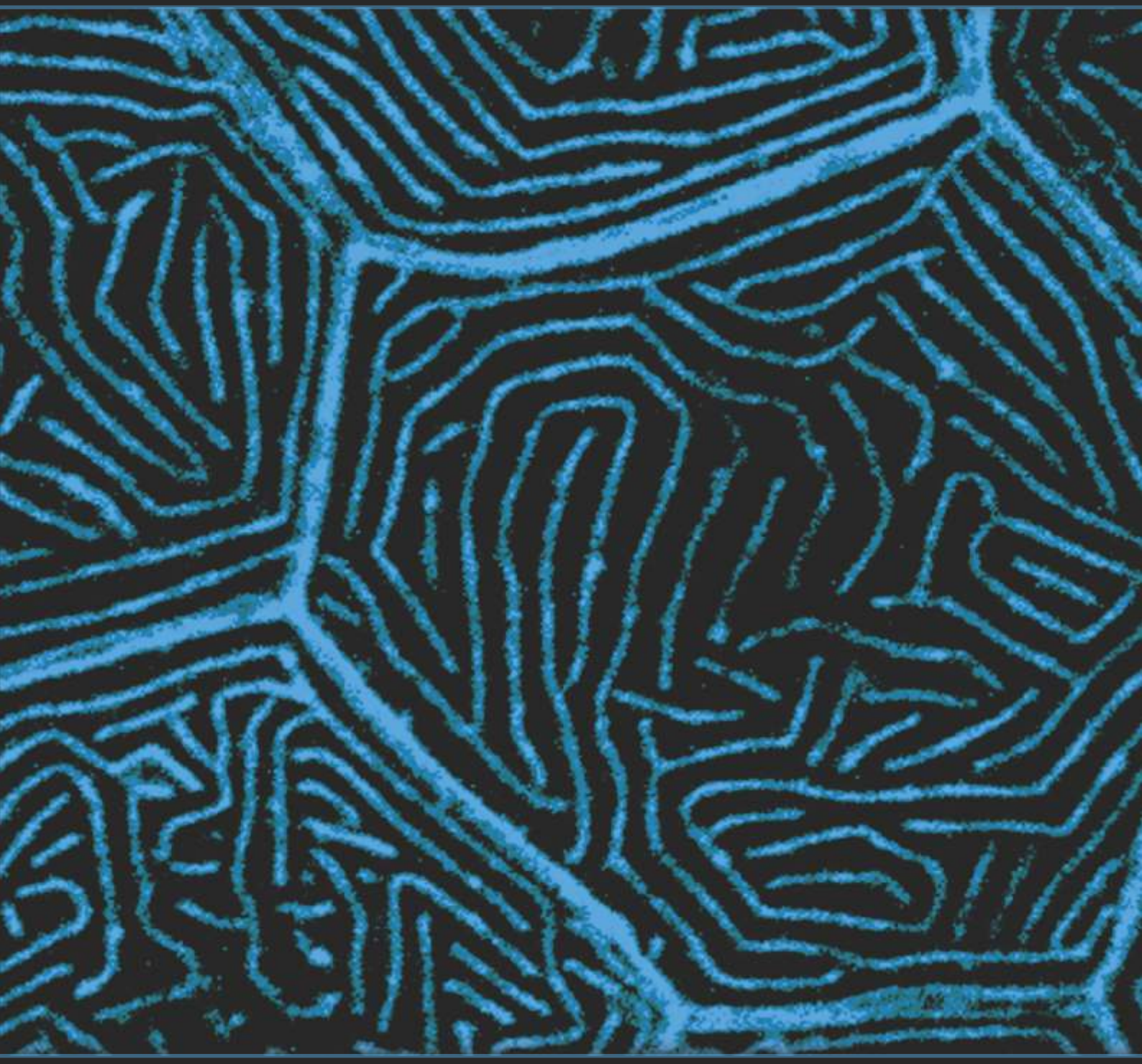
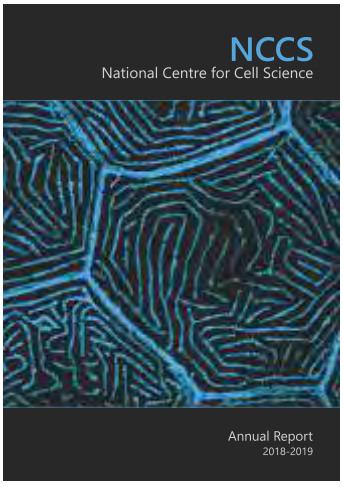
NCCS

National Centre for Cell Science



Annual Report

2018-2019

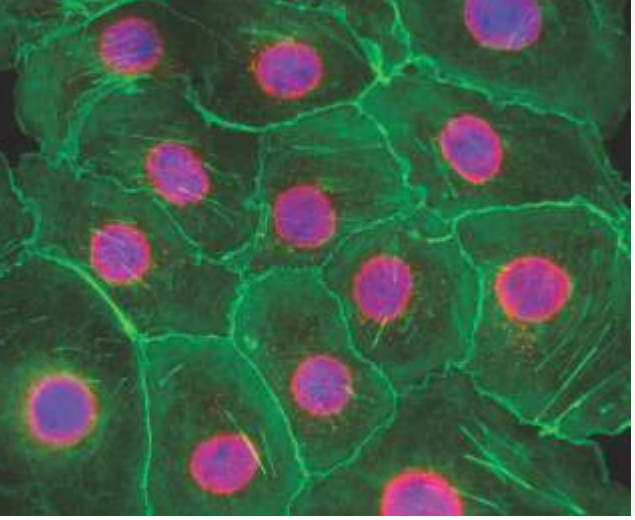


Cover page image

Confocal microscopic image showing actin-rich microridges present on the apical surface of zebrafish peridermal cells. Microridges are stained with fluorescently-labeled phalloidin. (Image courtesy of Indrasen Magre and Jomon Joseph)

National Centre for Cell Science

Annual Report 2018 - 2019



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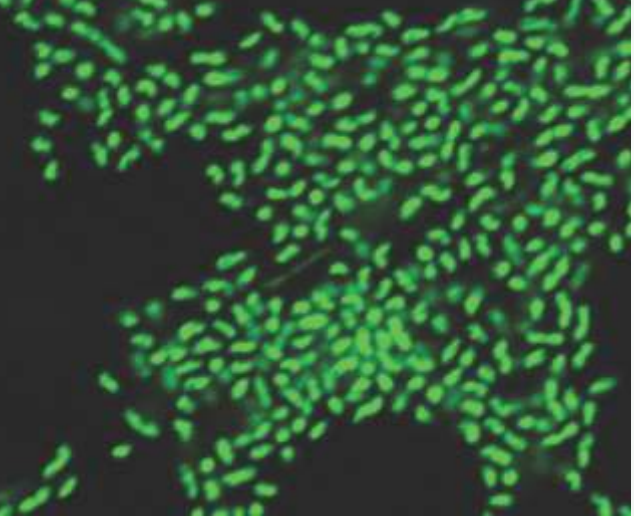


Mandate of NCCS

- To receive, identify, maintain, store, grow and supply:
  - Animal and human cell cultures.
  - Newly developed and existing (typed) cell lines.
  - Hybrid cells including hybridomas.
  - Tissues, organs, eggs (including fertilized ones) and embryos.
  - Unicellular, obligate pathogens, parasites and vectors.
  - Plasmids, genes and genomic libraries.

- To develop, prepare quality control and supply culture media, other reagents and cell products independently and in collaboration with industry and other organizations.

- Research and development.

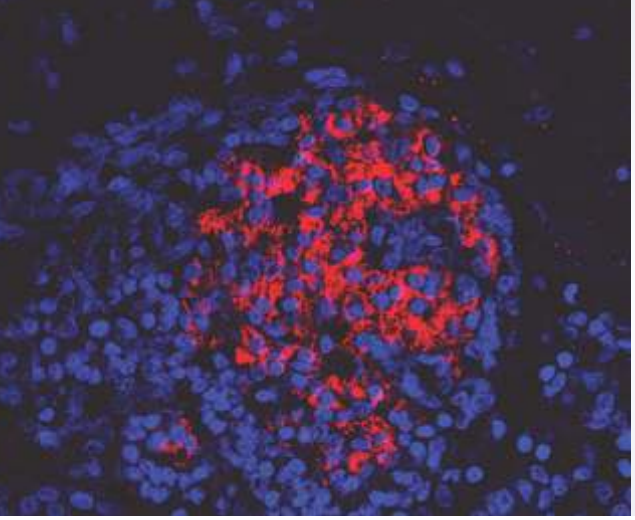
- To establish and conduct postgraduate courses, workshops, seminars, symposia and training programs in the related fields.

- To serve as a National Reference Centre for tissue culture, tissue banking and cell products, data bank etc., and to provide consultancy services to medical, veterinary and pharmaceutical institutions, public health services and industries etc. in the country.

- To provide and promote effective linkages on a continuous basis between various scientific and research agencies / laboratories and other organizations, including industries within the country.

- To participate in programs conducted for the betterment of society and advancement of science and technology in the country.

- To collaborate with foreign research institutions, laboratories and other international organizations in the areas relevant to the objectives of the facility.



Summary of NCCS Activities for the Unacquainted

NCCS carries out research in cell biology, which involves the study of cells, the 'basic unit of life'. The bodies of all animals, including humans, are composed of trillions of different types of microscopic cells. These cells, in turn, are composed of a variety of molecules, including DNA, RNA, proteins, and several others, which determine the structure, properties and biological activities of the cell. Cellular activities are also influenced by other determinants, including interactions between these molecules, as well as interactions of the cells with the environment and molecules outside the cell, with each other, and with microorganisms that they encounter. All these molecules, interactions and other factors that influence the functioning of cells, collectively determine the functioning of the animal as a whole. Consequently, to gain essential insights into how the body functions under conditions of health and disease, it is necessary to study the nuances of how cellular activities operate at the molecular level and decipher all the determinants involved. We carry out such studies at NCCS to address challenging questions about human health, especially those related to cancer, diabetes, infectious diseases, functioning of the immune system, regeneration of bone and other tissues, gut microorganisms in health and disease, stem cell biology, etc. Through achieving the proximal goal of understanding the basic biology of cells, we aspire to eventually contribute towards improvements in methods for diagnosis, and treatment regimens / therapeutics for management of diseases. Our studies hold special relevance for this purpose, since they are mainly focused on the Indian population. While engaging in basic research, we also explore possibilities for translating our promising breakthroughs into tangible benefits for the people through collaborations with clinicians. Transfer of medically useful technologies like 'large scale expansion of human skin culture for the treatment of burns, vitiligo and non-healing ulcers' & 'bone marrow cryopreservation' to Government medical colleges and hospitals exemplify our success on this front. The details of the research carried out at NCCS over the past year are described in the research reports of the individual scientists in the annual report that follows.

NCCS also has service-oriented components which play a big role in facilitating high quality research not only at NCCS, but also at other organizations. One of the aims of NCCS is to function as a national cell repository for animal cell lines, which are essential to study the biology of cells. Cell lines are different types of cells obtained from animals, including humans, which are grown and maintained under laboratory conditions. This cell repository provides cell lines to cell biologists from academic and research institutions across the country. Therefore, a significant proportion of cell lines-based research in India is dependent on the cell repository at NCCS, and is also supported by the training and guidance provided by NCCS to develop the skills required to handle cell lines.

The National Centre for Microbial Resource (NCMR) plays a big role in preserving the nation's microbial biodiversity, by serving as a national depository for microorganisms. It has successfully undertaken the enormous task of obtaining several different microorganisms from a variety of environments across India, preserving them in the laboratory in the form of 'cultures', and characterizing them to identify them and to explore their potential for application in biotechnology. The MCC is the largest individual collection of microorganisms in the world and is instrumental in India being internationally ranked as the country with the fourth largest collection of microbial cultures. It also facilitates high-quality research in microbiology in universities, colleges, other research institutions, and industries all over the country, by supplying authentic microbial cultures and providing related services, such as identifying

microorganisms using cutting-edge techniques. Further, MCC has been recognized by the World Intellectual Property Organization (WIPO) in Switzerland, as an International Depository Authority (IDA) for the deposit of microorganisms to fulfill the requirements of the patent procedure in 55 countries.

In addition to carrying out research and extending services as mentioned above, NCCS also contributes immensely to capacity building of the nation and human resource development through several teaching, training & outreach activities that benefit students, researchers & academicians from various organizations across the country, as well as the general public. NCCS conducts the Ph.D. (biotechnology) coursework for students registered with the S. P. Pune University. The NCCS scientists also visit various educational organizations to deliver lectures and provide hands-on training for students in their own organizations. For example, 'Edu-Bridge', an ongoing teaching programme initiated by NCCS, enables the scientists to teach fundamental concepts of science through lectures & hands-on activities to students of the Jankidevi Bajaj College of Science (JBCS), Wardha. Students and faculty members from educational institutions across India also visit NCCS throughout the year, which provides them the opportunity to learn about cutting-edge science, techniques and instruments that they may not have exposure to at their own institutions. Furthermore, the scientists at NCCS provide valuable mentorship and training in research to Ph.D. students and other students who carry out short-term research projects at NCCS every year as summer trainees (selected from among the Indian Academy of Sciences Summer Research Fellows) and project trainees (from various academic institutions).

NCCS serves to educate the general public and students about diverse topics in science by organizing various outreach activities. This includes public talks by eminent scientists, including Nobel laureates, open day at NCCS on the National Science Day (with public talks by eminent speakers & displays), contribution of material for 'Vigyan Rail' (the science exhibition on wheels initiated by the Government of India), display of exhibits at various science exhibitions like the India International Science Festival, articles published in newspapers and magazines in English as well as Indian languages, science-themed talks & discussions broadcast through All India Radio, participation in science documentaries for telecast on national channels like the DD National channel, DD Bharati, Lok Sabha TV & Rajya Sabha TV, etc.

From the Director's Desk

I am pleased to present the Annual Report of the National Centre for Cell Science (NCCS), Pune, for 2018-19.

This year has seen a major change, with our former Director, Dr. Shekhar Mande taking charge as DG, CSIR and Secretary, DSIR. We bid farewell to him in October 2018, with our best wishes for his future. The responsibility of carrying the mantle forward as Director, In-Charge was subsequently handed to me by the Department of Biotechnology. It has been a pleasure to have had the opportunity to take on this responsibility.

Like earlier years, the NCCS scentists are continuously engaged in pursuing cutting-edge research in cell biology and allied areas, such as cancer biology, immunology, stem cell biology, 3D culture, computational and structural biology, neurobiology, microbiology, nanotechnology etc. I am pleased to state that our research has led to fruitful outcomes over the last year, as is evident from over eighty research publications, many in leading peer reviewed international journals like The New England Journal of Medicine, Journal of Biological Chemistry, Nanoscale, PLoS Biology and Stem Cell Reports, etc., as well as seven patent applications being filed, and success at bringing in extramural funding to the tune of over rupees forty-two crores.

One of the major initiatives that commenced this year was the Pune Bio-Cluster project, a collaborative endeavour between NCCS and IISER, Pune. This is aimed at creating opportunities for researchers to benefit from high-end facilities, such as the state-of-the-art bio-imaging and cryo-electron microscope facilities being developed on the campus of both the institutions as part of the cluster, as well as from the expertise of the two institutions. The project also proposes to provide a platform to develop animal models for understanding the progression of human diseases. Given the rich research and academic ecosystem that Pune and its surrounding areas are blessed with, this project aspires to benefit stakeholders from several research organizations, academic institutions, industries, biotechnology entrepreneurs, and clinicians in and around Pune and Maharashtra, who are involved in biomedical research. We thus hope to encourage sharing and better utilization of national resources, and trust that this project will pave the way for various meaningful collaborations.

While acknowledging the importance of basic research, we also recognize the need to explore possibilities for scaling up and translating promising findings of basic research. To this end, an industry-academia meet was successfully organized, to encourage a dialogue between the stakeholders in both these sectors, on strategies to facilitate technology innovations & scale up in academic institutions. Furthermore, NCCS also partnered with various industries this year, to share our strengths and expertise through collaborative endeavours.

To further build on our experience with serving as a national cell repository over three decades, I have recently proposed to develop a state-of-the-art GMP-compliant national cell banking facility and repository services, which could provide a platform for the safe deposit and supply of characterized cell lines and cultures for use by the biopharma industry and academic organisations, by applying for funding through the National Biopharma Mission under the DBT, BIRAC and World Bank program.

I am happy to introduce two new faculty members through this year's annual report, Dr. Gaurav Das and Dr. Akanksha Chaturvedi. Dr. Das's research focuses on the neural circuit basis of feeding behavior, and his research expertise will further strengthen our neurobiology group, a relatively new addition to NCCS. Dr. Chaturvedi, who has joined very recently, will explore the interplay between innate and adaptive immune receptor

signaling in regulating B-cell responses. Her expertise in B-cell biology, a hitherto unexplored area at NCCS, will further expand the scope of our research in immunology.

In addition to strengthening our research, we continue to work towards providing quality services, and training the next generation of scientists through our academic programmes. The impact of the latter is evident from the fact that 23 of our students received Ph.D. degrees from the S. P. Pune University (SPPU) and the Maulana Abul Kalam Azad University of Technology, West Bengal, and 23 students submitted their theses to the S. P. Pune University this year. With 33 research scholars having registered as Ph.D. students with the University during this year, we had a total of 135 registered Ph.D. students as on 31st March, 2019. Furthermore, many college students received research training at NCCS during this year, including 35 project trainees & 21 Science Academies' Summer Research Fellows.

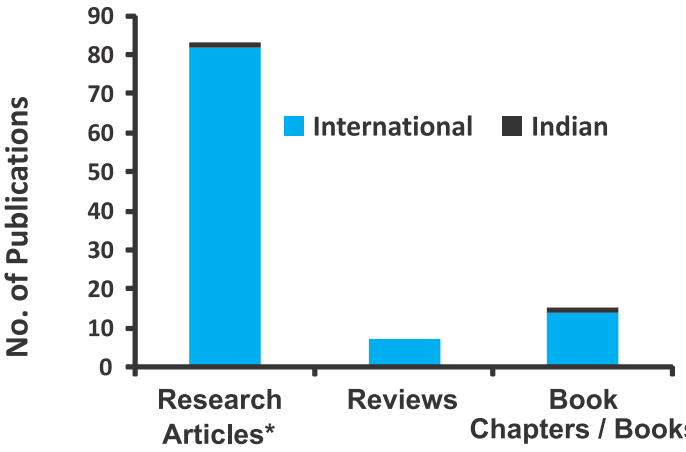
The National Cell repository of NCCS has also continued to play an important role in supporting cell biology research across India, by providing over three thousand cell lines to over five hundred organizations in the country during this year. Further, it has created a state-of-the-art infrastructure for the characterization and authentication of cell lines. The Centre of Excellence for 'National Centre for Microbial Resource (NCMR)', has also been playing a major role in serving as a depositary for microbial cultures from diverse environments, including those microorganisms that could produce druggable compounds for disease management. In the future, we hope to begin the Indian Human Microbiome Initiative, a pan-India project on a hitherto unprecedented scale, which will leverage the extensive expertise of NCMR in microbiome research.

I invite you to learn more about our research and other activities, which are covered in the annual report that follows.

Gopal C. Kundu
Director, In-Charge

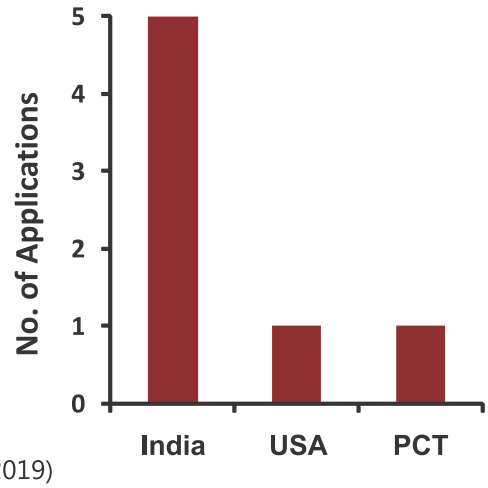
Major Highlights (2018-19)

PUBLICATIONS



* Total citations = 190 (from Google Scholar, as on 31 Aug, 2019)

PATENT APPLICATIONS FILED

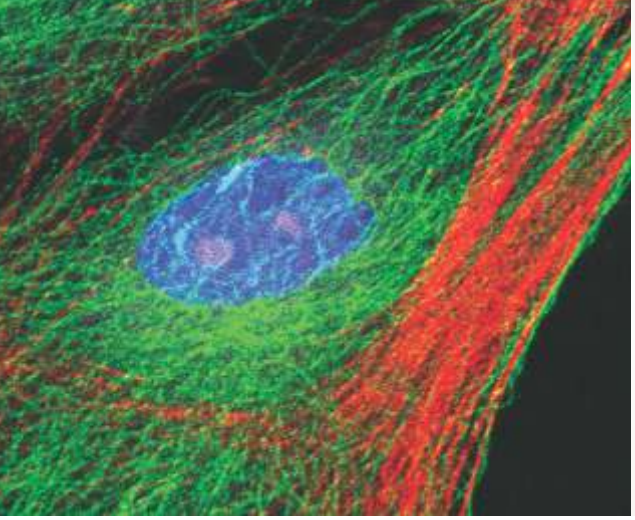


SIGNIFICANT SCIENTIFIC CONTRIBUTIONS

The NEW ENGLAND JOURNAL of MEDICINE	**Evidence of Artemisinin-Resistant Plasmodium falciparum Malaria in Eastern India.**
JBC JOURNAL OF BIOLOGICAL CHEMISTRY	**The SCF^{FBXO46} ubiquitin ligase complex mediates degradation of the tumor suppressor FBXO31 and thereby prevents premature cellular senescence** Srinadh Choppara, Sankaran Ganga, Rajeshkumar Manne, Paul Dutta, Shailza Singh, and Manas Kumar Santra
PLOS BIOLOGY	**Noncoding RNA Ginir functions as an oncogene by associating with centrosomal proteins**
JBC JOURNAL OF BIOLOGICAL CHEMISTRY	***Aspergillus fumigatus* conidial metalloprotease Mep1p cleaves host complement proteins** Rajashri Shende, Sarah Sze Wah Wong, Srikanth Rapole, Rémi Beau, Oumaima Ibrahim-Granet, Michel Monod, Karl-Heinz Gührs, Jayanta Kumar Pal, Jean-Paul Latgé, Taruna Madan, Vishukumar Aimanianda, and Arvind Sahu
Nucleic Acids Research	**MIR100 host gene–encoded lncRNAs regulate cell cycle by modulating the interaction between HuR and its target mRNAs** Qinyu Sun, Vidisha Tripathi, Je-Hyun Yoon, Deepak K Singh, Qinyu Hao, Kyung-Won Min, Sylvia Davila, Richard W Zealy, Xiao Ling Li, Maria Polycarpou-Schwarz ... Show more
STEM CELL REPORTS	**Clathrin-Mediated Endocytosis Regulates a Balance between Opposing Signals to Maintain the Pluripotent State of Embryonic Stem Cells** Yadanalli V. Narayana, Chetan Gadgil, Rohini D. Mote, Raghav Rajan, and Deepa Subramanyam

MAJOR AWARDS / HONOURS	Recipients
NASI-Platinum Jubilee Chair Distinguished Professor	1
Elected as Fellow of the Indian Academy of Sciences, Bangalore	1
J.C. Bose National Fellowship	3
Tata Innovation Fellowship	2
SwarnaJayanti Fellowship	1
National Bioscience Award	1
Selected as Member of the 38th Indian Scientific Expedition to Antarctica	1

BENEFICIARIES OF THE ACADEMIC PROGRAMMES	
Students awarded with the Ph.D. degree	23
Science Academies' Summer Research Fellows & Project Trainees	56



Human Resource Development

The beneficiaries of the NCCS academic programmes during the year 2018-19 are as follows:

Fourteen Research Fellows joined NCCS, and thirty-three research scholars registered for a Ph.D. with the University during this year, taking the total number of registered Ph.D. students to one hundred and thirty-five, as on 31st March, 2019. Twenty-three students submitted their theses to the University for evaluation and twenty-three students were awarded with a Ph.D. degree during the said year.

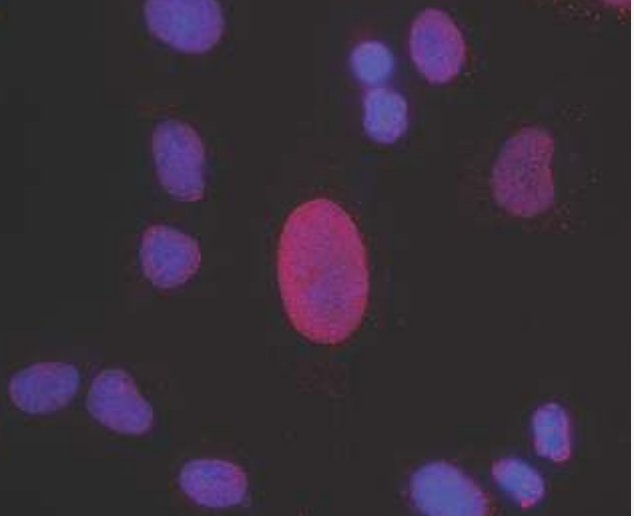
NCCS also conducts training programmes for students every year, as given below:

a) 6-months' project training is imparted twice a year, i.e. during January-June and July-December.

b) Summer training is conducted for 2 months during May-June. The summer trainees are selected from among the Indian Academy of Sciences Summer Research Fellows of the respective year.

The number of students who received training under these programmes during 2018-19 is as follows:

Project Trainees : 35
Summer Trainees : 21



Cell Repository

The Team

Dr. Punam Nagvenkar, Scientist D
Dr. Rahul Patil, Scientist C
Mrs. Tanuja Bankar, Technical Officer C
Mrs. Medha Gode, Technical Officer C
Mrs. Nivedita Bhave, Technical Officer C
Mrs. Anjali Patekar, Technical Officer B
Mr. Dharmendra Bulbule, Technical Officer A
Mr. Nitin Sonawane, Technician C
Mr. Bhimashankar Utage, Technician C
Mr. Vikas Mallav, Technician B
Mr. Yogesh Kumbhar, Assistant Technician

Training Program

National Hands-on Training Workshop on "Basic Cell Culture Technology"

14-17 May, 2018

No. of Participants trained

- Faculty: 4
- Ph.D Scholars: 10
- Technical: 6

NCCS has been functioning as a National Cell Repository for cell lines in India since its inception. The repository manages the expansion, cryopreservation and distribution of cell lines to researchers in academia and government as well as private research institutions in India. In the year 2018-19, three thousand seven hundred and one cell lines were supplied to five hundred and eight organizations across the country.

The repository team organized two National hands-on training workshops on "Basic Cell Culture Technology" as listed below, which included modules for important cell culture techniques related to cell line maintenance, expansion, cryopreservation and revival. A total of 40 early career researchers, including doctoral students, young faculty and technical staff from 32 academic and non-academic institutions from all over the country, were selected and imparted training.

External Scientists Trained

- Institutes (Name, City, Country)
  - The Maharaja Sayajirao University of Baroda, Vadodara, Gujarat
  - Naga Hospital Authority, Kohima, Nagaland
  - Indian Institute of Technology, Madras, Chennai, Tamil Nadu
  - Panjab University, Chandigarh
  - Manipal College of Pharmaceutical Sciences, MAHE, Manipal, Karnataka
  - Indian Institute of Technology (BHU) Varanasi, Uttar Pradesh
  - National Institute of Pharmaceutical Education and Research, Mohali, Punjab
  - Savitribai Phule Pune University, Pune, Maharashtra
  - St Anthony's College, Shillong, Meghalaya
  - Jankidevi Bajaj College of Science, Wardha, Maharashtra
  - University of Madras, Chennai, Tamil Nadu
  - National Institute of Technology Tiruchirappalli, Tamil Nadu
  - Tilak Ayurved Mahavidyalaya, Pune, Maharashtra
  - National Centre for Cell Science, Pune, Maharashtra
  - National Institute for Research in Reproductive Health, Mumbai, Maharashtra

Training Program

National Hands-on Training Workshop on "Basic Cell Culture Technology"

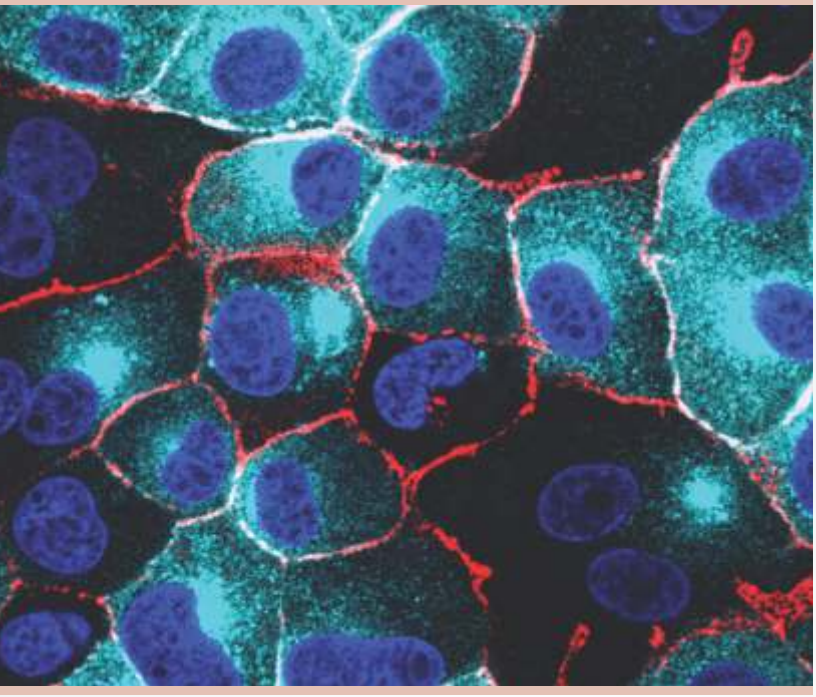
29 Oct - 01Nov, 2018

No. of Participants trained

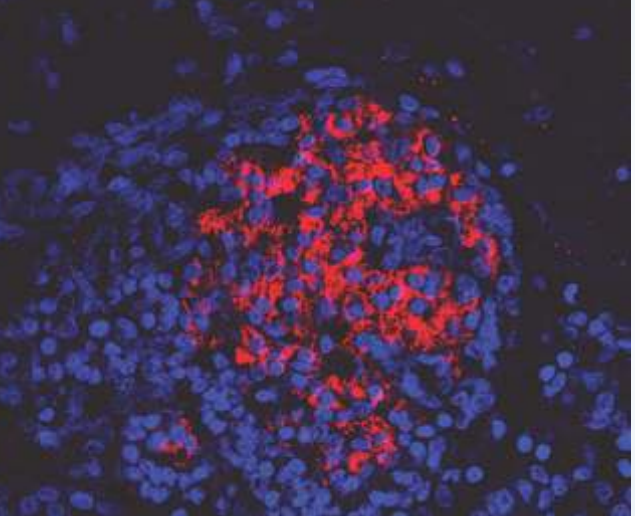
- Faculty: 3
- Ph.D Scholars: 16
- Technical: 1

- Institutes (Name, City, Country)
  - University of Calicut, Thenhipalam, Kerala
  - Saurashtra University, Rajkot, Gujarat
  - All India Institute of Medical Sciences, Jodhpur, Rajasthan
  - Alagappa University, Karaikudi, Tamil Nadu
  - ICAR-Indian Institute of Horticultural Research, Bengaluru, Karnataka
  - Sikkim University, Gangtok, Sikkim
  - MAEER's Maharashtra Institute of Pharmacy, Pune, Maharashtra
  - Rajiv Gandhi Institute of IT & Biotechnology, Bharati Vidyapeeth, Pune, Maharashtra
  - Shivaji University, Kolhapur, Maharashtra
  - Indian Institute of Science Education and Research, Pune, Maharashtra
  - CSIR-National Chemical Laboratory, Pune, Maharashtra
  - M. S. University of Baroda, Vadodara, Gujarat
  - Rani Durgavati University, Jabalpur, Madhya Pradesh
  - Dr. Harisingh Gour Vishwavidyalaya, Sagar, Madhya Pradesh
  - Savitribai Phule Pune University, Pune, Maharashtra
  - Government Ayurvedic College, Nanded, Maharashtra
  - Bharati Vidyapeeth College of Pharmacy, Kolhapur, Maharashtra

The cell repository team also participated in the celebration for the National Science Day on February 28th, 2019. Different types of cell lines were shown to the visitors and informed about the importance of their use in research. Our services for cell line authentication by Short Tandem Repeat (STR) analysis and Mycoplasma testing are well utilized by both in-house scientists and external users.



Research Reports



Index of Research Reports

Sharmila Bapat

sabapat@nccs.res.in

Understanding Cellular and Molecular Attributes during Tumor Growth

Objectives of the study

- Correlation between histopathological and molecular traits during tumor growth

Summary

Background

During the multistep progression of solid cancers, tumor size is linked with tumor staging, metastasis and overall survival of patients. Hypoxic conditions in a tumor reportedly induce metabolic reprogramming of cells, and favor *de novo* angiogenesis and metastases. Ovarian cancer is an extremely aggressive disease in which the stage at which these processes are triggered is poorly understood. Additionally, there is a limited understanding about tumor cell quiescence and dormancy. In the present study we profiled several molecular markers that correlate with the processes of hypoxia, metabolic reprogramming, metastases and vasculogenic mimicry during tumor development.

Main findings of the study

A sub-cutaneous tumor growth model for ovarian cancer was generated in immune-compromised NOD-SCID mice, based on increasing tumor volumes (Fig.1a). Briefly, this comprised of tumors in the following groups; group A: 0-≤0.625cm^3 (20-22 days), group B: >0.625-≤0.5cm^3 (25-28 days), group C: >0.5-≤1.69cm^3 (30-32 days), group D: >1.69-≤4cm^3 (35-40 days), group E: >4-7.8cm^3 (45-50 days) (Fig.1b). Whole slide imaging of H&E stained tumor sections identified discrete tumor cell, stromal, vascular and necrotic areas.

Lab Members

Gaurav Soman, *SRF*
Sagar Varankar, *SRF*
Madhuri More, *SRF*
Snehal Nimdeokar, *SRF*
Komal Patil, *Project JRF*
Gunjan Shukla, *Project Assistant*
Anuj Mavlankar, *Project Trainee*
Arpita Wagle, *Project Trainee*
Vaishnavi Jadhav, *Project Trainee*
Avinash Mali, *Technical Officer A*

Collaborator(s) - National

Dr. Mohit Kumar Jolly, *Indian Institute of Science, Banglore, India.*
Dr. Judith Clements, *Queensland University of Technology, Brisbane, Australia.*

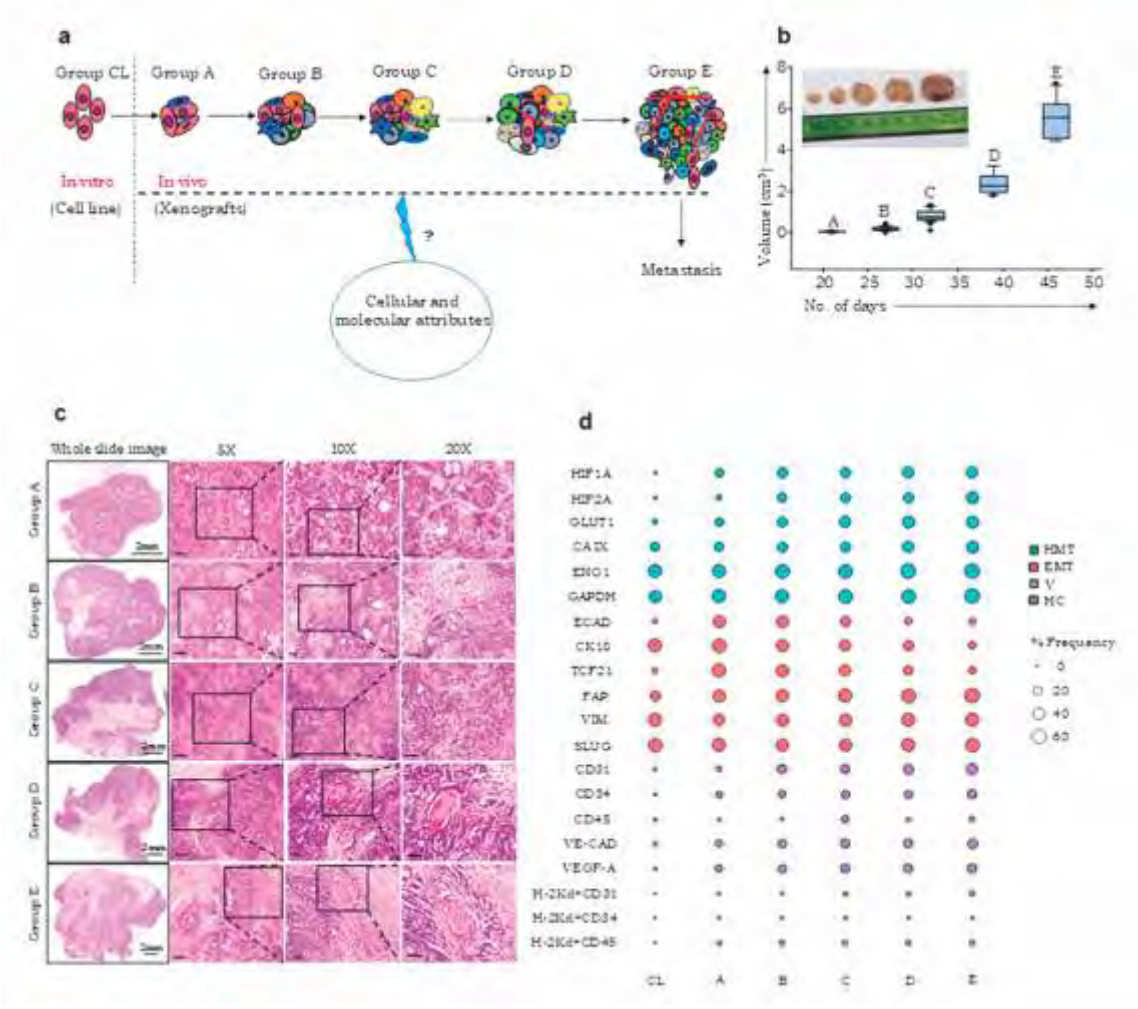


Fig.1: Correlation of tumor histopathology and molecular traits in ovarian cancer. a) A schematic depicting tumor growth model, Group CL represents in vitro cultured cells and Group A, B, C, D & E are xenografts of various sizes with different generation time; b) Volume based categorization of A4 xenografts, Group A: 0-≤.0625cm^3, Group B >0.0625cm^3–≤0.5cm^3, Group C >0.5cm^3–≤1.69cm^3, Group D >1.69cm^3–≤4cm^3 and Group E >4cm^3–≤7.8cm^3. The longest and shortest diameters of a tumor were measured using a vernier caliper and volumes were calculated by using a formula V=1/2*(L*(W)^2); c) Representative tissue images of tumor cross-sections depicting differential tumor tissue architecture during tumor growth, 4µm thick formalin fixed and paraffin embedded sections were stained with Hematoxylin and Eosin. Scale bar - Whole slide image-2mm, 5x magnification- 250µm, 10x magnification - 100µm, 20x magnification - 75µm; d) A weighted dot plot depicting flow cytometry based expression analyses of hypoxia, metabolic stress, EMT and vasculogenesis markers along with host contribution to the tumor. The size of a dot denotes percent frequency of marker expression as represented in the legend panel.

Further scanning at higher magnification revealed Group A tumors to be devoid of vascular and necrotic regions, and correlated with low expression of hypoxic markers HIF1A, HIF2A and target genes GLUT1 and CA IX (Fig.1d). Vasculature formation is initiated in group B tumors and their enhanced in group C, D and E tumors, which was further confirmed by high expression of endothelial molecules CD31, CD34, human leucocyte antigen CD45 and vascular endothelial growth factor, VEGF-A. Expression of vasculogenic mimicry marker VE-Cadherin indicates possible role of tumor cells in vascular network formation. Although larger tumors were more vascularized, higher extent of necrotic lesions in these tumors indicates that the rate of tumor cell proliferation overpowers the rate of blood vessel formation (Fig.1c). The presence of necrotic lesions indicates insufficient blood vasculature to supply diffused oxygen and nutrients, which suggests onset of hypoxia that correlated with upregulated expression of hypoxia inducible factors in xenografts. Metabolic stress in tumor cells was also suggested vide increased expression of CA IX, which is involved in maintaning intra and extra-cellular pH of cells, and of glycolytic enzymes Enolase1 and GAPDH in xenografts that indicates high glycolysis rate. Since hypoxia is reported to induce phenotypic plasticity, we profiled the expression of epithelial and mesenchymal markers. Cultured A4 cells expressed mesenchymal markers FAP, VIM, SLUG and epithelial marker CK18 accompanied by low levels of other epithelial

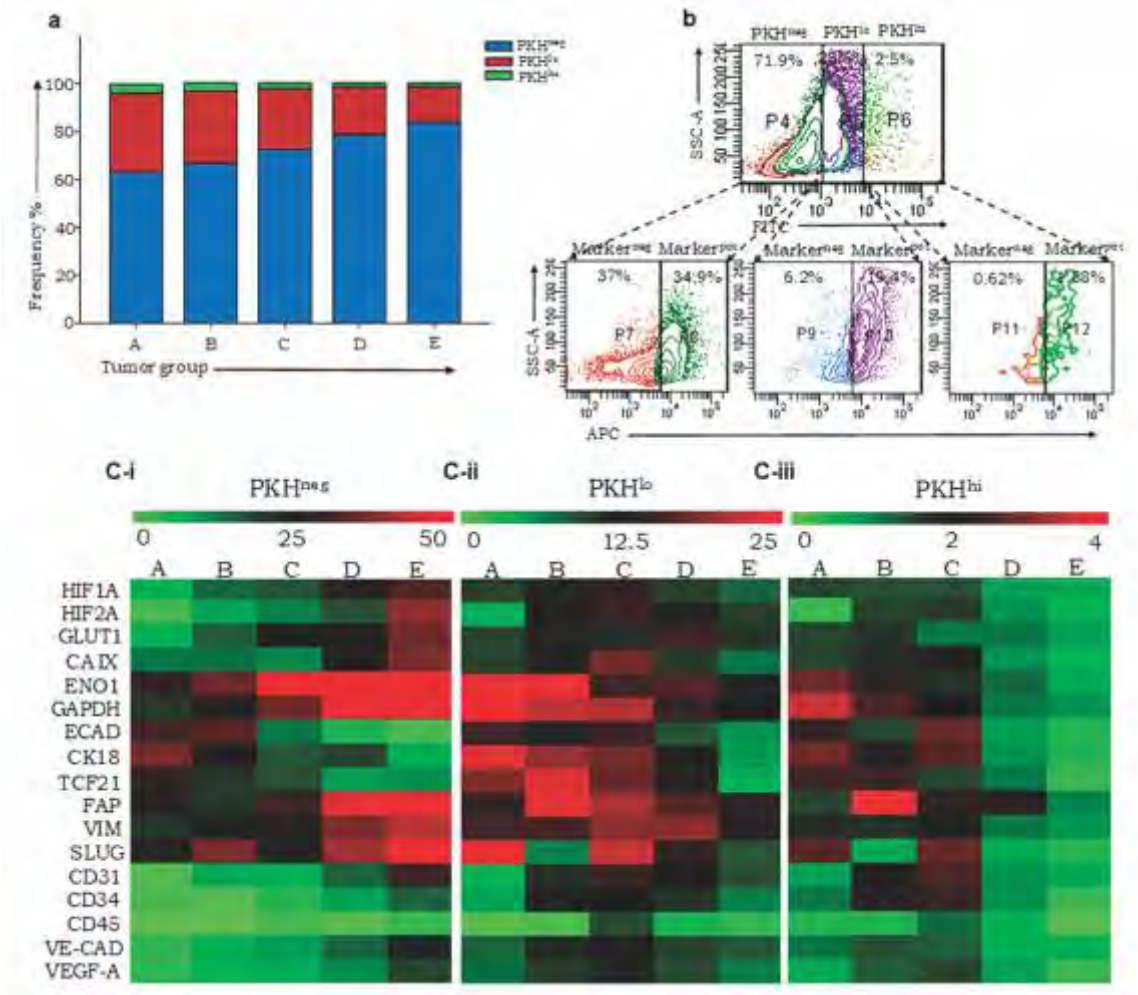


Fig.2: Evaluation of molecular traits and proliferative hierarchy during tumor growth. a) Flow cytometry-based quantification of PKH^{neg}, PKH^{lo} and PKH^{hi} fractions during tumor growth. Vital fluorophore PKH67 was used for pre-labelleing of cells; b) A schematic representing resolution of proliferative hierarchy across marker negative and positive population; c) Heat-maps depicting protein expression of molecules involved in hypoxia, metabolic stress, EMT and vasculogenesis modules in PKH^{neg}, PKH^{lo} and PKH^{hi} fractions across tumor groups A, B, C, D and E.

molecules ECAD and TCF21. Epithelial characteristics were induced on xenotransplantation in tumor groups A and B along with co-expression of mesenchymal markers, but consequently were lowered with increasing tumor size. There was not complete loss of either epithelial or mesenchymal properties indicating partial epithelial to mesenchymal transition (EMT; Fig.1d).

