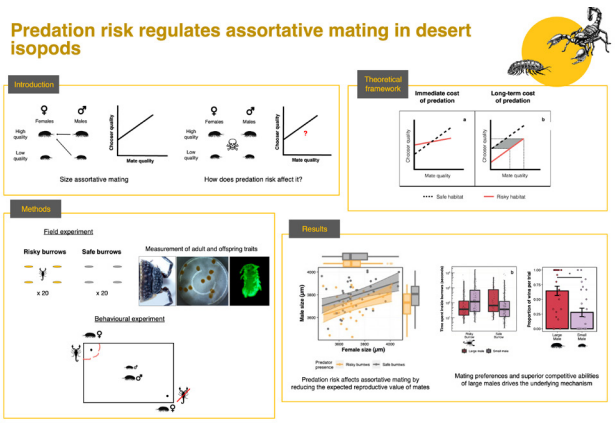
Predation risk regulates assortative mating in a desert isopod

Keywords: Predator-prey interactions, reproductive behavioural ecology, ecosystem functioning, field ecology, mesocosm experiments

Abstract:

Animals exhibit size assortative mating (SAM), but how predation affects it remains largely unknown. We hypothesized that predation risk may turn prey less choosy, thereby disrupting SAM, or reduce the reproductive value of mates, maintaining SAM but with different size ratio between mates. We tested these hypotheses in desert isopods in the Negev desert. They are crustaceans that live in burrows and exhibit male mate choice. We conducted a manipulative field experiment by digging burrows and introducing live scorpions near half of them. We found that isopods under predation risk maintained SAM, but males were on average smaller for a given female size. Fewer isopod pairs were formed in risky sites but there were no differences in female sizes and progeny number, size, and age near and away from scorpion burrows. Therefore, we find that males anticipated future costs of predation leading to an equal fitness choice between high quality mates in risky sites and lower quality mates in safer sites. A complementary behavioural experiment revealed that bigger males prefer safe burrows and won more male-male contests indicating competition to be the driving mechanism (Torsekar VR, Zaguri M and Hawlena D. 2022. Predation risk regulates prey assortative mating by reducing the expected reproductive value of mates. Ecology, p.e3869). Finally, in a follow up field experiment we investigated whether isopods proactively choose habitats that match their own quality, thereby exhibiting 'prudent habitat choice'. Preliminary results suggest that indeed smaller individuals prefer risky habitats without first competing for safer habitats (Torsekar VR, Lajmi A and Hawlena D, Prudent habitat choice in response to predation risk in desert isopods. In Prep.). Overall, our findings highlight that predation risk weakens SAM by affecting male-male competition, and this may be driven by habitat choice rather than mate choice.



Predation risk regulates assortative mating in a desert isopod
Credits: Viraj R Torsekar

PDF 40
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Indian Institute of Science, India
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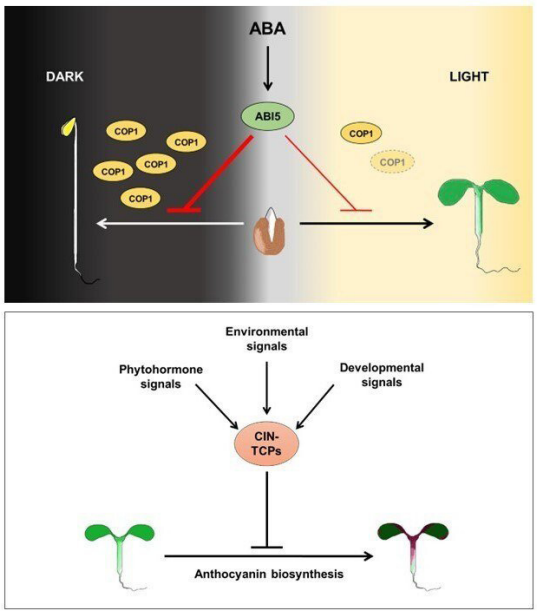
Lights, Colors, and Resilience: integration of environmental cues with adaptive responses in plants under abiotic stress conditions

Keywords: Photobiology, hormonal signaling, flavonoids, abiotic stress, agriculture

Abstract:

Under stress conditions, plants accumulate the phytohormone abscisic acid (ABA) which enhances their survival by inhibiting seed germination and controlling post-germination seedling growth. Light is an environmental signal that has a tremendous influence on early seedling development. However, the effect of light on ABA-induced post-germination growth arrest has not been clearly understood. We identified that ABA-mediated inhibition of early seedling development in Arabidopsis is greater in darkness as compared to light conditions. CONSTITUTIVELY PHOTOMORPHOGENIC1 (COP1), a protein that is prevalent in darkness and suppresses light signaling, was found responsible for the enhanced ABA sensitivity in dark conditions. COP1 activates ABA-responsive gene expression by promoting the binding of the prominent ABA-responsive transcription factor ABSCISIC ACID INSENSITIVE 5 (ABI5) on its target promoters. COP1 interacts with the master light signaling factor ELONGATED HYPOCOTYL5 (HY5) and mediates its proteasome-mediated degradation. We identified that HY5 suppresses ABA response during post-germination development, acting downstream to COP1. Together, these findings unveil the molecular interactions between light and ABA signaling pathways during early seedling development.
In addition to the adjustments in growth and development, plants accumulate protective flavonoid compounds, including red-blue-colored anthocyanin pigments, to enhance stress tolerance. The biosynthesis of flavonoids is tightly controlled, as their overaccumulation can inhibit plant growth. We have identified that members of the TEOSINTE BRANCHED1/ CYCLOIDEA/ PROLIFERATING CELL FACTORs (TCP) family transcription factors play a key role in controlling anthocyanin biosynthesis. We have characterized several loss- and gain-of-function Arabidopsis mutants and found that CINCINNATA-like TCPs act as suppressors of anthocyanin accumulation. Using genetic, biochemical, and molecular approaches, we demonstrate that the CIN-TCP protein TCP4 directly activates the transcription of MYB-LIKE2 (MYBL2), a well-known inhibitor of anthocyanin biosynthesis genes, which leads to the suppression of anthocyanin levels. Our findings establish a novel component in the regulatory mechanism of flavonoid biosynthesis in plants.



Light-mediated control of early seedling growth arrest and TCP-mediated control of anthocyanin biosynthesis in plants during stress conditions

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Nishad Matange: nishad@iiserpune.ac.in and/or
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The Young Investigators' Meeting brings together India's best early-career life science researchers, postdoctoral fellows from around the world and India, renowned Indian and international scientists, and administrators for five days of interactions focusing on biology and careers in Indian science.

Ahmedabad University

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