We further explored the association of these differentially expressed markers within a label-chase based regenerative hierarchy (using the vital fluorophore PKH67 which binds to lipid bilayer of a cell membrane and partitioned equally into daughter cells upon cell division). Such label-chase resolves differential regenerative potential in xenografts using flow cytometry to identify PKH^{hi} cells as quiescent cancer stem cell containing fraction which retains high intensity of the label, PKH^{lo} that represents transiently amplifying progenitor cells which undergo few cell divisions and retain some label, while PKH^{neg} are differentiated cells that undergo complete quenching of the label. Large size tumors are more differentiated with depleting levels of progenitor and stem cell populations (Fig.2a). Profiling of such PKH^{hi}, PKH^{lo} and PKH^{neg} fractions for hypoxia, metabolic stress, EMT and vasculogenesis markers (Fig.2b) identified high expression of hypoxia and metabolic stress markers HIF1A, HIF2A, GLUT1, CA IX, ENO1, GAPDH and mesenchymal markers FAP, VIM and SLUG within in PKH^{neg} fractions of larger tumor (Groups C, D & E; Fig.2c-i), while epithelial markers ECAD, CK18 and TCF21 along with hypoxia and metabolic stress markers dominated PKH^{lo} fraction suggesting transiently amplifying nature of these population (Fig.2c-ii); and PKH^{hi} fraction showed prominent expression of FAP along with ENO1, GAPDH, ECAD, CK18, TCF21, Slug and

CD31 molecules indicating possible stem cell like properties of these molecules (Fig.2c-iii).

Significance

Histopathological characterization of tumor growth allowed resolution of size- and latency-associated differences in tumor tissue architecture that reflects on specific pathways and functionalities. Further validation of molecular features and evaluation of regenerative potential would help in identifying possible drug targets for improved disease management.

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Cancer, Chemotherapy and Metabolic disorders

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Objectives of the study

- Unraveling the mechanism behind HCC associated hypercholesterolemia
- Consequence of elevated cholesterol level on the cancer cell survival upon anticancer drug treatment

Summary

Background

Metabolic disorders diabetes and obesity alter the risk of developing variety of cancers, and the associations are biologically plausible. The World Health Organization (WHO) predicts that the diabetic and obese population will double from the year 2000 to 2030 and the epidemiological data clearly establishes a link with cancer. Obesity or Type 2 Diabetes Mellitus promoted influx of nutrients (sugars, free fatty acids), pro-inflammatory cytokines, adipokines, and insulin resistance cause chronic low grade inflammation in the liver. This can accelerate developmental cascade of liver diseases like nonalcoholic fatty liver disease (NAFLD), non-alcoholic steatohepatitis (NASH) and cirrhosis, ultimately leading to hepatocellular carcinoma (HCC).

Cancer cells rewire their cellular metabolism to enhanced glucose uptake to support rapid reproduction. Hyperglycemia, a common manifestation of diabetes or obesity, renders an advantageous access of glucose to cancer cells, thus, directly or indirectly contributing to the risk and progression of tumors by regulating various cellular factors. Interestingly, the effect of different nutrients on tissue gene expression and serum proprotein-convertase-subtilisin-kexin

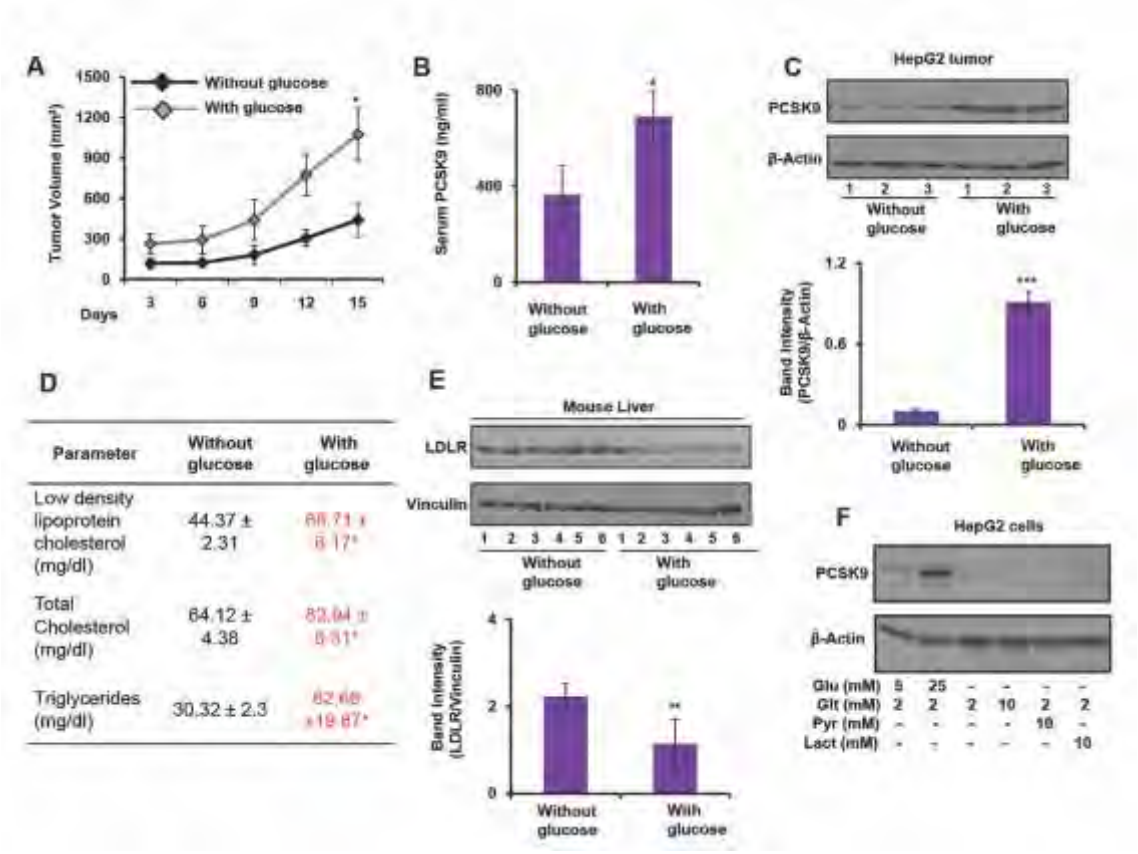

Fig. 1: Elevated serum LDLc in glucose fed mice correlates with increased PCSK9 level. A) Tumor progression after injecting HepG2 cells (5×10^6) subcutaneously in mice fed with glucose. B) Individual serum samples collected were subjected to ELISA to quantify circulatory PCSK9 levels. C) Tumor tissue lysates from three representative samples were resolved by SDS-PAGE and PCSK9 protein levels were analyzed by immunoblot. Band intensities were measured by densitometry and normalized with β-Actin. D) Serum lipid parameters. E) Liver tissue lysates from six samples from each group were resolved by SDS-PAGE and LDLR protein levels were analyzed by immunoblot. Band intensities were measured by densitometry and normalized with Vinculin. F) HepG2 cells were treated with indicated concentrations of glucose (Glu), glutamine (Glt), pyruvate (pyr) and lactate (lact) for 12 h and expression of PCSK9 was analyzed by western blot. Bar graphs represent mean ± SEM; n=3; *p< 0.05, **p<0.01 denote significant differences in the groups

type-9 (PCSK9) has been studied extensively. PCSK9 has been implicated in development of hypercholesterolemia by regulating hepatic low density lipoprotein receptor (LDLR) level. There is a tight correlation between serum PCSK9 and LDLc levels in humans as PCSK9 is a post-transcriptional inhibitor of LDLR. Various nutrients either did not change or lowered serum PCSK9 in healthy human subjects. However, the role of glucose in the regulation of PCSK9 expression remains elusive. Considering the co-existence of HCC and metabolic syndromes which are often associated with the persistent nutritional over-load; altered PCSK9 regulation is indeed a possibility. On these lines, we hypothesized that glucose could have effect on PCSK9 expression in HCC tumor which may have implications in altering LDLc level in the host.

Findings of the study

1. PCSK9 expression is increased upon supplementation of glucose in vivo: Findings imply that glucose supplementation modulates PCSK9 and LDLR levels in mice with and without HepG2 xenograft. PCSK9 derived from tumor-graft increases on glucose feeding, and is likely to be associated with development of hypercholesterolemia in xenograft-bearing mice.

2. Glucose modulates PCSK9 expression in HCC cells: Findings suggest that induction of PCSK9 expression is specific to glucose availability and uptake.

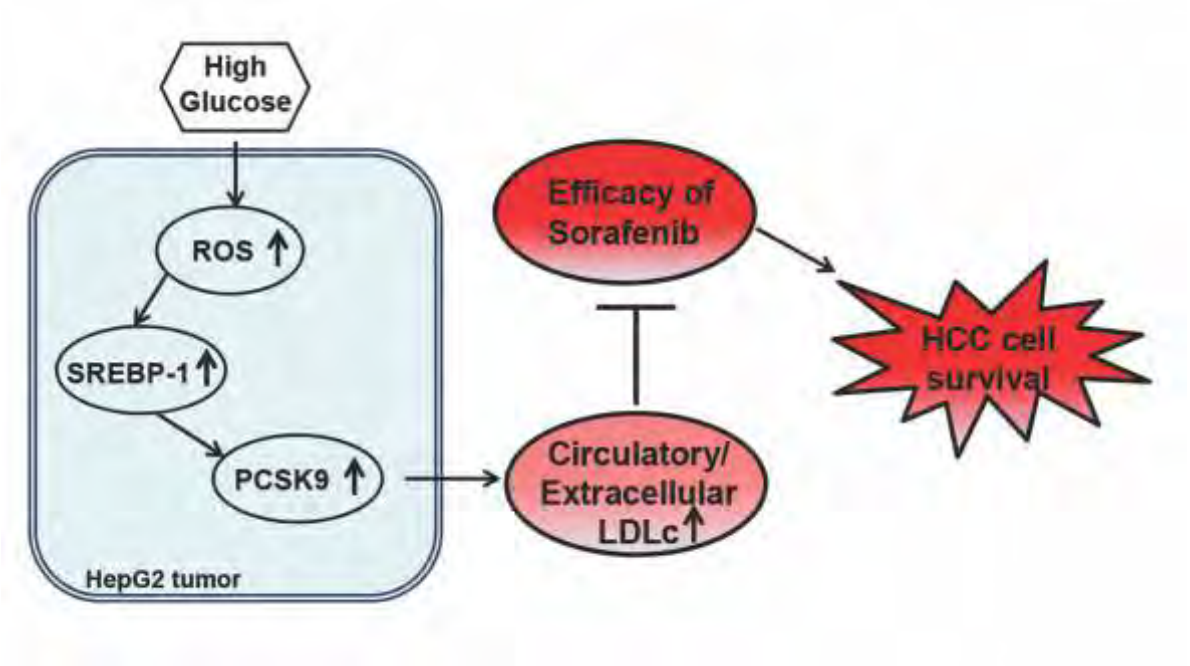

Fig. 2: Schematic illustration Proposed model demonstrating HG-driven changes in HepG2 tumor leading to increased expression of PCSK9 and associated hypercholesterolemia which can further lead to HCC cell survival by decreasing the efficacy of sorafenib.

3. Glucose stimulates PCSK9 expression via ROS and SREBP-1: Results indicate a potential role of glucose stimulated ROS and SREBP-1 in PCSK9 regulation.

4. Extracellular LDLc decreases efficacy of sorafenib: Observations indicate that hypercholesterolemia can hamper sorafenib-induced cell killing and promote HCC cell survival.

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Understanding the potential functions of scaffold / matrix region binding protein (SMAR1)

Objectives of the study

- To decipher the mechanism of hTERT repression by SMAR1.
- To understand the role of SMAR1 in inhibition of cancer stem cell population.
- To understand the role of small compound in inhibition of hTERT via SMAR1 stabilization.

Summary

Background

The interphase nucleus is characterized by the presence of nuclear matrix which provides basic shape and structural integrity to the nucleus. It mainly comprises of nucleic acids and proteins as the interacting partners and is important for various cellular processes like replication, transcription, splicing, DNA damage repair and recombination. Amongst different factors involved in compaction and tethering of chromatin to nuclear proteins, Scaffold / Matrix binding proteins (MARBPs) play a central role. SMAR1 (Scaffold / Matrix attachment region 1) is one such nuclear matrix-binding protein identified from double positive mouse thymocytes (Chattopadhyay et al. 2000 *Genomics*). SMAR1 is a known chromatin modifier which recruits HDAC1/mSin3a repressor complex to cyclin D1 promoter and thereby inhibiting its transcription (Rampalli et al. 2005 *Mol Cell Biol*). Interestingly, SMAR1 is also reported to interact with p53 and play a decisive role between cell cycle arrest and and apoptosis (Sinha et al, 2010 *EMBO*). SMAR1 is also known to be a stress response protein, wherein it regulates the acetylation status of Ku70 by interacting with HDAC6 (Chaudhary et al. 2014 *Cell Death and Disease*). Additionally, SMAR1 was reported to

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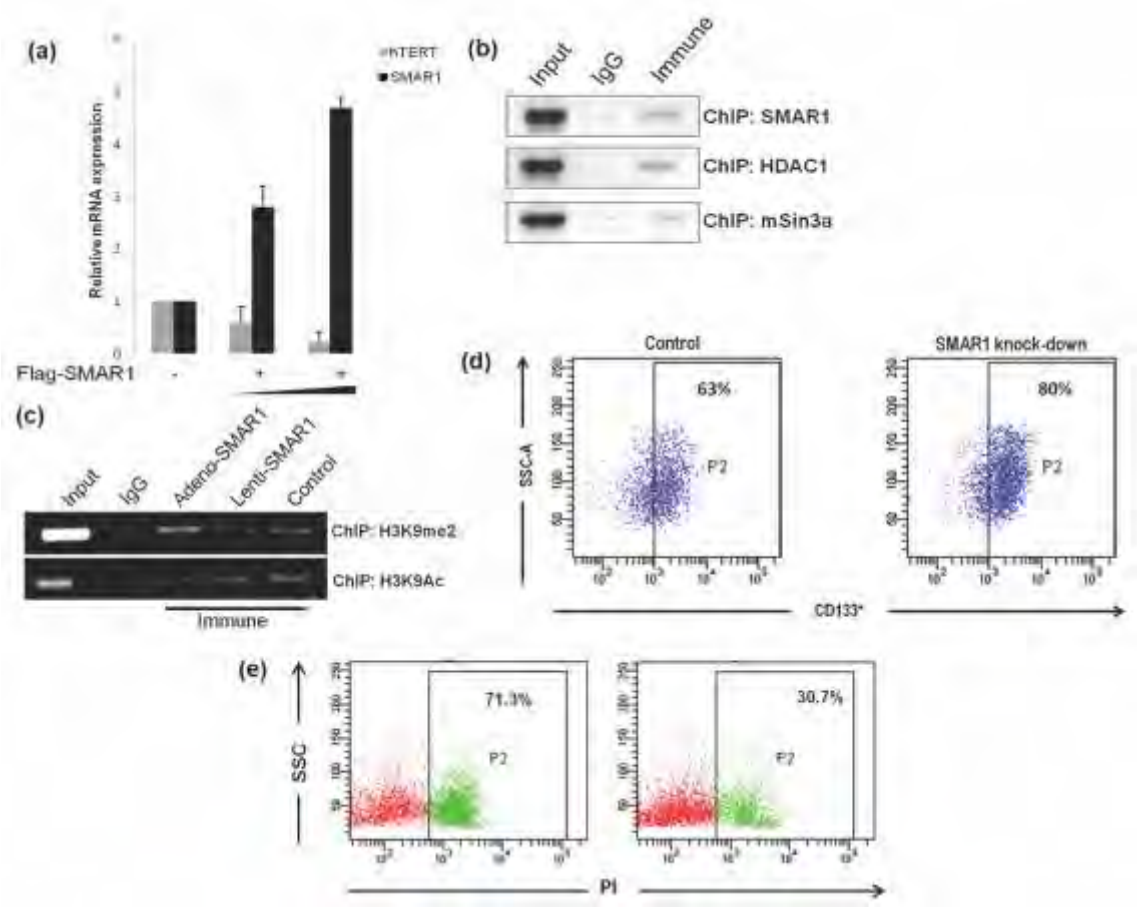

Fig. 1: SMAR1 acts as a transcriptional repressor of *hTERT*. (a) SMAR1 represses the transcription of hTERT (b) SMAR1, HDAC1 and mSin3a bind to the hTERT promoter as shown by chromatin immunoprecipitation (c) SMAR1 over-expression causes an increase in the H3K9me histone repressive mark and SMAR1 knock down causes an increase in the H3K4Ac activation mark (d) FACS shows that SMAR1 knockdown causes an increase in the $CD133^{+}$ expression (e) SMAR1 knock down makes cells resistant to anoikis as shown by reduction in the PI staining.

negatively regulate alternative splicing by modulating the acetylation status of Sam68 by recruiting HDAC6 (Nakka et al. 2015 *PNAS*). ChIP-seq analysis suggested that SMAR1 binds and regulate miR-371-373 which is an important miRNA cluster involved in cancer and metastasis (Mathai et. al. 2016 *Scientific Reports*). We have also reported that SMAR1 governs the switch between effector T cells and regulatory T cells by allowing the commitment of T cells to Th2 lineage and suppressing the Th1 and Th17 lineage commitment. (Mirlekar et.al. 2015 *Mucosal Immunology*, Mirlekar et. al. 2017 *Frontiers in Immunology*). It has also been observed that with the progression in grades of breast carcinoma, there is a drastic reduction in levels of SMAR1 (Singh et al, *2007 PLoS One*). Recently we reported that in higher grades of colorectal cancers, reactivation of Wnt/β-Catenin results in proteasomal degradation of SMAR1 through D boxes (Taye et. al. 2018 *Oncotarget*). The proteosomal machinery that is involved in degradation of SMAR1 involves CDC20, which is an E3 Ubiquitin Ligase that mediates this degradation. (Paul et. al. 2017 *Cell Death and Disease*). Amongst many different functions of SMAR1, one such study involving the role of SMAR1 in repression of hTERT will be discussed in brief.

Main findings of the study

Role of SMAR1 in repression of hTERT and inhibition of cancer stem cell trait in colorectal cancer

Telomerase re-activation is one of the hall marks of cancer cells. More than 85% of solid tumors exhibit indefinite proliferation of cells due to reactivation of this enzyme. Telomerase, is an RNA-dependent DNA polymerase, and is responsible for maintaining the length of the telomeres in an actively dividing cancer cells. The reactivation of this enzyme imparts the immortal phenotype that is so typical of a cancer cell. Telomerase is a holo-enzyme, containing a protein moiety and RNA. The catalytic subunit is the hTERT (human Telomerase Reverse

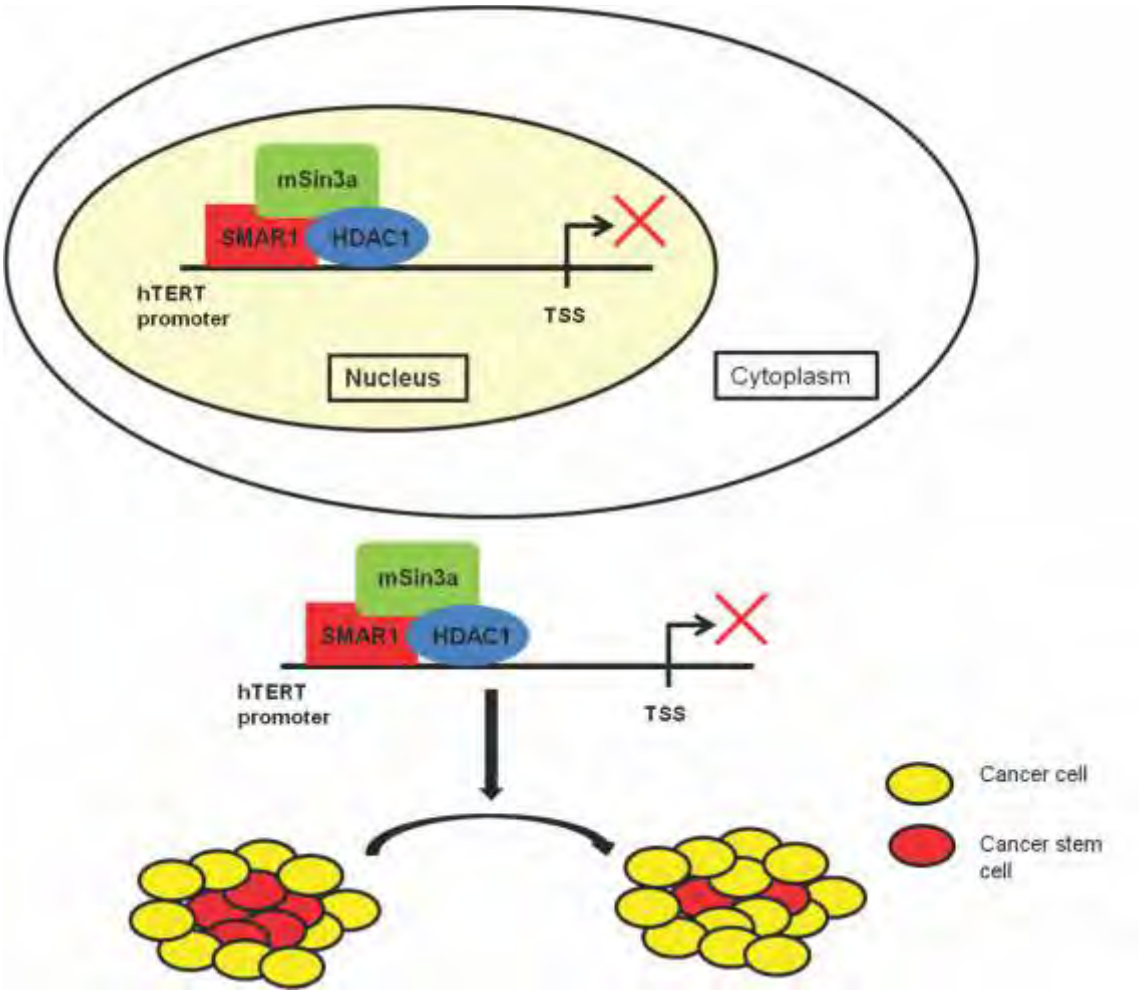

Fig. 2: Proposed model. SMAR1 recruits HDAC1/mSin3a co-repressor complex onto the hTERTpromoter and brings about epigenetic repression of hTERT expression. This leads to inhibitionof cancer stem cell trait in colorectal cancer cells.

Transcriptase) and the RNA entity is hTR (human Telomeric RNA). Reports suggest that only the hTERT is enough to cause reactivation of telomerase in any primary cell. Higher grades of cancer exhibit elevated expression of hTERT and this gives a cancer cell an advantage of replicative immortality. We show that SMAR1 negatively regulates the transcription of hTERT. SMAR1 recruits the HDAC1/mSin3a co-repressor complex at the hTERT promoter and alters the histone marks to bring about repression of hTERT by deacetylating the histones.

Along with imparting indefinite proliferative potential to a cancer cell, hTERT performs several other non-canonical functions which are crucial in successful tumor progression. One such function of hTERT is maintaining the stem cell population in the tumor. We find that SMAR1 acts as a negative regulator of cancer stem cell trait. $CD133^{high}$ cells exhibit lower levels of SMAR1 as compared to the $CD133^{low}$ cells. Also SMAR1 knock down enhances the $CD133^{+}$ population in colorectal cancer cells. Moreover, knock down of SMAR1 leads to enhanced potential for colonosphere formation. We also find that SMAR1 knock down makes the colorectal cancer cells resistant to anoikis. We thus propose SMAR1 as a novel transcriptional repressor of hTERT and thus the cancer stem cell phenotype. We also propose the use of isothiocynate derivative, SCS-OCL-381, as a SMAR1 stabilizing compound. We find that SCS-OCL-381, stabilizes SMAR1 protein expression and in turn brings about transcriptional repression of hTERT.

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Molecular mechanisms integrating the adaptive and innate immune receptor signaling in B cells

Summary

Antibody responses are initiated by B cells that recognize and respond to foreign antigens through antigen-specific B cell receptors (BCRs). In addition to the BCRs, B cells also express various germline encoded innate immune system receptors. For example, Toll like receptors (TLRs) that recognize highly conserved motifs present in microorganisms, called pathogen associated molecular motifs (PAMPs). This dual expression allows B cells to not only sense antigens, but also survey their environment for danger signals associated with the presence of pathogens. How the BCR and TLRs function independently of one another is known in considerable molecular details. We know little about the mechanisms that integrate BCR and TLRs signaling at subcellular and molecular levels. Although both BCR and TLRs initiate signal independently, in response to antigens and PAMPs, B cells are able to integrate both antigen-specific and danger signals into a qualitatively and quantitatively unique molecular response. The goal of my lab is to determine the cellular and molecular mechanisms by which BCR signaling regulates cross-talk with intracellular TLRs to modulate B cell responses, and how intracellular BCR signaling fine-tunes B cell activation in particular B cell metabolic pathways. In addition, we also plan to understand how inappropriate B cell activation by TLR ligands potentially results in autoimmunity and tumorigenesis.

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Structural and Functional Studies on Components of the Nuclear Pore Complex

Objectives of the study

- Reconstitution of minimally interacting regions of Nup93 subcomplex to understand their roles in assembly of the NPC.
- X-ray crystallographic and/or cryo-EM studies on reconstituted complexes of Nups.
- Analysis of the Nups in regulating transport activity and NPC assembly.

Summary

The nuclear pore complexes (NPCs) embedded in nuclear membrane bilayer solely mediate transport of all kind of macromoleculeS between nucleus and cytoplasm, and regulate nearly most cellular processes such as gene expression, mitosis, cell differentiation etc. Additionally, alternations in NPC and its associated proteins have been linked to several human diseases. We earlier demonstrated that the NPC composition is very species specific and thus may vary in architecture among the species. Each mammalian NPC is comprised of ~30 different proteins called nucleoporins (Nups) that are arranged in multiple copies to yield a size of 65 MDa (yeast) or 125 MDa (vertebrate). In order to understand the molecular mechanisms of NPC assembly formed by these ~30 nups and its versatile functions, the high-resolution structures are highly desired but complexity and the size of the NPCs pose tremendous challenges. A rational strategy therefore would be to disintegrate the components of NPC based on their structural and functional specificity and employ integrative approaches to learn about the roles of Nups in NPC assembly and cellular physiology.

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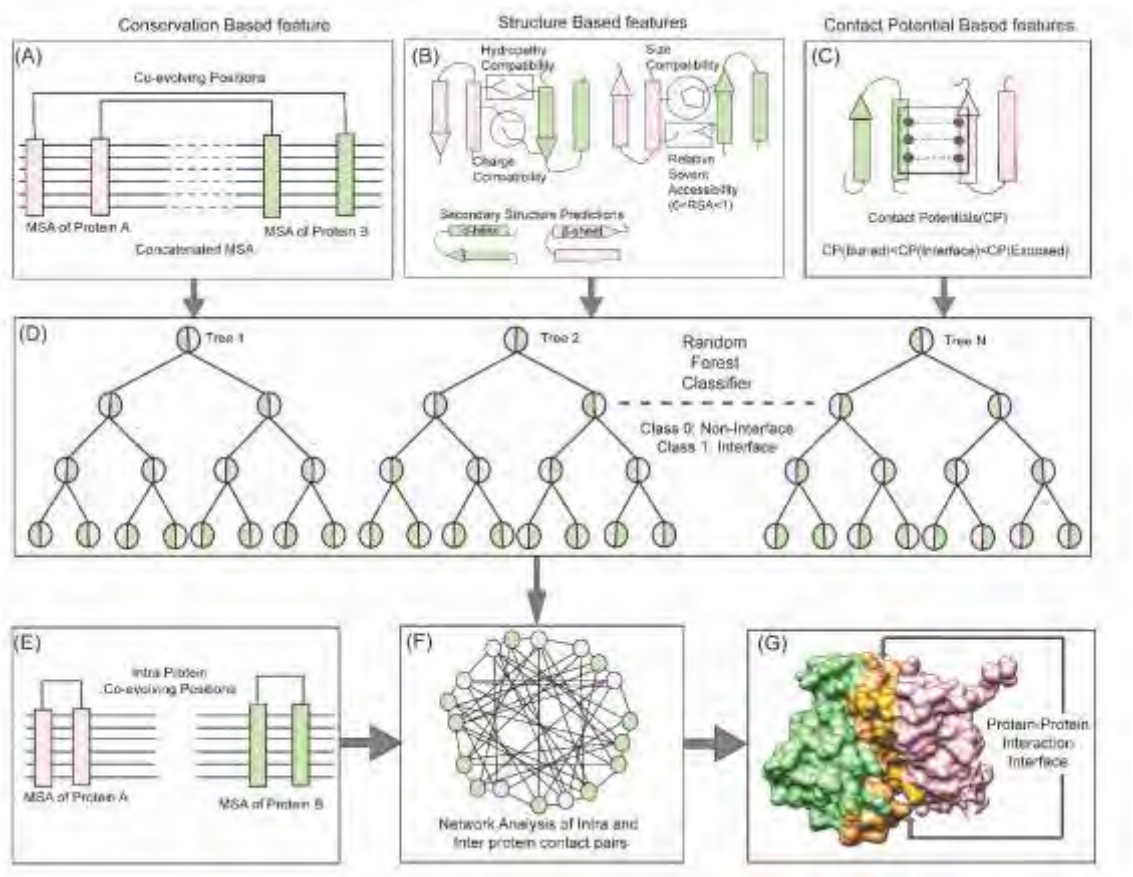

Fig. 1: CoRNeA pipeline for predicting co-evolving contact forming residues in interacting pair of proteins. The method for predicting the protein-protein interaction interface consists of three levels. The top panel depicts the features used for machine learning pipeline. (A). Conservation based (coevolution) (B) Structure based (Charge, Size, Hydropathy, Secondary structure and Relative solvent accessibility) and (C) contact potential- based features (both for buried and exposed residues). (D) Random forest classification where pairwise values for both proteins are considered depicted in half green and pink circles for binary classification (Class 1: protein interface, Class 0: non interface). The bottom panel depicts the application of network analysis by combining intra and intra protein contact predictions for reducing the false positives. (E) Prediction of intra contacts of Protein A and B. (F) Combined network analysis of inter and intra predicted contacts. (G) Interface prediction for PDB ID: 1H9D

Our laboratory routinely utilizes various structural biology tools such as X-ray crystallography, Cryo-EM and computational methods to understand the versatile functions of NPCs, such as how Nups interact with each other to form entire NPC assembly, how they participate in nucleocytoplasmic transport, gene regulation and cell differentiation functions.

Very recently we attempted to decipher protein-protein interactions of NPC by using computational tools and since no such method was available, my group generated a new hybrid pipeline for the prediction of protein-protein interaction interfaces from the amino acid sequence information which is based on the framework of co-evolution, machine learning (random forest) and network analysis named CoRNeA trained specifically on eukaryotic protein complexes (Figure 1). We use conservation, structural and contact potential as major group of features to train the random forest classifier. We also incorporate the intra contact information of the individual proteins to eliminate false positives from the predictions keeping in mind that the amino acid sequence also holds information for its own folding and not only the interface propensities. Our prediction on example datasets shows that CoRNeA not only enhances the prediction of true interface residues but also reduces false positive rates significantly. Overall, we have an entirely new framework for a method that can predict interprotein interactions of ~30 Nups within NPC and thus can lead us to undertake reconstitutional and structural studies on multiprotein complexes.

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Neurobiology of nutrient specific memories and behaviour in *Drosophila*

Objectives of the study

- To find neural circuitry underlying protein and lipid reinforced memories.
- To determine how nutrient specific brain circuitry interact with each other.

Summary

Memories of past feeding experiences are critical in making food choices. Such memories can guide choice towards a particular food source that redresses current nutrient deficiencies. However, it is not well understood how individual nutrient components from a food source are encoded in the brain and remembered. We will use novel behavior paradigms to assay for nutrient specific learning and to understand the neural circuit basis of forming, storing and recalling nutrient specific information. Our preliminary results suggest that flies seem to remember an odour coupled with the consumption of an amino acid for a day at least.

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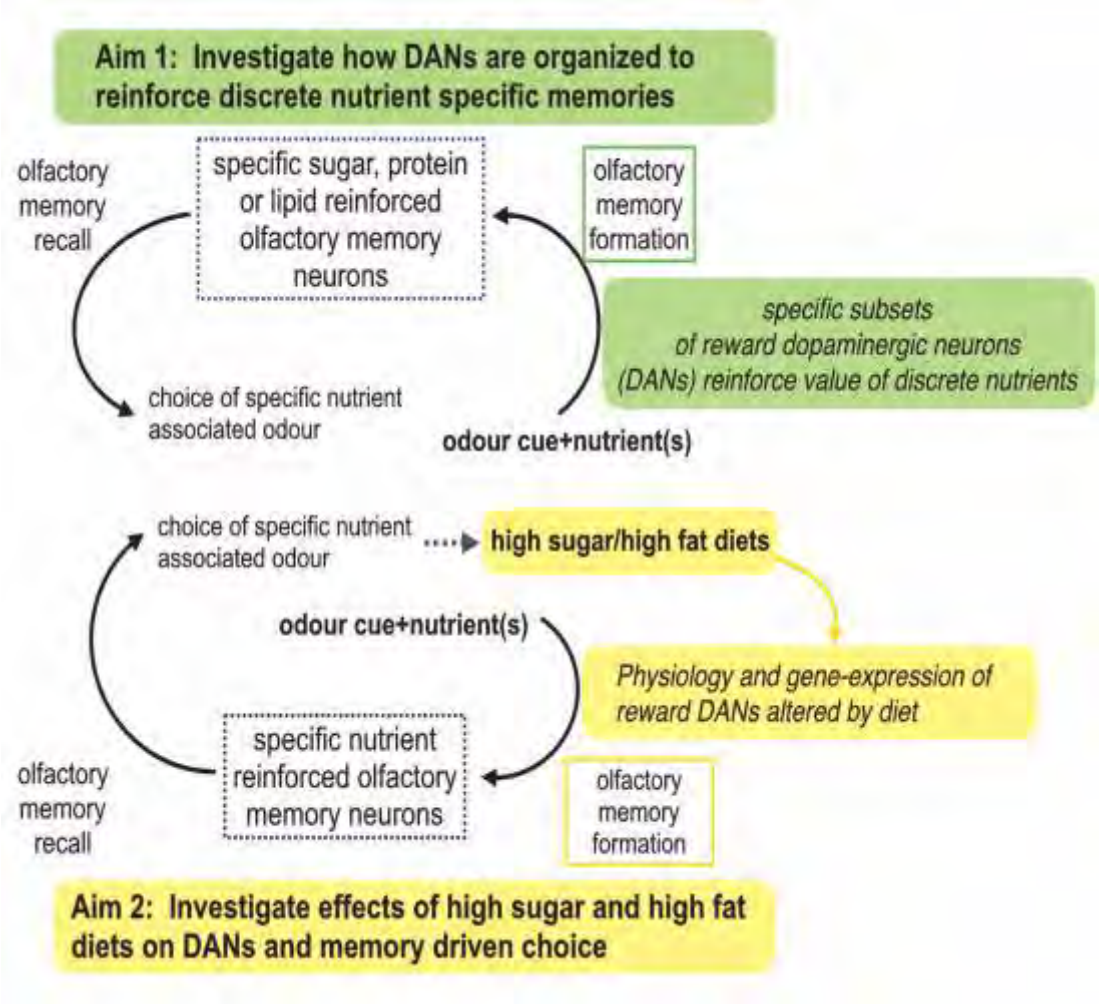

Fig. 1: Graphical abstract of the project.

Fig. 2: Two food choice assay in Drosophila.

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Inter-cellular transfer of Ran GTPase occurs through exosomes

Objectives of the study

- Investigating the detailed mechanism of inter-cellular transfer of Ran GTPase through exosomes.
- Studying the exosomal recruitment of proteins by Ran GTPase.
- Identification and characterization of sequence determinants regulating recruitment of proteins into exosomes.

Summary

Although exosomes are recently appreciated to be means of inter-cellular communication in multiple scenarios, how do cells sort different cargos into exosomes is not well understood. Ran GTPase has well-established function in nucleo-cytoplasmic transport. Serendipitously, we found that Ran gets transferred from one cell to another. This transport occurs through exosomes in a GTP- and CRM1-dependent manner. Consistent with this conclusion, intereference with the exosome formation by specific depletion of TSG101 significantly impaired inter-cellular Ran transfer (Fig. 1). Consistent with its well-known function in CRM1-dependent nuclear export of cargo molecules, we hypothesize that Ran-CRM1 axis plays a role in recruitment of cargos into the exosomes. Based on the results obtained, we propose the following working model (Fig. 2). We speculate that the RanGTP-CRM1 axis may regulate the recruitment of a cargo that contains NES or NES-like sequence. However, such an interesting possibility needs to be tested in future experiments. The RanGTP-CRM1-Cargo complex may be originating from the nucleus or independently assembled in the cytoplasm. Intercellular communication through exosomes has great implications in diseases such as cancer, and overexpression of Ran is

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associated with multiple cancers. Understanding the potential function for Ran is important for both basic and clinical aspects of inter-cellular communication.

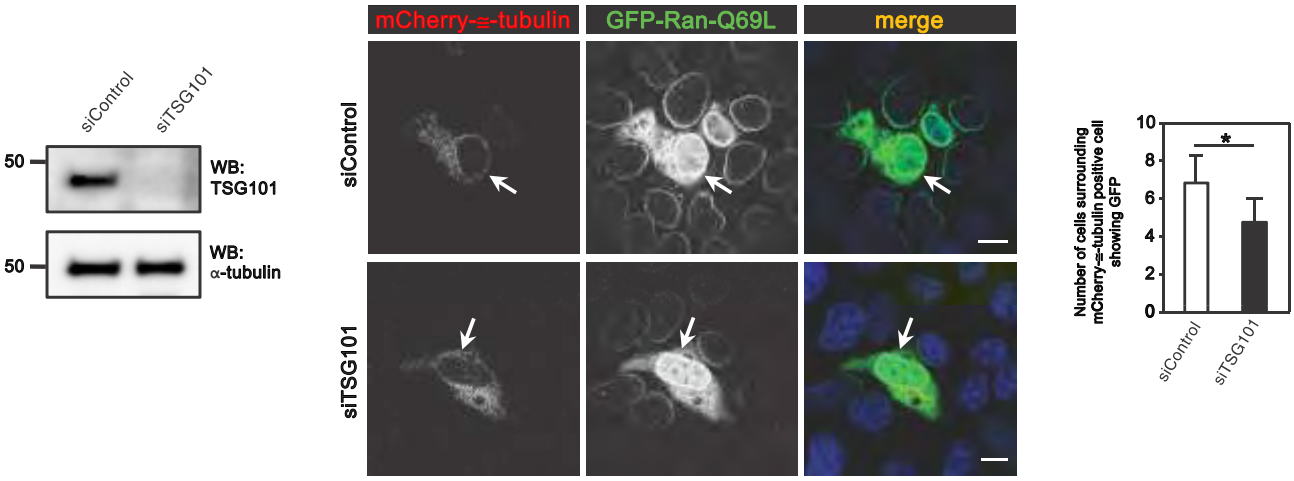

Fig. 1: Inter-cellular transfer of Ran occurs through exosomes

HeLa cells were transfected with control (siControl) or TSG101-specific (siTSG101) siRNA (40 nM) for 48 h and re-transfected with each siRNA (40 nM) for 24 h. Then the cells were co-transfected with GFP-Ran-Q69L and mCherry-α-tubulin (transfection marker) for transient Ran transfer assay. The extent of TSG101 depletion was monitored by western blot analysis (left panel). The number of GFP-positive recipient cells (green) surrounding mCherry-α-tubulin expressing donor cells (red, indicated by arrow) were analysed. DNA was stained with Hoechst 33342 (blue). Relative extent of GFP-Ran-Q69L transferred to the recipient cells was calculated from three independent experiments and plotted (right panel). Data are presented as mean ±SD, P-value was calculated using Student's t test and * indicates $P < 0.05$.

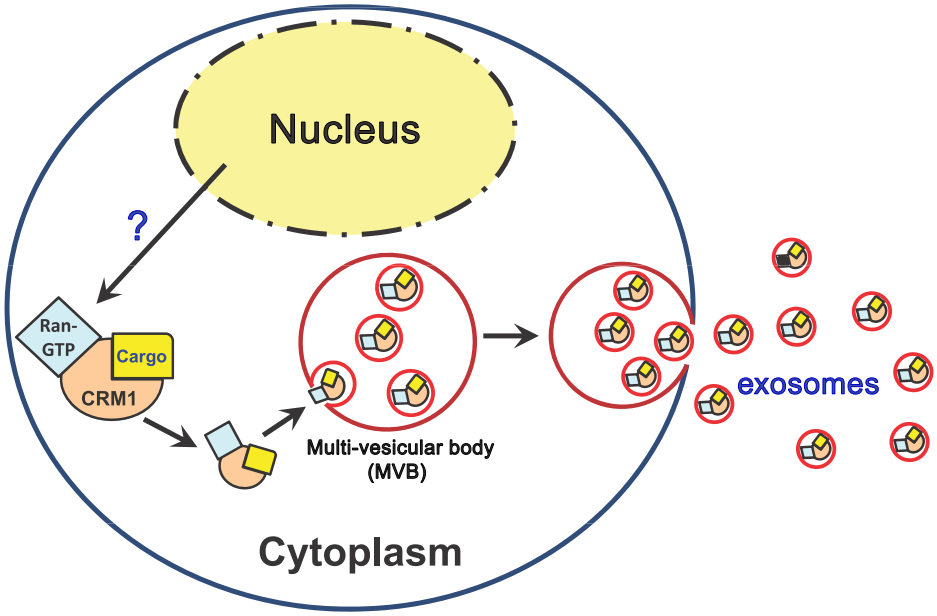

Fig. 2: Working model for Ran's function in exosomes

RanGTP-CRM1 axis might regulate the recruitment of a subset of cargoes into the exosomes from the cytoplasm. RanGTP-CRM1-Cargo complex may be sorted into the intra-luminal vesicles of the multi-vesicular bodies (MVBs) generated due to inward budding. The MVBs eventually fuse with the plasma membrane to release the intra-luminal vesicles, which are the 'exosomes'. The RanGTP-CRM1-Cargo complex may originate from the nucleus (?) or be assembled in the cytoplasm.

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IgA specific to region VI of EBL-175 confers tissue protection in Malaria infection

Objectives of the study

- To determine whether or not ligand specific IgA observed against malarial antigens confers benefits to infected host.

Background

In order to develop an effective vaccine against malaria, it is important to separate or understand specific immunological responses important in 'tissue protection' vs 'reduction of parasitaemia'. The definition of protection against malaria need not necessarily mean the inhibition of parasitaemia but protection of mucosal surfaces that can prevent sequestration of parasites at remote locations including brain and lungs. Naturally acquired antibodies to *P. falciparum* have been shown to play a key role in immunity against malaria. However, it is still not clear which type of response is important in mucosal surface protection *vis-a-vis* increase in parasitaemia, despite a number of immuno-epidemiological studies that have attempted to correlate the occurrence.

The homology between region VI of EBA-175 of *P. falciparum* (PfrVI) and EBA-140 of *P. berghei* (PbrVI) has helped us to examine the protective role of the IgA against the peptide sequences derived from this domain on the onset of experimental cerebral malaria and lung inflammation. Our data suggests that this IgA can play an important protective role in vivo.

Findings

Among the immunoglobulin subtypes the IgM, IgG and IgE were all implicated in the adverse pathology associated with rosette formation, placental malaria

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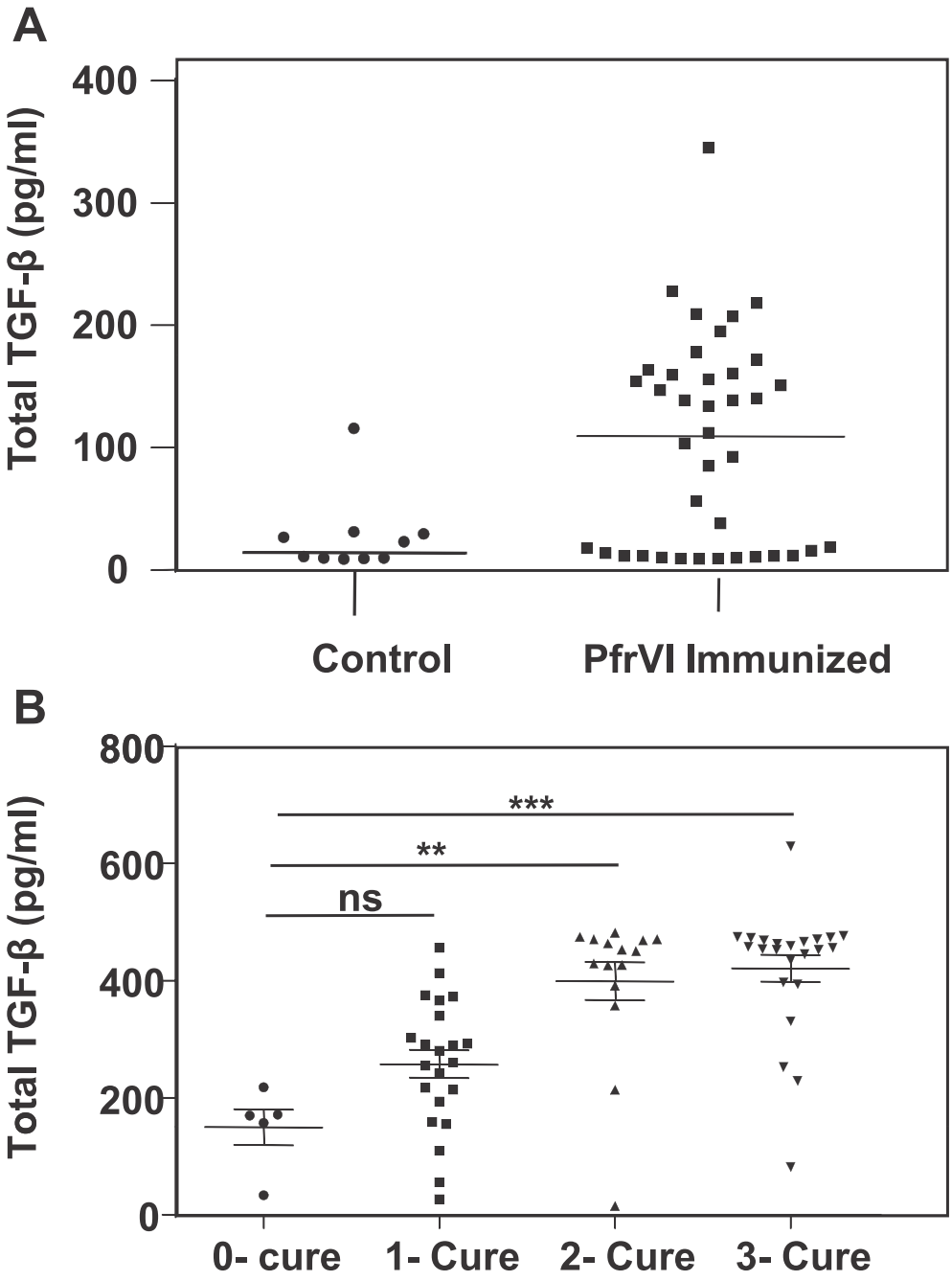

Fig. 1: Total TGFβ concentrations:

(A) Total TGF β level in PfrVI immunized mice: The symbols represent individual values for serum obtained from control and PfrVI immunized mice after day 4. The horizontal lines represent the mean values for the groups. The graph here represents the data of one of three independent experiments. The symbols *, ** and *** represent $p<0.05$, $p<0.01$ and $p<0.001$ relative to controls under the same conditions. n=40 for PfrVI immunized mice, n=10 for control.

(B) Total TGF β level in semi immune mice: The symbols represent individual values for serum obtained from control, 1- cure, 2- cure and 3- cure mice after 2nd day of infection till the parasitaemia reaches 4-5%. The horizontal lines represent the mean values for the groups. The graph here represents the data of one of three independent experiments. The symbols *, ** and *** represent $p<0.05$, $p<0.01$ and $p<0.001$ relative to controls under the same conditions.

and severe malaria while certain IgG subtypes were found to be protective to the host, the IgA subtype has not been investigated in detail. Malaria is known to induce hypergammaglobulinemia in which IgG is produced in excess and its advantages *vis-a-vis* disadvantages are unclear. Our earlier work has identified two peptide sequences that belong

to region VI (rVI) of *P. falciparum* (PfrVI) elicit the IgA referred as Mpep3 (1388 to 1401) and Mpep4 (1408-1424). The IgA specific to this Mpep3/Mpep4 could inhibit the *in vitro* invasion of *P. falciparum* merozoites and also found to improve the overall cerebral pathology of *P. berghei* ANKA infected mice. In this study, we have attempted to understand the role of region VI sequences of *P. berghei* ANKA i.e. EBL-140 (equivalent of EBA-175) in parasitaemia progression vs. tissue pathology.

***P. berghei* peptides elicit IgA:** The PfrVI is conserved among all the EBLs and we could identify the peptides of *P. berghei* ANKA strain that have homology with the PfrVI. The synthetic versions of the peptides labeled as Mpep3 and Mpep4 were earlier shown to elicit IgA response upon immunization while the same homologous to *P. berghei* has remained unexplored. We have synthesized two peptides viz. Pb1 and Pb3 of the EBA 140 rVI and the antiserum generated against these peptides showed abundant IgA with a relatively low IgG. This is sharp contrast to the Mpep3 and Mpep4 peptides which had elicited only IgA.

Pb1/Pb3 immunization improves pathology: The goal is to understand whether or not immunization with the Pb1 and Pb3 peptides can offer protection against parasitaemia build-up or better pathology or both. To investigate this, we have challenged the C57BL/6 mice immunized with Pb1& Pb3 peptides with a *P. berghei ANKA* (PbA-1). The lungs of all immunized mice are much better compared to the control mice. The lung pathology is focused mainly due to the association of IgA, the predominant immunoglobulin class in lung secretions, with mucosal immunity in contrast to blood plasma, where IgG is highly abundant. We have specifically examined for lung edema, hemorrhages and thickened septa filled with congested capillaries, infected red blood cell, and leukocytes (iRBC). We have set a 60% reduction in adverse pathology as the criteria with power set at 80% confidence level. Based on these criteria, the pathology of unimmunized control mice showed an extreme congestion of the alveolar space while, the immunized mice have a normal like appearance despite the high parasitaemia. It is relevant to mention that the Pb1 immunized mice have always shown a high level of IgA, in comparison to Pb3 immunized mice which have shown a significant IgG along with IgA. Overall this data suggests the importance of the peptide (Pb1) and thereby, Pb1 specific IgA, in preventing the adverse tissue pathology associated with the infection, very much akin to the Mpep3/Mpep4 immunized mice data shown in earlier published report.

TGF-β secretion increase with multiple infection cycles: The overall severity of disease depends on the delicate balance of inflammatory response, which is controlled by various pro- and anti-inflammatory cytokines. The TGF-β has both pro- as well as anti-inflammatory properties. TGF-β was also reported to specifically induce the IgA class switch. Therefore, to identify whether there is any increase in the TGF-β levels among the infected mice, we have quantified the total TGF-β in mice immunized with PfrVI and challenged them with PbA-1. The serum was collected every alternate day post challenge and analyzed for IgA, IgG and total TGF-β. We observed the positive increase in the total TGF-β levels among the mice subjected repeated infection and cure cycles.

Similarly, we have also examined the status of total TGF-β in serum of semi-immune-mice, generated by repeated infection-cure cycles resembling an endemic like population (Fig. 1). A clear increase in the TGF-β levels among 2- and 3-cure mice is observed in comparison with the 0- and 1-cure mice as shown in. As mentioned above, in 2- and 3-cure mice, the $CD19^{+}PfrVI$ specific IgA is also high in comparison to the 0- and 1-cure mice, suggesting that there is a significant positive correlation between TGF-β and IgA which is helping the host from the ill effects of possible tissue damage caused by the parasite.

Summary

IgA is found to be present in serum and breast milk of individuals of endemic area and is significant only among the individuals who had multiple clinical attacks of malaria. However, the antigen that elicited the IgA has been elusive and the anti-malarial IgA does not seem to recognize synthetic peptides derived from various blood stage antigens. Much like the endemic population, out observations, unambiguously highlights the following points (i) It is possible to isolate and study the B-cells representing the IgA subclass after immunization with the antigen (ii) It is also clear that the laboratory endemic experiments can, in principle, pave the way for simulation of human endemic situations to study the evolution of useful IgA while it is important to identify all other IgA eliciting antigens of Malaria parasite (iii) The presence of TGF-β appears to skew the immune response towards IgA as the number of episodes of recovery and re-infection increases. Our observation correlates with the research published by Deshpande and co-workers, where they have studied various cytokines to determine the severity of malaria in endemic areas of central India.

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Structural and Functional Insights into GluK3-kainate Receptor Desensitization and Recovery

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Objectives of the study

- Structure elucidation of GluK3 receptors trapped in multiple functional states.
- Understanding the conformational changes underlying receptor transitions.
- Elucidating the role of N-linked glycans in modulating GluK3 receptor functions.

Summary

GluK3-kainate receptors are atypical members of the iGluR family that reside at both the pre- and postsynapse and play key role in regulation of synaptic transmission. For better understanding of structural changes that underlie receptor recovery from desensitized state, GluK3 receptors were trapped in desensitized and resting/closed states and structures analyzed using single particle cryo-electron microscopy. We show that receptor recovery from desensitization requires major rearrangements of the ligand binding domains (LBD) while the amino terminal (ATD) and transmembrane domains remain virtually unaltered. While, the desensitized GluK3 has domain organization as seen earlier for another kainate receptor-GluK2, antagonist bound GluK3 trapped a partially "recovered" state with only two LBD domains in dimeric arrangement necessary for receptor activation. Using structures as guide, we show that the N-linked glycans at the interface of GluK3 ATD and LBD likely mediate inter-domain interactions and attune receptor-gating properties. Mutational analysis also identifies putative N-glycan interacting residues. These results provide a molecular framework for understanding gating properties

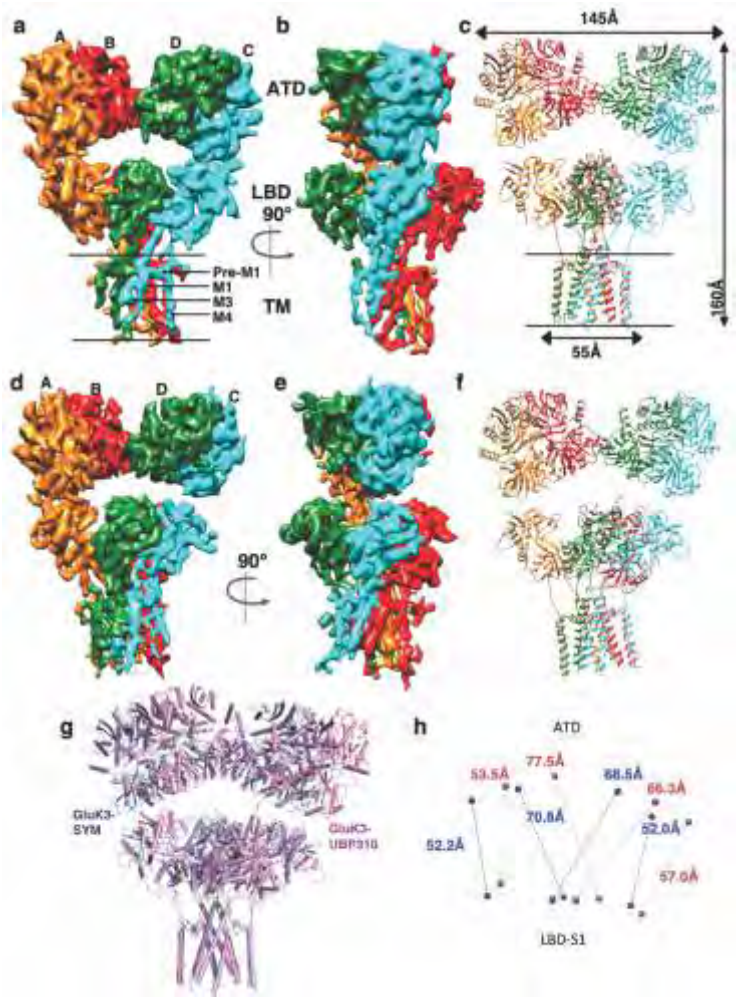

Fig. 1: Cryo-EM density map and fitted model for the agonist and antagonist bound GluK3. Segmented and colored cryo-EM density map at 7.4 Å for agonist 2s,4R-4-methylglutamate-bound (a-c) and at 7.7 Å for antagonist UBP310 bound $GluK3_{EM}$ (d-f), a and d show the front view of receptor, perpendicular to the overall two-fold axis of molecular symmetry with each subunit colored uniquely; b and e are 90° rotated view of a and b; c and f show the fitted atomic model colored to show four receptor subunits as in a-b and d-e. Panel g-h show reorientation of the extracellular domains during transition from agonist-bound to antagonist bound state. g shows front view (perpendicular to the global 2-fold axis of symmetry) of the full-length GluK3 receptor structure in complex with SYM (in cyan), superposed on the UBP310 structure (magenta) by aligning the TMD regions. Distances between center of masses, shown as spheres between ATD and LBD-S1 lobe of each subunit in SYM (blue) and UBP310 (red) bound receptor is measured and indicated in panel h.

unique to GluK3 and identify role of N-linked glycosylation in their modulation.

Kainate receptors are comparatively less studied than AMPARs and NMDA receptors but the current advancement in KAR knowledge indicates that they are involved in multifunctional neuronal activity and have a profound role in health and diseases. Using a multi-pronged approach, combining cryo-EM, X-Ray crystallography, electrophysiology, we studied GluK3 Kainate receptor structure in desensitized and closed state (Fig. 1). Primarily, three major states exist in the gating cycle of glutamate receptor ion channels namely; resting, activated and desensitized state. Binding of agonist to the resting state receptor leads to a short-lived active state, which immediately relaxes to a desensitized state in order to relieve the strain caused by activated state onto linkers between LBD and TM. It quickly rearranges to a more energetically favorable desensitized conformation, where the LBDs acquire a quasi 4-fold symmetry. Removal of agonist or binding of antagonists in *in vitro* conditions allows the receptor to go in resting/closed state by rearranging LBD to a dimeric state, which leads to re-positioning of the linkers between LBD and TM. It is well established that kainate receptors recover slower than AMPA receptor. Also, the desensitized state in kainate receptors is ~100 fold more stable than their AMPA counterpart. Further, N-glycans by virtue of their large size, position and chemical composition could mediate both intra and inter–domain interactions within the same subunit or other subunits in a tetramer. These interactions would potentially modulate receptor functions. Our GluK3-SYM and GluK3-UBP310 complex structures combined with electrophysiology based functional assays; identify structural elements on receptor surface, which potentially interact with N-glycans at Asn 247 and Asn 402 near the ATD-LBD interface (Fig. 2). These interactions would likely impede receptor recovery from desensitized state since the desensitized to resting state transition requires large-scale movements of the distal and proximal LBD domains in order to regain the dimeric configuration. The distal domains are stabilized in the desensitized state likely by inter-domain interactions mediated by N-glycans at Asn 247 and Asn 402 apart from other protein-protein interactions. Our results provide a plausible explanation

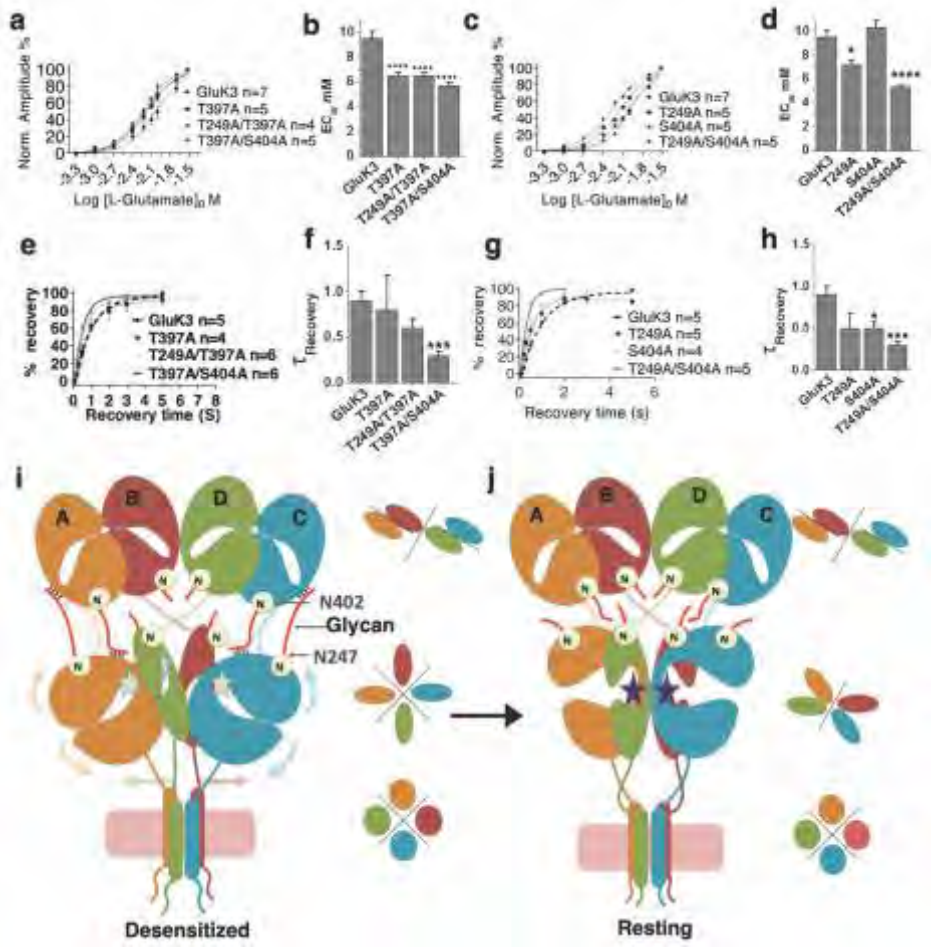

Fig. 2: Model depicting effect of N-glycans on the receptor recovery from desensitized state via interdomain interactions at the ATD-LBD interface. N-glycans modulate GluK3 gating properties. Panels **a-h** show electrophysiological characterization of the various N-glycan mutants. Panels **a-d** show concentration-response curves evoked by 100 ms application of glutamate at concentrations ranging from 30 μM to 30 mM normalized to the 30 mM glutamate-evoked current amplitude. Panels **e - h** show two-pulse glutamate (30 mM) recovery experiments for the indicated mutants and wild type GluK3 receptors recombinantly expressed in HEK293 cells. The amplitude of the second glutamate application in a two-pulse experiment is reported as a normalized percentage of the first glutamate application and is plotted against interpulse intervals. Recovery rates (τ_{rec}) were calculated with a single exponential association fit. Error bars indicate the SEM and P values < 0.05 were considered statistically significant and are reported (* = p < 0.05, ** = p < 0.01, *** = p < 0.001, **** = p < 0.0001). Inter-domain interactions at the ATD-LBD interface mediated by N-glycans (thick red lines) at Asn 247 and Asn 402 positions are shown in a desensitized GluK3 receptor in panel **i**. Panel **j** shows a schematic for "fully-recovered" receptor where the N-glycan mediated interactions (depicted in black lines) would be broken due to rearrangements at the LBD layer. These interactions likely contribute in impeded receptor recovery from desensitized state since the desensitized-resting state transition requires that LBD domains return to dimeric configuration. These transitions would restore 2-2-4 symmetry for ATD, LBD and TM domains respectively in closed/resting state **(j)** from 2-4-4 symmetry observed in desensitized state **(i)** shown in cartoon for various domains.

for the low potency of glutamate, which might be due to a partially recovered resting state in GluK3, reducing the efficacy of bound ligand in channel opening. This could also explain why the GluK3 receptors desensitize faster even at sub-saturating glutamate concentrations. Disruption of the N-glycan mediated interactions likely allows full-recovery leading to slower desensitization, higher glutamate potency and faster recovery from desensitized state (Fig. 2).

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Role of Tumor and Stromal Heterogeneity in Breast Cancer Progression: An Emphasis on Tumor-associated Macrophages

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Objectives of the study

- To study tumor heterogeneity by establishing Patient Derived Xenografts (PDXs) model from breast cancer patients.
- To delineate the role of Tumor Associated Macrophages (TAMs) in regulating Cancer Stem Cell (CSC) mediated tumor growth in orthotopic breast cancer model.
- To delineate the signalling mechanism by which TAMs regulate CSC dependent breast tumor progression.

Summary

Tumors exhibit both cancer and stromal heterogeneity limiting the efficacy of anticancer therapy. This heterogeneity contributes to radio and chemotherapy resistance. Stromal heterogeneity is due to existence of different subsets of macrophages and fibroblasts and heterotypic signaling mediated context-dependent activation of different stromal cell types. Many anticancer drugs have failed to reach clinical trials due to lack of adequate preclinical models. Patient-derived xenografts (PDXs) are important models for validation as they mirror histological and molecular features of patient's tumor. We have recently developed breast cancer specific PDX models. These PDX models will be used to identify potential drug targets and therapeutically relevant biomarkers using genomics and proteomics approaches.

Tumor stroma comprises of various tumor cells, endothelial cells, fibroblasts, and immune cells like tumor associated macrophages (TAMs). Tumor cells evade immunosurveillance by inhibiting antigen presentation pathways and secreting higher levels of anti-inflammatory cytokines thereby polarizing the

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macrophages into M2 phenotype, promoting tumor growth and angiogenesis. Tumor derived cytokines like CCL-2, and CCL-5 act as chemo-attractants and facilitating monocytes / macrophages recruitment into the tumor microenvironment from surrounding tissues. TAMs are characterized by using surface markers such as CD163 and CD206 and by their ability to express high levels of IL-10, TGF-β, PGE-2, arginase activity, VEGF, MMPs, EGF and uPAs. Thus, TAM-derived cytokines interact with cancer cells and aid proliferation, angiogenesis and metastasis. Cancer Stem Cells (CSCs) possess the ability of self-renewal and differentiation through symmetric and asymmetric divisions. CSCs hypothesis states that tumor progression and relapse is due to a small subpopulation present within the tumor, known as cancer stem cells. CSCs are identified in various cancers by expression of different markers like $ALDH^+$, $CD44^+CD24^-$, $CD133^+$, $CD44^+CD24^+ESA^+$, Sca-1 for breast, brain, and pancreatic cancer stem cells respectively. Studies have reported the co-localization of TAMs with CSCs and correlated enhanced infiltration of TAMs with higher malignancy. Studying the interplay between the TAMs and CSCs in breast cancer will shed light on knowledge facilitating cancer immunotherapy. Based on the above background information, we sought to study the role of TAM-derived cytokines and how that promote breast tumor progression through enhancing CSC phenotype.

Work done

In the present study, we have evaluated the tumor and stromal heterogeneity and transcriptional stability by establishing different generations of PDXs (Fig 1A). Histopathologic analysis of serial generations of PDXs has indicated that many of histologic features were retained in higher generations of PDXs. Immunofluorescence analyses using specific markers have revealed that many of them have retained their pattern of expression from G1 to G4 (Fig 1A). Time required for tumor generation gradually decreased after initial engraftment into NOD/SCID female mice (Fig. 1B). To study the transcriptional stability of these tumors in different generations of PDXs, we have performed transcriptome analysis of primary tumor and different generations of PDXs. RNA sequencing data has revealed that gene expression of patient tumors correlate with PDXs (Fig 1C). We have observed that higher passages of PDXs were slightly deviated from primary tumors. Then, we analysed differentially expressed genes between the primary tumors and different generations of PDXs. Interestingly we have found that most of differentially expressed genes are related to stromal

processes such as inflammation and extracellular matrix proteins (Fig 1D).

TAMs are the key players in stromal compartment which regulate tumor progression by regulating inflammation. In this study, we have explored interaction between macrophages and breast cancer cells and its effect on macrophage activation and subsequent effect on breast cancer stem cell (CSC) enrichment. Macrophage activation was performed by treating macrophages (RAW) with conditioned Media (CM) of breast cancer cells (4T1). We observed that there is a change in morphology of TAMs compared to control. Further, we observed that breast cancer cell derived CM enhances the expression of IL-6 in TAMs through p38 MAPK activation. We further examined the role of TAM derived IL-6 on CSC enrichment in breast cancer. Treatment with recombinant IL-6 showed increased ALDH1 activity and Sca-1 expression along with CSC associated transcription factors Sox-2, Oct3/4 and Nanog in 4T1 cells, indicating a critical role of IL-6 in CSC enrichment. Further, treatment with CM of TAMs enriched CSC population in 4T1 cells as confirmed by enhanced ALDH1 and Sca-1 expression. Interestingly, this effect was abrogated when CM of TAMs are neutralized with IL-6 antibody, suggesting that TAMs enhance CSC phenotype through IL-6 expression (Fig 2A). It has been well documented that IL-6 activates STAT3 pathway. It was observed that 4T1 cells upon treatment with IL-6 or CM of activated RAW exhibited higher phosphorylation of STAT3, which was abrogated upon blocking the function of IL-6. Furthermore, blocking STAT3 pathway using its specific inhibitor, Stattic resulted in abrogation of CSC enrichment in IL-6 or CM of activated RAW treated 4T1 cells. Thus our data suggests that TAM derived IL-6 may enhance CSCs through STAT-3 pathway. To understand the role of TAM derived IL-6 on breast tumor growth, we treated 4T1 tumor-bearing mice with CM of activated RAW with or without IL-6 blocking and observed the tumor growth. The results revealed that mice treated with CM of activated RAW showed enhanced tumor growth as compared to control, whereas the increase in tumor size was abrogated when function of IL-6 is blocked (Fig. 2B, C). Moreover, tumor volume and tumor weight data support earlier data. (Fig. 2D, E). In summary, our findings suggest that breast cancer cells enhance IL-6 expression in TAMs through p38 pathway, which in turn enriches breast CSCs by upregulating CSC specific transcription factors through STAT3 activation leading to breast cancer progression (Fig. 2F).

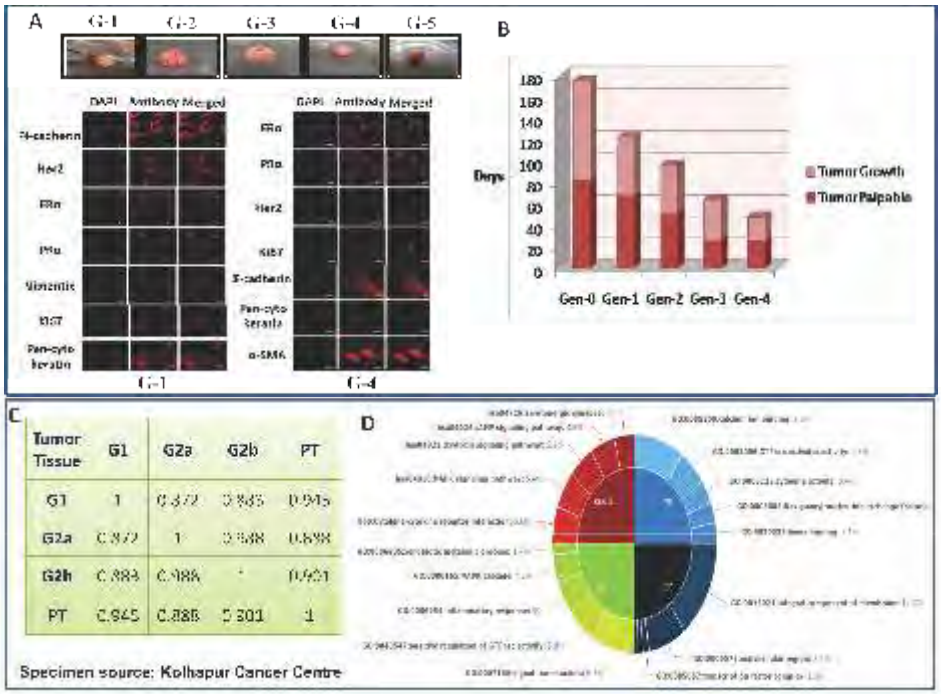

Figure1: Breast cancer patient-derived xenografts (PDX) exhibit tumor heterogeneity and transcriptional stability. (A) Ablated tumors (top) and primary cultures derived from tumor sections of G1 and G4 were stained with N-cadherin, Her2, ERα, PRα, Ki67, pan-cytokeratin and vimentin and immunofluorescence analyses were performed (bottom). (B) Tumor growth pattern in terms of palpability and time to tumor burden of PDXs after initial engraftment into NOD/SCID female mice. (C) Correlation of gene expression between the primary tumor and different generations of PDXs by GeneSpring. (D) Gene Ontology analysis for functional annotation of genes differentially expressed between primary tumor and different generations of PDXs.

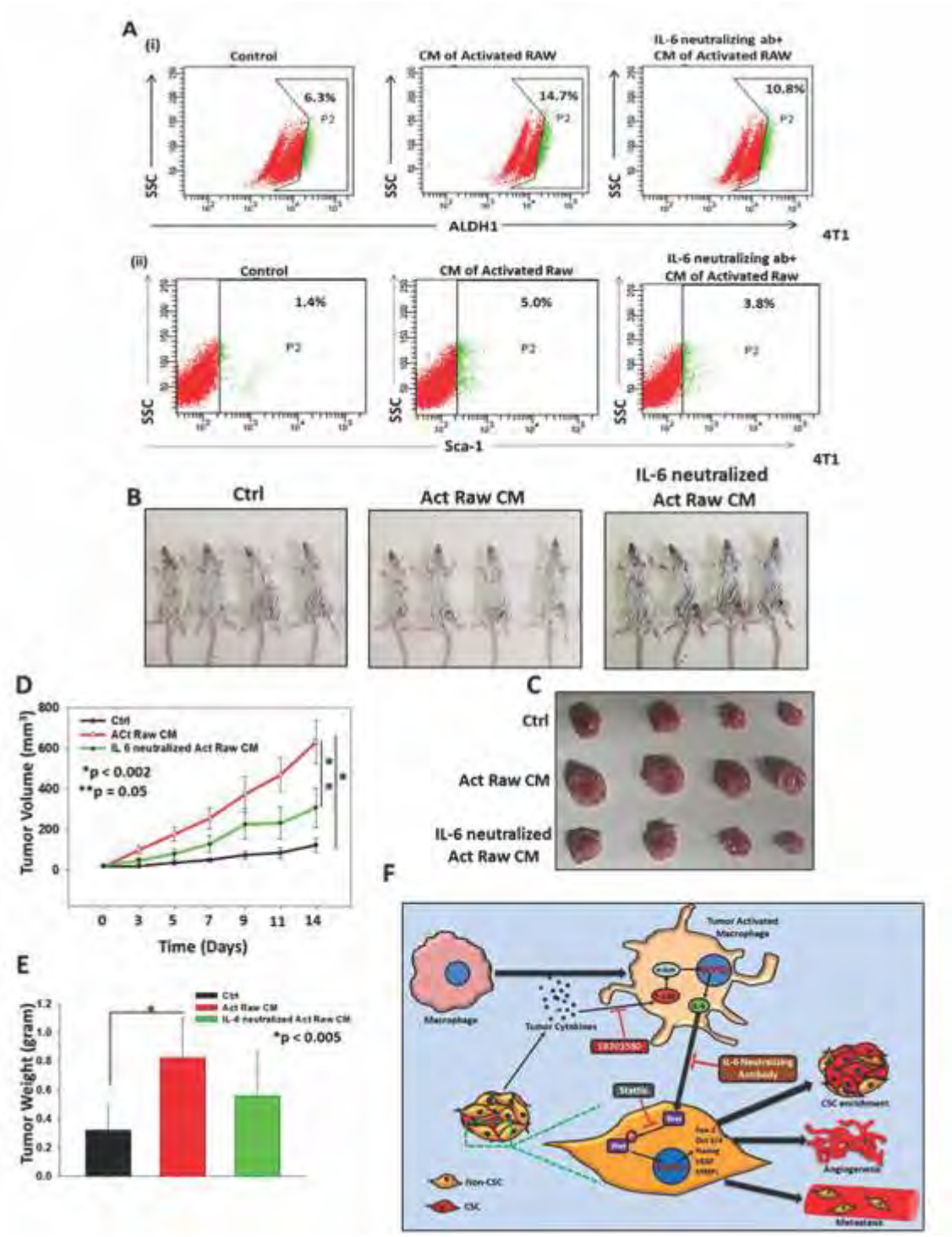

Fig. 2: TAM derived IL-6 enriches CSC phenotype in breast cancer. **(A)** FACS analysis of **(i)** Aldefluor activity and **(ii)** Sca-1 expression in 4T1 cells either untreated or treated with CM of activated RAW or IL-6 neutralized CM of activated RAW. 4T1 breast cancer cells ($5x10^3$) were injected in right mammary fat pad of female Balb/C mice. After tumor development (2-3 mm), mice were intra-tumorally injected with CM of activated RAW or IL-6 neutralized CM of activated RAW for every alternate day, along with tumor measurements for two weeks. **(B)** Images of tumor bearing mice. **(C)** Physical appearance of excised tumors. **(D)** Line graph depicts the tumor growth in terms of mean tumor volume ± SE (n=6). **(E)** Excised tumors were weighed and analyzed statistically. Bar graph represents mean tumor weight ± SD (n=6). **(F)** Schematic representation of breast cancer cell induced IL-6 expression in TAMs and TAM-derived IL-6 mediated CSC enrichment via STAT3 activation.

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Role of transcription factor T-bet and RORγt in $CD4^+$ T cells during neuroinflammation and neuronal autoimmunity.

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Objectives of the study

- To determine how inflammation in the peripheral system affects the central nervous system (CNS).
- To determine what the components involved in the transmigration of inflammatory $CD4^+$ T cells into the CNS are.
- To determine how the immune system cross-talks with the nervous system during inflammation and autoimmunity.

Summary

We investigated how transcription factor T-bet and RORγt expression in pathogenic Th1 and Th17 control its pathogenicity in neuroinflammation and neuronal autoimmunity. T-bet regulates the migration of neuronal antigen-specific Th1 and Th17 cells explicitly into the CNS whereas RORγt expression controls the apoptosis of neuron during neuronal autoimmunity. Apoptosis of neuron in the CNS was independent of the host-derive iNOS molecule and required IL-23-IL-23R signaling in neurons. This study provides a distinct molecular mechanism used by pathogenic Th1 and Th17 cells and may help in designing a better strategy to control neuroinflammation and neuronal autoimmunity

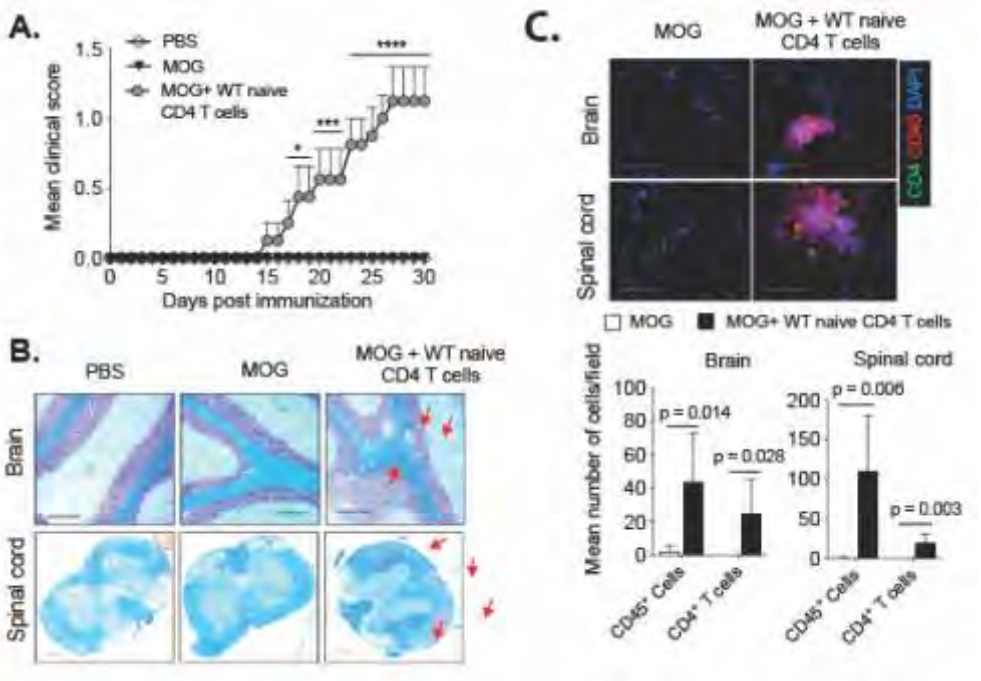

Fig. 1: T-bet expression in $CD4^+$ T cells control BBB damage and cause Experimental Autoimmune Encephalomyelitis (EAE). $T\text{-bet}^{-/-}$ mice were given *s.c.* injection of myelin oligodendrocyte peptide 35-55 (MOG peptide) in complete Freund's adjuvant (CFA), and *i.v.* injection of pertussis toxin (PTx) on day 0 and 2. On the day of MOG peptide injection, wild-type purified naive $CD4^+CD25^-$ T cells (2 X 10^6 cells/mouse) were adoptively transferred. Control mice received PBS emulsified in CFA plus two injections of PTx. **(A)** EAE clinical score was monitored and plotted. **(B)** A representative Luxol-fast blue staining of $T\text{-bet}^{-/-}$ mice brain tissues at day 30 of MOG injection is shown. **(C)** A representative image of the brain and spinal cord tissues stained for CD45 (red), CD4 (green) and nuclear stain DAPI (dark blue) is shown (upper). Mean number of $CD4^+$ and $CD45^+$ cells per field were quantitated and plotted (lower). Data are representative of three independent experiments with 3-5 mice in each group. * p <0.05, *** p < 0.001, **** p < 0.0001, One-way ANOVA followed by Bonferroni test **(A)**; Student's t-test **(C)**; Original magnification 100x **(B)**, 400x **(C)** Error bar represents ± S.E.M. **(A)** S.D. **(C)**; Scale bar 300 m **(B)** and 100 µm **(C)**.

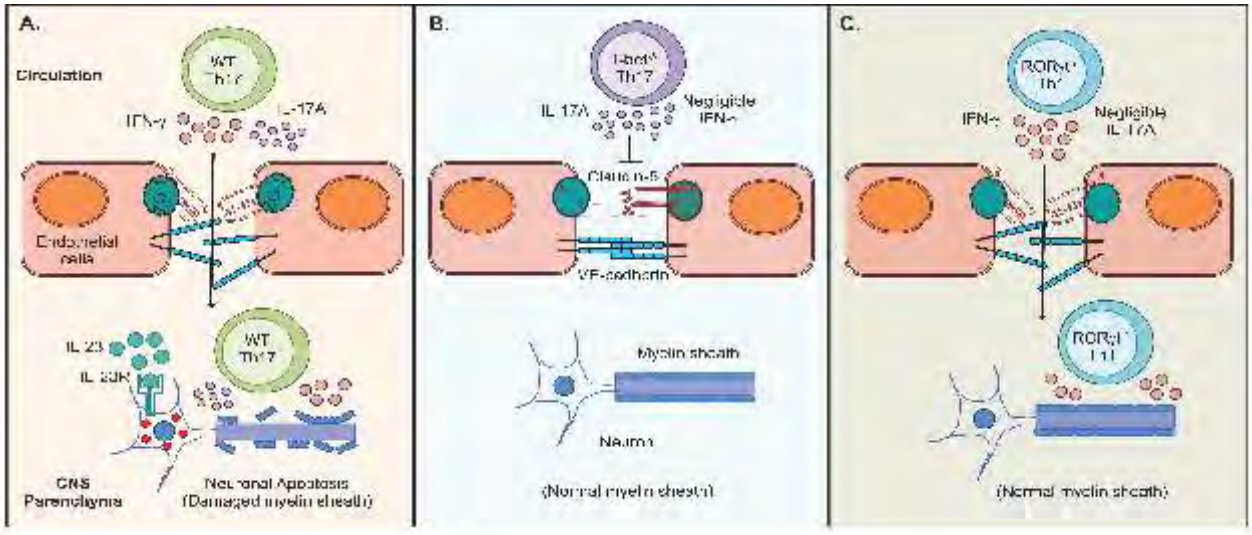

Fig. 2: Differential role of T-bet and RORγt in promoting blood-brain barrier (BBB) disruption, CNS transmigration, and induction of neuronal damage. **(A)** The majority of highly pathogenic myelin-specific Th17 cells express RORγt and T-bet and produce both IL-17A and IFN-γ. The local production of IFN-γ in these cells act on BBB endothelial cells and induce the junctional disorganization of critical molecules such as claudin-5, VE-cadherin, and ZO-1 leading to increased vascular permeability and transendothelial migration of these cells across the BBB into the CNS. In the CNS parenchyma, RORγt induces the expression of IL-23R on β-III tubulin$^+$ and NeuN$^+$ neurons. In the inflamed CNS, locally produced IL-23 act on IL-23R-expressing neurons and induced apoptosis in neurons. **(B)** The $T\text{-bet}^{-/-}$ myelin-specific Th17 cells generated in the presence of IL-23 produce substantial amounts of IL-17A but lack IFN-γ. Due to the absence of T-bet and its target IFN-γ these cells could not damage BBB and unable to enter into the CNS. Similarly, in MOG-immunized $T\text{-bet}^{-/-}$ mice, where lack of $T\text{-bet}^{+/+}$ $CD4^+$ T cells impairs the breach of BBB. **(C)** The $ROR\gamma t^{-/-}$ myelin-specific Th1 cells are $T\text{-bet}^{+/+}$ and produce IFN-γ but lack IL-17A. The locally produced IFN-γ by these cells act on BBB endothelial cells and disrupt the junctional molecules and allowed these cells to transmigrate across the BBB into the CNS parenchyma. Although $ROR\gamma t^{-/-}$ Th1 entered into the CNS parenchyma, but due to lack of RORγt expression, these cells failed to induce IL-23R on neurons and did not induce apoptosis. Similarly, when $ROR\gamma t^{-/-}$ mice immunized with MOG/CFA and PTx or $ROR\gamma t^{-/-}$ naive $CD4^+$ T cells were transferred into $T\text{-bet}^{-/-}$ recipients, where $ROR\gamma t^{-/-}$ $CD4^+$ T cells breached BBB and entered in the CNS parenchyma but failed to induce EAE.

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Differential influence of USP and its mechanism of action during mesoderm induction and subsequent differentiation into its derivatives

Objectives of the study

- To gain a mechanistic understanding about USP's influence during mesoderm induction and subsequent differentiation to its derivatives.

Summary

Embryonic development involves precise and fine-tuned orchestration of events in a temporo-spatial manner. The key players during the same include the signalling molecules, their cross-talk, genetic and epigenetic modulators etc. commensurate with the stage of development. Mesoderm, the middle of the three embryonic germ layers during gastrulation, gives rise to cells of various vital systems including haematopoietic, cardiovascular, reproductive, excretory, urogenital etc. during early development. Embryonic stem cells (ESCs) derived from the inner cell mass of blastocyst do represent an elegant *in vitro* model to unravel the complex molecular events underlying these developmental proceedings. Using ESCs, we have already demonstrated temporal and differential influence of Wnt during Mesoderm induction and also its downstream haemato-endothelial fate specification and cardiomyogenesis. While exploring further to identify specific targets of Wnt during this differentiatial cell fate modulation, we came across a deubiquitinase (DUB/USP) that was having multiple TCF/LEF binding sites. Gene expression analysis of the USP showed its expression to be significantly higher during differentiation and its further up-regulation seen under Wnt activation condition suggested it to be a downstream effector molecule of canonical Wnt activation. Further investigation following establishment of USP deficient and efficient ESC clones and assessing USP's attributes during cell fate specification revealed an

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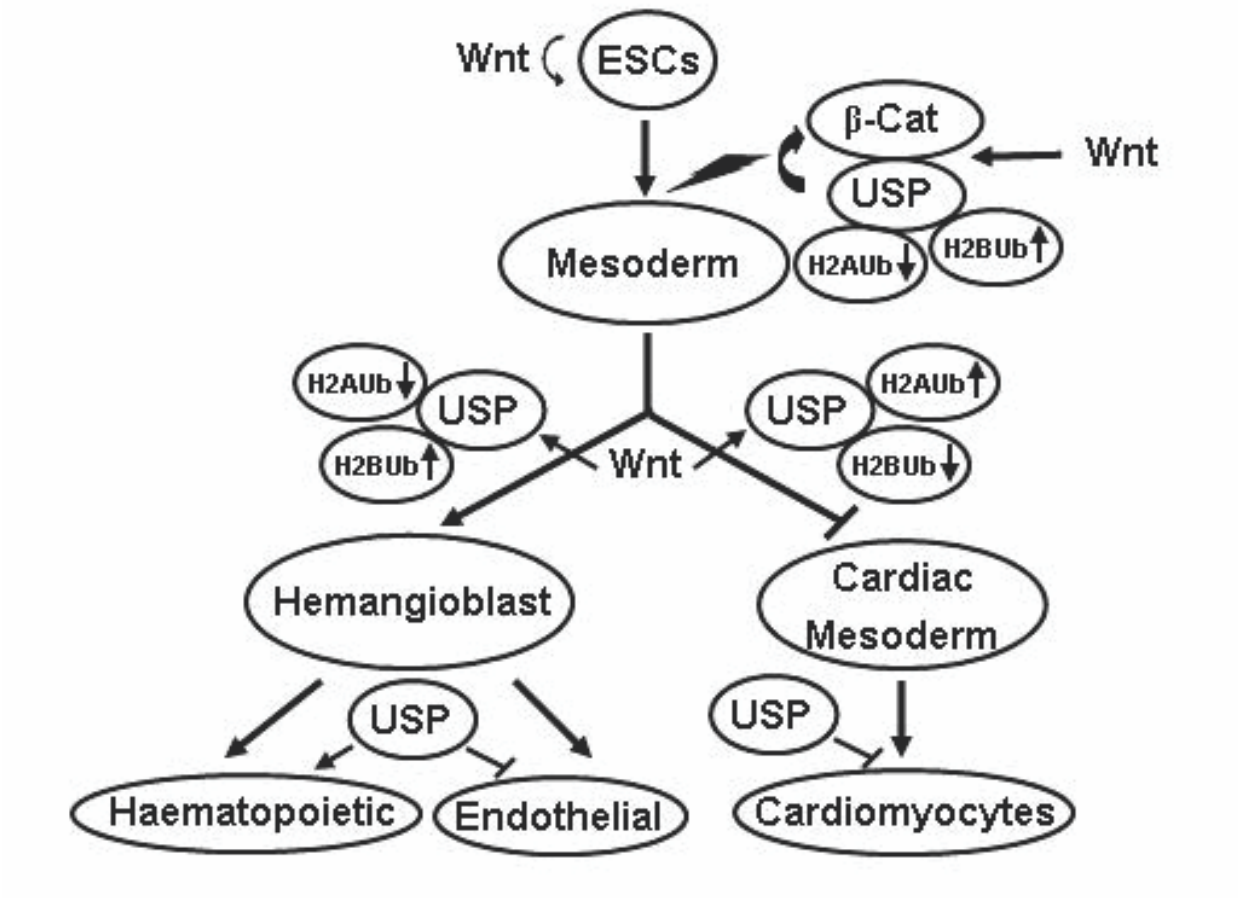

Fig. 1: Wnt-USP link and histone ubiquitination dynamism during mesoderm specification and differentiation.

interesting paradigm of differential fate modulation during mesodermal induction and subsequent differentiation. Accordingly, we intended to chalk out the mechanistic basis underlying its action. Corroborating with Wnt influence, our findings not only demonstrated the interaction between USP and β-catenin, but also revealed β-catenin expression to be modulated by USP, deciphering thereby an interesting feedback loop operational during Wnt/USP mediated cell fate decision. While mesoderm induction was pronounced under USP efficient condition, it further promoted hemangioblast specification at the expense of cardiomyogenic progenitor specification and further differentiation. Additionally, it displayed a positive modulatory effect directing induced hemangioblasts towards haematopoietic lineage at the expense of endothelial ones. Moreover, our investigation also delineated the importance of USP catalytic activity underlying this modulation. To further delineate the mechanistic basis underlying the DUB activity and its influence during ESCs differentiation, we could ascertain its chromatin association and thus ascribing it as a chromatin modulating enzyme. Interestingly, USP was found to be associated with deubiquitinating both H2AUb and H2BUb, where differential recruitment of both in the promoters of mesodermal genes dictated various mesodermal fates choice (Fig. 1). Considering the multifaceted role of Wnt during early development, further investigation would shed light on the relevance of USP -β-catenin interaction and involvement of other DUBs during the same.

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Studies on Expansion, Cryopreservation and Differentiation of Hematopoietic, Mesenchymal and Induced pluripotent Stem cells isolated from Umbilical cord tissues

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Objectives of the study

(Out of the 3 ongoing projects, the project on neutrophils will be described here)

- To establish *in vitro* system for generation of neutrophils from HSCs.
- To elucidate the mechanism involved in their cell fate decision.

Summary

Chemotherapy-induced neutropenia causes severe infections in patients, which are often fatal. Transfusion of *in vitro*-generated neutrophils could supplement the currently available methods to treat neutropenia. We have optimized a 14days protocol for differentiation of neutrophils from hematopoietic stem cells (HSCs)/mononuclear cells (MNCs) isolated from apheresis-derived peripheral blood (APBL) and umbilical cord blood (UCB). Neutrophils generated were morphologically, phenotypically and functionally (migration and phagocytosis) similar to human primary neutrophils. Morphology of *in vitro* generated neutrophils as observed by Wright's and Giemsa staining is depicted in Fig.1A. Expression of CD66b and CD15 on both UCB and Apheresis derived neutrophils was analyzed by flow cytometer. It was found to be similar with human primary neutrophils (Fig.1B). Generated neutrophils were found to be functional as determined by their migratory ability towards fMLP chemoattractant (Fig.1C) and by engulfing *E.coli* Bioparticles (Fig.1D). Label-free quantitative proteomics analysis of *in vitro* generated neutrophils showed significant upregulation of the peptidyl arginine deiminase typeIV protein (PADI4), which plays a key role in neutrophil extracellular trap (NET) formation (Fig.2A). NET formation in UCB derived neutrophils after fMLP

stimulation and their inhibition by Cl-amidine (PADI4 inhibitor) is shown in Fig.2B. Whereas, NET formation by apheresis derived neutrophils and their subsequent inhibition by PADI4 inhibitor is depicted in Fig.2C. NADPH oxidase and autophagy were found to be involved in NETosis process. Our MNCs data also show that the HSCs isolation is not absolutely essential for neutrophil generation, making this protocol applicable to clinics that do not have facilities to isolate HSCs.

Highlights

- Functional neutrophils can be generated *in vitro* from HSCs.
- MNCs can directly be used to generate neutrophils by eliminating HSCs isolation step.
- *In vitro* generated neutrophils express PADI4 and possess NET forming ability.
- NADPH oxidase and autophagy play a crucial role in *in vitro* generated neutrophils.

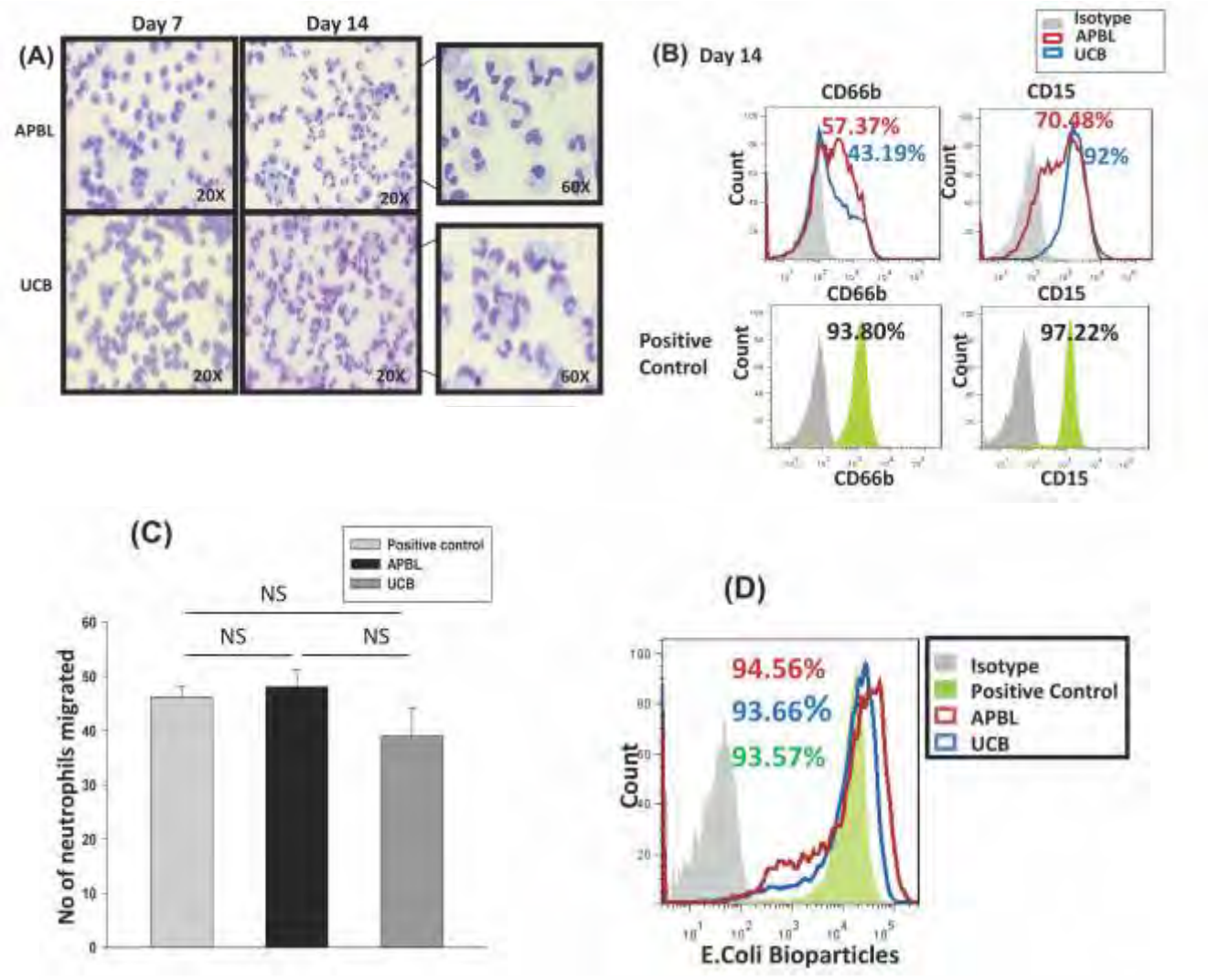

Fig. 1: A) Representative images of Wright's and Giemsa-stained cultures on day7 and day14 showing the maturation of cells from granulocyte precursors towards multilobed neutrophils cells. Images were taken at 20X and 60X. B) Representative histogram plots of phenotypic surface marker CD66b, and CD15 of cells analyzed by flow cytometry on day14, Human peripheral blood isolated neutrophils were used as positive control. C) Graph showing the numbers of cells that migrated through 3µ inserts towards chemoattractant fMLP. Mean values of numbers of migrated cells were calculated from random fields of inserts stained with Wright's and Giemsa. Data are from three different donors. NS: Non significant D) Representative histogram plots showing phagocytosis of fluorescently-labeled *E.coli* bioparticles by cultured and primary human neutrophils (positive control).

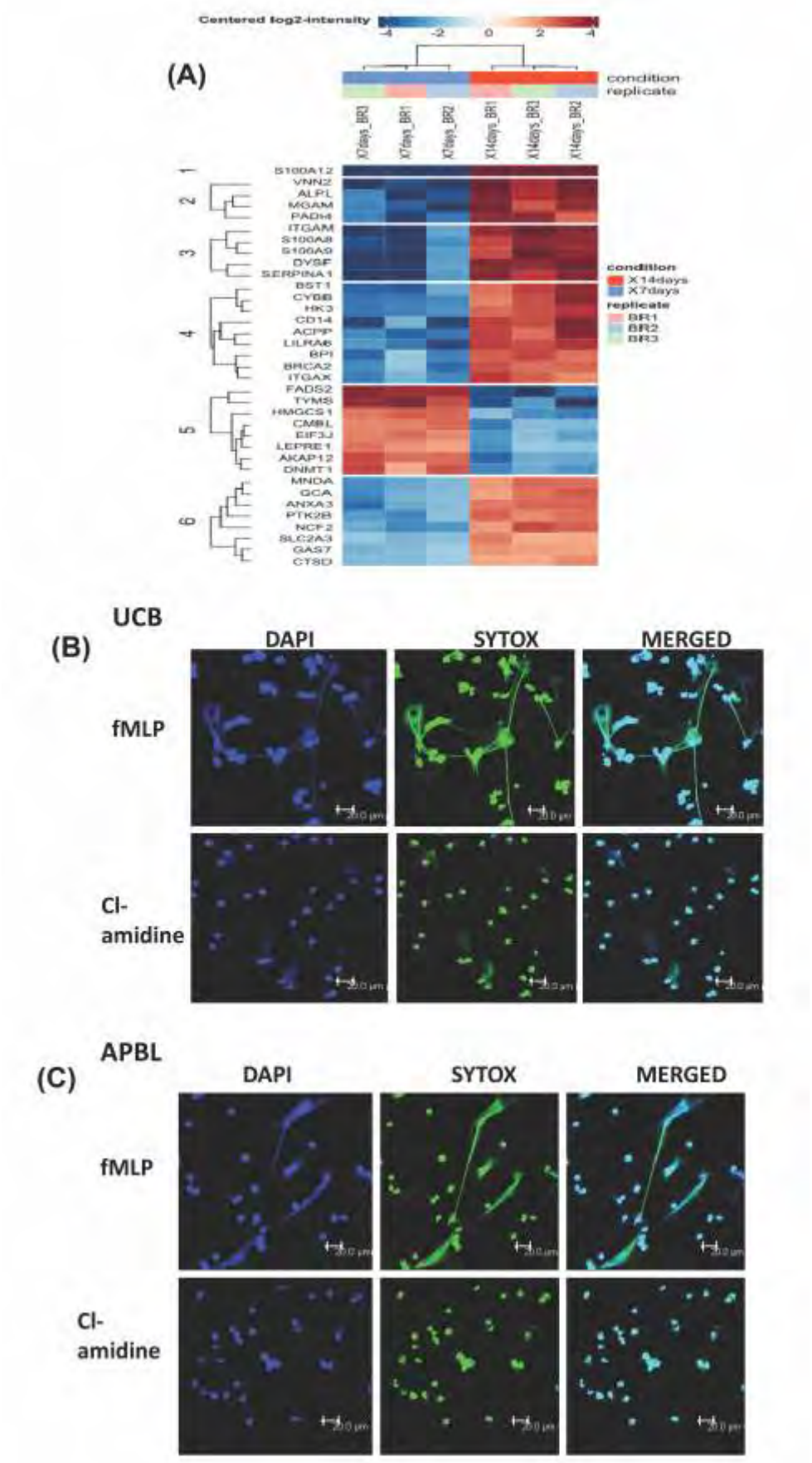

Fig. 2: A) Heat map of the top 35 differentially expressed proteins with p-values above 0.05. Representative confocal images show the NET formation and their reduction upon Cl-amidine treatment in B) UCB and C) APBL derived neutrophils. (DNA-DAPI,Blue; Extracellular DNA- SYTOgreen, Green), Scale bars=20 µm.

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Role of protein synthesis in Huntington's disease

Objectives of the study

- To study the role of protein synthesis in cells expressing pathogenic Huntingtin protein

Summary

Huntington's disease (HD) is a severe neurodegenerative disorder caused by poly Q repeat expansion in the Huntingtin (Htt) gene. While the Htt amyloid aggregates are known to affect many cellular processes, its role in translation is not addressed. Here we report pathogenic Htt expression causes protein synthesis deficit in cells. We find a functional prion-like protein, the translation regulator Orb2 to be sequestered by Htt aggregates. Coexpression of Orb2 can partially rescue the lethality associated with poly Q expanded Htt. These findings can be relevant for HD as human homologs of Orb2 also can be sequestered by pathogenic Htt aggregates. Our work suggests that translation dysfunction could be one of the contributors in the pathogenesis of HD and new therapies targeting protein synthesis pathways might help alleviate disease symptoms.

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Deciphering the structure and function of hypoxia protein Rv0081 protein in *Mycobacterium tuberculosis*

Objectives of the study

- Structure determination of Rv0081
- Biophysical and biochemical characterization of Rv0081

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Summary

The transcription factor Rv0081 of *Mycobacterium tuberculosis* controls the hypoxic gene expression and acts as a regulatory hub in the latent phase of tuberculosis infection. We successfully solved the structure of hypoxia protein Rv0081 at 2.9 Å resolution. Although, Rv0081 is crystallized in various buffer conditions but all crystals diffracted ~ 3 Å or less resolution. Despite that, we successfully solved the structure. We observed through structural analysis of Rv0081 that it belongs to well known metal dependent transcription repressor ArsR/SmtB family. Furthermore, we were surprised to observe that Rv0081 is devoid of metal binding residues and does not possess any cysteine residue (s), suggesting an alternate mechanism of gene regulation unlike ArsR/SmtB family. Moreover, our structural and biochemical analysis suggests the molecular basis for the recognition of self-regulatory DNA sequence and we explained the plausible mechanism of regulation of Rv0081 in the latent phase of tuberculosis infection. This work has been published as entitle: "Structural basis of hypoxic gene regulation by the Rv0081 transcription factor of *Mycobacterium tuberculosis*" in FEBS Lett. 2019 May; 593(9):982-995 and the structure of Rv0081 has been deposited in Protein Data Bank as PDB ID: 6JMI.

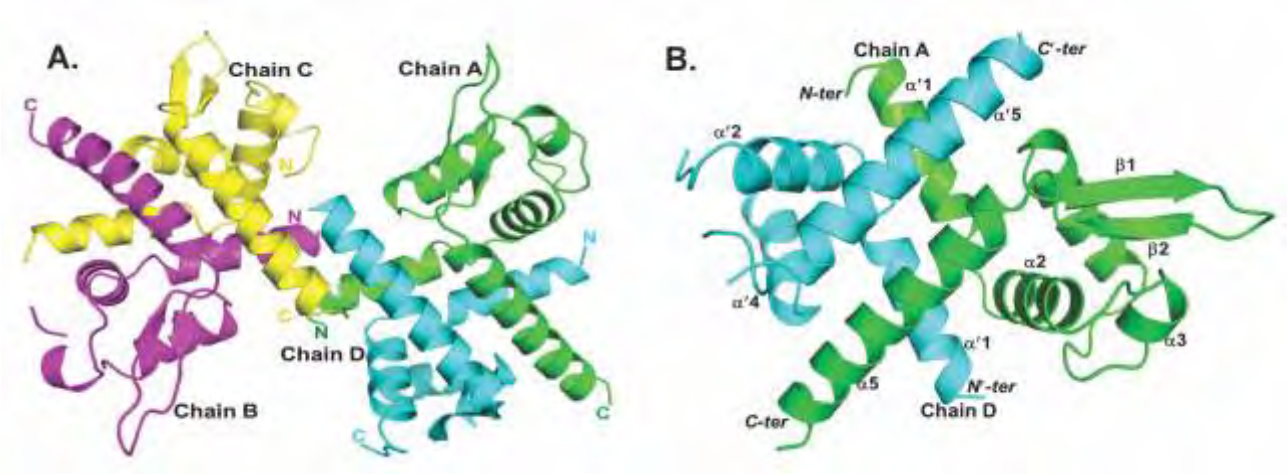

Fig. 1: Structure of the Rv0081 dimer: The structure of Rv0081 is typical of the ArsR/SmtB family of metal-dependent transcriptional repressors. (A) Crystal asymmetric unit contains four identical chains as shown in four different colors. The extremities of the polypeptide chains at either of the N- and C- termini make up the interface between two dimers. At this stage it is not clear if the tetrameric assembly is biologically relevant or not. (B) Two monomers possess an extensive monomer-monomer interface, clearly suggesting that the biological assembly is that of a dimer. The interface is principally made up of the first and the last helices. (Ref: Structural basis of hypoxic gene regulation by the Rv0081 transcription factor of *Mycobacterium tuberculosis*" in FEBS Lett. 2019 May; 593(9):982-995).

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Host cell factors in HIV pathogenesis and identification of new anti-viral lead molecules

Objectives of the study

- Role of viral regulatory proteins Tat and Nef in HIV pathogenesis.
- Differential gene expression studies to identify molecular mechanism of HIV-1 induced T-cell apoptosis.
- Identification of novel molecules with anti-HIV activity and their potential for use as microbicides.

Summary

Human immunodeficiency virus is the causative agent of acquired immunodeficiency syndrome (AIDS), the incidence of which has reached pandemic levels worldwide. The therapeutic regimen being used at present can reduce the viral load significantly but is not the ultimate answer to AIDS patients as a therapy for cure from HIV is yet to be identified. Our group has been working on different aspects of HIV pathogenesis, related to host-virus interactions, immune response and drug discovery. The primary objective is to gain more understanding of the virus and its interaction with the host cell, which may lead to new antiviral strategies.

The Human Immunodeficiency Virus Type 1 encodes a 27 KDa protein, Nef, which has come a long way from being termed as a negative factor to being one of the most important proteins of HIV-1. However, its role in HIV-1 replication and gene expression remains to be clearly understood. We have shown earlier that cellular HSP40 and HSF-1 proteins interact with viral Nef protein and positively regulate HIV-1 replication. Although involvement of different heat shock protein family members in viral pathogenesis has been

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reported earlier, a clear understanding of their role in viral replication and infectivity remains to be elucidated. We have initiated a comprehensive study of all the HSP protein family members during HIV infection. Our expression profiling results targeting HSP family members and their isoforms indicate that a significant number of genes belonging to HSP40 family are differentially expressed during infection. The differential expression profile of selected HSP40 isoforms has now been validated in HIV-1 infected human PBMCs. We have also checked the effect of these selected isoforms on HIV-1 LTR promotor driven gene expression by silencing and over-expression study. Here, we find that over-expression of some of the isoforms enhances LTR driven promotor activity while overexpression of some other isoforms reduce LTR driven promotor activity significantly, which also correlated well with virus production analysis based on p24 antigen capture ELISA. We have also checked the expression of HSP70 isoforms at the mRNA level, using gene specific primers and found that known heat inducible isoforms like HSPA1A, HSPA1B and HSPA6 get highly upregulated during HIV-1 infection as well. We further observed through overexpression and silencing experiments with different isoforms that few of them are involved in regulation of viral replication and infectivity. The mechanism of action is currently being elucidated. We have been also studying the role of HSP70 binding protein; HspBP1, a co-chaperone molecule of HSP70. Our studies have clearly shown that HspBP1 inhibits HIV-1 LTR mediated gene expression and viral replication. We have reported earlier that HspBP1 inhibits HIV-1 gene expression and replication by restricting p65 from binding to NF-κB enhancer sequence on the viral promoter. We have also observed that HIV-1 down-modulates the expression of nucleotide exchange factor, HspBP1. As we were curious to understand if this regulation occurs through the promoter of HspBP1, which has not been characterized till date, we have created different constructs of upstream sequences of HspBP1 UTR region. Our initial results indicate that a small segment of DNA (-70 to +30) around the transcriptional start site shows core promoter activity. This could potentially be termed as the core promoter of HspBP1. Our initial results also suggest that HIV-1 down regulates the activity of the above-mentioned promoter construct, however, individual viral proteins did not down-regulate this promoter activity.

In recent times, HSP90 has also emerged as an important cellular factor for viral pathogenesis. The ability of HSP90 to perform diverse range of functions arises from its differently compartmentalized five isoforms, thus each of them taking part in unique as well as similar cellular processes. In cytoplasm, HSP90 is expressed as two inducible isoforms i.e. HSP90AA1 and HSP90AA2 (together known as Hsp90α) and one constitutive isoform HSP90AB1 (HSP90β). Other than the cytosolic isoforms, HSP90 also has one endoplasmic isoform HSP90B1 and one mitochondrial isoform TRAP1 (Tumor Necrosis Factor Receptor-Associated Protein-1). We have now initiated studies to look at the role of HSP90 isoforms in viral replication and infectivity. The dose dependent over-expression studies with the isoforms have shown differential modulation of LTR driven gene expression and viral replication in presence of different HSP90 isoforms. Further we are trying to elucidate the molecular mechanism through which the selected isoform acts on HIV-1 life-cycle. These findings are particularly important because it can steer the orientation of future studies as well as may provide a therapeutic target to inhibit HIV-1 infection.

In addition to above, we are currently also trying to functionally characterize the role of Death associated protein Kinase (DAPK/ZIPK) that has been shown to interact with Nef protein both *in vitro* and *in vivo*. Our initial results suggest that ZIPK down regulates HIV-1, whereas viral Nef protein down regulates expression of ZIPK in infected cells, the molecular mechanism of which is being currently elucidated. Furthermore, HIV-1 infection is known to be associated with the hijacking of a number of cellular factors including non-coding RNAs. Mammalian miRNAs are small non-coding RNAs that are potent regulators of gene expression. Although there is significant literature suggesting that host miRNAs play a fairly important role in HIV-1 infection, however, a comprehensive elucidation of the role of micro RNAs in HIV-1 replication and infectivity remains to be done. Thus, we have initiated identification of deregulated miRNAs through bioinformatic analysis of existing GEO database. Selected miRNAs from this list is currently being functionally characterized including looking at the role of their targets. Finally, we have also initiated studies on cellular stress response during HIV-1 infection. The host unfolded protein response (UPR) modulation by HIV-1 has not been studied well and the detailed mechanism remains to be characterized. Our study aims to monitor the effect of HIV-1 on the host UPR as well as to analyze the effect of these modulations on the viral replication, production and infectivity. Finally, we have been also involved in identification of novel anti-HIV molecules and study of their potential use as microbicides. Selective modulation of several host factors has shown promising result in suppressing

HIV-1 replication as well as the rebound of the latent provirus in recent times. In this direction, our group has been involved in exploiting HSP90's role in HIV-1 replication and as a potential therapeutic target. For this, in collaboration with BIT, Mesra, we have identified several new lead anti-HIV molecules which seem to act by inhibiting HSP90. Further systematic studies of these novel HSP90 inhibitors in combination with currently used ART regimen may help us to combat HIV-1 more efficiently.

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Metabolomic profiling of Idli Batter Fermentation

Objectives of the study

- To identify the important metabolites generated during the fermentation of idli batter by gas chromatography mass spectrometry.
- To perform volatomic profiling of the fermentation of idli batter.

Summary

Different metabolites generated during the fermentation process impart various nutritional properties and also attribute to the taste and flavor of the fermented foods. Metabolomic profiling of very few fermented foods has been reported. To get a detailed picture of idli batter fermentation, metabolomic and volatomic profiling of its fermentation was performed alongwith the microbial diversity and functional analysis.

Using the derivatization approach, 124 metabolites were detected by gas chromatography mass spectrometry. Of these, 41 compounds which included various important acids, sugars, sugar alcohols, amino acids and sterols were found to be statistically significant. These compounds impart beneficial properties as food additives, preservatives and flavoring agents, short chain fatty acids, trans fatty acids, saturated long chain fatty acids, antifungal compounds, antioxidants, etc. Different metabolites were generated at different times implying presence of a peculiar succession of metabolites during the idli batter fermentation. Thus, the fermentation appears to occur in two major phases, early and late phase of fermentation.

Employing the head-space solid phase microextraction method, 107 volatile compounds were detected during idli fermentation. Of these, 61 known

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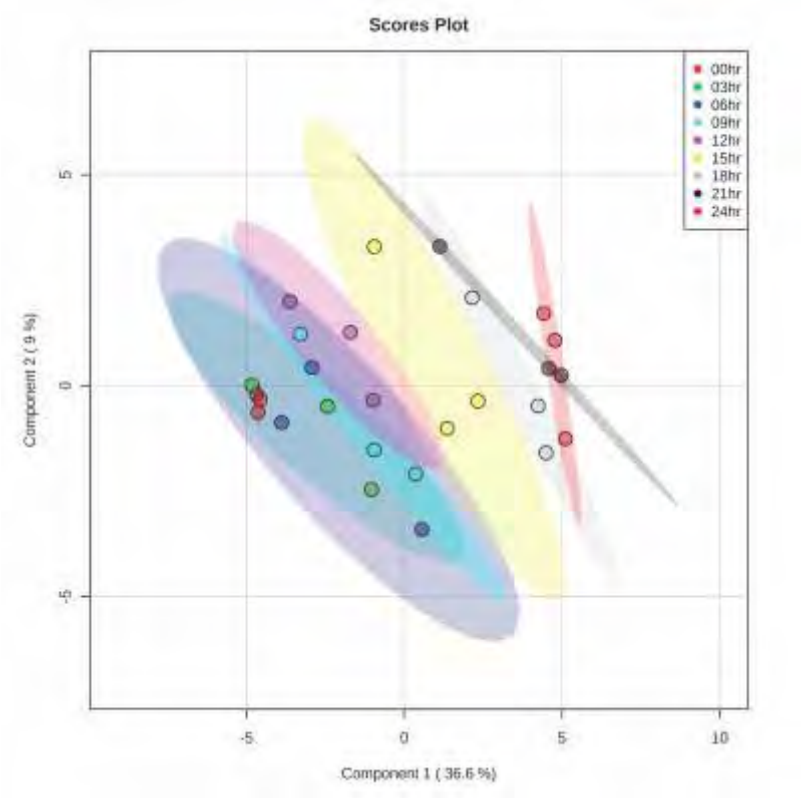

Fig. 1: Partial least square discriminant analysis (PLS-DA) showing separation of different time points of fermentation based on the top two components.

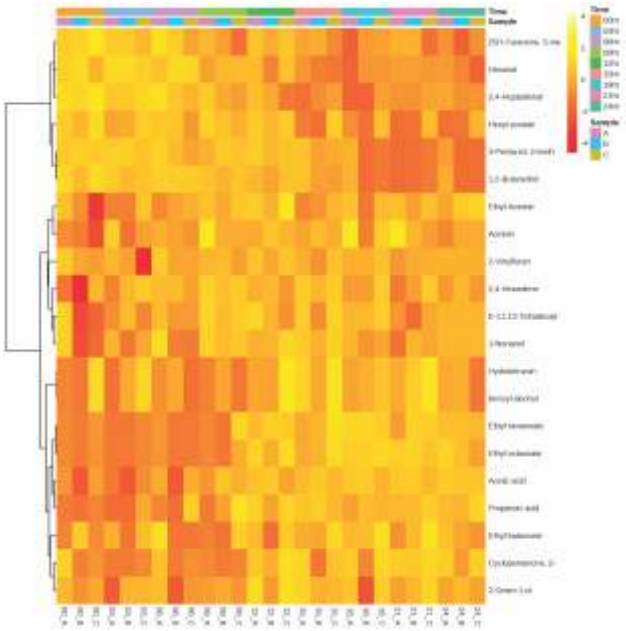

Fig. 2: Heatmap showing the abundance of important volatile metabolites during the idli batter fermentation

flavouring agents were identified. Few volatile organic compounds (VOCs) such as hexanal, hexyl acetate, 1,2 butanediol, 2, 4 heptadienal, etc were expressed highly in the early phase of fermentation. The known flavoring agents such as ethyl acetate, ethyl hexanoate, ethyl octanoate, acetoin, acetic acid, benzyl alcohol, 2-vinylfuran were found to be expressed more in the later phase of fermentation. Thus, the VOC profile and thereby the flavor and aroma of idli batter is different in the early amd late stages of fermentation. This distiction of VOCs generated at different times of fermentation provide idli cakes with a characteristic flavor and aroma.

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Identification of potential targets and biomarkers for multiple myeloma using quantitative proteomics and molecular approaches

Objectives of the study

- Investigation of bone marrow interstitial fluid proteome alterations associated with multiple myeloma using quantitative proteomics.
- Investigation of serum proteome alterations associated with multiple myeloma using quantitative proteomics.
- Identification and validation of potential biomarkers for Multiple Myeloma using bone marrow mono nuclear cells (BM MNCs).

Summary

Multiple myeloma (MM) is a plasma cell cancer that accounts for nearly 10% of all haematological malignancies. In MM, malignant plasma cells expand and accumulate in the bone marrow and lead to bone resorption and over production of antibodies. It is one of the most dominant hematological malignancy in the Indian subcontinent, where 4 out of every 100,000 people are detected with MM every year. Despite several years of research in the area of hematological oncology, MM still remains as an incurable plasma cell malignancy with poor prognosis. Most importantly, there is no reliable protein marker available for MM diagnosis. Considering the restricted and economically limited facilities such as genetic testing and imaging for the diagnosis of MM, identifying the novel targets and reliable markers can be highly useful for diagnosis as well as prognosis and it will also be useful for better understanding of the MM disease pathophysiology. Mass spectrometry (MS) based proteomics serves as an excellent approach that provides the information about protein markers including alterations and modifications in the protein levels of patient's clinical samples including tissues and body fluids.

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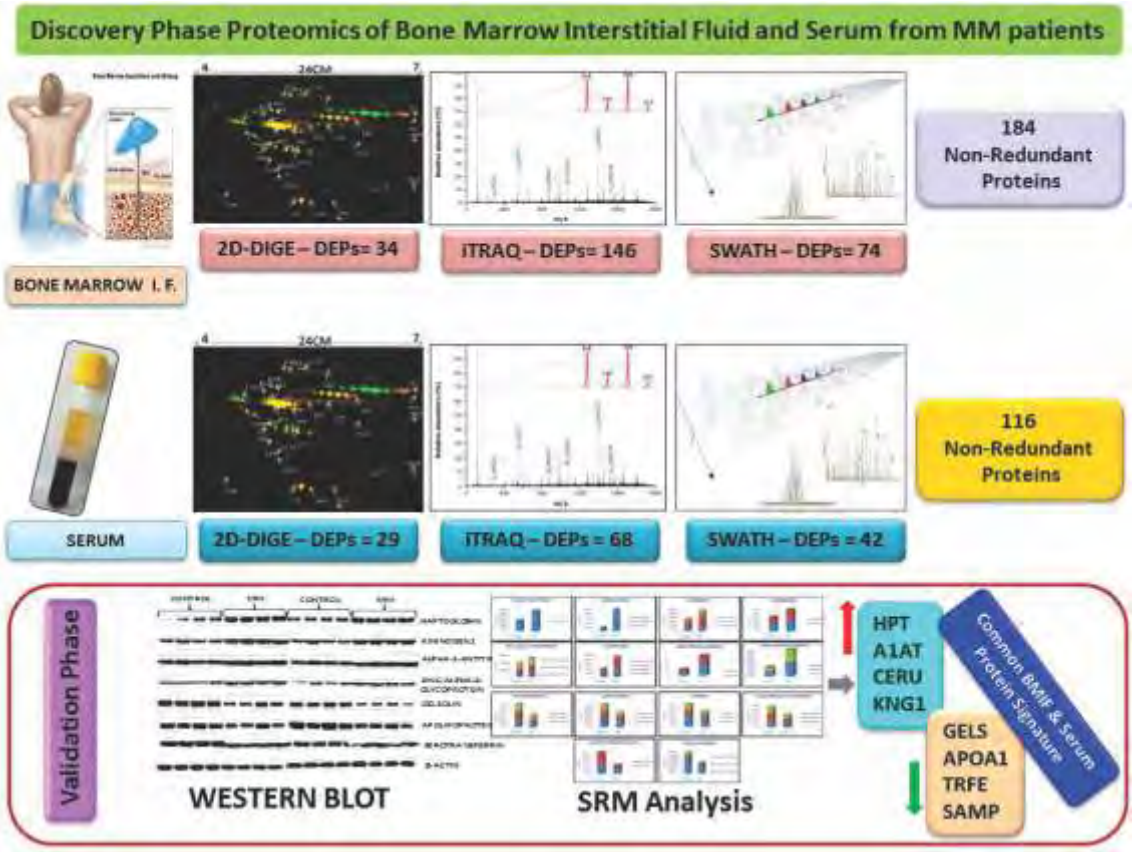

Fig. 1: An experimental design and overall results obtained for quantitative proteomic analysis of BMIF and serum samples of multiple myeloma and controls. In the discovery phase, 184 and 116 non-redundant differentially expressed proteins were identified for BMIF and serum respectively using multipronged quantitative proteomic approaches. A common BMIF and serum protein signature consisting of 8 significant proteins was identified and validated in a fresh cohort of samples.

Globally, many research groups have tried to explore and identify different potential biomarkers and targets for various cancers using MS based proteomic approaches. However, limited studies explored the identification and understanding of the potential candidate markers using proteomic approaches in MM.

In this present work, we used MM bone marrow interstitial fluid (BMIF), serum, BM mono nuclear cells and respected controls for identification of diagnostic and therapeutic biomarkers. Differential proteomic analysis was performed using multipronged approaches viz. 2D-DIGE, iTRAQ and SWATH. In BMIF study, we identified 184 differentially expressed proteins out of which 101 proteins were up-regulated and 83 proteins were down-regulated (Fig. 1). Biological context of these dysregulated proteins was deciphered using multiple bioinformatics tools like PANTHER, DAVID, IPA and LENS. Validation experiments were performed for the significant proteins in a new cohort of samples using immunoblotting and LC-MS based SRM assays. Similarly, in the study of serum proteome alterations, our quantitative proteomic analysis resulted in alteration of 116 proteins in which 51 proteins showed increased expression and 65 proteins showed decreased expression (Fig. 1). Validation experiments of the selected significant proteins are consistence with quantitative data. Interestingly, 8 proteins were shown similar pattern of expression in both MM serum and MM interstitial fluid (Fig. 1). These results strongly suggest that these 8 common proteins can be useful as potential theranostic markers for MM.

Further, proteomic analysis of BM MNCs yielded a total of 892 proteins using SWATH analysis in which 222 proteins were differentially expressed. Based on the literature, we selected two differentially expressed proteins viz. Plasma cell induced resident ER protein (MZB1) and Voltage dependent anion channel 3 (VDAC3). Although MZB1 and VDAC3 proteins were reported in few cancers, still its role in MM is unknown. In this study, we validated MZB1 and VDAC3 proteins as MM targets in BMIF, serum samples and performed functional studies to understand the role of these proteins in MM. Validation results in

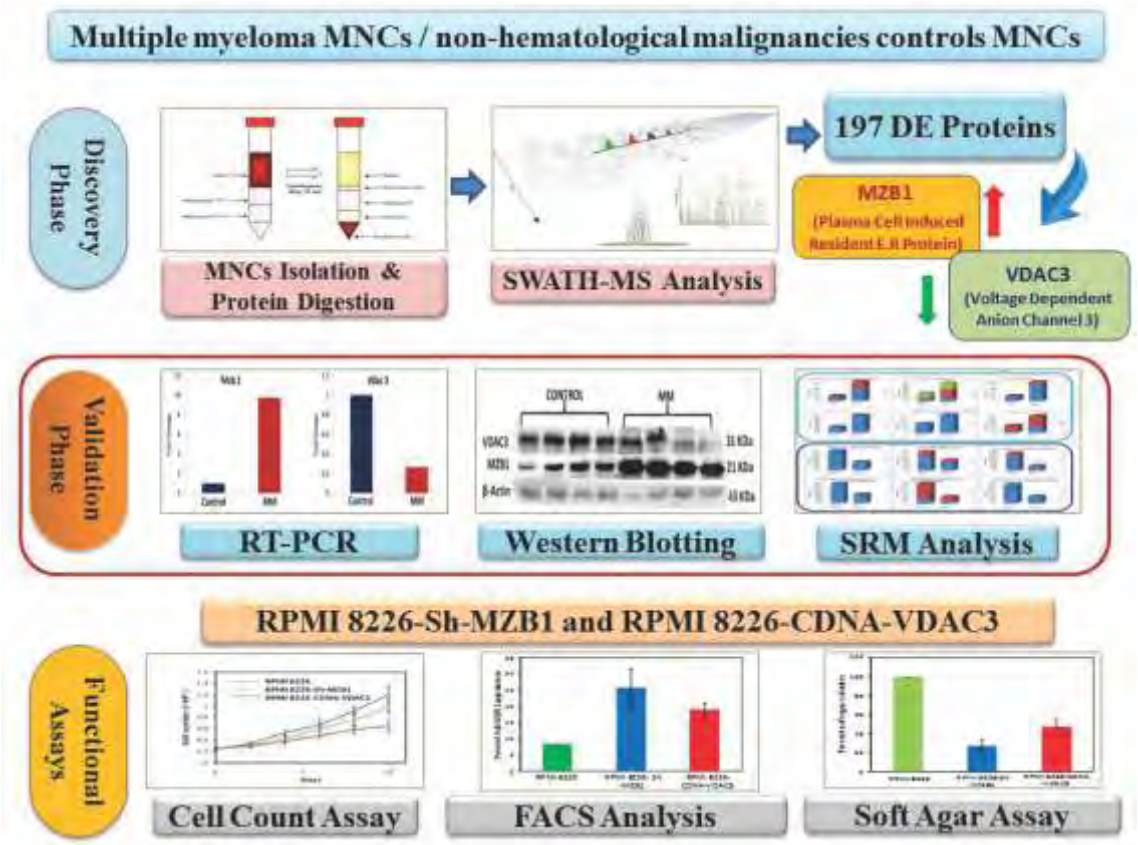

Fig. 2: A flowchart depicting experimental design and overall results obtained for multiple myeloma MNCs proteomic analysis. In the discovery phase, 197 differentially expressed proteins were identified using SWATH based quantitative proteomics. An up-regulated protein MZB1 and a down-regulated protein VDAC3 were selected for validation as well as functional studies based on literature review and being unexplored in terms of MM.

a new cohort of samples using western blot and SRM are consistent with quantitative proteomics data. Furthermore, knock down of MZB1 and over expression of VDAC3 in the RPMI 8226 cell line proves that these proteins could be better theranostic targets for MM (Fig. 2). In future, we are also identifying therapeutic targets for MM through global proteomic analysis and molecular approaches.

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Assessment of the prophylactic efficacy of homoeopathic formulation of curcumin in the villages in the Belonia Division (Tripura) and Pallahara Division (Angul, Odisha)

Objectives of the study

- To check the efficacy of Nanocurcumin as an anti-malarial drug.
- To check prophylactic efficacy of Nanocurcumin.

Background

Malaria is a mosquito borne infectious disease and two major areas of concern are control on multidrug resistant property of parasites and development of new drugs. Curcumin is naturally occurring compound obtained from *Curcuma longa*. It is used to treat many diseases, as it has been shown to possess anti-inflammatory, antioxidant, anti-cancerous and anti-malarial properties. In the present study homeopathic formulation of curcumin and its dose potency for control of malaria was estimated.

To evaluate the effect of homoeopathic drugs on malaria, the experiments were performed on male C57BL6 mice aged 6-8 weeks. The 1st experiment and 2nd experiment were performed after *Plasmodium berghei* ANKA infection in these mice. The 3rd experiment was performed to check prophylactic efficacy of the drugs. Infection and drug treatment were carried out through the following procedures:

Experiment I:
33 male C57BL/6 mice aged 6-8 weeks were taken and infected with 1x104 P. berghei ANKA infected RBCs per mouse and then randomly divided according to the following groups:

1. Infected, PBS treated - 5 mice
2. Infected, Curcuma longa 30C treated - 7 mice

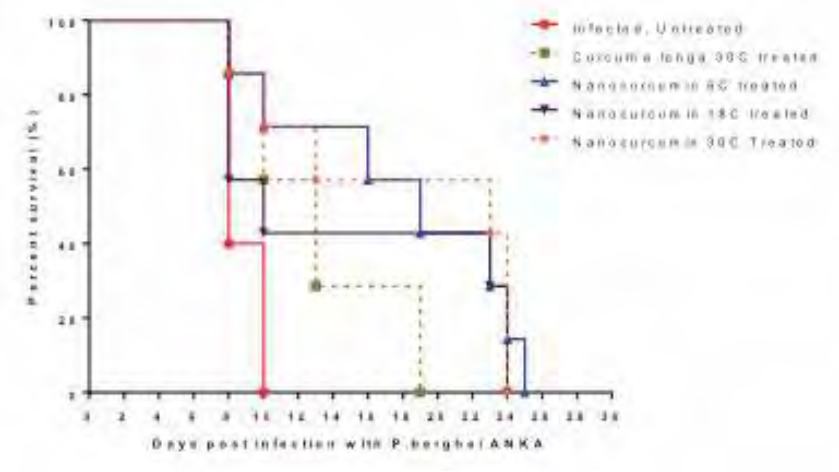

Fig1: Survival curve of animals after infection with *P. berghei* ANKA and treatment with respective homeopathic formulations.

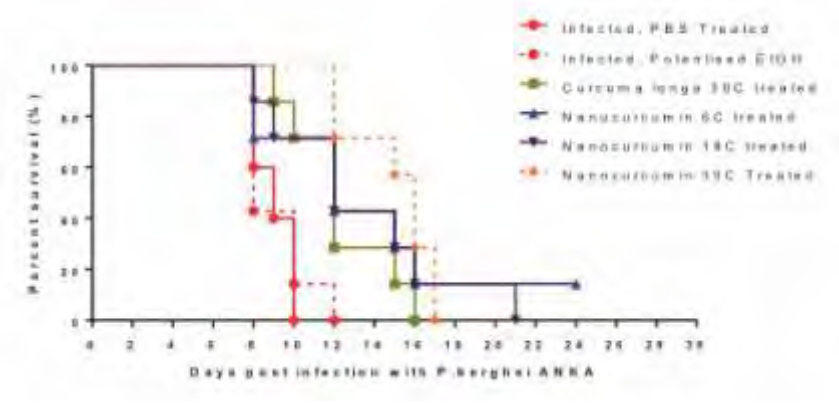

Fig 2: Survival curve of animals after infection with *P. berghei* ANKA and treatment with respective homeopathic formulations.

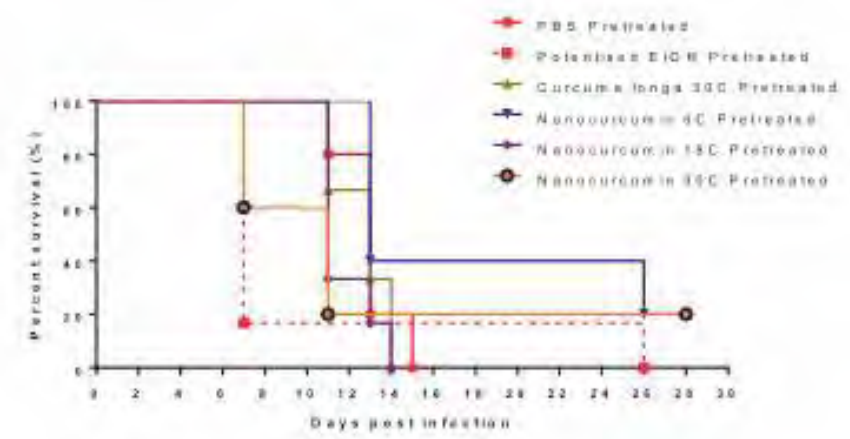

Fig 3: Survival curve of animals after infection with *P. berghei* ANKA and treatment with respective homeopathic formulations (Prophylactic experiment).

3. Infected, Nanocurcumin 6C treated - 7 mice
4. Infected, Nanocurcumin 18C treated - 7 mice
5. Infected, Nanocurcumin 30C treated - 7 mice

The animals were given the respective drugs treatments (50ul drug diluted with 150 ul PBS) twice daily for 6 days followed by parasitemia in the blood and survival was noted.

Results and Discussion Experiment-I:

After infecting each male C57BL6 mouse with (1x104) P. berghei ANKA infected RBCs, parasites occurrences were observed daily by preparing blood smear. When parasite appearance was confirmed, mice were treated twice in a day for 6 days with the respective drugs treatment (50µl drug diluted with 150 ul PBS).

To observe Parasitemia, blood smears were taken at 7th, 11th, 14th and 20th day post-infection.

It was observed that only 40% of the animals belonging to the infected untreated group were alive by 8th day post infection and all the animals belonging to this group died by 10th day post infection.

In comparison, in the Curcuma longa 30C treated group 85 % of the animals were alive by 8th post infection, 30% were alive by day 15th post infection and the remaining of the animals died later by the 19th day, post infection.

In the Nanocurcumin 6C treated group, 85 % of the animals were alive by 8th day post infection, 70% were alive by day15th post infection, and the animals survived up to 25th day post infection.

Similarly, in the Nanocurcumin 18C treated group, about 60 % of the animals were alive by 8th day post infection, about 40 % were alive by day 15th post infection, and the surviving animals survived till about 24th day post infection.

85 % of the animals treated with Nanocurcumin 30C potency were alive on day 8th post infection, about 60 % were alive by day 15th post infection and the surviving animals survived till about 24th day post infection.

Experiment II:

40 male C57BL6 mice age 6-8 weeks were taken and infected with 1x104 P. berghei ANKA infected RBCs per mice and then randomly divided according to the following groups:-

1. Infected, PBS treated - 5 mice
2. Infected, Potentised Ethanol treated - 7 mice
3. Infected, Curcuma longa 30C treated - 7 mice
4. Infected, Nanocurcumin 6C treated - 7 mice
5. Infected, Nanocurcumin 18C treated - 7 mice
6. Infected, Nanocurcumin 30C treated - 7 mice

The animals were given the respective drugs treatment (50ul drug diluted with 150 ul PBS) twice daily for 6 days followed by Parasitemia in the blood and survival was noted.

Result and Discussion Experiment-II:

After infecting each male C57BL6 mice with (1x104) P. berghei ANKA infected RBCs, parasites occurrences were observed daily by preparing blood smear. When parasite appearance was confirmed, mice were treated twice in a day for 6 days with the respective drugs treatment (50ul drug diluted with 150 ul PBS). To observe Parasitemia, blood smears were taken at 6th, 7th and 8th day of post-infection

It was observed that 60% animals belonging to infected untreated group were alive by 8th day post infection. Whereas, all the animals from this group died by 10th day post infection.

In infected ethanol treated group only 40% of animals were alive by 8th day post infection. Surviving animals were survived until about 12th day post infection.

Whereas, in the Curcuma longa 30C treated group it was observed that, 85% animals were alive by 9th day post infection. About 30% were alive by 14th day post infection. In addition, remaining animals survived until 17th day post infection.

75% animals were alive in the Nanocurcumin 6C treated group, by 8th day post infection. About 40% animals belonging to this group were alive by 14th day post infection. Whereas, surviving animals survived till about 25th day post infection.

Similarly, in the Nanocurcumin 18C treated group, 85% animals were alive on 8th day post infection. Only 40% animals were alive on 14th day post infection. Rest surviving animals belonging this group survived till 22th day post infection.

In Nanocurcumin 30C treated group 90% animals were alive by 8th day post infection. About 70% animals were alive by 14th day post infection and surviving animal survived around 18th day post infection.

Experiment III (Prophylactic Action Experiment):

35 male C57Bl6 mice aged 6-8 weeks were taken and then randomly divided according to the following groups:

1. Infected, PBS treated - 5 mice
2. Infected, Curcuma longa 30C treated - 6 mice
3. Infected, Nanocurcumin 6C treated - 6 mice
4. Infected, Nanocurcumin 18C treated - 6 mice
5. Infected, Nanocurcumin 30C treated - 6 mice

The animals were given the respective drugs treatment (50ul drug diluted with 150 ul PBS) twice daily for 6 days following infecting them with 1x104 P. berghei ANKA infected RBCs per mice followed by, Parasitemia in the blood and survival of the animals was noted.

Result and discussion Experiment-III:

35 male C57Bl6 mice age 6-8 weeks taken and randomly divided in to 6 groups. The animals were treated with the respective drugs treatment (50ul drug diluted with 150 ul PBS) twice daily for 6 days followed by infecting them with 1x104 P. berghei ANKA infected RBCs per mice. To observe Parasitemia, blood smears were taken at 9th and 11thday of post-infection.

It was observed that 80% animals belongs to infected PBS treated group were alive by 11th day post infection. Whereas, all the animals belonging to this group died by 15th day post infection.

In infected ethanol treated group only 20% animals were alive

by 11th day post infection. Whereas, surviving animals survived till 26th day, post infection.

Whereas, In the Curcuma longa 30C treated group, 70% animals were alive by 11th day post infection. About 20% were alive by 13th day post infection and remaining animals were died later by 15th day post infection.

In the Nanocurcumin 6C treated group, 80% of the animals were alive by 12th day post infection, 40% were alive by day 24th post infection, and the remaining animals from this group survived till 27th day post infection.

Only 30% animals were alive in the Nanocurcumin 18C treated group by 11th day post infection. Whereas, Rest surviving animals belonging this group survived till 14th day post infection

In Nanocurcumin 30C treated group 60% animals were alive by 10th day post infection. About 20% animals were alive by 22th day post infection and surviving animal survived around 29th day post infection.

Summary

Among the different treatment groups, based on the first two experiments performed, it was observed that in the group that was treated with Nanocurcumin 6C, on an average a larger percentage of the animals survived for a longer period as compared to the rest of the groups. When Nanocurcumin homoeopathic formulation was administered to mice as a prophylactic for 6 days followed by infection, it was observed that 40% to 60% of the animals survived for a longer period by suppressing the parasite growth to some extent and animals treated with Nanocurcumin 6C and 30C potencies survived the longest. However, even though because of pre-treatment there was initially some suppression of the parasite levels in the blood of the infected animals, eventually the drug potencies used could eliminate the rising parasitemia in the blood and the animals died after surviving for a longer period of time. Further, for investigating the molecular basis of animal survivability by suppression of the parasite in the blood, blood samples from each treated group of mice have been taken and mRNA has been extracted and converted to cDNA for observing the changes in the expression of different genes by RT-PCR. We would futher investigate the molecular basis of animal survivability by altering the parasite load.

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Understanding the molecular basis of complement regulation

Objectives of the study

- To examine functional modularity in complement regulators.
- To understand the molecular basis of complement regulation.

Summary

Background

The complement system is an essential effector system of innate immunity. Although classically it is known for its direct action on pathogens, it is also critically involved in boosting the pathogen-specific adaptive immune responses as well as other processes such as cell differentiation and polarization, tissue regeneration, lipid metabolism, and removal of immune complexes and apoptotic cells. The system is tightly regulated by multiple regulatory proteins, as inappropriate activation is known to result in host tissue destruction. The major proteins that regulate complement activation belong to a family dubbed as regulators of complement activation (RCA). These proteins are exclusively composed of complement control protein (CCP) modules and are located on the cell surface as well as in the fluid phase. Notably, defects in the functioning of these RCA proteins are linked to various diseases such as age-related macular degeneration, atypical hemolytic uremic syndrome, and dense deposit disease.

The central step in complement activation is the formation of bimolecular enzymes formed by a non-catalytic (C3b/C4b) and a catalytic (Bb/C2a) subunit termed C3 convertases (C3bBb/C4b2a), which initiate all the downstream effector function of complement. The RCA proteins regulate these enzymes by

Architecture of the functional units

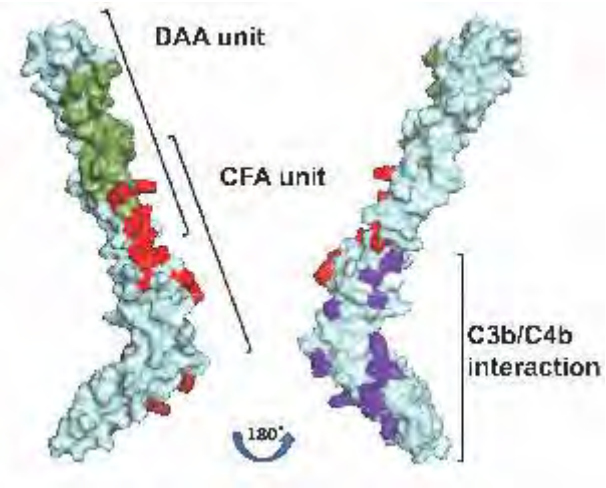

Fig. 1: Modelled structure of four-domain DAF-MCP chimera named decay cofactor protein (DCP) showing spatial arrangements of functional units for decay-acceleration activity and cofactor activity. Our data show that: i) functional unit for each of the regulatory activity is formed only by 2 successive CCP domains wherein each participates in the function, albeit CCP2 has a bipartite function, ii) dual function composition requires that domains are arranged in a specific order - decay-acceleration activity (DAA) unit followed by cofactor activity (CFA) unit, and iii) interaction of the terminal domains of RCA with C3b and C4b is critical for the optimal CFA as well as DAA.

two molecular activities dubbed decay-acceleration activity and cofactor activity. In decay-acceleration activity, the RCA protein binds to the convertase and irreversibly dissociates it into its subunits, while, in cofactor activity, the RCA protein binds to the noncatalytic subunit of the convertase and recruits serine protease (factor I) to cleave and inactivate it, thus ceasing its ability to form C3 convertase. The present study was designed to answer whether functional modularity exists in these proteins, i.e., whether individual CCPs or multi-CCP units are capable of imparting a specific function to the protein and whether joining them would add new functional capabilities.

Functional modularity in the RCA proteins

Among the human RCA proteins, decay-accelerating factor (DAF; CD55) harbors only decay-acceleration activity, while membrane cofactor protein (MCP; CD46) possesses only cofactor activity, and both these proteins are composed of four CCP modules, which are arranged in extended arrangements. Thus, to determine the functional unit for decay-acceleration activity in DAF and cofactor activity in MCP, we utilized the domain swap strategy. Our data showed that domains D2 and D3 along with the charged inter-domain linker are enough to drive the decay-acceleration of the C3 convertases. Further, the data also pointed out that in MCP, cofactor activity is primarily mediated by the M2 and M3 domains along with its inter-domain linker. Additionally, we established that C-terminal domains that enhance the avidity of the molecule for C3b/C4b are required for the optimal activities. To provide a proof of principle, we composed a four-CCP DAF-MCP chimera with robust decay-acceleration and cofactor activities, named DCP (decay cofactor protein) (Fig. 1). Hence, we show that CCP functional units can be linked together to design a dual-activity regulator.

Insights into the molecular basis of complement regulation

The molecular mechanism responsible for decay or dissociation of the C3 convertase enzyme by RCA proteins is not clear. Our data demonstrated that D2D3 modules form the decay unit. We thus modelled the ternary complex of the C3 convertase (C3bBb) with D2D3 domains. Upon interface analysis, we found that D2 and D3 interact with both catalytic as well as non-catalytic subunits of the convertase. Previous studies have suggested that a stable conformation of the metal ion-dependent adhesion site (MIDAS) in the catalytic subunit is critical for maintenance of a high-affinity conformation of the C3 convertase. Our modeling data show that D2 and D3 majorly interact with two loops and a helix, which are away from the MIDAS site. We thus propose that interaction of D2D3 with these loops/helix results in allosteric changes in the MIDAS site, leading to decay of the convertase.

The current model of cofactor activity based on the structural and biochemical data suggests that during this process, the RCA protein binds to the non-catalytic subunit (C3b/C4b) and provides a platform for docking of the protease (factor I), which then cleaves this subunit, resulting in its inactivation. Our data revealed that M2M3 domains of MCP form the cofactor unit. Our efforts to model a ternary complex of M2M3 with C3b and the protease showed that M2M3 interact with C3b as well as the protease. The interaction sites for C3b are located primarily in the M3 domain, and the interaction sites for the protease are located in both M2 as well as M3 domains. Based on our modelling data we propose that interaction of M2M3 with the C3b on one face results in bridging of its CUB-MG2 domains, and with the protease on the other face results in reorientation of the protease and cleavage of scissile bonds in the CUB domain of C3b.

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F-box protein FBXO16 functions as a tumor suppressor by attenuating nuclear β-catenin function

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Objectives of the study

- To identify the cellular substrate(s) of F-box protein FBXO16
- To decipher the cellular function of FBXO16

Summary

Human genome has 69 genes, which code for F-box proteins. This class of proteins facilitates the ubiquitination of their substrates. Dependening the nature of ubiquitination, the fate of the ubiquitinated proteins would be decided. Previous studies suggested that F-box proteins migh have crucial role in various diseases including cancer. However, function of majority of F-box proteins remains elusive. In this study, we have identified cellular targets and function of an unexplored F-box protein, F-box protein 16 (FBXO16). It functions as a putative tumor suppressor. It is a component of the SCF (SKP1-Cullin1-F-box protein) complex, which targets the nuclear β-catenin protein to facilitate proteasomal degradation through the 26S proteasome. In addition, it inhibits epithelial-to-mesenchymal transition (EMT) by attenuating the nuclear level of β-catenin. Therefore, depletion of FBXO16 leads to increased levels of β-catenin, which then promotes cell invasion, tumor growth, and EMT of cancer cells. Furthermore, FBXO16 and β-catenin share an inverse correlation of cellular expression in clinical breast cancer patient samples. In summary, we propose that FBXO16 functions as a putative tumor suppressor by forming an SCF^{FBXO16} complex that targets nuclear β-catenin in a unique manner for ubiquitination and subsequent proteasomal degradation to prevent malignancy. This work suggests a novel therapeutic strategy against human cancers related to aberrant β-catenin activation.

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Major findings

Aim 1: To identify the cellular substrate(s) of F-box protein FBXO16

FBXO16 interacts with β-catenin

The cellular function of FBXO16 is poorly understood. To discover its cellular function and physiological substrates, we performed coimmunoprecipitation followed by mass spectrometry to identify its interacting partners. Results demonstrated that FBXO16 interacts with 117 cellular proteins, and β-catenin was found to be the most represented candidate, with coverage of six unique peptides. We performed coimmunoprecipitation experiments to validate the mass spectrometry finding. We detected the physical interaction of FBXO16 and β-catenin (Figure 1A).

Aim 2: To decipher the cellular function of FBXO16

β-Catenin is known to be involved in progression and metastasis of breast cancer, and we were intrigued to draw up a correlation between β-catenin and FBXO16 in the context of breast cancer. Accordingly, using different breast cell lines, we discovered an inverse relationship between β-catenin and FBXO16 levels. For a clinical perspective, we then checked the correlation of FBXO16 and β-catenin expression in the breast cancer patient samples. Immunohistochemical analysis demonstrated a significant converse correlation of FBXO16 and β-catenin expression with increased levels of β-catenin and concomitant attenuation of FBXO16 in higher grades of breast cancer patient samples (Figure 1B). Furthermore, the TCGA database demonstrated a close association of higher FBXO16 expression with disease-free survival (Figure 1C). Collectively, our findings suggested that FBXO16 might function as a putative tumor suppressor by limiting nuclear β-catenin activity.

FBXO16 promotes ubiquitylation and proteasomal degradation of β-catenin through SCF complex

Being an F-box family member, we presumed that FBXO16 might regulate the stability of β-catenin at the posttranslational level. To test that, we performed a series of experiments. First, we found a significant attenuation of nuclear β-catenin following ectopic expression of FBXO16 (Figure 1D). Further, FBXO16-mediated reduction of β-catenin was significantly blocked in the presence of MG132, indicating that β-catenin stability is indeed regulated at the posttranslational level by FBXO16 through the 26S proteasome. Furthermore, Figure 1F shows the presence of a notable high mass ladder of ubiquitylated β-catenin

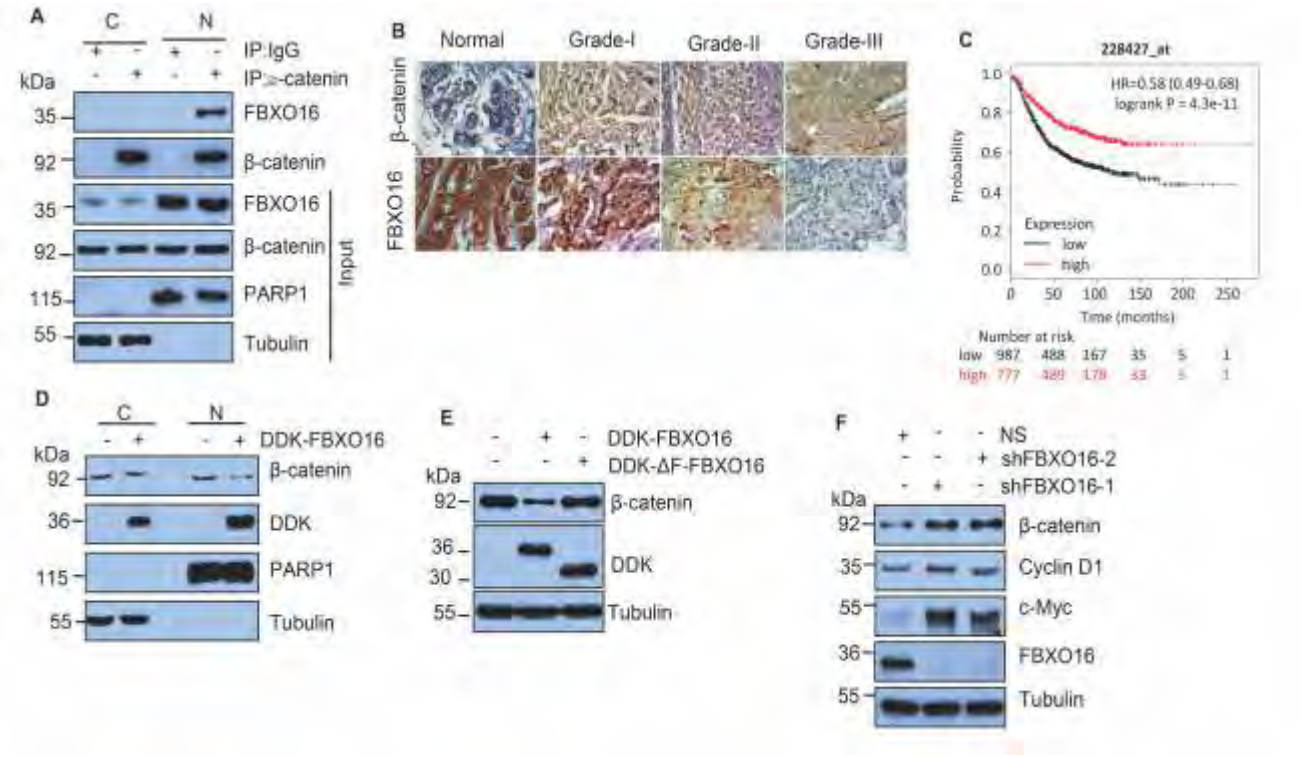

Fig. 1: FBXO16 facilitates proteasomal degradation of nuclear β-catenine.

(A) Nuclear and cytoplasmic fractions were immunoprecipitated with either anti-β-catenin antibody or IgG. Immunoprecipitates and input lysates were separated on SDS-PAGE and immunoblotted for the indicated proteins. Cells were grown in the presence of 5 μM MG132 for 6 h before harvesting. (B) Expression levels of β-catenin (top row) and FBXO16 (bottom) in samples of normal and different grades of breast cancer. (C) Kaplan-Meier plot depicting overall survival of breast cancer patient cohorts with different levels of FBXO16 expression. Red trace represents comparative higher expressions of FBXO16. (D) Fractionated cell lysates of MDA-MB-231 cells expressing either vector control or DDK-FBXO16 were immunoblotted using the indicated antibodies. PARP1 and tubulin were used as nuclear and cytoplasmic loading controls, respectively. (E) Whole-cell protein extracts of MDA-MB-231 cells expressing either vector control or DDK-FBXO16 or DDK-ΔF-FBXO16 for 48 h were immunoblotted for the indicated proteins. (F) Whole-cell lysates of MCF7 cells expressing either NS or FBXO16 shRNAs were immunoblotted for the indicated proteins.

exclusively in the nuclear fraction, suggesting that FBXO16 facilitates proteasomal degradation of nuclear β-catenin.

Typically, F-box proteins associate with SKP1 to form an SCF complex through their F-box motif and bring their substrates to the complex for ubiquitylation. To examine whether FBXO16 complies with this, wild-type and F-box-deleted FBXO16 (ΔF-FBXO16) were overexpressed in MDA-MB-231 cells. Results demonstrated that ΔF-FBXO16 is incompetent to reduce the expression of β-catenin (Figure 1E). In addition, we found that FBXO16-mediated β-catenin degradation is independent of its activating signals like Wnt3a induction and EGF stimulation.

Typically, F-box proteins recognize phosphorylated substrates as a mark for promoting their ubiquitylation. It is paradigmatic that GSK3 β-imparted phosphorylation on threonine 41 of β-catenin conduces its proteasomal degradation. So, we questioned whether FBXO16-mediated β-catenin degradation is GSK3β dependent. Results demonstrated that, despite administering GSK3β inhibitor BIO, FBXO16 degraded β-catenin. To further substantiate this observation, we ectopically coexpressed the T41A mutant of GFP-β-catenin and FBXO16 in MCF7 and found that FBXO16 degraded the phosphorylation-defective mutant of β-catenin equivalently to wild type, indicating that GSK3 β-mediated β-catenin phosphorylation is

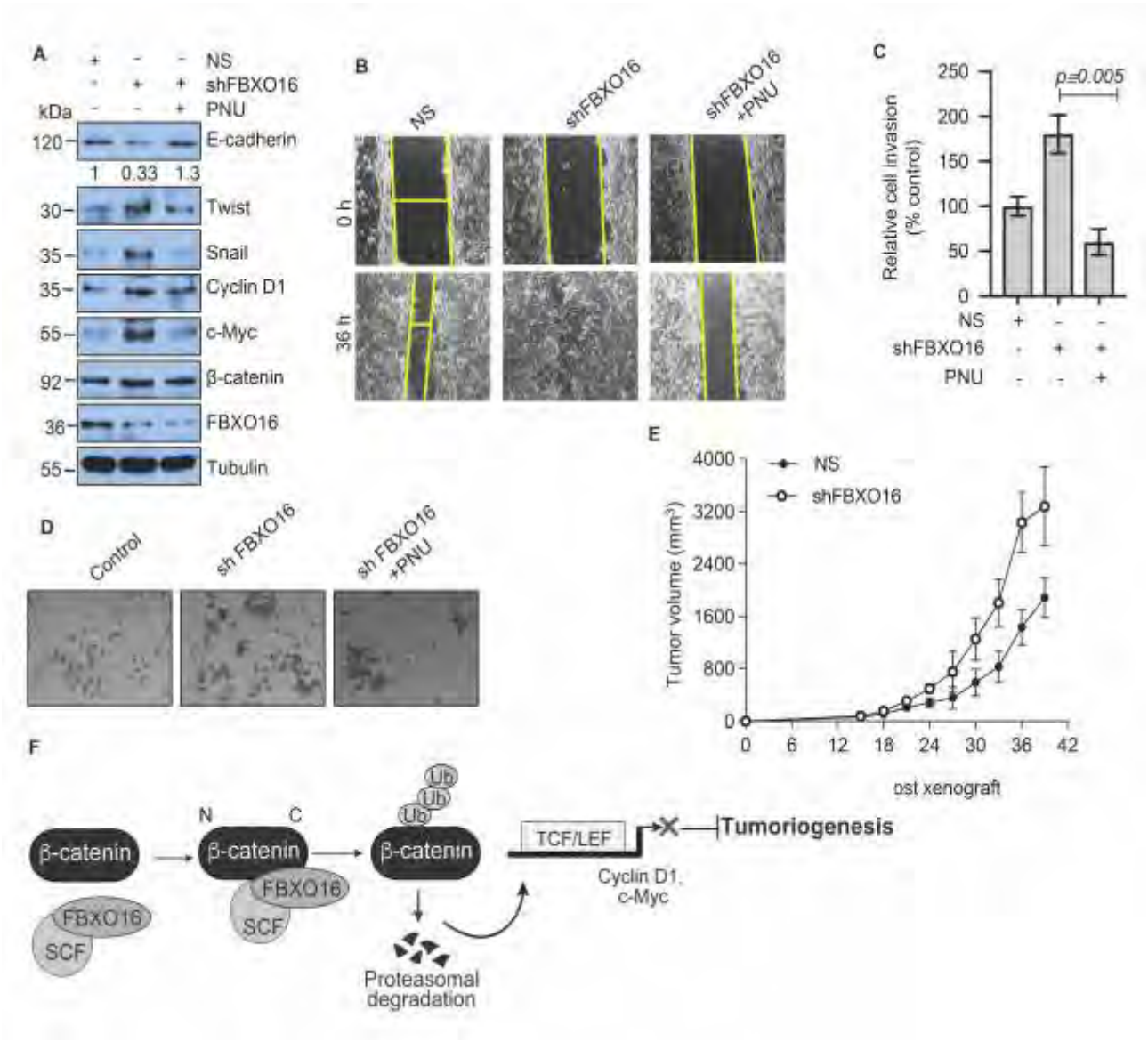

Fig. 2: FBXO16 functions as putative tumor suppressor through suppressing the function of nuclear β-catenin.

(A) Whole-cell protein extracts of MCF7 cells stably expressing either NS or FBXO16 shRNA were immunoblotted for the indicated proteins. (B) Scratch would healing of MCF7 cells expressing either NSor FBXO16 shRNA for 30 h in the absence or presence of 500 nM PNU. (C) Invasion of MCF7 cells expressing either NS or FBXO16 shRNA in the absence or presence of 500 nM PNU. (D) Soft agar colony formation assay of MCF7 cells expressing either NS or FBXO16 shRNA in the presence or absence of the β-catenin inhibitor 500 nM PNU. A total of 5000 cells were used for this assay. (E) NOD-SCID mouse xenograft growth of MCF7 cells expressing either NS or FBXO16 shRNA. Five mice were used for each group. (F) Model depicting the tumor-suppressive activity of FBXO16 through the regulation of β-catenin.

not required for its recognition and degradation by FBXO16. A recent study showed that PKCδ also plays an important role in β-catenin degradation. Hence, we checked PKCδ's role in this aspect and found that FBXO16-mediated β-catenin degradation was independent of PKCδ. Moreover, we found that the interaction between β-catenin and FBXO16 was phosphorylation independent.

βTrCP was the first discovered F-box protein to degrade β-catenin. Hence, we asked whether FBXO16-mediated degradation of β-catenin was βTrCP dependent. We observed that ectopically expressed FBXO16 degraded β-catenin equally in both wild type and βTrCP-depleted MCF7 cells. Collectively, our results demonstrated that FBXO16-mediated β-catenin degradation might be independent of GSK3β, PKCδ, and βTrCP.

Next, we questioned whether FBXO16 maintains the basal level of β-catenin. Depletion of FBXO16 in MCF7 cells using two unrelated shRNAs resulted in increased β-catenin levels, with no apparent change at mRNA levels (Figure 1F).

FBXO16 inhibits tumorigenesis by regulating β-catenin levels β-Catenin is an exemplary regulator of EMT in development and diseases. Our results convincingly demonstrated that FBXO16 promotes degradation of nuclear β-catenin and vetoes upstream controller Wnt signaling as well. This cellular interplay stoked us into assessing the expression of EMT hallmarks in the presence of FBXO16. We found that silencing FBXO16 in MCF7 cells resulted in mesenchymal morphology and increased the expression of EMT regulators (Figure 2A), which was restored using the β-catenin-TCF/LEF binding inhibitor, PNU.

As EMT is a key process of metastasis, we looked into the migratory potential and invasiveness of the cells following depletion of FBXO16. We observed that depletion of FBXO16 significantly increased scratch wound healing compared to the wild type cells (Figure 2B). Furthermore, the addition of PNU suppressed the migratory potential of FBXO16 depleted cells, suggesting that elevated levels of β-catenin in FBXO16-depleted cells are responsible for enhanced cell migration (Figure 2B). In addition, we examined the invasion of MCF7 cells following depletion of FBXO16. Significant enhanced invasion was observed following depletion of FBXO16, which was robustly inhibited following treatment with PNU (Figure 2C).

The nuclear accumulation of β-catenin is a hallmark of malignant progression through the activation of many oncogenes. We found that the mRNA levels of crucial oncogenes, such as CCND1 and MYC, were increased in FBXO16-depleted cells because of increased β-catenin levels. Next, we performed a series of experiments to check whether FBXO16 has any role in cancer cell proliferation following epletion of FBXO16 in MCF7 cells. Soft agar assays demonstrated that depletion of FBXO16 resulted in the formation of more colonies, which was notably inhibited by PNU (Figure 2D). Conversely, soft agar colony formation assays demonstrated that numbers of colonies were significantly attenuated upon ectopic expression of FBXO16 in MDA-MB-231 cells. These encouraging observations prompted us to further check tumor growth as xenografts in NOD-SCID mice. Our results demonstrated that tumor growth was markedly increased following depletion of FBXO16 (Figure 2E). Collectively, our findings suggested that FBXO16 may function as a putative tumor suppressor by limiting the activity of nuclear β-catenin (Figure 2H).

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Role of RNA-protein interactions in *Plasmodium falciparum* infection

Objectives of the study

- To characterize the role of RNA binding proteins in gene regulation of *P. falciparum*.
- To delineate the functional role of host proteins (PIP4K2A and Ago2) in *P. falciparum*.

Summary

P. falciparum is a causative agent for malaria and has a complex life cycle in human and mosquito hosts. During its life cycle, the malarial parasite *Plasmodium* goes through different asexual stages in human blood, and asexual and sexual stage in mosquito. Expression of stage-specific proteins is important for successful completion of its life cycle and requires tight gene regulation. In case of *Plasmodium*, due to relative paucity of the transcription factors, it is postulated that post-transcriptional regulation plays an important role in stage-specific gene expression. We had previously identified human PIP4K2A as one of the proteins that associate with specific plasmodium transcripts to regulate its expression. Although miRNA-mediated gene regulation has been well-established to function in post-transcriptional regulation in many eukaryotes, existence of such a phenomenon or the presence of miRNA-associated factors in *Plasmodium* remains unclear. A number of miRNAs are shown to be imported into *Plasmodium falciparum* from erythrocytes and role of these miRNAs is not understood. We hypothesized that along with the miRNAs, components of miRISC are also imported into the parasite as miRNP complex. We envisaged that such a complex may be functional in regulating gene expression in *Plasmodium*. We

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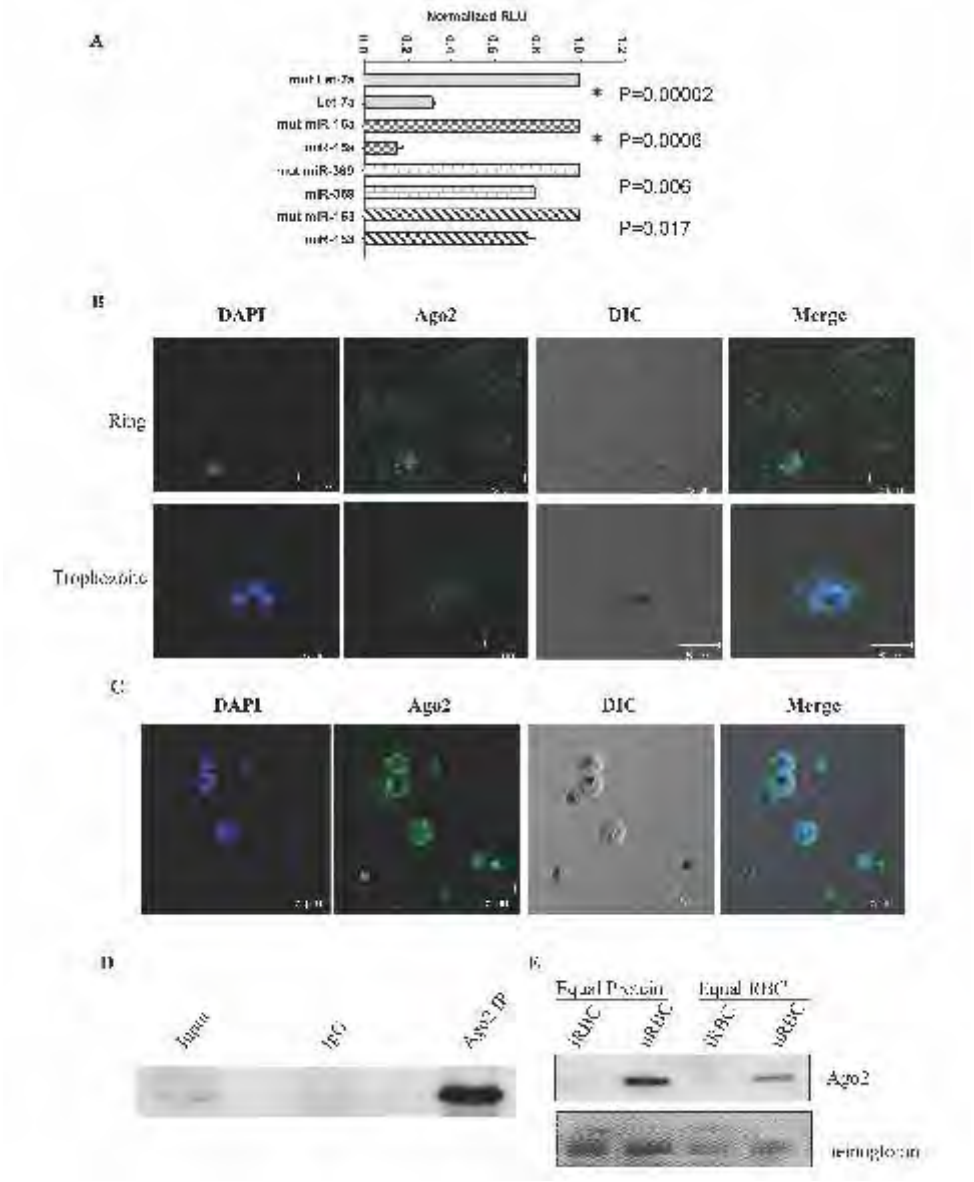

Fig 1. RBCs miRNA can regulate reporter containing *P. falciparum* 3'UTR target in HEK 293T by importing the RISC components. *In vivo* translation efficiency was measured by Dual Luciferase reporter assay. Plasmid containing the miRNA target site downstream of the Luciferase ORF was transfected into HEK293 cells along with pSUPER-miRNA, or mutant miRNA target site. The luciferase value was normalized with renilla and the relative luciferase levels are plotted with the mutant miRNA-target combination set to one. **(A)** The graph represents the average of three independent biological repeats with the error bars indicating the standard error of mean and indicates *p* values. **(B)** Plasmodium infected erythrocytes were fixed with paraformaldehyde and immunostained with two different antibodies against Ago2 (green). Nucleus stained with DAPI (blue). **(C)** Erythrocytes are lysed with saponin and *P. falciparum* parasites were isolated from them. The parasites were then stained for Ago2 (green), Nuclei (DAPI, blue). The dense black spots in the parasites are the polymeric hemozoin pigment inside the parasite **(D)** Immuno-precipitation (IP) of Ago2 from *P. falciparum* whole cell extract. Western blot of Ago2 before and after IP by rabbit mAgo2 antibody, mouse IgG was used for control immunoprecipitation **(E)** Western blot analysis of Ago2 depleted in RBCs post *P. falciparum* infection. Percoll synchronized *P. falciparum* at schizont stage were purified by magnetic separation. Same number of infected and non-infected RBCs were lysed by 0.15% saponin and the supernatant (Only RBC lysate) was assessed for hAgo2. Equal amount of total protein was loaded in the first two lanes while equal volume (corresponding to extract from equal number of RBCs) of the lysate were loaded in the right two lanes. Hemoglobin levels were used as normalization control (lower panel).

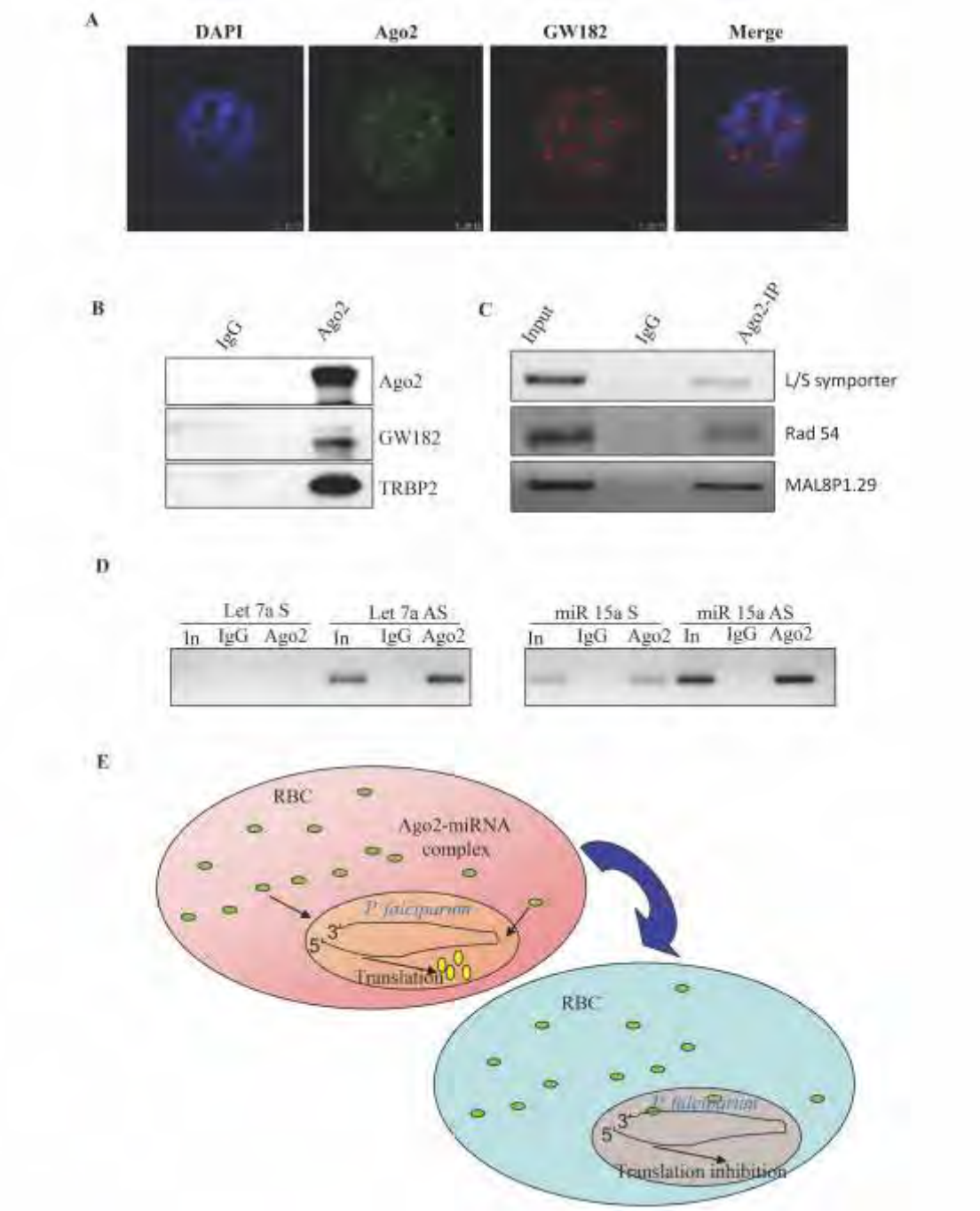

Fig 2. hAgo2 is imported into *P. falciparum* and interacts with RISC components, miRNA and their target mRNA.. (A) Immunofluorescence staining of GW182 (red) and hAgo2 (green) in *P. falciparum* parasite. Phase contrast shows location of parasites and food vacuole containing hemozoin (dark pigment). (B) hAgo2 in *P. falciparum* lysate was immunoprecipitated and the immunoprecipitate was analyzed for the presence of hAgo2 (upper panel) and interacting member of RISC (Lower panel) by western blotting. Mouse IgG was used for control immunoprecipitaion. hAgo2-RNA interaction in *P. falciparum* by UV crosslinked RNA immunoprecipition followed by RT-PCR. RIP was performed by incubating 2.5 μg of antibody with ~200 μg of *P. falciparum* extract and the Ago2 associated immunoprecipitated RNA was isolated and analyzed by RT-PCR for (C) *P. falciparum* mRNA (D) human miRNA. The specific miRNA and the *P. falciparum* transcripts that are analyzed are indicated and IgG was used for control RIP. (E) Schematic representation of miRNP import in to *Plasmodium falciparum*. The miRNA as a complex along with RISC members Ago2, GW182, TRBP2 and hnRNP is imported into the parasite. The miRNP complex, then associates with specific plasmodium transcripts containing the target sequence to regulate gene expression.

show that specific miRNAs present in RBCs are taken up by the parasite, which could potentially target mRNAs from *Plasmodium falciparum*. We find that human RBCs not only contain hAgo2, but is also imported into *Plasmodium falciparum* (Fig 1). The imported hAgo2 is localized to specific regions within the parasite cell. In the parasite, hAgo2 exists as in a complex with specific human miRNAs like let-7a and miR15a which can potentially target the *Plasmodium* genes *Rad54* and *Lipid/sterol:H+ symporter* respectively. We show that hAgo2 associates with *Rad54, Lipid/sterol:H+ symporter* and other *P. falciparum* transcripts (Fig 2). Collectively, these data suggest that *Plasmodium* imports the functional components of RBCs miRISC complex, which can regulate the gene expression in the parasite.

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Understanding the mechanism of transformation elicited by a novel long non-coding RNA – Ginir

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Objectives of the study

- To perform differential gene expression and pathway analyses of Ginir over-expressing cells by whole transcriptome sequencing.
- To evaluate the network of Ginir interacting proteins in mouse cells.
- To determine the human homologue of Ginir noncoding RNA.

Summary

The recent surge of information regarding evolutionary conservation, functionality, and annotation of sequences from the mammalian genome has revealed that a bulk of the transcriptome is noncoding and includes small and long noncoding RNAs (lncRNAs). In our lab, we have identified a long noncoding RNA pair, which we named Genomic Instability Inducing RNA (Ginir)/antisense RNA of Ginir (Giniras). The Ginir and Giniras transcripts together are involved in maintaining cellular growth and homeostasis in normal mouse cells like NIH/3T3 cells. Our studies have shown that this RNA pair is expressed in a spatiotemporally regulated manner during mouse embryonic development and is enriched specifically in the brain. Using various *in vitro* and *in vivo* assays to decipher functionality of this ncRNA pair we have established role of Ginir ncRNA as a dominant oncogene. Further, RNA pull-down experiments followed by Mass Spec analyses have led to identification of various interacting protein partners for Ginir ncRNA which have been experimentally validated. One of the interacting proteins for Ginir identified by us is a centrosomal protein 112 (Cep112). Next using co-immunoprecipitation studies, we have provided experimental evidence of a novel protein-protein interaction of Cep112 with breast cancer type 1 susceptibility protein (Brca1), a

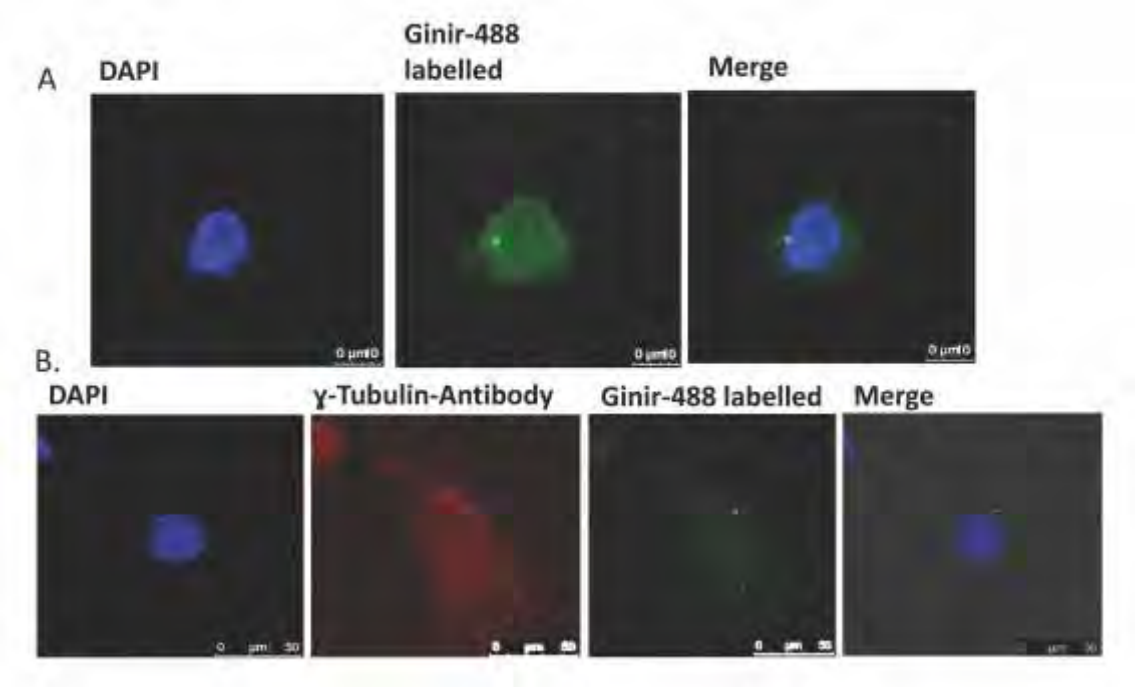

Fig. 1: Immuno-FISH analyses of Ginir ncRNA in human Glioma cells. A. Ginir localizes to centrosomes as detected by LNA-FISH using Ginir probe. B. Co-localization of Ginir ncRNA with beta-tubulin as detected by immune-FISH.

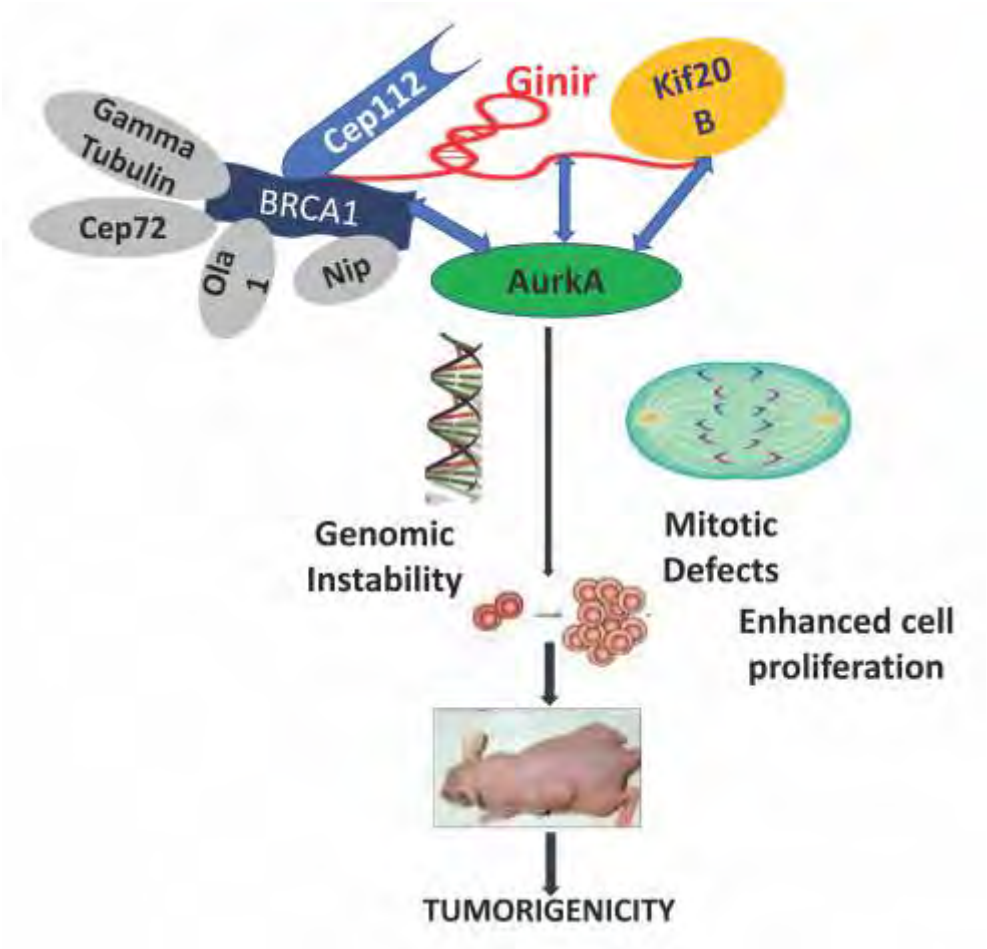

Fig. 2: Model depicting protein interactors of Ginir ncRNA. The effects of protein interactions on oncogenic role of Ginir in mouse cells.

protein well known for its role in genome surveillance (Panda *et al*, Plos Biology, 2018). Our data revealed that interactions between Cep112-Brca1 proteins were perturbed in the presence of excessive levels of Ginir RNA, which resulted in aberrant mitosis and drove cells towards neoplastic transformation. Next, by Mass-Spec analysis we identified a microtubule associated protein Kif20b as an interacting protein partner of Ginir RNA. Kif20b is a member of the kinesin 6 superfamily of proteins, also known as M-phase phosphoprotein 1 (MPP1 or MPHOSPH1). It is an important molecular motor protein required for completion of cytokinesis. Further, we focused on determining the interaction network for Kif20b and found that this protein had the potential to interact with proteins involved in cell cycle regulation like Aurora kinase A (Aurka). Our data clearly indicated role of Kif20b in cytokinesis and we further demonstrated its localization and interaction with Aurka at mid-body during cell division signifying the role of this interaction in regulation of cell division. Mechanistic studies with Ginir ncRNA function indicated that Kif20b and Aurka interaction was disrupted in Ginir over-expresseing cells and their aberrant association contributed to the dysregulated mitosis. Importantly, we confirmed presence of human homologue of Ginir by sequence analysis and our expression studies showed that it was specifically expressed in lung carcinomas and in neuro-epithelial tumors like glioma. Interestingly, we were able to detect presence of Ginir ncRNA on Chromosome 16 in human species. Its localization was found to be centrosome associated as confirmed by us using immuno-FISH wherein we performed single cell FISH using Ginir specific probes followed by immune-fluorescence using beta-tubulin antibody (Fig. 1A and B). Interestingly, the localization of Ginir on centrosomes was restricted only to specific phases of the cell-cycle. In summary, we have specifically deciphered interaction of Ginir RNA with proteins important in cell-division and thereby demonstrated a pivotal role of Ginir ncRNA in mitosis. A schematic depiction explaining the mechanistic involvement of Ginir in cell division in mouse cells is exemplified in Fig 2. Collectively, our studies indicate that the Ginir nc-RNA is conserved across evolution and is associated with cellular hyper-proliferation indicating an important role for Ginir/Giniras pair in cell growth regulation and cancer.

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Lonar Lake Microbial Ecology

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Objectives of the study

- Delineating the overall prokaryotic community structure and function of Lonar Lake and inflow.
- Shotgun sequencing of Lonar Lake metagenome and deciphering the genome diversity employing metagenomic genome reconstruction.

Summary

Lonar Lake is a world-famous soda lake, located in southern peninsula of Indian subcontinent (Aurangabad, Maharashtra, India). This is the only soda lake in the world which is formed by meteor impact on basaltic terrain. The lake has a single notable major perennial inflow popularly called as 'Dhara' and do not have any outflow of water (endorheic basin). Despite the prevailing harsher conditions, this soda lake harbor diverse communities dominated by still uncultured poly-extremophiles or haloalkaliphilic microbes, mostly prokaryotes that are well adapted to survive and grow under highly saline and alkaline conditions. Despite the extensive efforts, the characterized prokaryotic lineages cultured from soda lakes is limited to around 70 species spanning across 30 different genera. The shotgun metagenome sequencing of the Lonar Lake metagenome and high-throughput genome reconstruction can generate enormous genomic and functional information about the microbial communities of this unique ecosystem. A total of 170Gb (341757513 metagenomic reads, 250x2) data was generated from 12 sediment samples employing Illumina Hiseq 250 x 2 pair end sequencing. After quality filtering, 150 GB shotgun metagenome data (299025621 metagenomic reads) was used for subsequent community analysis and metagenomic genome reconstruction.

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Overall prokaryotic diversity of Lonar Lake inflow

Using community structure analysis based on the shotgun metagenome sequencing, 46 prokaryotic phyla and 203 prokaryotic genera were recovered cumulatively from all samples. The phylum retrieved in our survey included the phyla belonging to the major super phylum groups like FCB group, PVC group and Terrabacteria group and also the microbes belonging to Archaeal super phylum TACK group. Among the bacterial phyla, the Proteobacteria with average read abundance of (48%), Firmicutes (4.7%), Actinobacteria (4.4%), Choloroflexi (3.9%), Bacteriodetes (3.8%), Planctomycetes (3.08%), Verrucomicrobia (1.6%), Gemmatemonadetes (1.5%), Dienococcus-Thermus (0.5%), Nitrospiraea (0.65%) were predominant bacterial phyla across all the studied samples. The average percent read abundance of the Firmicutes was 6.8% in Lonar Lake, (almost 3 times) to that of average percentage read abundance of Firmicutes (2.5%) in inflow. However, the average percentage read abundance of Acidobacteria in the inflow (7.1%) was almost five times (5x) higher to that of the Lonar Lake (1.6%). Overall, Archaeal abundance was higher in Lonar Lake sediments in comparison to the inflow. The prokaryotic genera *Marinobacter, Alkalimonas, Haliea, Chromatocurvus and Idiomarina* were exclusive present in Lonar Lake and were absent in inflow metagenome.

Metagenomic genome reconstruction and high throughput genome recovery

Using the metagenomic genome reconstruction, 67 near-complete (≥90% complete, <5% contamination) metagenome-assembled genomes (MAGs) were constructed. The 67 good quality metagenomic bins were thoroughly annotated and we could retrieve the six MAGs (LS1 bin60, LS1 bin65, LS2 bin24, LS3 bin 30, LS3 bin13, LS3 bin55) classified as photoautotrophs based on presence of genes (pufA, pufB) for light-harvesting complex 1 alpha and beta chains. The presence of pufM gene that encodes a key photosynthetic reaction centre protein universally found in purple bacteria, and the genes for sulfide/thiosulfate oxidation (SoxA, SoxX, SoxY, SoxZ) in the two metagenomic bins (LS1 bin60 and LS3 bin 30) pointed their origin from Purple Sulphur bacteria. Both the bins were taxonomically assigned to class Gamma-proteobacteria which affirmed their origin from purple sulfur bacteria.

Metagenome assembled genomes of acetogens having genes for Wood-Ljungdahl pathway

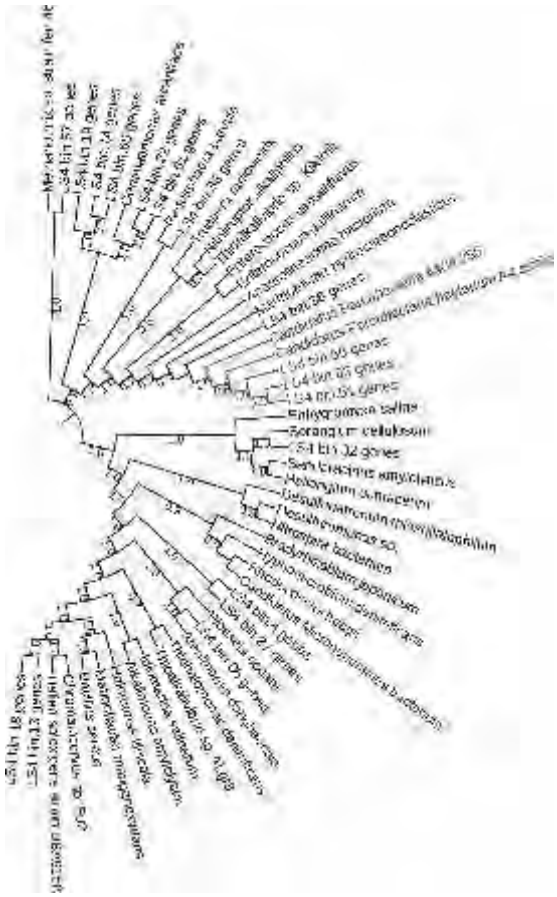

Fig. 1: The phylogenomic analysis of CPR MAGs (Metagenome Assembled Genomes) displaying the clustering of CPR MAGs with Parcubacterial reference genomes (shown in blue color) included for phylogenomic tree construction. Bootstrap value of the clades remains above 0.9 on the bootstrap scale of 0-1.

We scanned our 67 good quality metagenomic bins for the presence of acsB, cdhC, cdhD, cooS, cdhE (key genes encoding enzymes of Wood-Ljungdahl pathway) and confirmed the presence of these genes in five MAGs (LS1.bin29, LS3.bin61, LS5.bin46, LS5.bin9, LS5.bin68). However, the detailed analysis of these metagenomic bins resulted in the recovery of an archaeal MAG (LS5.bin9) that also possessed the genes (mcrA; mcrB, mcrG, mcrC, mcrD) encoding for methyl-coenzyme M reductase (enzyme complex present only in methanogens) and also the encoding potential for CODH/ACS complex. The presence of these two complexes in the same genome affirms the presence of the Wood-Ljungdahl pathway in this methanogen from Lonar Lake.

Recovery of four CPR genomes and Genomic insights into CPR biology

In taxonomic analysis of 12 metagenomes, a substantial proportion of reads (around 4% for all samples) were assigned to the candidate phyla, a radiation of major lineages largely representing uncultured groups. This prompted us to look for the possible CPR genomes in our metagenomic bins. For detection of the CPR genomes in our metagenomic bins, we used CPR scan which is based on existing training file set of 797 known CPR genomes. Using CPR scan, we recovered four CPR genomes with all CPR bins having CPR-Scan confidence of 100%. The four CPR bins showed the completeness of the 80% (LS4_bin51), 76% (S2_bin81), 64.9 % (LS4_bin56), 50% (LS4_bin63), with contamination > 0.1%, as assessed by CheckM. The phylogenomic tree was constructed based on the metagenomic bins recovered in this study and the reference genomes derived from PATRIC web server using the genome-based tree building program PhyloPhlan. The phylogenomic analysis of the four putative CPR bins placed them within the clade of the Parcubacteria (well-known super-phylum of CPR sub-division) with very high bootstrap values of above 0.9 (bootstrap scale 0 to 1). This further confirmed the authenticity of our identified CPR bins. The KEGG annotation and pathway mapping of the four CPR bins revealed the complete lack of the genes related to the TCA (tricarboxylic acid) cycle suggesting them to be obligate fermenters.

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Molecular Simulation to Biochemical Network Perturbation in Infectious Disease: Stability and Stochasticity in Synthetic Circuit

Objectives of the study

- Drug target identification through systems biology approaches: metabolic network analysis and inhibition studies performed through kinetic modeling.
- Identification of inhibitors against the identified target based on pharmacophore modeling, docking and molecular dynamics study.
- *In vitro* and *in vivo* testing of the selected compounds.

Summary

Cutaneous leishmaniasis, with 1.5 million new cases, is the most common form of leishmaniasis and has always been neglected as a major public health problem due to its non-fatality. However, disfigurement, scars and difficulty to cure in immunocompromised individuals are the consequences of the disease. The current therapy regime technique (chemotherapy) is inadequate and has been hampered by various side effects, toxicity, drug resistance and high cost. Due to the increasing global burden of leishmaniasis, it is clear that the requirement to develop novel, more effective and affordable anti-leishmanial drugs is desirable. Moreover, more effective molecular drug targets with therapeutic value are also needed.

The glyoxalase system of *Leishmania* is a ubiquitous thiol-dependent detoxification pathway that protects against cellular damages caused by a-ketoaldehydes, especially, methylglyoxal (MGO). MGO is an unavoidable byproduct of glycolysis and being a highly reactive compound, it reacts with amino groups of arginine and lysine and irreversibly forms advanced glycation end products (AGEs) leading to the increase in reactive oxygen and nitrogen

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species (ROS and RNS) level. ROS and RNS are extremely reactive entities and cause modification of various enzymes, leading to their degradation. In *L. donovani*, MGO has been shown to inhibit cell growth at higher concentration (IC50: 1mM). High activity of GLOI in tumor tissues and its role in the regulation of cellular growth has been reported previously. Besides this, GLOI specific inhibitors have been reported selectively toxic to proliferating cells due to increased accumulation of MGO leading to inhibition of DNA synthesis.

The glyoxalase system comprises of two enzymes, glyoxalase I (GLOI) and Glyoxalase II (GLOII) and catalyzes the formation of S-D-lactoyl glutathione and D-lactate. Glyoxalase system of *Leishmania* possesses an unusual thiol metabolism in which instead of glutathione, trypanothione ($T[SH]_2$) is used. Also, the metal cofactor is nickel (Ni^{+2}) instead of zinc. Thus, both the cofactors of *Leishmania* GLOI (LmGLOI) are different from those of mammalian glyoxalases. This difference in cofactor dependence is also reflected in differences between the active sites of the human and LmGLOI, suggesting that the latter may be a target for anti-leishmanial therapy.

Hence, from above discussion, we hypothesize that if the activity of GLOI is inhibited, it may cause the accumulation of MGO inside the parasite that, subsequently, will damage the parasite by reacting with its proteins, nucleic acids and lipids. Therefore, the purpose of the current project is to design novel compounds against GLOI by applying bioinformatics and systems biology approaches and test them *in vitro* to check their therapeutic potency against *Leishmania major*.

Model Reconstruction and Network topology

Initially, A directed master network, **M**, was built from **iAC560** by removing all transport and exchange reactions, self-loops, currency metabolites (ATP, ADP, CO_2, etc.), electron carriers ($NADP^+$, NADPH, NAD, NADH), Waters (H_2O), and electron transporters (H^+, PO_4^{+3}, HCO_3^-) and all reversible reactions were converted to two irreversible backward and forward reactions. This model consisted of 226 metabolites (Table1, Figure 1). Further, to get a deeper insight of the leishmanial metabolic network, the master model, **M**, was subdivided into 7 small directed bipartite graphs (M1, M2, M3, M4, M5, M6, and M7). The network topology of all networks was analyzed in Cytoscape and is summarized in Table 1. Further, betweenness centrality calculated for each node in M network pointed out important metabolites. In our M model several of these metabolites (HTA, MG, Pyr, $T[SH]_2$) with high betweenness centrality were part of M7 model (FBA model) suggesting the importance of FBA model.

Curvature distribution

For each vertex in all directed graphs, we computed Forman curvature (Fv), Out Forman (Fo), In Forman (Fi), Out Forman-Ricci (FRo), In Forman-Ricci (FRi) curvatures, total Forman and Forman-Ricci flow. It was observed that most of the nodes and edges were comprised of negative curvature values. Although, the distribution of Forman curvature of both nodes and edges was broad, the peaks with high frequency were concentrated towards (or at) 'zero'. Interestingly, nodes with higher Forman curvature were found to be related to glycolysis, MG metabolism and $T[SH]_2$ metabolism pathways. Furthermore, these metabolites were also spotted as important vertices from Forman curvature plot of nodes in 'M' model (Figure 1).

The correlation between Forman curvatures and betweenness centrality, closeness centrality, In-degree and Out-degree were computed in 'M' model (Table 2, Figure 1). A high negative correlation was observed for Fi and FRi with and In-degree (Figure 1). Moderate negative correlation was reported for Fi, FRi, Fo with betweenness centrality (Figure 1). Interestingly, In-degree and Out-degree have also shown moderate correlation with betweenness centrality but the R-value was shifted to positive side than the negative one (Table 2). For small scale models, only M7 indicated high negative correlation for Fo and FRo with betweenness centrality. It was found similar to the correlation for betweenness centrality and In- and Out-degree for M7 model (high positive correlation). However, other models only showed moderately positive correlation for the same (Table 2).

Flux balance analysis

Since our focus for performing FBA was to investigate the importance of glyoxalase pathway in redox metabolism, we refrained our model from genome-based construction and kept it at simple metabolic level. The proposed stoichiometric model accounts for the reactions of glycolysis, glyoxalase pathway, and thiol metabolism. The reconstructed model resulted in a network consisted of 109 reactions that included 48 main reactions, 22 transport reactions and 24 exchange reactions (Table 3). Our aim was to observe the effect of metabolism of MGO through Glyoxalase pathway on the system; hence, we focused on the formulation of objective functions (OF) by taking into account the metabolites only used in the model. The system was investigated in two scenarios, first, functional GLOI (Glyoxalase I), and second, nonfunctional (absent from the system) GLOI.

After simulation, in second scenario the flux rate was found to be more or less similar for glycolysis but only upto the synthesis

of GA3P and DHAP. In fact, the flux through TPI enzyme (DHAP synthesis) was more than that of scenario 1 that probably contributed to the synthesis of MGO. It is noticeable that MGO was produced at twice the rate than the previous case. This higher level of accumulation of MGO was found to contribute to equal level of the formation of AGEs and $MGO^{\bullet-}$ free radicals (Figure 1). It was worth noticing that in case of inactive GLOI, the flux moved from glycolysis to for the synthesis of MGO. In the model, this resulted into negligible flux through the rest of the glycolysis pathway. Although in real network, pyruvate production will be happening at normal rate except for that the inactivation of GLOI should lead to the increased level (~1.5 fold) of accumulation of MGO. It was observed that, inactivation of GLOI caused the 'zero' flux through the rest of the glyoxalase pathway.

Kinetic modeling and Computer simulation

Initially two kinetic models for glyoxalase pathway, inhibited and non-inhibited, were built (Figure 1) and appropriate rate laws and initial concentrations were assigned to each reaction (Table 4 and 5). Time course simulation was ran in COPASI (version 4.22) using LSODA algorithm to inspect the MGO consumption in the model. Higher GLOI activity was observed in non-inhibited model when compared to the inhibited one. Parameter scanning on both the models revealed that when initial concentration of MGO was raised to 2, 4, 6, 8, and 10-fold, it led to the similar level of accumulation of MGO in inhibited system (Figure 1). This has, consequently, affected the rate of synthesis of S-lactoylglutathione and D-lactate (Figure 1).

Since, MGO damages proteins by modifying Arginine (Arg) and Lysine (Lys) residues forming AGEs, we introduced Arg and Lys modification reactions to the models to know the effect of MGO. Due to high level of accumulated MGO increased level of formation of AGEs was observed (Figure 1), hence, supporting our hypothesis from systems perspective and exhibiting the importance of GLOI.

Further, as we mentioned earlier, MGO, by reacting with Arg and Lys, promotes the formation of ROS and RNS. Therefore, to understand the link between high concentration of MGO and ROS/RNS formation, we extended our models to higher level and introduced other reactions related to the formation of various free radicals (Figure 1). Interestingly, when comparison was made between inhibited and non-inhibited models, our extended model showed that accumulation of MGO has influenced the formation of ROS/RNS, especially, $MGO^{\bullet-}$ radical and modified Lys were observed at higher concentration in inhibited model than that of the non-inhibited one (Figure 1).

Molecular modelling, simulation and pharmacophore features selection

Further, for searching potent inhibitors for LmGLOI, a number of thiosemicarbazone and benzimidazole derivatives were retrieved from various online databases, *viz.*, Pubchem, Drugbank, ZINC, ChEMBL, etc. After applying ADMETox filters and molecular docking calculations, top 8 GLOI-ligand complexes were selected (Table 6, Figure 2) and subjected to MD simulation. Analysis of binding modes of these complexes have revealed that all the ligands have maintained interaction with active site residues and the binding modes obtained after MD simulation were more or less similar to those obtained after docking. (Figure 2). RMSD for the backbone atoms for GLOI and ligand bound GLOI were plotted to understand the relative stability of the GLOI-ligand complexes. Hydrogen bonds between ligand-GLOI have demonstrated that all ligands were interacting with the active site by forming at least one H-bond and ligand distance from Ni^{+2}-was observed to be within the range. The rmsd plot of backbone of GLOI and ligand suggested that all the 8 complexes were stable throughout the simulation cycle without much fluctuation (Figure 2). Although, hydrogen bonds plots between ligand-GLO I have demonstrated that all ligands were interacting with the active site by forming at least one H-bond, rmsd of backbone and rmsd in terms of interaction diagram of ligand-GLO I has suggested that only two complexes, C1 and C2, were stable throughout the simulation cycle without much fluctuation. Furthermore, the ligand distance from Ni^{+2} was observed to be within the range (Figure 2). These two compound-GLO I complexes were further subjected to extended MD simulation for up to 100ns to inspect their structural and interaction stability. Our results revealed that only C1-GLO I complex exhibited stable behaviour in terms of rmsd. Also, in the interaction diagram of ligand-GLO I, it was observed that C2 deviated from GLO I active site and fluctuated even after coming into the contact of GLO I (Figure 2). Same was noted in case of C2-GLO I complex when the two structures from 10ns and 100ns were superposed. Hence, our molecular modelling and simulation analysis suggested that C1 can be, further, used as an active hit against *Leishmania*.

Next, based on C1 binding modes in GLO I active site, a 6 point pharmacophore model was developed using Phase (Figure 2). This model was, further, used for database screening against ZINC drug-like database. The screened compounds were then docked against GLO I. Table 7 shows top 10 compounds selected from pharmacophore based virtual screening.

Expression and purification of LmGLO I

After reconstitution and transformation of construct into BL21 strain, the cells were grown at 37°C for 24 hrs. The plasmid DNA was isolated and digested by restriction enzyme followed by its gel electrophoresis (Figure 2). Further, *glo1* gene was expressed by giving 1mM IPTG induction for different time point upto 5 h (Figure 2). The purified GLO I protein through Ni-NTA resin column was found to be ~24kDa in size.

Anti-promastigote activity of compounds and

Compounds C1 and C2 were procured and tested against *L. major* promastigotes and raw cell line of macrophages post 48 h of treatment and their IC50 values were calculated in order to define their efficacy. Between the two compounds, C2 showed little inhibition and its IC50 against *Leishmania* parasite could not be calculated (IC50 > 1000 µM). However, C1 exhibited promising antileishmanial activity. Its IC50 value was calculated as 105 µM (Figure 2). At this concentration, macrophages have shown ~80% cell viability at IC50 value of C1 (Figure 2). Furthermore, in SEM analysis, promastigotes treated with both the compounds have shown remarkable morphological changes. Both the compounds were able to cause size reduction, membrane blebbing and loss in motility in the parasite (Figure 2).

C1 induced cell-division arrest and apoptosis in L. major

To quantify the percentage of pseudodiploid leishmanial cells, flowcytometric analysis was performed after cell permeabilization and PI labeling. C1 treated leishmanial promastigotes demonstrated 17.12% increase in sub-G0/G1 phase when compared with untreated parasites (Figure 2). This increase was accompanied by decrease in the number of cells in S and G2/M phase (4.78% and 0.11%, respectively) in comparison to untreated cells (18.57% and 4.95%, respectively). While in case of MIL treated parasite lower values were obtained (sub-G0/G1: 10.19%, S: 1.06%, and G2/M: 0.18%). Moreover, in C1 treated parasites, percentage annexin V-positive, PI-negative population was found to be 8.69% that is higher than MIL treated parasite (1.16%) (Figure 2). The anti-leishmanial activity of C1 was observed as apoptosis driven due to the lower percentage of PI-positive population (4.23%).

Efficacy of C1 in L.major infected mice

As mentioned, the drug C1 was administered orally in different groups (5, 10, 20 and 40 mg/kg/body weight/day). The swelling in the foot pad was monitored post treatment and it was observed that in the groups who received C1 did not show any difference in the lesion size unlike the control group administered with water showing gradual increase in lesion size (Figure 2). To confirm the efficacy of C1, treated and untreated mice were euthanized and their lymph nodes were collected to find parasitic burden. It was noted that in all treated groups the parasitic load found to be decreased as compared top untreated mice (Figure 2). Moreover, it was noted that at higher dose (40 mg) the compound showed little toxic effect that caused weakening of mice. Our results indicate that C1 has healing effect in infected mice and reduced the parasitic burden in mice. Henceforth, we suggest C1 as potent anti-leishmanial hit and by further modification it could be possible to develop novel and effective compounds.

TABLES:

Table 1. Topological properties of the Networks

Model	No. of metabolites	Clustering Coefficient	Network diameter
M	226	0.038	31
M1	39	0.026	17
M2	81	0.022	13
M3	23	0.118	8
M4	23	0.051	17
M5	27	0.046	12
M6	36	0.017	8
M7	33	0.010	12

Table 2: Summary of R-values for different models.

	R-value													
	Fi		FRi		Fo		FRo		Fv				Between ness Centrality	
	Between ness Centrality	In-degree	Between ness Centrality	In-degree	Between ness Centrality	Out-degree	Between ness Centrality	Out-degree	Between ness Centrality	Closeness Centrality	Deg-ree	Clustering Coefficient	In-degree	Out-degree
M	-0.457	**-0.855**	-0.388	**-0.672**	-0.422	-0.215	-0.294	-0.014	**-0.688**	-0.060	-0.091	-0.146	0.387	0.403
M1	-0.335	-0.069	-0.490	-0.114	-0.394	-0.210	-0.230	-0.040	-0.350	0.109	-0.312	-0.117	0.062	0.330
M2	-0.140	**-0.851**	-0.289	-0.570	-0.206	-0.122	-0.276	-0.062	-0.409	-0.337	-0.704	-0.198	0.155	0.434
M3	-0.134	**-0.816**	-0.360	-0.599	-0.299	-0.127	-0.265	0.160	-0.347	-0.444	0.0281	-0.576	0.226	0.277
M4	-0.263	**-0.970**	-0.508	**-0.776**	-0.264	-0.131	-0.264	-0.054	**-0.596**	-0.209	-0.572	-0.426	0.290	0.469
M5	-0.614	**-0.941**	0.017	0.160	**-0.698**	-0.498	-0.039	-0.023	**-0.849**	-0.116	**-0.854**	-0.057	0.504	0.544
M6	-0.297	**-0.945**	-0.169	**-0.807**	-0.438	-0.001	-0.027	0.249	**-0.520**	-0.449	**-0.782**	-0.459	0.372	0.424
M7	**-0.847**	**-0.920**	**-0.766**	**-0.860**	**-0.865**	-0.600	**-0.658**	-0.177	**-0.897**	-0.240	**-0.903**	-0.242	**0.793**	**0.670**

Table 3. Properties of FBA model constructed from M7 model

Property	Count
Reactions	48
Transport reactions	22
Exchange reactions	24
Metabolites	86
Compartments	1

Table 4. Reactions and rate law assigned in each model

	Model			
	Non-inhibited		Inhibited	
	Reaction	Rate Law	Reaction	Rate Law
R1	MG + TSH2 -> HTA	K_1*MG*T[SH]$_2$	MG + TSH2 -> HTA	K_1*MG*T[SH]$_2$
R2	HTA -> MG + TSH2	K_2*HTA	HTA -> MG + TSH2	K_2*HTA
R3	HTA -> SDLTSH (GLOI)	(Vm1*HTA)/ (Km1+HTA)	HTA -> SDLTSH ; MG (GLOI)	(Vm1*HTA)/ (Km1+HTA+Km1*(HTA/Ki)^2
R4	SDLTSH -> DL + TSH2 (GLOII)	(Vm2*SDLTSH)/ (Km2+SDLTSH)	SDLTSH -> DL + TSH2 (GLOII)	(Vm2*SDLTSH)/ (Km2+SDLTSH)

Table 5. Parameter values and initial concentrations used in the models

Parameter	Value	Metabolite	Initial Conc. (M)
K1	0.0056 $M^{-1}s^{-1}$	Methylglyoxal (MGO)	0.00332
K2	0.016 s^{-1}	Trypanothione (TSH2)	0.9
Km1	3.2E-05 M	--	–
Km2	3.9E-05 M	--	--
Vm1	0.000159 Ms^{-1} (Calculated)	--	--
Vm2	2.3E-09 Ms^{-1}	--	--
Ki	3.2E-06 M	--	--

Table 6. Molecular descriptors of selected top 8 compounds

Comp No.	Docking Score	MW	RO5	PAINS Filter
C1	-7.746	232.34	0	Pass
C2	-7.15	259.35	0	Pass
C3	-8.002	301.36	0	Pass
C4	-7.595	238.28	0	Pass
C5	-7.592	293.32	0	Pass
C6	-6.694	247.35	0	Pass
C7	-6.588	246.30	0	Pass
C8	-6.587	227.22	0	Pass

Table 7. Top 10 compounds selected on the basis of their docking score after pharmacophore based screening and molecular docking

	ZINC ID	Docking score	MW
1	ZINC72199852	-11.229	311.519
2	ZINC06188149	-10.577	337.224
3	ZINC72199240	-10.537	255.624
4	ZINC04749669	-10.307	341.363
5	ZINC71689273	-10.059	279.378
6	ZINC13496706	-10.006	299.252
7	ZINC13496705	-9.887	303.671
8	ZINC71688725	-9.804	265.352
9	ZINC18066480	-9.675	303.671
10	ZINC71690425	-9.579	255.288

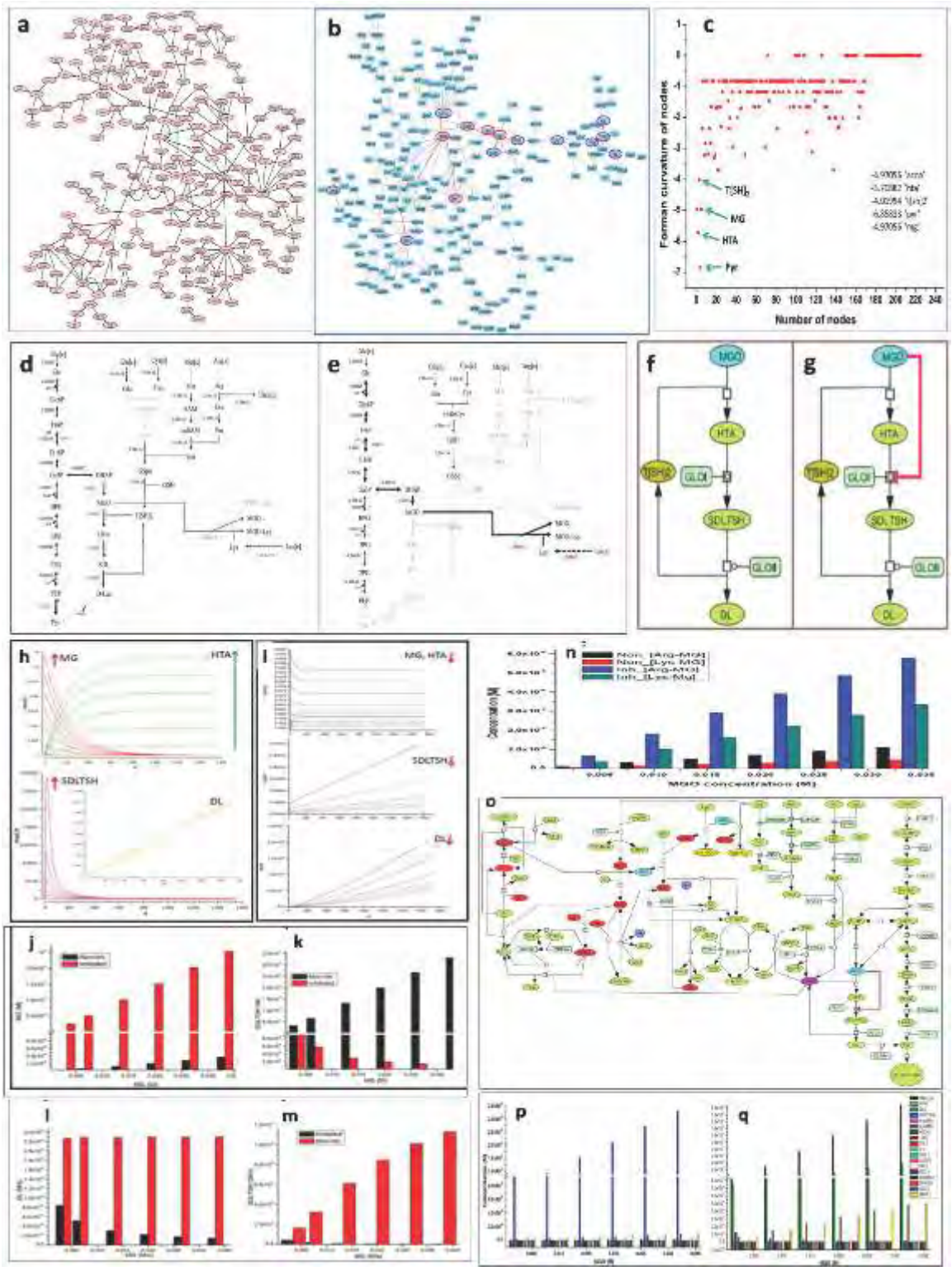

Figure 1. Illustration of node identification and kinetic simulation: (a) Reconstructed master model post removing currency metabolites and self-loops, (b) Depiction of internal connectivity in Master model showing the components connection by *backbone* forming high curvature nodes (encircled in red color). (c) Metabolites with high curvature values are labeled and pointed with green arrows. Reaction fluxes for (d) scenario 1 (Functional GLOI), and (e) scenario 2 (Non-functional GLOI). Solid thick black arrows represent the direction of main flux flow through the model. Gray arrows are an indication of undetermined (zero) flux through the respective reaction. Dotted arrows represent the transport of the metabolites. (f and g) Two basic small scale models constructed to study the inhibition kinetics of GLO I. Concentration (h, i, j, k, l and m) vs Time plot of 2, 4, 6, 8, and 10 folds increased MGO concentration and its effect on its accumulation in non-inhibited and inhibited models. (n) Effect of 1, 2, 4, 6, 8, and 10 folds increased MGO concentration on the formation of modified Arg and Lys. (o) Hybrid model of accumulation of MGO. Substrate level inhibition (red line) of SDLTSH synthesis leads to the increased formation of various free radicals including $MGO^{\bullet-}$ ions. Illustration the effect of increased concentration of MGO in hybrid model (p) Non inhibited, (q) Inhibited

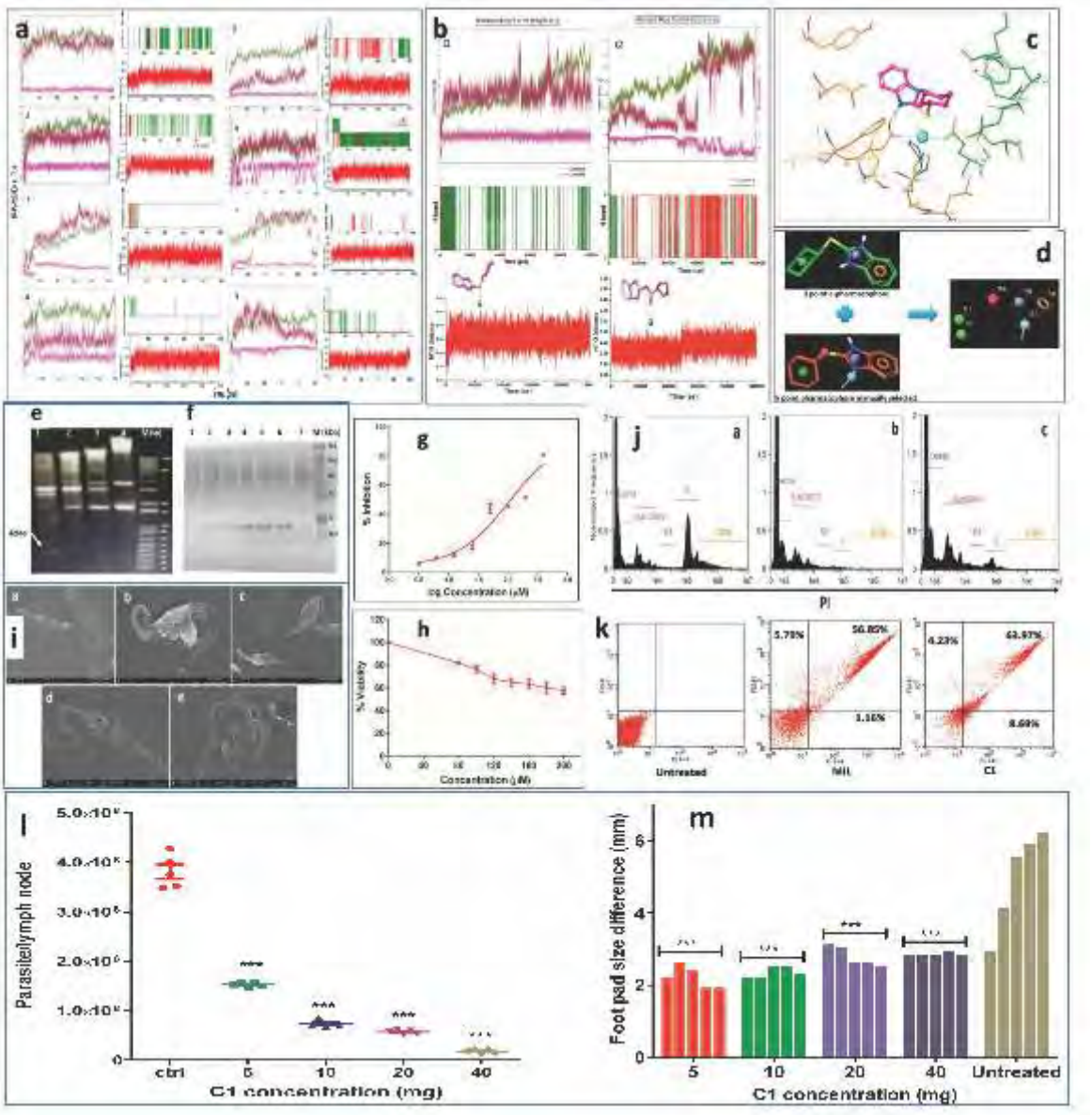

Figure 2. (a) Comparison of root mean square deviation (RMSD) of backbone atoms (left), and hydrogen bond and potential energy as a function of time for 8 systems as the function of simulation time (upper and lower panel, right, respectively). (b) Evaluation of time course simulation of C1 and C2 with GLO I complex for 100 ns. (c) Depiction of binding interaction between C1 and GLO I and (d) Pharmacophore features selection on the basis of these bindng interactions. A 3 point pharmacophore was designed automatically using e-pharmacophore tool. To include metal binding feature (negative feature, N4) and H-bond donor (D1) features to 3-point e-pharmacophore model, a 5-point model was developed manually. Then, these two models were merged to generate a 6-point pharmacophore model. Gel electrophoresis of *glol* gene and GLO I protein. (e) Indicating the location of *glol* gene. Lane 1: NdeI+NotI; 2: NdeI; 3: NotI; 4: Construct with GLOI; 5: DNA molecular weight marker. (f) SDS-PAGE indicating the location of GLOI protein. Lane 1: Noninduced 5 h; 2: Induced 1 h; 3: Induced 2 h; 4: Induced 3hr; 5: Induced 4 h; 6: Induced 5 h; 7: Untransformed BL21 strain 5 h; M: Protein molecular weight marker. Testing the efficacy and cytotoxicity of C1 (g) IC50 calculation of C1 against *L. major* parasite. (h) Cytotoxicity of the C1 over Raw macrophage cell line. Morphological analysis of untreated and treated leishmanial promastigotes through SEM. (i) untreated (a), (b and c) C1 treated, and (d and e) C2 treated. (j) Cell cycle analysis of *L. major.* (a) untreated; and treated (b) MIL; (c) C1. (k) Apoptosis analysis of untreated and treated (MIL and C1) *L. major.* (l) Foot pad size difference in C1 treated and untreated groups. (m) Parasite load assay of the C1 treated and untreated groups. Every dot indicates one mice. P-value was calculated by comparing treated groups with control and significance is indicated in the figure as ***p<0.0001

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Combinatorial role of DYRK1A and DSCR1 during neurogenesis in Down syndrome

Objectives of the study

- Developing tools to study role of Human Chromosome 21 genes during neurogenesis.

Summary

Individuals with Down syndrome (DS) show impaired intellectual development. Section from the brains of aborted DS fetuses show reduced brain volume, brachycephaly and reduced number of neurons. These observations indicate defective neurogenesis. However, exact cause of reduced neurogenesis remains unknown. Several mouse models of DS have contributed significantly in understanding neurobiology of DS but several important differences in neurogenesis and limitations of generating complete trisomy of human chromosome 21 has proven to be a major hindrance.

Recent invention of induced pluripotent stem cells (iPSCs) by somatic cell reprogramming using defined factors has opened up possibilities to model diseases in a dish. In a major achievement, we were able to recapitulate major in vivo brain phenotypes in a dish, such as reduced neurogenesis, using isogenic pair of DS and normal human induced pluripotent stem cells (hiPSCs).

Human Chromosome 21 (HSA21) harbors about 550 genes. It has been postulated that triplication of genes is present in region 21q22.1 to 21q22.3 (Down Syndrome Critical Region (DSCR) are involved in learning and memory deficit. Dual-specificity tyrosine -(Y)-regulated kinase 1A (DYRK1A), Down

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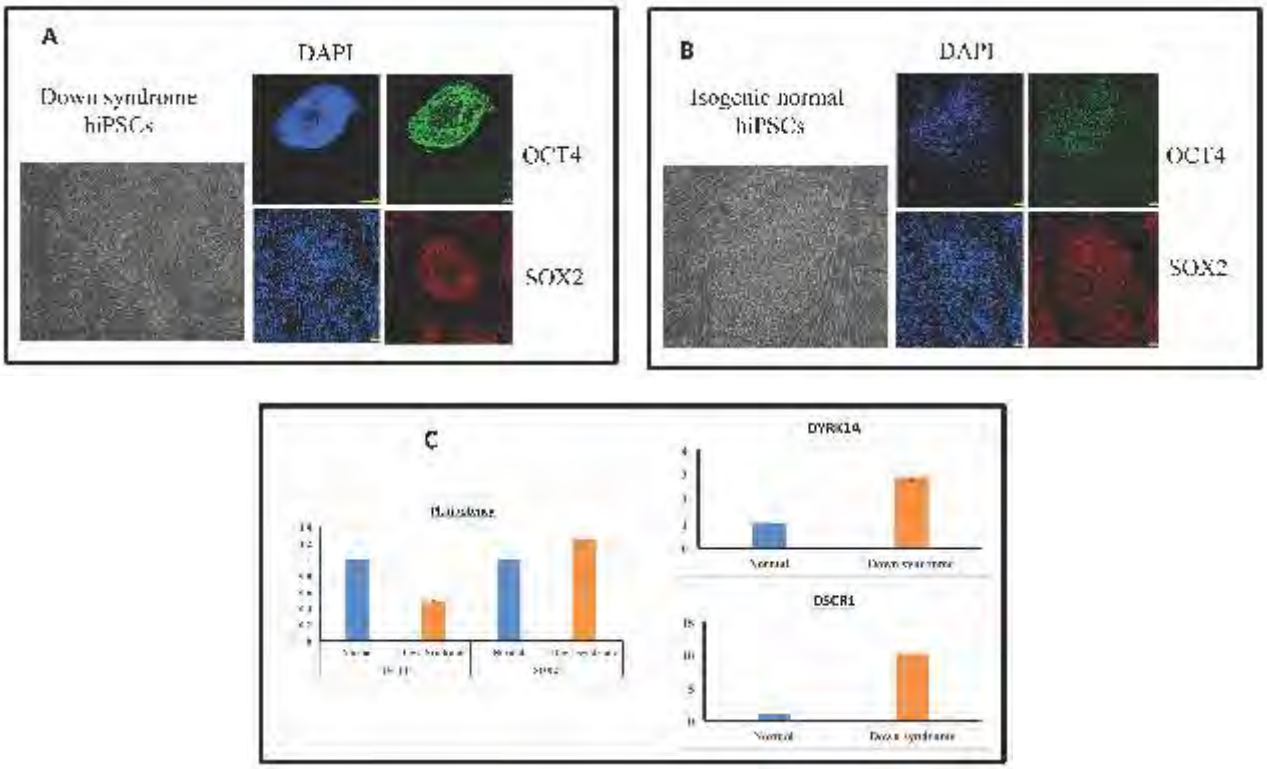

Fig. 1: Down syndrome and Isogenic normal human iPSCs. (A) Down syndrome human iPSCs bright field image, and immunostaining with pluripotency genes OCT4 and SOX2. (B) Isogenic normal human iPSCs bright field image, and immunostaining with pluripotency genes OCT4 and SOX2. (C) Quantitative expression analysis of pluripotency associated transcript Oct4 an Sox2 as well as HAS 21 associated genes Dyrk1a and DSCR1.

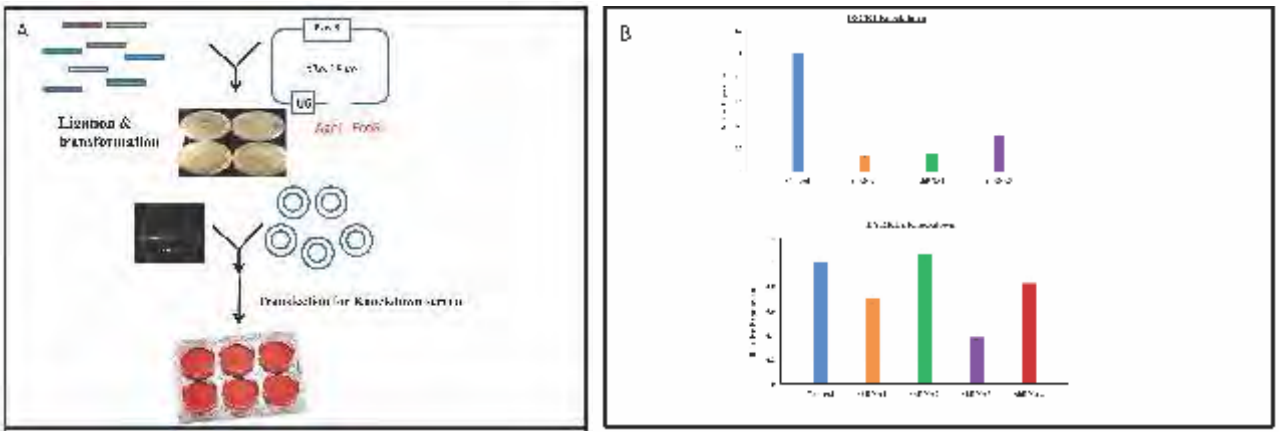

Fig. 2: Generation of inducible knockdown hiPSCs. (A) Schematics of cloning and screening of gene specific shRNA. (B) Quantitative analysis of DSCR1 and DYRK1a expression after shRNA mediated knockdown.

Syndrome Critical Region Gene 1 (DSCR1) also referred as regulator of calcineurin1 (RCAN1) are present in DSCR. Overexpression of DYRK1A has been shown to cause premature differentiation of neural progenitors, causing depletion of progenitor pool. DSCR1 in a study performed in Ts1cje mice, it was observed that ameliorating expression levels of either one i.e. DYRK1A or DSCR1 failed to rescue neurogenesis but simultaneously reducing expression of DYRK1A and DSCR1 rescued neurogenesis. These observations indicate that genes present on Chr21 not only play role individually but also in combination to affect neurogenesis.

Thus, in order to study the role of genes present on HSA21, individually and in combination we sought to develop shRNA based knockdown system to allow examining role of these genes.

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Mechanism of breast cancer stem cell (BCSC) radio-resistance: Role and regulation of antioxidant and DNA damage repair pathways

Objectives of the study

- Isolation and characterization of BCSCs from Breast cancer cell lines and clinical Samples as well as establishment of mammospheres.
- Elucidation of the Keap1-Nrf2 pathway and its downstream regulators in radio-resistance of BCSCs.
- Understanding the role of BRCA 1 and DNA damage repair mechanisms in radio-resistance of BCSCs and the relation between Nrf2 and BRCA1 in resistance and recurrence of tumor.

Summary

Radioresistance due to the presence of cancer stem cells (CSCs) is a recurring problem in radiotherapy in breast cancer, either used alone or in conjunction with other therapies such as surgery and chemotherapy. As enhanced antioxidant defense mechanisms and DNA repair are suggested as underlying mechanisms, we aimed to investigate the role of Keap1-Nrf2, BRCA 1 and DNA damage repair pathways and their correlation if any in BCSC radioresistance using adherent MCF-7 cells and their mammospheres irradiated with single dose (6 Gy) and fractionated doses (2 Gy for 3 consecutive days) of γ-radiation. We observed that, mammospheres treated with fractionated doses, showed increased expression of the embryonic stem cell markers SOX2, KLF4 and NANOG, increased radioresistance as seen by colony formation assays and lower levels of ROS. Since nuclear factor-erythroid 2 related factor 2 (Nrf2) is a master regulator of all the antioxidant defences whose expression is shown to be increased in many types of cancers as well as in chemoresistance in BCSCs, we next checked the levels of Nrf2 and its downstream targets HO-1 and NQO1 in MCF-7 cells treated with fractionated dose. Knockdown of Nrf2 showed a

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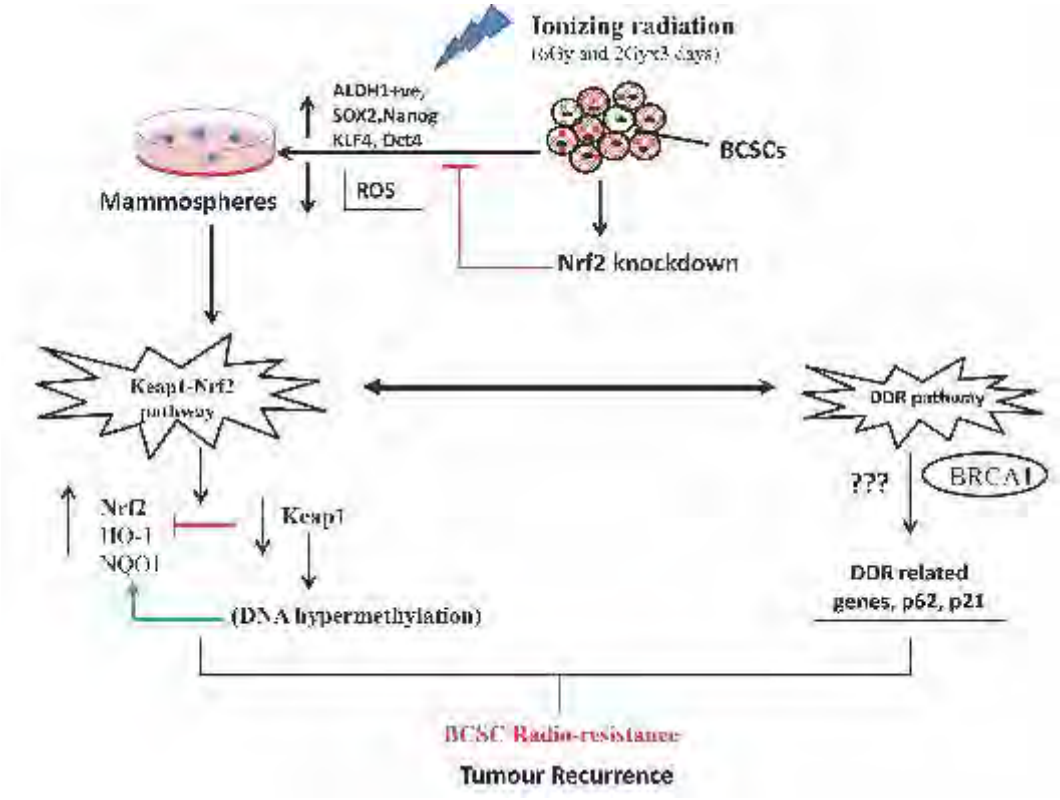

Fig: Schematic representation of Nrf2 pathway in radio-resistance of BCSCs: Elevated expression of Nrf2 in irradiated mammospheres enhances radio resistance via increasing BCSC population. Hypermethylation of keap1 promoter stabilizes Nrf2 and increase in the expression of antioxidant enzymes.

decreased expression of OCT4, SOX2, KLF4 and NANOG in these cells suggesting that Nrf2 might play a role in elevation of BCSCs population after irradiation. Keap1 is responsible for the constant degradation of Nrf2 under normal condition, we hypothesized that the stabilization of Nrf2 might be due to the disruption of Keap1 -Nrf2 binding, we further checked the expression of Keap1 as well as the negative regulator of Nrf2, Bach1 in adherent cells and mammospheres irradiated with single and fractionated doses of radiation. Low levels of Keap1 were observed in both adherent and mammospheres irradiated with single and fractionated doses. These low levels could either be due to epigenetic modification or post transcriptional modification, so we next treated adherent MCF7 cells with azacytidine, an inhibitor of methylation and irradiated these cells. We found an increase in the expression of Keap1 in cells treated with azacytidin even after irradiation with fractionated dose of radiation. This is the first report where the role of Nrf2 in breast cancer stem cell radioresistance is being studied.

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Trafficking in stem cells: a story of cell fate determination.

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Objectives of the study

- To uncover components of the vesicular transport machinery that play a role in the maintenance of pluripotency.
- To understand the role of molecules involved in vesicular transport in mammalian development.

Summary:

Pluripotent embryonic stem cells possess the ability to differentiate into cell types belonging to all three germ layers. These cells provide a useful model system to study cell fate changes and choices in early mammalian development. Pluripotency in embryonic stem cells is known to be regulated by numerous factors, including epigenetic modifications, small non-coding RNAs, and more recently, the process of intracellular trafficking.

Vesicular transport or trafficking is required for the accurate transport of molecules within a cell. A number of studies have shown that alterations in the process of intracellular trafficking can affect the acquisition of pluripotency through reprogramming assays. However, a detailed analysis of the role of trafficking in the maintenance and acquisition of pluripotency remains to be carried out. It is towards this goal that the following aims have been proposed.

Main findings:

- Our screening results demonstrate that clathrin-mediated endocytosis (CME) is essential to maintain the pluripotent nature of mouse embryonic stem cells.

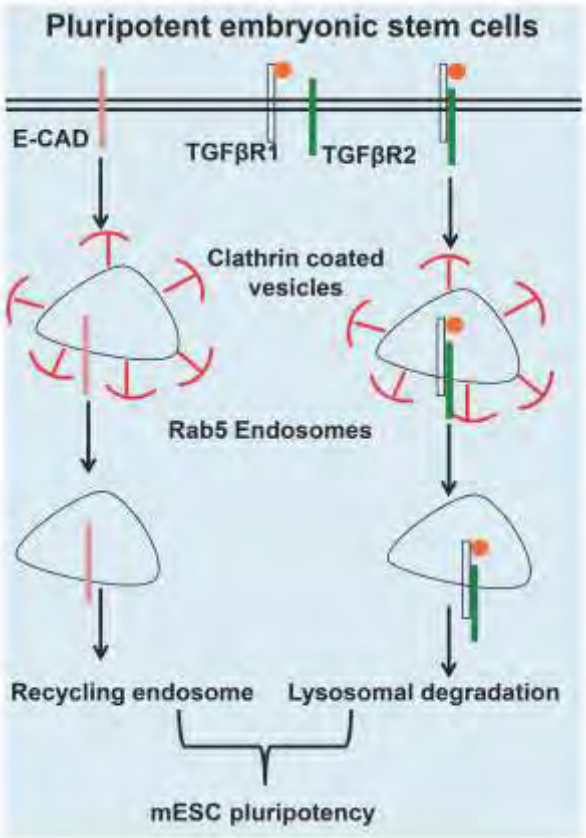

Fig. 1: Model demonstrating that clathrin-mediated endocytosis (CME) is necessary to maintain mouse embryonic stem cell (mESC) pluripotency by regulating the trafficking of E-CAD and TGFβR1. E-CADHERIN is internalized in a clathrin-dependent manner and is recycled back to the membrane. TGFβR1 is internalized and targeted to the lysosome for degradation. Maintaining a balance between E-CADHERIN levels and TGFβR1 signalling is essential to maintain the pluripotent state of stem cells.

- CME regulates the internalization and recycling of the cell-cell adhesion molecule, E-CADHERIN in embryonic stem cells.
- CME also regulates the internalization and targeting of the Transforming Growth Factor beta receptor 1 (TGFβR1) for lysosomal degradation.
- Loss of CME results in a loss of pluripotency characterized by decreased E-CADHERIN and enhanced TGFβR1 and MEK signaling.
- CME thus balances the actions of these two opposing molecules, E-CADHERIN and TGFβR1 in maintaining the pluripotent state of embryonic stem cells (Fig. 1).

Our results demonstrate that clathrin-mediated endocytosis plays a role in regulating the fate of pluripotent stem cells by modulating the differential trafficking of molecules (Narayana et al., Stem Cell Reports, 2019). We have also previously shown that caveolin-mediated endocytosis is absent in pluripotent stem cells, and that components of this pathway are actively repressed in embryonic stem cells, and are expressed upon differentiation (Mote et al., Scientific Reports, 2017). Together our results suggest that the fate of embryonic stem cells may be dependent on the activity of specific intracellular trafficking pathways.

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Gene regulatory functions of mammalian long noncoding RNAs [lncRNAs] during quiescence-proliferation axis.

Objectives of the study

- Characterize complete lncRNA signature associated with cellular quiescence and proliferation.
- Delineate regulatory mechanisms through which lncRNAs orchestrate these processes.

Summary

A large portion of the eukaryotic genome is transcribed into RNAs that do not code for proteins. These interesting molecules, formally known as noncoding RNAs (ncRNAs) that bypass the central dogma for the flow of genetic information in cells, have been under constant scrutiny for their existence for several decades. Although the discovery and functional characterization of small ncRNAs have dominated the field of RNA biology over the past several decades, long noncoding RNAs [lncRNAs] are the least explored emerging regulatory molecules. Although the function of a large number of lncRNAs is still not known, there is clear evidence for their importance in physiology, embryology and development with numerous novel gene regulatory functions, including their role in contribution to high degree of complexity observed in multicellular organisms. Various studies have revealed their active role in controlling multiple regulatory layers including chromosome architecture, chromatin modulation and epigenetic modification, transcription, RNA maturation, splicing and translation. Based on the current evidences, lncRNAs can perform their function by physically interacting with DNA, RNA and proteins, thereby regulating complex network of gene expression by acting as signals (for integrating spatiotemporal, developmental, and stimulus-

Lab Members

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Collaborator(s) - Industry

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specific cellular information), decoys (the ability to sequester a range of RNA-dependent effectors and protein partners), guides (for proper localization of chromatin-modifying complexes and other nuclear proteins to specific genomic loci to exert effects), and scaffolds (for bringing two or more proteins into discrete complexes).

Elucidating the different mechanism of action of lncRNAs will not only provide the basic biological understanding of cellular function but also a critical nexus for revealing the basis of lncRNAs in disease etiology and their use as targets in subsequent drug design. Most importantly, the fact that mammalian transcriptome comprises several thousand lncRNAs with diverse signatures, the question that whether all of them have biological purpose still stands unanswered. Thus a comprehensive knowledge of their function would greatly facilitate our current understanding of various cell regulatory networks and disease mechanisms.

We have generated a pipeline where we established the inputs as RNA-Seq data of diploid lung fibroblasts at early, mid and late stages of quiescence entry and exit. Additionally, we also incorporated earlier known annotations from RefSeq/GENCODE and the new annotations from MiTranscriptome assembly. The RNA-Seq data were aligned to the genome and assembled into transcripts by TopHat and Cufflinks, respectively. Additionally, with the known annotations, we considered transcripts with high conservation and diverse tissue expression. Finally, from this group we only selected the intergenic transcripts for further evaluation. In our initial analysis, we have focused on highly conserved and diversely expressed lncRNAs because it can provide an exciting avenue for *in vivo* study of the role of lncRNAs in development and carcinogenesis. From our RNA-seq data, we obtained approx. 2500 differentially expressed transcripts, out of which 38 showed a significant GFOLD upon quiescence entry and 141 transcripts showed significant GFOLD upon quiescence exit. Additionally, to understand the role of mammalian lncRNAs in cellular proliferation, we performed a comprehensive expression analysis of approx. 17648 lncRNA genes in synchronized mammalian cell lines (HeLa, U-2 OS). Interestingly, we identified approx. 733 lncRNAs that display cell cycle stage specific expression pattern, indicating their involvement in the regulation of the respective stages of the cell cycle. To further corroborate active transcription of the lncRNAs, we intersected intervals surrounding the transcription start sites (TSSs) with ENCODE ChIP-seq data for H3K4me3, RNA PolII binding sites from 13 cell lines. Maximal enrichment of these marks at the TSSs of these genes but not at randomly shuffled control regions suggested that the assembled lncRNAs possess actively regulated promoters. So, finally, we have identified several previously uncharacterized lncRNAs that are differentially expressed during quiescence entry and exit. Furthermore, their functional characterization is in progress.

To summarize, we have generated a catalog of approximately 733 lncRNAs that display cell cycle-regulated expression dynamics. A transient knockdown experiment for a few candidates revealed severe cell cycle defects upon depletion, strongly suggesting their potential role in coordinating the cell cycle program. This is a powerful starting point to begin investigating the function of lncRNAs during cell cycle and to determine their mechanism of action. It is important to identify the protein interactors of these lncRNAs and other cell cycle regulators that associate with these RNAs towards the execution of various events during the cell cycle program.

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Studies on regulation of IL-3 receptor expression on human T helper cells

Objectives of the study

- To study the expression of IL-3R on human Th cells.
- To investigate the role of various cytokines on regulation of IL-3R expression on human Th cells.
- To study the role of IL-3 on differentiation of human Th cells.

Summary

IL-3, a cytokine secreted by activated T lymphocytes is known to regulate the proliferation, survival, and differentiation of haematopoietic cells. IL-3 has also been implicated in other biological processes such as angiogenesis and proliferation and survival of neuronal progenitor cells. Previously, we have demonstrated the novel role of IL-3 in regulation of bone remodelling. IL-3 inhibits mouse osteoclast differentiation and diverts the cells towards macrophage lineage. IL-3 also inhibits human osteoclast differentiation and diverts the cells towards dendritic cell lineage. Recently, we have also shown that IL-3 has anti-inflammatory and immunomodulatory properties and protects bone and cartilage loss *in-vivo* in arthritic mice by up-regulating regulatory T cells. These results suggest that IL-3 has regulatory role in mouse T helper (Th) cells. However, the role of IL-3 in development of human Th cells is not yet delineated. Examining the expression level of specific cytokine receptor on the cell surface is crucial for understanding the cytokine function. In the present study, we investigated the regulation of IL-3 receptor (IL-3R) expression on human Th cells.

We first examined the expression of IL-3R on human peripheral blood-derived $CD3^{+}CD4^{+}$ Th cells by FACS. We found that human Th cells lack surface

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Garima Pandey, *JRF*
Satish Pote, *Tech. Officer A*
Lekha Goyal, *DST Woman Scientist*
Amruta Barhanpurkar, *DST Woman Scientist*
Ashwini Dhamanage, *Research Associate*
Milanjeet Kour, *Research Associate*

Collaborators

Brig Yogesh Sharma, *AFMC, Pune*
Anil Ulemale, *Veterinary College, Shirwal*
Gyan C. Mishra, NCCS, Pune

expression of IL-3R, however, it was clearly seen at intracellular level. Responsiveness of naive Th cells to various stimuli such as cytokines and chemokines is regulated by T cells activation signals. Therefore, we examined the expression of IL-3R on anti-CD3 and anti-CD28 activated Th cells at 48 and 96 hours. We observed that after T cell receptor (TCR) stimulation the percentage of IL-3R positive cells was increased at 48 hours and significant increase was seen at 96 hours (Fig. 1A). The median fluorescence intensity was also increased at both the time points (Fig. 1B). These results indicate that IL-3R surface expression is dependent on TCR signaling. We further observed that TCR stimulated human Th cells activate STAT-5 in response to IL-3.

Cytokines mediated regulation of IL-3R have previously been reported in other cells such as endothelial cells, monocytes and eosinophils. Therefore, we evaluated the effect of various cytokines such as IL-2, IL-3, IL-4, IL-5, IL-7, IL-9, IL-10, IL-12 and TGF-β1 on IL-3R expression. We found that the percentage of IL-3R positive cells in activated Th cells was significantly enhanced by IL-4 and IL-7 (Fig. 2A and 2B). We also found that IL-4 and IL-7 regulate IL-3R expression independently.

Since IL-4 and IL-7 are known to be involved in differentiation of Th2 cells, we speculated that IL-3R positive cells are Th2 cells. Therefore, we differentiated naive Th cells into different Th cell subsets including Th1, Th2, Treg and Th17, and determined the percentage of IL-3R on these cells. We found that IL-3R expression was higher in Th2 cells and very low on Th1, Treg and Th17 cells. GATA-3 expression was also observed on IL-3R positive Th2 cells. We also examined the percentage of $CCR4^+CRTH\text{-}2^+$ on IL-3R positive and negative Th cells. We observed that the percentage of $CCR4^+CRTH\text{-}2^+$ cells were significantly higher in IL-3R positive fraction. These results demonstrated that IL-3R expressing cells belong to Th2 lineage. We further checked whether IL-3 could influence Th2 differentiation. We found that IL-3 in the presence of IL-4 significantly enhanced the percentage of $IL\text{-}4^+$ and $IL\text{-}4^+IL\text{-}13^+$ secreting cells. However, IL-4 alone showed no effect on $IL\text{-}4^+IL\text{-}13^+$ secreting cells. In addition, IL-3 in absence or presence of IL-4 enhanced the percentage of IL-5 secreting cells. These results indicate that IL-3 regulates differentiation of Th2 cells.

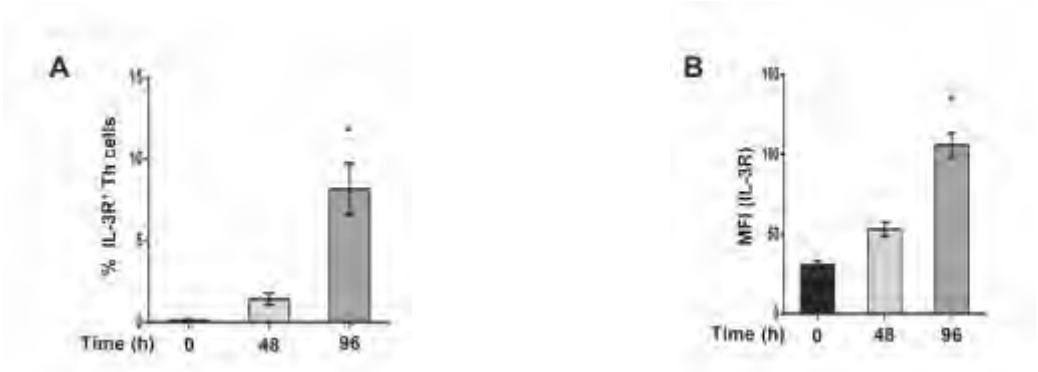


Fig. 1: IL-3R expression in resting and TCR-stimulated Th cells. Naive Th cells were activated with anti-CD3 and anti-CD28 coated activation beads for 48 and 96 hours, and percentage of IL-3R positive Th cells was evaluated by FACS (A). MFI of IL-3R expression on activated Th cells (B). Results are presented as mean ± SEM from 2-3 independent experiments, *p < 0.05 versus unstimulated cells.

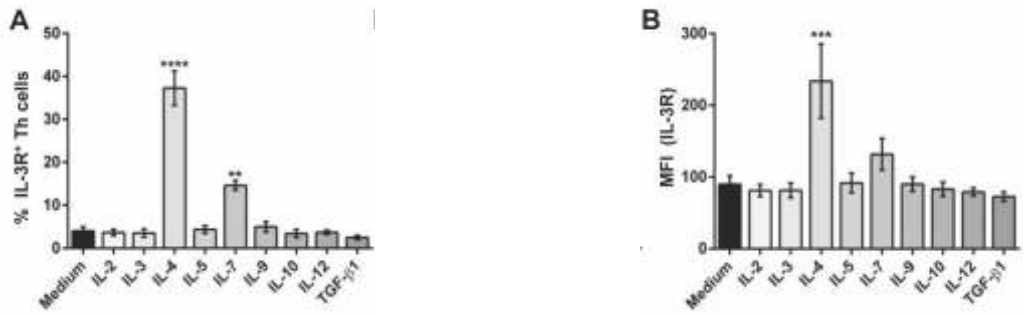
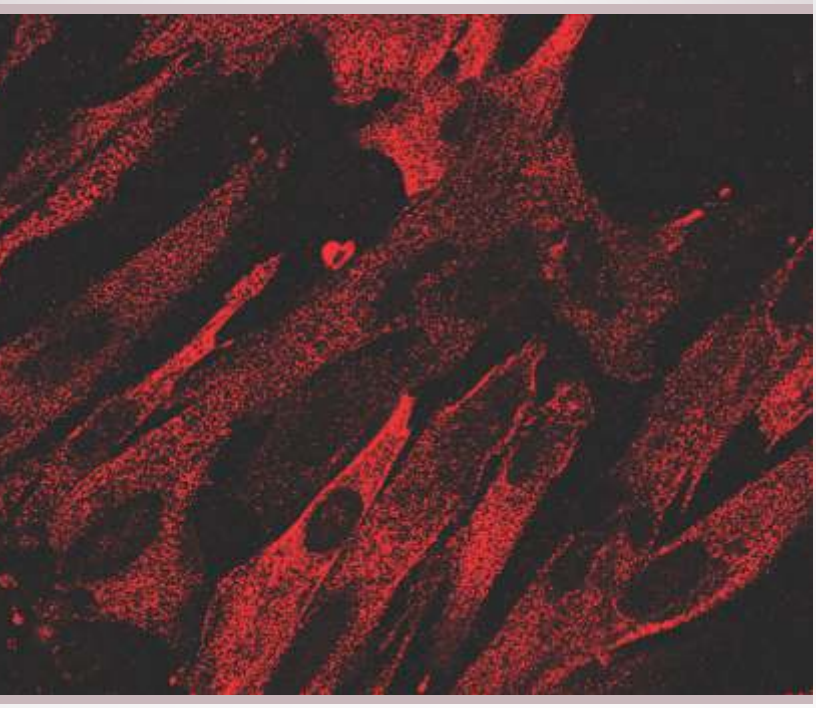


Fig. 2: Cytokine mediated regulation of IL-3R expression. Naive Th cells were activated with anti-CD3 and anti-CD28 beads and incubated with or without 25 ng/ml of each IL-2, IL-3, IL-4, IL-5, IL-7, IL-9, IL-10, IL-12 and 5 ng/ml of TGF-β for 4 days. The percentage of IL-3R positive Th cells (A) and MFI of IL-3R (B) was evaluated. Results are presented as mean ± SEM from 2-4 independent experiments. **p < 0.01, ***p < 0.001 and ****p < 0.0001 versus unactivated cells.



Support Units & Other Facilities

Experimental Animal Facility

Dr. Ramanamurthy Boppana

(Scientist In-Charge)

The Experimental Animal facility (EAF) is a core service department of the Institute providing a wide range of services in the area of Laboratory animal Experimentation for Research and Development programs. The facility is registered with the "Committee for the Purpose of Control and Supervision of Experiments on Animals" (CPCSEA) and operates in compliance with the guidelines laid down by the Committee. The mandate of the animal facility is to breed, maintain and supply laboratory animals viz. inbred and mutant mice, rats, rabbits etc. for the ongoing research projects of the Institute. The following is the list of various laboratory animals maintained at the facility:

MICE:

- BALB/cJ
- C57BL/6J
- DBA/2J
- DBA/1/J
- 129/SvJ
- FVB/NJ
- SWISS#
- BALB/c*
- NZB
- AKR#
- CF1
- CD1
- Genetically engineered mutant mice (knock-out, transgenic and mutant mice - 43 lines)

RATS: WISTAR

RABBITS: NEWZEALAND WHITE

* BALB/c with cataract mutation # Outbred

Defined procedures are followed in the maintenance of the laboratory animals.

The Team

Dr. Rahul M. Bankar
Mr. Md. Shaikh
Mr. A. Inamdar
Mr. Prakash T. Shelke
Ms.Vaishali Bajare
Mr. Mahavir Rangole
Mr. Rahul B. Kavitake
Mr. Ganesh B. Yadav
Mr. Sanjay Gade
Mr. Harshal G. Gaonkar
Mr. Dilip B. Thorat

The breeding program for the propagation of the inbred mice is planned and executed to meet the needs of Scientists of the Institute for the conduct of animal experiments. Complete scientific as well as technical support is extended as per demand to the Scientists and their group members for the conduct of experiments under Institutional Animal Ethics Committee (IAEC) approved projects.

The total number of 56 mice strains including inbred, outbred, and mutant and hybrids are being maintained at the Experimental Animal Facility. The foundation/nuclear colonies of mice are housed in Individually Ventilated Caging systems. Genetic monitoring using standard protocols for mutant mice and select microsatellite markers for the major inbred strains is carried out regularly by PCR.

As a part of human resource development, the facility conducts training/course work for the research fellows of the Institute in the area of Laboratory Animal Experimentation and Ethics. During the year 2018-19, a total of 44 fellows underwent the course which comprised of both theory and practical sessions.

Proteomics Facility

Dr. Srikanth Rapole (Scientist In-Charge)
rsrikanth@nccs.res.in

Technical Staff

Mr. M. V. Vijayakumar, *Technical officer C*

Dr. Venkateshshwarlu Naik, *Technician B*

The proteomics facility is a core service facility of the institute with an objective to provide mass spectrometric analysis of biological samples. The following is the list of various instruments available at the facility:

Orbitrap Fusion Tribrid LC-MS/MS system

Orbitrap Fusion Tribrid LC-MS/MS system (Thermo Scientific) combines the best of quadrupole, ion trap and Orbitrap mass analysis in revolutionary tribrid architecture to provide unprecedented depth of analysis and ease of use. The system enables analyzing the most challenging low-abundance, high-complexity samples to identify more compounds faster, quantify more accurately and elucidate structures more thoroughly. This system is capable of multiple dissociation techniques viz. CID, HCD, and ETD with ion trap or Orbitrap detection at any level of MS^n maximize flexibility for research applications. The system performs a wide variety of analyses, from in-depth discovery experiments to characterization of complex PTMs and comprehensive qualitative and quantitative workflows. The number of samples analyzed is approximately 638 samples including 28 external samples from April-2018 to March-2019.

4800 LC-MALDI-TOF/TOF

4800 LC-MALDI TOF/TOF system (Sciex) is a tandem time-of-flight MS/MS system combined with nano LC and robotic spotter that is used for high-throughput proteomics research. The system identifies proteins by determining accurate masses of peptides formed by enzymatic digestion. Additionally, the system can more definitely identify and characterize proteins by isolating and fragmenting a molecular ion of interest and measuring the fragment ion masses. The number of samples analyzed is 36 samples from April-2018 to March-2019.

4000 Q-Trap LC-MS/MS

AGILENT GC-MS

4000 Q-Trap LC-MS/MS system (Sciex) is a hybrid triple quadrupole/linear ion trap mass spectrometer. The system is ideal for proteomic applications, metabolomic applications and lipidomic applications. The number of samples analyzed is 96 samples including 20 external samples from April-2018 to March-2019.

Gas Chromatography Mass Spectrometry (GC-MS) system (Agilent) with 7890B GC and 5977A MSD provides unmatched sensitivity for ultra-trace analysis, and increased performance. It is highly suitable for volatile and semi-volatile compounds. GC-MS set-up is used for identifying volatile metabolites involved in cancer.

Bioinformatics and High Performance Computing Facility

Dr. Shailza Singh
(Scientist In-Charge)

The bioinformatics facility at NCCS provides access to high-performance computing resources and programming expertise. The compute infrastructure serves scientists at NCCS to master the informatics needs of their research in a proficient and cost-effective manner.

Hardware Infrastructure

SGI Altix XE 1300 Cluster
Head Node:
SGI Altix XE 270 Serve.
Dual Quad Core XEON 5620 @ 2.4GHz / 12MB cache,12GB Memory,5 x 2TB SATA Disk @ 7.2K RPM RAID 5

Compute Nodes:
SGI Altix 340 Servers
2 x HEXA Core XEON 5670 @ 2.93GHz / 12MB cache, 24GB Memory, 250GB SATA Disk @ 7.2K RPM, Dual Gigabit Ethernet Card

SGI Cluster Software Stack:
SLES Ver 11
SGI ProPack 7
SGI Foundation Software Ver 2.0
Interconnect:
24-Ports Gigabit Ethernet Switch

GPU Computing HP Proliant SL6500
2x Intel Xeon X5675 @3.06GHz/6 core/12MB L3 Cache
96 GB (8 GB x 12) PC3 – 10600 (DDR3 – 1333) Registered DIMM memory
2 x 1 TB hot Plug SATA Hard Disk @7200 rpm
Integrated Graphics ATI RN50/ES1000 with 64 MB memory
2x NIVIDIA Tesla 2090 6 GB GPU computing module

Specialized Workstations:
HP Elite 8200 CMT PC
Second generation Intel core i7-2600 processor 3.40 GHz, 8M cache, 4 cores/8 threads
Integrated 4 port SATA 6GBs controller

Integrated Intel HD graphics

HP Z800 High End Work Station (2 in number)

2x Intel Xeon E5649 6 core @2.53 GHz, 80 watt 12MB cache
5.86GTs QPI, DDR3 1333 MHz, HT Turbo
NVIDIA Quadro FX380 Graphics with 256MB memory
SATA 6 GBs controllers with RAID 0/105 & 10 support
19" LCD wide Display with Windows OS

HP Z820 High End Work Station

2x Intel Xeon E5-2690@2.9GHz, 8 core/20MB L3 cache
8 GTs QPI, DDR3 1600 HT Turbo 2 with vPro support
NVIDIA Quadro 4000 Graphics with 2GB DDR memory
SATA 6 GBs controllers with RAID 0/105 & 10 support
22" LCD wide Display with Windows OS

High End Desktop (4 in number)

HP workstations of Intel Core 2 Duo @3.00GHz with 8 GB of DDR2 memory, 320 GB of SATA storage and 19" LCD wide Display with Linux/Windows OS

HP Elite Desktop of Intel i7 processor, 3.4GHz with 16GB RAM, 2TB SATA storage and 21.1" LCD wide display with Windows 8.1 Professional OS.

Desktop Computers

Desktop computers with Intel core 2 duo processor @1.8Ghz to 2.8GHz with 2 GB to 4 GB of DRR2 memory, 160GB to 320GB of SATA storage with 17" wide LCD display and with Windows XP OS

iMAC: For running specialized software like Biojade

Printer: HP Laser jet M1136MFP, Canon Network Printer, HP laserjet pro 8000 color printer

APC UPS 10 KVA for supporting the HPCF

Software infrastructure

The Bioinformatics Facility at NCCS has procured several software for scientific research having commercial and/or academic license. These are:

Sequence analysis: BLAST, CLUSTAL-W, MEGA, Eisen

Molecular Modeling: Modeler

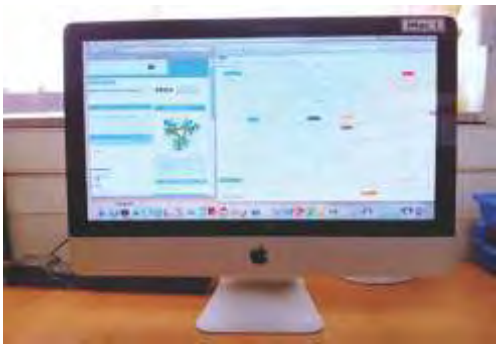
Molecular Docking: AUTODOCK, HADDOCK, ClusPro

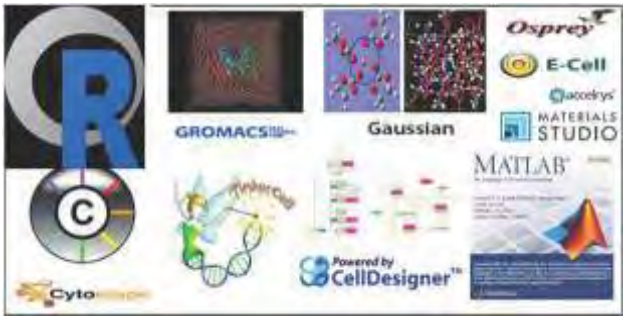
Pharmacophore Modeling: Auto Pharmacophore generation, Receptor-ligand pharmacophore generation, 3D QSAR pharmacophore generation, Steric Refinements with excluded volumes.

Network Modeling: CellDesigner

Toxicity Prediction: Molinspiration, DSSTox, PreADMET Toxicity Prediction

QSAR: Create Bayesian Model, Recursive Partioning Model, Multiple Linear Regression Model, partial least squares model, genetic function approximation model, 3D QSAR model. Intelligent QSAR using molecular fragments of interest and their





features, evaluation of descriptors from template scaffold to form relationship with the activity.

Molecular Dynamics: CHARMM, GROMACS, NAMD, MOIL

Molecular Visualization: Rasmol, MolMol, WinCoot, Swiss PDB viewer, MolScript, VMD

ab initio modeling: GAUSSIAN

Systems Biology Tools: Virtual Cell, M-cell, Cell Designer, GEPASI, Cytoscape, Osprey, E-Cell, SimBiology

Artificial Intelligence: SVM^{light} and SNNS

Material Modeling and Simulation: Material Studio 5.5

Graphs and Graphics: Sigma Plot, GNU Plot, Corel Draw and Adobe PhotoShop

Statistical packages: MATLAB and R

Workshops conducted at the Bioinformatics and High Performance Computing Facility:

1. In-house "Applications of Computational Biology" training for graduate students. This was organized to help the students to develop a computational framework for gene survey of the biological sequences, which includes structure prediction, phylogenetic analyses, motif prediction, network modeling, molecular docking, protein-protein interaction etc. The workshop helped them to derive inferences about biological mechanisms and develop hypotheses for further experimental testing.
2. Workshops are regularly conducted for the students enrolled in the PhD coursework. 48 students (from NCCS, ARI, NIV, and Departments of Biotechnology, Botany and IBB from Savitribai Phule Pune University) enrolled in the PhD Coursework-2018, received training through this programme.

   Dates: 25/9/18, 28/9/18, 5/10/18, 6/10/18, 9/10/18, 12/10/18, 4/12/18, 7/12/18, 11/12/18, 14/12/18

The training included:

1) Different types of structure representation and implications - PyMol, Chimera
2) Surface calculation and implications: Hydrophobic, charge representation
3) Secondary structure prediction
4) Structure based alignment
5) Binding pocket prediction - Castp; Glycosylation, phosphorylation sites prediction
6) Modeller - homology modeling, threading
7) Energy Minimisation
8) Validation of models - Procheck, Whatif, Verify 3d
9) Auto dock VINA

A National Level Workshop on 'Systems Biomedicine and Network Pharmacology' was organised for 25 students and faculty members from outside NCCS on 27th March 2019. This workshop, jointly organised by NCCS and NASI-Pune Chapter, was supported by DBT, NASI and Schrodinger.

Library

The Team

Mr. Krupasindhu Behera, *Technical Officer*

Mr. Rameshwar Nema, *Technical Officer*

The NCCS library is listed in the Union Catalogue of Biomedical Serials in India created by the National Institute of Science Communication and Information Resources (NISCAIR), New Delhi.

The NCCS library has an extensive collection in frontier areas of biotechnology. The library's priority is to support the research activities of NCCS. Therefore, the collection is expanded in consultation with the NCCS faculty. The library's print collections are growing by approximately 500 volumes per year. The library holds approximately fourteen thousand five hundred eighty-seven bound journals, three thousand six hundred fifteen books, and two hundred eighty-five Ph.D. theses of students of NCCS. It subscribes to twenty scientific journals and twenty-eight other periodicals in print form.

The staff and students are provided access to 734 online publications, including journals and the online book series, Methods in Enzymolgy, which are published by various publishers, including Springer, John Wiley, Nature Publishing group, Mary & Libert, Oxford, Elsevier, Science Direct, etc., through DeLCON, the online journal consortium of DBT. The library also subscribes to eight additional online journals related to research areas of interest to the NCCS faculty and students. Furthermore, the library regularly purchases books on popular science and other topics, and magazines, in English and Hindi for general reading.

The library is equipped with the Linux-based SLIM21 library software for its housekeeping operations, and Web-OPAC for online searching of the library documents. Additional facilities in the library include CD-ROMs for a number of books, journals and Ph.D. theses, and a local area network providing access to the internet for PubMed search and other associated activities.

The library personnel are involved in providing library-related information for the NCCS website (English), including library holdings, services, useful links and other relevant information. During the period under review, they have created a digital archive of the Ph.D. theses submitted by the NCCS research scholars to the University, and the NCCS publications published during the said year, which are accessible through the NCCS intranet. In addition to the above, the library also provides in-house services for scanning manuscripts and Ph.D. theses using the iThenticate antiplagiarism software, prior to their submission to journals and the Savitribai Phule Pune University. The library has also set up an open access repository for the research publications of the NCCS scientists, which is available on the following link - http://nccs.sciencecentral.in

Computer Section

Dr. M.V. Krishnasastry

(Scientist In-Charge)

The computer department provides various computing and network infrastructure. It also routinely provides support in the setup and configuration of servers, desktops, laptops, printers, scanners, software and network services, along with their maintenance.

The department provides secured network services, including the design of campus wide LAN/WAN solutions, intranet solutions, as well as providing computing services to ongoing R&D projects. It has installed two internet links, viz. 100 Mbps bandwidth from NKN and 10 Mbps from Tata communications Ltd. The internet facilities are extended to all institute users, as well as visitors to the guest house and students' hostel. The present network security system has been upgraded with the latest Sophos UTM firewall CR-1500XP and Sophos Antivirus with Intercept-X for desktops and laptops, to provide a cohesive secured environment.

Technical Support Services provided:

- Wired and wireless networking solutions & services to desktops, laptops and mobile phones.
- Wi-fi network for conferences, seminars and meetings.
- Internet connectivity to all scientists, staff and students through NKN and Tata links.
- Computer hardware infrastructure procurement, installation, configuration and maintenance.
- Web services, including design and maintenance of the NCCS intranet and website, and its management.
- User support services, including new desktop specifications, software and hardware installations, printers, scanners and all other computer related devices.
- E-mail service to all staff members.
- Technical support for video conferencing / SKYPE / DROPBOX / VPN access.
- Management of virtualised high performance servers for hosting services like WWW, DNS, E-mail, DHCP and Proxy.

The Team

Mr. Rajesh Solanki *(Technical Officer)*

Mr. Shivaji Jadhav *(Technical Officer)*

Mrs. Rajashri Patwardhan *(Technical Officer)*

Mrs. Kirti Jadhav *(Technical Officer)*

- Network management and maintenance of high speed routers, switches and WL access points.

New Initiatives:

1. Installation and configuration of CISCO core switch - Nexus 9300 completed

The existing 3COM core switch 7754 was installed in 2007-08 and it has reached the end of its life. A new core switch i.e. Nexus 9300 from Cisco Systems has been installed and configured with 3 software modules, namely Cisco Enterprise Management for LAN, CISCO Prime Infrastructure for complete lifecycle management of converged wired and wireless network, and Cisco ISE for network device administration.

2. Configuration of New Domain environment

A new Virtual machine with Windows 2016 server has been configured as an active directory domain controller. The new domain 'nccsdbt.gov' has been established. All the desktop PCs of the institute were brought into this domain. This helps in centralized configuration and management of all PCs. Desktops with non-compatible operating systems were upgraded to the Win-10 Pro. OS for Domain configuration.

3. Animal House Fiber Connectivity restored

A new single mode fiber optic cable has been laid and configured, connecting the animal house to the server room.

4. Additional Sophos Antivirus Licenses installed

Additional 100 numbers of Sophos Antivirus licenses with Intercept -X have been installed with the software on all desktops and laptops.

5. Server for Salary software

A separate desktop server for the 'Saral PayPack' Salary Software has been setup for preparation of salaries. The Paypack software takes care of staff salary process that includes TDS and EPF, NPS deductions. Initial training to use this software has been given to Mrs. Smita Deshmukh of the Administration Section

6. Renewal of Tata Internet Connectivity

The 10 Mbps (1:1) Internet Leased Line used for E-mail / DNS traffic from TATA Communications was renewed for 1 year i.e. 2018-2019.

General Assistance

Regular maintenance and up-dating of the NCCS website and intranet website is done by the computer section. This section also uploads tenders / corrigenda on the CPP Portal. Several operating systems and common application software were installed / updated on user computers at NCCS. These include MS Office 2010, Adobe Suite X, Sigma Plot Suite 12.0 and Reference Manager 12.0. This section also provided network configuration and software support during installation of LED 5 display screens on the NCCS campus, to display information about the institution, including seminar / event / talk notifications.

Technical support provided

- 10th Annual meeting of Proteomics Society, India (PSI) & International Conference on Proteomics for Cell Biology and Molecular Medicine (12-14 December 2018).
- National Level Workshop for Image Analysis (6-8, March 2019).
- Emerging Trends in Disease Model Systems (25-26th March, 2019).
- Parliamentary Committee visit in April 2018.
- NCCS YouTube Channel for streaming of NCCS Public Talks etc.

Other Facilities

1) FACS Core Facility

The Team

- **Dr. Arunkarthick S.** *(Facility In-Charge)*
- Mr. Amit Salunkhe *(Technician C)*
- Ms. Ashwini Kore *(Technician B)*
- Mr. Dnyaneshwar Waghmare *(Technician B)*
- Mr. Atul Khirwale *(Operator provided by BD and posted in NCCS under BD-NCCS STEM CELL CoE)*

FACS Facility Instrument Installation and Configuration Details

The FACS Core Facility has a total of six instruments, out of which three are analysers and three are sorters. All six flow cytometer machines are of Becton Dickinson (BD).

Instrument Name	Instrument Sr. No.	Date of Installation	Lasers & Colours
FACS Calibur	E97500465 (Nov.2006)	12/06/2007	2 Lasers, 4 Colours (Blue 488 nm, Red 633 nm) 2b-2r
FACS Canto II (Old)	V96300124 (Oct.2006)	12/06/2007	3 Lasers, 8 Colours (Blue 488 nm, Red 633 nm, Violet 405 nm) 4b-2r-2v
FACS Canto II (New)	V96301326 (Feb.2011)	31/05/2011	3 Lasers, 8 Colours (Blue 488 nm, Red 633 nm, Violet 405 nm) 4b-2r-2v
ARIA III SORP	P6BO00001 (Feb.2011)	17/03/2011	5 Lasers, 16 Colours (Blue 488 nm, Red 640 nm, Violet 405 nm, UV 355 nm, Yellow Green 561 nm) 3b-2r-4v-3uv-4yg
ARIA II SORP	P5I400001 (Feb.2009)	28/04/2010	(SP)4 Lasers, 11 Colours (Blue 488 nm, Red 640 nm, Violet 405 nm, UV 355 nm) 5b-2r-2v-2uv
ARIA III STD	P9O600008 (Feb.2011)	11/11/2011 (Upgraded & installed)	5 Lasers, 11 Colours (Blue 488 nm, Red 633 nm, Violet 405 nm / UV 375 nm, Yellow Green 561 nm) 3b-2r-4yg-2violet/yg

The usage of the six instruments over the period under consideration is summarized below:

IMMUNOPHENOTYPING & CELL CYCLE analysis:

Equipment	Surface / Intrace-llular staining	DNA Cell cycle	CBA flex	CBA	After Office Hrs.	Total Samples Acquired
FACS Calibur	811	3130	–	–	–	3941
FACS Canto II (Old)	6420	12	–	–	4211	11643
FACS Canto II (New)	9373	10	–	229	–	9612

STERILE SORTING:

EQUIPMENT	SORTING	ACQUISITION **
FACS AriaII SORP	252	775
FACS Aria III SORP	229	876
FACS Aria III Standard	260	680

** Includes analysis of samples that require UV laser, as we do not have UV analyzers.

Samples from external users:

Since the workload of samples from external users has increased, NCCS has made a policy and has been charging users outside NCCS for their samples since June 2012. The charges are lower for academic and research institutes than those for private organizations. Institutes / companies like Rasayani Biologies Pvt. Ltd., IISER Pune & IRSHA utilized this facility from April 2018 - March 2019. Around 411 samples were acquired for Surface / Intracellular staining and DNA cell cycle analysis.

Other activities of the FACS core facility

a) FACS Canto-II training:

This facility organized in-house training in batches on Canto-II during the period under report.

35 students from NCCS received training during three sessions: 22-23 March 2018, 3-4 May 2018 and 28-29 May 2018. 26 students from NCCS received training during three subsequent sessions: 30-31 August 2018, 17-18 September 2018 and 15-16 November 2018.

b) Workshops organized:

The facility organized a workshop on the Attune Nxt Flow cytometer, in association with personnel from Invitrogen during 21-25 May 2018. 18 people from NCCS participated in this workshop.

c) Technical Seminars Organized:

The FACS facility organized three technical seminars during this year.

Sr. No.	Date	Details of the demonstration session
1	21/05/2018 to 28/05/2018	Demonstration of 'Attune Nxt Flow cytometer' by Invitrogen.
2	13/11/2018 to 20/11/2018	Demonstration Hands-on workshop on "Imaging Flow cytometer - AMNIS MARK II" by Merck Life Science Pvt. Ltd
3	01/03/2019	Demonstration of BD Rhapsody Express workflow (part of BD Rhapsody single cell analysis system).

e) National Science Day: During the 'open day' organized at NCCS on the National Science Day (28 February, 2019), the FACS facility organized a demonstration of FACS machines, and displayed a poster entitled 'NCCS Flow Cytometry Core Facility, for the benefit of the visitors.

f) Bioplex Machine shifting: The Bioplex instrument from Dr. Giridhari Lal's laboratory was recently shifted to FACS core Facility.

g) Parliamentary Standing Committee's visit to the FACS Facility

Members of Parliament (MPs) from the Hon. Parliamentary Standing Committee for Science and Technology learning about the instruments at the FACS facility and their applications, during their visit to NCCS on 27 April 2018.

2) Bio-Imaging facility

The Team

Dr. Arunkarthick S. *(Facility In-Charge)*

Dr. Ashwini Atre, *Technical Officer A*

Mrs. Trupti P. Kulkarni, *Technician B*

Ms. Ketakee Pawar, *Laboratory Manager*
(Pune Bio-Cluster Project)
Ms. Leena Thomas, *Laboratory Associate*
(Pune Bio-Cluster Project)

The Bio-imaging facility has three scanning confocal laser microscopes, which includes Zeiss LSM 510 Meta, Olympus FV10i and Leica TCS SP5 models. All the systems are inverted microscopes and have a wide range of lasers. The systems can be used for doing FRET, FRAP, 3D imaging and reconstruction and live cell imaging, which are required for most cell biology research. All three instruments are used by in-house users as well as by users from neighbouring organizations.

i) Zeiss LSM510 META :-

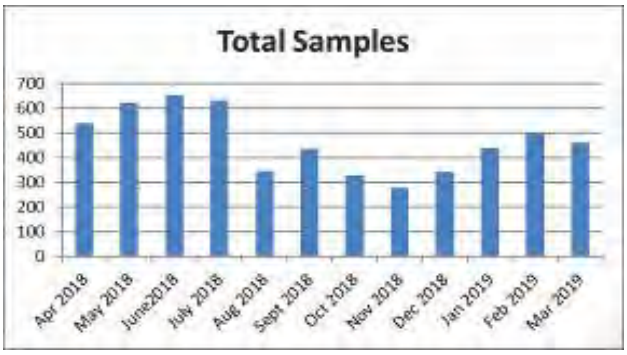
Advanced Spectral Confocal Microscope, Zeiss LSM510 META:This system comprising of fully motorized and computer controlled Inverted Fluorescence microscope is used for confocal imaging regularly. The Lasers available are Blue Diodelaser (405 nm), multi-line Argon ion laser (458/477/488/514 nm), 543 nm He-Ne and 633 nm He-Ne. The spectral detect or permits separation of upto eight emission signals, even if the fluorescence spectra are strongly overlapping.

ii) Leica SP5 II :-

This is a high-end Broadband Confocal Laser Scanning Microscope with 3 PMT's, 2 Hybrid detectors and AOBS technology equipped with CO_2 incubator, fully motorized, automated and computer controlled microscope Leica DMI 6000. The Lasers are Blue Diode Laser 405 nm, Argon ion Laser with 458/488/476/496/514 nm lines, DPSS 561 nm, He-Ne 594 nm and He-Ne 633 nm with incubation chamber for live cell experiments as well as FRET and FRAP experiments. The software for Confocal imaging 3D imaging and reconstruction, Time lapse, colocalization, FRET (SE & AB), FRAP are also available.

iii) Olympus FLUOVIEW FV10i :-

The FLUOVIEW FV10i microscope from M/s Olympus has a compact design and does not require a dedicated darkroom. This is an easy to use and self-contained confocal microscope equipped with four lasers [405, 473, 559 and 635 nm].



Usage of Microscopes during 2018-19:

The numbers of samples imaged during this year were approximately 5518 in-house, plus 39 samples received from various other institutes. The above graph shows the month wise details of number of samples imaged during last year in NCCS confocal microscopy facility.

Other activities of the Bio-Imaging Facility:

a) Workshops / Training Programs Conducted:

- Training on 'Confocal Fluorescence Microscope' was imparted to staff from the D.Y. Patil University. 14th March, 2019. (No. Of Participants: 5).
- A National Level Hands-on Training Workshop on 'Microscopy Image Analysis' was organized under the aegis of the Pune Bio-Cluster Project. 6 - 8 March, 2019. (No. of Participants: 25).
- Training Workshop on 'Light Microscopy': Zeiss LSM 510 Meta Confocal laser scanning microscope, Inverted microscope & Apotome Microscope. 7 – 9 August, 2018. (No. of Participants: 18).

b) Technical Seminars: Nineteen technical seminars were organized during this year.

c) Demonstration of Microscopes: Demonstration of five different high-end microscopes was organized during the said year, as listed below.

Sr. No.	Date	Details of the demonstration session
1	17/09/2018 to 28/09/2018	The demonstration of Olympus FV3000 Confocal Laser Scanning Microscope system.
2	03/10/2018	Demonstration of Cilika digital microscope.
3	11/10/2018 to 19/10/2018	Demonstration of High Content Analysis System: Invitrogen CellInsight HCS CX7 LED
4	26/11/2018 to 07/12/2018	The demonstration of Nikon A1R-HD Confocal Microscope.
5	17/12/2018 to 05/01/2019	Demonstration workshop of ONI - Nanoimager (Super Resolution Microscope).

d) **Image analysis training:** The bio-imaging facility provided training to students regarding post- acquisition analysis of images and data using the ImageJ, IgorPro and Matlab softwares.

e) **Planning for a new Bio-Imaging Facility:** The team from the bio-imaging facility have been working towards getting the new microscopy facility set up. They are in process of ordering new high-end microscopes like Multiphoton Fluorescence Microscope, Spinning Disk High resolution Microscope, Super resolution microscopes and High Content Image Analysis system, as well as renovations, ordering of furniture and other necessary items, etc.

f) Outreach:

- **National Science Day:** During the 'open day' organized at NCCS on the National Science Day (28 February, 2019), the bio-imaging facility organized a demonstration of microscopes available at the facility for the visitors. They were shown interesting cell images and videos acquired with the microscopes, and were given information about the microscopes and their features. Additionally, personnel from the companies, Zeiss, Leica and Olympus, were invited to display their microscopes at NCCS to further educate the public about the different types of microscopes available.
- Dr. Arunkarthick conducted a workshop on 'Quantitative Microscopy Image Analysis' for B.Sc & M.Sc students and faculty members, under the Edu-Bridge program at the J. B. College of Science, Wardha, during 22-23rd February 2019.
- The bio-imaging facility participated in the open day organized at NCCS, as a prelude to the 4th India International Science Festival (IISF-2018), on 21st September 2018.

3) DNA sequencing facility

The Team

Dr. Yogesh Shouche (Facility In-Charge)

Dr. Abhay Bajaj, *Scientist In-Charge, NCMR*

Dr. Sarang Satoor, *Technical Officer*

Mr. Mandar Rasane, *Technician*

Mr. Vikas Patil, *Technician*

The central sequencing facility of NCCS is located at the National Centre for Microbial Resource (NCMR) and houses two instruments from Applied Biosystems (3730 and 3730xl), along with sequence and data analysis software. This facility caters to the needs of research institutions and industrial clients across the country. The facility offers services related to sequencing of plasmids, PCR products and cloned inserts; primer walking; and genotyping and fragment analysis in addition to Ribosomal RNA (rRNA) gene of bacteria/Internal Transcribed Sequence (ITS) of fungi for molecular identification; to researchers from NCCS and other organizations. NCMR offers this sequencing service for identifying bacteria, archaea and fungi using respective universal primers for each type of organism. Additionally, the facility serves as the back-bone of culture authentication and identification for NCMR's preservation activities.

Over the year 2018-19, nearly 39928 sequencing reactions were run on the machine. The facility provided support to the internal institutional research activity by delivering 20909 sequencing reactions. 418 services (5910 reactions) against payment were provided to 109 different academic and research institutions across the country. Bacterial identification using 16S rRNA gene sequencing and fungal identification using the ITS/18S/LSU region sequence were mainly performed. For the identification of bioprospection cultures stored in the biobank at NCMR, 4625 cultures were processed. Also, 1408 cultures (8485 reactions) were validated for general deposit in the culture collection during this year.

a) Name of the machine : ABI 3730XL DNA Analyzer.
b) Number of samples (reactions) run on the machine during the said period (416 96-well plates): ~ 39928.
c) No. of in-house users: 29.
d) No. of extramural users who benefited: 109 different institutions / universities across the country.

4) Protein crystallization and X-ray diffraction facility

The Team

Dr. Radha Chauhan

Dr. Janesh Kumar

A new state of the art X-ray diffraction facility for single crystals was setup in July 2018. This facility is equipped with a Rigaku FRX generator with a HyPix 600 detector and an Oxford cryojet cooling system. This facility is also capable of screening crystals directly from crystallization plates. Additionally, a sophisticated protein crystallization facility is being setup with capabilities of protein crystallization at different temperatures, robotic crystallization of proteins, including membrane proteins, stereomicroscope for visualization, and various tools for freezing protein crystals in liquid nitrogen for either in house X-ray diffraction data collection or at a synchrotron.

5) IVIS Imaging System

The Team

Dr. Gopal C. Kundu *(Facility In-Charge)*

Dr. Mahadeo Gorain, *Technician.*

The IVIS imaging system facility is a common central facility. The instruments at this facility provide bioluminescent and fluorescent imaging of cells, as well as whole small animals under in-vitro and in-vivo conditions. The IVIS imaging instrument was used by more than 22-25 research scholar and scientist in various laboratories in this institute, and

collaborators in different research institutes. The scholars used bioluminescence as well as fluorescence imaging for different strains of mice (NOD/SCID/ NUDE/ C57/Balb/C etc), as well as 1.5 ml eppendorf tubes and different type of tissue culture plates (i.e. 96 well, 24 well and 12 well etc), for in-vitro studies.

The Xenogen IVIS-Spectrum System is capable of imaging bioluminescence and fluorescence in living animals. The system uses a novel in-vivo biophotonic imaging to use real-time imaging to monitor and record cellular and genetic activity within a living organism. A light-tight imaging chamber is coupled to a highly-sensitive CCD camera system.

This IVIS Imaging System includes a custom lens with a 5-position carousel and adjustable field of view (FOV) of 4-26 cm, more uniform light collection, and improved resolution with single cell sensitivity for in-vitro use. An integrated fluorescence system and 24-position emission filter wheel allow easy switching between fluorescent and bioluminescent spectral imaging, while a laser scanner provides 3D surface topography for single-view diffuse tomographic reconstructions of internal sources. A 25 mm (1.0 inch) square back-thinned CCD, cryogenically cooled to -90°C (without liquid nitrogen), minimizes electronic background, and maximizes sensitivity. This camera system is capable of quantitating single photon signals originating within the tissue of living mice. Up to five or six mice can be imaged simultaneously and an integrated isoflurane gas manifold allows rapid and temporary anesthesia of mice for imaging.

Standard filter sets for IVIS Imaging System

Fluorescence Filters

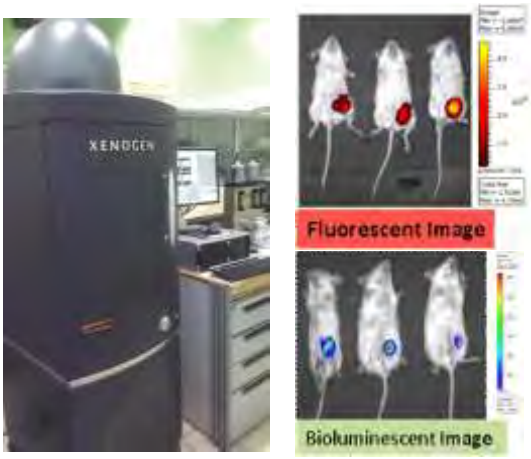
Set	Name	Excitation (nm)	Emission (nm)
1	GFP	445-490	515-575
2	DsRed	500-555	575-650
3	Cy5.5	615-665	695-770
4	ICG	710-760	810-875

Spectral Imaging Filters

Set	Excitation (nm)	Emission (nm)
5	560 nm	550-570
6	580 nm	570-590
7	600 nm	590-610
8	620 nm	610-630
9	640 nm	630-650
10	660 nm	650-670

Benefits and Features:

- High-sensitivity in vivo imaging of fluorescence and bioluminescence
- High throughput 6 mice) with 26 cm field of view
- High resolution (to 60 microns) with 3.9 cm field of view
- Dual 12-position emission filter wheels (24-position total) and 12-position excitation wheel
- A set of four filter pairs for fluorescent imaging come standard with the instrument, in addition to a set of four background filters for subtraction of tissue autofluorescence
- 25 x 25 cm alignment grid on the imaging platform ensures consistent accurate placement of animals for imaging
- Spectral imaging filters that acquire images at different wavelengths (ranging from 560 nm to 660 nm) facilitate 3D diffuse tomographic reconstruction & determination of the
- Depth and location of a bioluminescent reporter
- Heated animal shelf (up to 40˚ C)
- NIST traceable absolute calibrations
- Class I Laser Product



IVIS Imaging System

6) Central Sterilization Facility

The Team

Dr. Mohan Wani *(Facility In charge)*

Suresh Basutkar, *Technical Officer C (Lab)*

Narayan Kadlak, *Technician C*

Pramod Surve, *Technician C*

Gayatri Sagare, *Asst. Technician*

Kailash Bhandalkar, *Helper A.*

This facility is an infrastructure service department of the institute. It provides in-house services, such as washing, packing and sterilization of all the glassware and other research material, to all the research laboratories, the cell repository, the media section and the other service departments. It also supplies high-grade distilled water to all the sections of the institute. In addition to this, some technical staff members are also involved in the safe disposal of radioactive and biohazardous waste material.

Centre of Excellence for 'National Centre for Microbial Resource (NCMR)'

Yogesh Shouche

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Lab Members

Dilip Ranade, *Senior Consultants*
Milind Patole, *Senior Consultants*
Tapan Chakrabarti, *Senior Consultants*
Abhay Bajaj, *Scientist B*
Aehtesham Hussain, *Scientist B*
Amaraja Joshi, *Scientist C*
Amit Yadav, *Scientist C*
Avinash Sharma, *Scientist C*
Dhiraj Dhotre, *Scientist C*
Dhiraj Paul, *Scientist B*
Kamlesh Jangid, *Scientist D*
Mahesh Chavadar, *Scientist B*
Neetha Joseph, *Scientist C*
Omprakash Sharma, *Scientist D*
Praveen Rahi, *Scientist C*
Rohit Sharma, *Scientist C*
Shrikant Pawar, *Scientist C*
Tushar Lodha, *Scientist B*
Lucky Thakkar, *Technical Officer A*
Sonal Chavan, *Technical Officer A*
Abhijeet Pansare, *Technician B*
Ajay Paul, *Technician B*
Archana Suradkar, *Technician B*
Dharmendra Kumar, *Technician B*
Kunal Jani, *Technician B*
Madhuri Vankudre, *Technician B*
Mahesh Gudade, *Technical Assistant*
Mahesh Sonawane, *Technician C*
Mandar Rasane, *Technician C*
Mitesh Khairnar, *Technician B*
Nitin Narawade, *Technician C*
Prachi Karodi, *Technician B*
Shalilesh Mantri, *Technician B*
Shraddha Vajjhala, *Technician B*
Sonia Thite, *Technician C*
Sunil Dhar, *Technician B*
Swapnil Kajale, *Technician B*
Tushar Ghole, *Technician B*
Umera Patawekar, *Technician B*
Varinder Singh ,*Technician B*
Vikas Patil, *Technician B*
Vikram Mohite, *Technician B*
Vipool Thorat, Technician B
Vishal Thite, Technician C

Objectives

- The Complete characterization of the existing collection of 1.8 lakh isolates so as to increase their utility for investigators.
- To develop an infrastructure to facilitate services of the highest standard, such as the supply of authentic microbial cultures, identification of microorganisms, a deposit of microorganisms, their long-term protection and other related areas.
- To serve as a repository of meta-omics libraries and to develop and maintain a database of information about the "not yet cultured" organisms generated from high throughput meta-omics studies.
- To serve as International Depositary Authority for deposit of Micro-organisms under the Budapest Treaty for protection of intellectual property rights.
- To serve as Designated National Repository under the Biological Diversity Act 2002 of India.
- Stimulation of deposit of strains subject to publication and research in India to protect national investments.
- To become a global leader in the collection of microbial resource, its maintenance and ex situ conservation including patent cultures and thus safeguarding the enormous microbial diversity of our nation.
- Networking to increase the range of resources and expertise available to Indian researchers.
- To develop quality manpower with creative abilities in microbiology/ microbial biotechnology / technology management by providing both long and short-term training courses and workshops involving experts from across the globe.
- To undertake research in the relevant areas of microbial ecology and systematics so as to strengthen the services.

Summary

More than ~2,00,000 bacterial cultures collected from various ecological niches were preserved as safe deposit cultures. SOPs were designed and followed on a

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Sachin Pawar, Office Assistant
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Vishal Paygude, Office Assistant
Yogesh Kalbhor, Officer A
Anusha Priya, Junior Research Fellow
Ashwini Hagir, Project Assistant
Diptaraj Chaudhari, Junior Research Fellow
Gajanan Mane, Junior Research Fellow
Harshada Paralikar, Project Assistant
Kiran Kirdat, Junior Research Fellow
Meghana Gaikwad, Project Assistant
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Pratiksha Taskhedkar, Junior Research Fellow
Sayali Dongare, Junior Research Fellow
Shalaka Patil, Junior Research Fellow
Vikas Ghattargi, Project Assistant
Krishna Kumar Yadav, Junior Research Fellow

Collaborator(s) – National
Dr. Govind Rao, *Indian Agricultural Research Institute, New Delhi*
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Dr. Kamlesh Shukla, *Pt. Ravishankar Shukla University, Raipur*
Dr. Krishnappa Rangappa, *ICAR Research Complex for NER Region, Umiam*
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Dr. Nitin Adhapure, *Vivekanand Arts, Commerce and Science College, Aurangabad*
Dr. R. Sundarraj, *Institute of Wood Science and Technology, Bangalore*
Dr. Rajesh Barsaiya, *Radhav Agriculture H.S. School, Narsinghpur*
Dr. Shiv Mohan Singh, *National Centre for Antarctica and Ocean Research, Goa*
Dr. Vijay Tripathi, Jacob Institute of *Biotechnology and Bioengineering, Naini*
Dr. Yadvinder Singh, *Sri Guru Granth Sahib World University, Fatehgarh Sahib*

Collaborator(s) – International
Dr. Dalia Sukmawati, *University of Jakarta, Indonesia*
Dr. Eddie Cytryn, *Institute of Soil, Israel*
Dr. Rakesh Kumar Singh, *Florida State University, USA*
Dr. Ashvini Chauhan, *Florida Agricultural and Mechanical University, USA*

Collaborator(s) – Industry
Dr. Supriya Sarkar and Dr. Priyanka Saha, *Tata Steel, Jamshedpur, India.*

routine basis for the periodic preservation and passaging. They have been categorized on the basis of their screening for different bio-active compounds. All 7,938 pure 'Three Star' cultures have been identified either by 16S rRNA gene sequencing or by MALDI-TOF mass spectrometry. In addition, all normal category cultures are being processed for identification by 16S rRNA gene sequencing or MALDI-TOF since September 2013. Since then, a total of 24,179 (13,833 till 2017) normal cultures have been identified by 16S rRNA gene sequencing and 46,413 (30,501 till 2017) by MALDI-TOF analysis. Out of these cultures; total 10,468 cultures were identified by 16S rRNA sequencing in 2018 and 15,464 cultures were identified by MALDI-TOF.

The screening activity of 175,000 extracts led to the discovery of 16,000 bioactive extracts in different therapeutic areas, among which 1,000 bioactive microbial extracts randomly selected to represent each ecological niche, were subjected to fractionation. The crude ethyl acetate extracts for each isolate were subjected to de-replication for novel molecules or molecules with novel activity. Fractions with known compounds and known reported activities were omitted from further studies. During the process, 235 compounds were dereplicated and 51 bioactive compounds were purified. Eighty-two other structures have also been postulated from only 1000 of these active extracts. The exercise led to discovery of one Novel Chemical Entity (NCE), identification of known three compounds with novel activities (novel chemical activity (NCA)) and four probable NCEs (Figure 02).

NCMR actively processes microbial samples received under the various categories of deposits, identification and characterization services for the researchers in academia and industry across the globe. Cultures deposited under 'General Deposit' category are listed in NCMR catalogue and are accessible to public for academic and scientific research. The number of these publicly available cultures is growing steadily over the period of time since it started in 2010 and have cross the mark of 3200, out of which over 3000 are bacterial cultures and 730 are fungal cultures. In year 2018, NCMR accessioned 553 bacterial and 156 fungal cultures. The cultures deposited under 'Safe Deposit' category is maintained at NCMR under confidentiality and security agreement with depositor. So far, NCMR holds 52 cultures under 'Safe Deposit' category, out which 19 cultures were received in year 2018-19. Microorganisms deposited in an IDA fulfil the requirement of

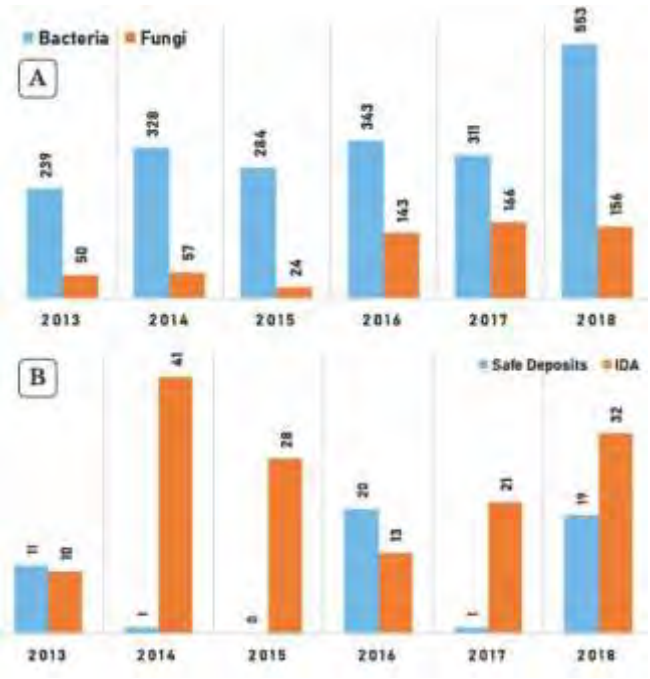


Fig. 1: Number of 'General Deposit' Cultures accessioned (A) and Number of 'Safe' and 'Patent' cultures (B) in 2018.

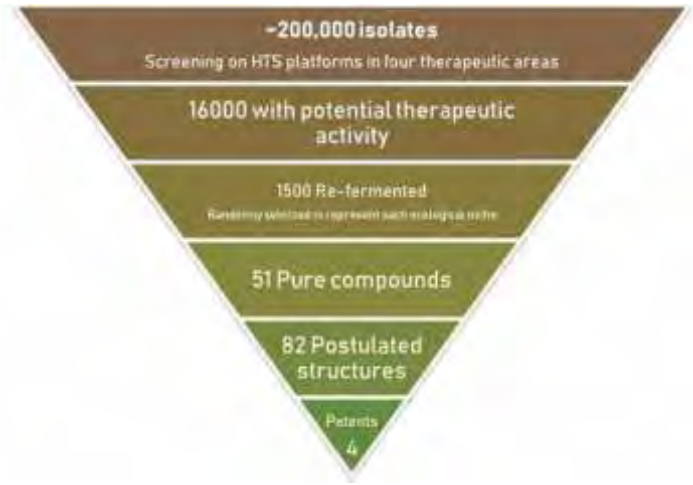
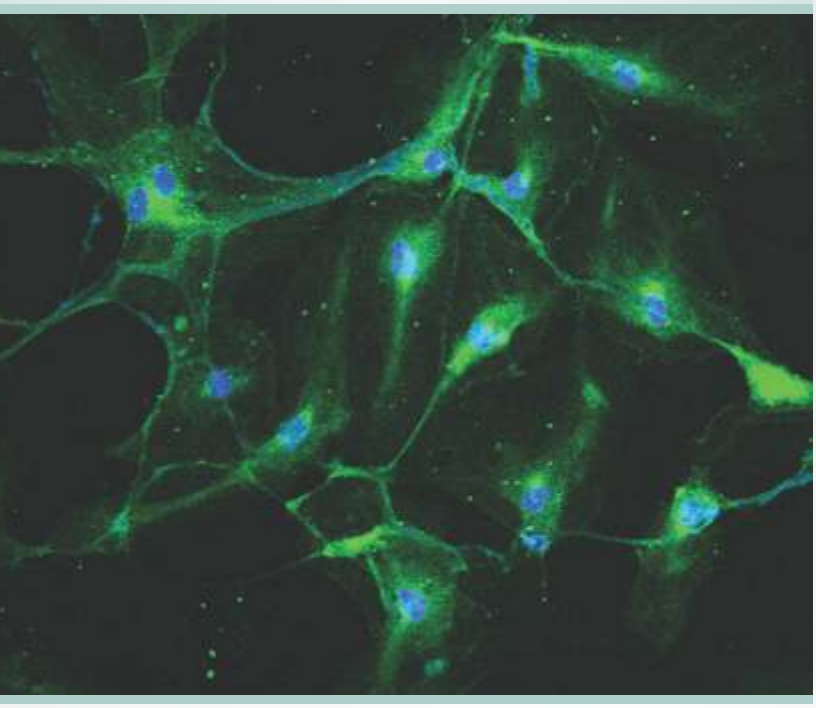


Fig. 2: Current Status of Leads obtained from Bioprospecting Project

deposit for the purposes of patent procedures in all states' signatory to the Budapest Treaty. So far, NCMR has accessioned 152 IDA cultures and 32 deposits were accessioned in year 2018-19. NCMR provides range of services involving identification of microbes including bacteria, archaea and fungi. Over One Crore rupees were earned through the inhouse facilities and expertise. NCMR has started supplying lyophilized and active stabbed cultures of bacteria and fungi to its customers. In 2018, total 394 bacterial and 150 fungal culrures were supplied to various customers. Additionally, as part of DBT's initiative to share the microbial cultures for the screening of additional bioactive compounds, NCMR has supplied 4369 Cultures to Dr. D. Y. Patil University, Pune and 8742 cultures to MES Aabasaheb Garware College, Pune. Last year, NCMR supplied 4300 bacterial cultures to DBT funded project at North Maharashtra University (NMU). NCMR Scientists are publishing papers in various aspects of Microbiology since 2009 and 34 research papers are published in 2018. Total 50 novel taxa have been published by NCMR since 2009, 4 of which were published in the 2018. As a part of research in microbial genomics and taxonomy, NCMR completed draft genomes of 20 bacterial species including one *Candidatus* bacterial species. Currently there are 12 extramural projects running in NCMR funded by either DBT, SERB-DST, Gate Foundation. Since 2016, NCMR faculty have been awarded project grants of ₹467.82 lakhs in total. In 2018, total 7 projects were sanctioned as compared to 2 in 2017 and 3 in 2016.



Other Information

Publications / Book Chapters / Patents

Publications of NCCS faculty

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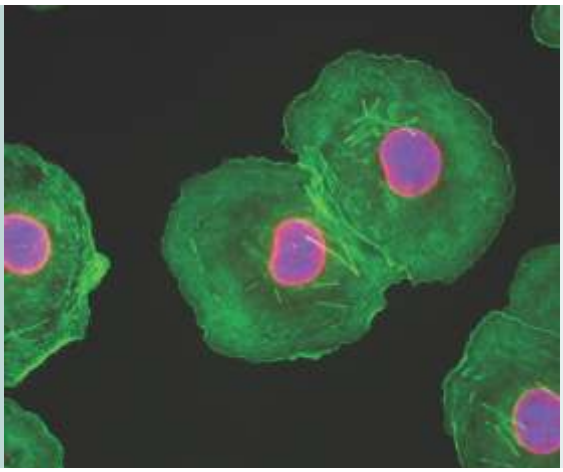
Patent Applications Filed

Sr.No.	Title	Inventors	Applicant	PCT/ Country	Patent No. (Filed)	Date of Filing
1	Novel Antiviral Drug Compunds and Composition Thereof	Debashis Mitra	NCCS	India	201821018105	15.05. 2018
2	A Novel Anti-Cancer Combination	Padma Shastry	NCCS	India	201821033349	05.09. 2018
3	A Novel Method for Detection of Cancer	Gopal C. Kundu, George F. Weber	NCCS	India	201821040459	26.10. 2018
4	Chimeric Transcripts and Peptides as Method of Diagnosis and Prognosis of High-Grade Serous Ovarian Cancer	Sharmila Bapat	NCCS	India	201821046394	07.12. 2018
5	A Novel Therapetic Intervention for Osteoporosis	Mohan R. Wani	NCCS	USA	16/208,322	03.12. 2018
6	A Novel Chimeric Protein Kinase C as an Immunomodulator	Shailza Singh, Dipali Kosey, Milsee Mol	NCCS	PCT	PCT/IN2019/050115	15.02. 2019
7	A Novel Anti-Cancer Combination	Dipti Athavale, Manoj K. Bhat	NCCS	India	201821039548	18.10.2018



Awards / Honours

Awards / Honours - NCCS Faculty

Sharmila Bapat

- TATA Innovation Fellowship from the Department of Biotechnology (April 2017 - March 2020).
- Nominated and elected as Council Member, Indian Academy of Sciences, Bangalore (2019 - 2021).

Samit Chattopadhyay

- J C Bose National Fellowship (extension).
- Took over the additional charge of Director CSIR-North East Institute of Science and Technology (NEIST), Jorhat, June 30, 2018.
- Convener, Sectional Committee, Indian National Science Academy (INSA) (2017 onwards).

Gopal C. Kundu

- Elected as Associate Editor, Molecular Cancer (IF 10.69) (2015-till date).

Girdhari Lal

- SwarnaJayanti Fellowship 2018, from Department of Science and Technology, Ministry of Science and Technology, Government of India.
- Elected as Vice President (West Zone) of Indian Immunology Society.

Nibedita Lenka

- Chairperson, Institutional Ethical Committee, OCT Therapies & Research Pvt. Ltd. Mumbai.
- Mentor, AICTE approved QIP Workshop on 'Recent trends in Biotechnology Related to Tissue Engineering', IITM, Chennai. January 7-11, 2019.

Debashis Mitra

- J C Bose National Fellowship.

Bhaskar Saha

- J C Bose National Fellowship.

Arvind Sahu

- Elected as a Fellow of the Indian Academy of Sciences, Bengaluru, India.

Manas Kumar Santra

- National Bioscience Award for Career Development, 2019, Department of Biotechnology, Government of India.

Vasudevan Seshadri

- Special recognition award for the talk on 'Development of insulin resistance animal models to understand diabetes', delivered at the 3rd International Diabetes Summit 2019, Pune.

Mohan Wani

- TATA Innovation Fellowship 2018 of the Department of Biotechnology (DBT), Govt. of India, New Delhi.
- Task Force Member, Expert Group on Stem Cell Research and Therapy, Indian Council of Medical Research (ICMR), New Delhi, 2018-2021.
- Task Force Member, Technical Expert Committee on Stem Cell and Regenerative Medicine, Department of Biotechnology (DBT), New Delhi, 2018-2021.

Awards / Honours - Other Scientists, Postdoctoral Fellows, Students & Technical Staff

- **G. C. Mishra** - NASI Platinum Jubilee Chair Distinguished Professor.
- **Jyoti Singh** - Wellcome Trust-DBT /IA Early Career Fellowship.
- **Abir Mondal** (Dr. A. Shiras's group): Best presentation award & travel fellowship; EMBO EMBL meeting on Exosome Biology, 2018, Heidelberg, Germany.
- **Akshay Gaike** (Dr. Y. Shouche's group): Best Poster Presentation Award - Human Microbiome Section at 'International Conference on Microbiome Research (ICMR 2018)' organized by NCMR-NCCS at Hyatt Regency Pune from 19-22nd Nov 2018.
- **Ameya Bendre** (Dr. J. Kumar's group): DBT-RA fellowship.
- **Amit Yadav** (Dr. Y. Shouche's group): Elected as 'Member of Central Council' of 'Indian Association of Mycoplasmologists (IAM), New Delhi in August 2018. Dr. Amit Yadav is a life member of IAM.
- **Ashwani Kumar** (Dr. S. Mande's group): Best Poster Award: 'Structural basis of hypoxic gene regulation by the Rv0081 transcription factor of *Mycobacterium tuberculosis*', Molecular Omics, Royal Society of Chemistry, UK, at the International Conference on Proteomics for Cell Biology and Molecular Medicine, Protein Society of India (ICPMM-PSI-2018), NCCS Pune, India; 12th -14th December, 2018.
- **Avinash Sharma** (Dr. Y. Shouche's group):
  - Wellcome Trust DBT-India Alliance Early Career Research Fellowship (2018), for studies on: 'Discovery of novel antimicrobials from uncultured microorganisms against the multidrug resistance bacteria.
  - Selected as a member of the 38th Indian Scientific Expedition to Antarctica (26 Jan - 6 May, 2019), to collect samples from this unique ecosystem for studying the 'Specific adaptations of previously unknown, psychrophilic prokaryotes from Antarctic environment'.
  - Awarded as Fellow of Society for Environment and Develpment, India (FSED) in 2018.
  - International Travel Grant by SERB, DST, India to attend ISME 2018, Leipzeig, Germany (August 12- August 17, 2018).
  - Awarded as Visiting Expert by The World Academy of Science (TWAS) to visit Department of Biology, State University of Jakarta, Indonesia, under TWAS Visiting Expert Programme (25 June to 11 July, 2018).

- **Bhavnita Soni** (DST-Inspire SRF in Dr. S. Singh's group):
  - Selected to make an oral presentation at the Biological

Engineering Society of India's Annual Conference (BESCON 2018); 26-27 October 2018.

- **Debasish Paul** (Dr. M. Santra's group):
  - ISCA Young Scientist Award (New Biology, 2018-2019),

awarded by the Indian Science Congress Association, Govt. Of India, at the 106th Indian Science Congress, Jalandhar, India, 7th January, 2019.

- **Diptaraj Chaudhari** (Dr. Y. Shouche's group):
  - Best Poster Presentation Award - Human Microbiome Section at 'International Conference on Microbiome Research (ICMR 2018)' organized by NCMR-NCCS at Hyatt Regency Pune from 19-22nd Nov 2018.
  - DST SERB Travel Award-PhD for attending International Society for Microbial Ecology -17 (ISME-17) at Leipzig, Germany from 11-17th Aug 2018
  - Best Oral Presentation Award at "National conference on Microbiome Research: Understanding the diversity to improve plant, animal, human and environmental health", Bhakta institute of Biotechnology, Uka Tarsadia University, Bardoli, Gujrat, India (Mar, 2019).
  - ISME Early Career Travel Award for the "National conference on Microbiome Research: Understanding the diversity to improve plant, animal, human and environmental health", Bhakta institute of Biotechnology, Uka Tarsadia University, Bardoli, Gujarat, India (Mar, 2019).
- **Fahima Munavar K** (Dr. N. Lenka's group): Selected participant to attend the 9th Bangalore-Benny Shilo Course on Developmental Biology, NCBS, Bangalore; 2019, January 1-11, 2019.
- **Kamlesh Jangid** (Dr. Y. Shouche's group): Academic Advisor, Beijing Key Laboratory of Biodiversity and Organic Farming, China Agricultural University, China. 2018 onwards.
- **Kunal Jani** (Dr. Y. Shouche's group):
  - ISME Early Career Travel Award for the "National conference on Microbiome Research: Understanding the diversity to improve plant, animal, human and environmental health", Bhakta institute of Biotechnology, Uka Tarsadia University, Bardoli, Gujarat, India (Mar, 2019).
  - Best Oral Presentation Award at "National conference on Microbiome Research: Understanding the diversity to improve plant, animal, human and environmental health", Bhakta institute of Biotechnology, Uka Tarsadia University, Bardoli, Gujrat, India (Mar, 2019).
  - FEMS Congress Attendance Grant for the 8th FEMS Congress of European Microbiologists", Glasgow, Scotland (2019).
  - Travel Fellowship Award - by INSA/CSIR/DAE-BRNS-CCSTDS Grant for the 8th FEMS Congress of European Microbiologists", Glasgow, Scotland (2019).
  - Science and Engineering Research Board (SERB) International Travel Support Grant for the 8th FEMS Congress of European Microbiologists", Glasgow, Scotland (2019).
- **Kusum Dhakad** (Dr. Y. Shouche's group): DST SERB Travel Award- PDF for attending International Society for Microbial Ecology -17 (ISME-17) at Leipzig, Germany from 11-17th Aug 2018.
- **Lekha Rani** (DST Woman Scientist in Dr. M. Wani's group): Young Investigator Award for the paper presented during the 2nd National Congress on Osteoarthritis: Update & Research Society for Osteoarthritis Research, organized by Arthritis Research and Care Foundation, Center for Rheumatic Diseases held at Pune, 31 August - 2 September, 2018.
- **Lumbini Yadav** (Dr. S. Mande's group):
  - Selected for participation in the 68th Lindau Nobel Laureate Meeting, 24-29 June 2018, Germany; & Post Lindau tour through DST-DFG programme to visit German research institutes and universities; 2 - 6 July, 2018.
  - Poster prize, awarded by the by American Chemical Society and Science and engineering research board, for good research work done during her NPDF tenure.

- **Madhuri More** (Dr. S. Bapat's group):
  Oral presentation award, at 'Stem Cells and Cancer - India 2019', Mumbai, 1st February, 2019

- **Meitei Heikrujam Thoihen** (Dr. G. Lal's group): Best Oral Presentation Award, 2nd Society of Inflammation Research Conference (SIRCON 2018), API Bhavan, Bangalore, 19th August, 2018.
- **Misha, K.R.** (Dr. J. Joseph's group): Best oral presentation award, 7th International Confernce on Molecular Signaling, co-organized by S.P. Pune University and NCCS, Pune, India, 23-25 January, 2019.
- **Mishra Amrita and Haldar Namrita** (Dr. G. Lal's group): Best Poster presentation Award, NCCS Retreat, 26 September 2018.
- **Nimma Ramakrishna** (Dr. G. C. Kundu's group): Third Best Poster Presentation. 4th International Conference on Translational Research (4th ICTR), Goa, 11-13 October, 2018.
- **NNV Radharani** (Dr. G. C. Kundu's group): Second Best Poster Presentation Award. 4th International Conference on Translational Research (4th ICTR), Goa, 11-13 October, 2018.
- **Nutan Chauhan** (Dr. S. Singh's group): Best Poster Award; National Conference on Emerging Trends in Disease Model Systems, NCCS-NASI Pune Chapter, 25-27 March 2019.
- **Osheen S.** (Dr. Rapole's group):
  - Best poster award: Intenational Conference of Proteomics for Cell Biology and Molecular Medicine; National Centre for Cell Science, Pune, India; 12 - 14 December, 2018.
  - Best poster award: 7th International Conference on Molecular Signalling, National Centre for Cell Science, Pune, India. 23 - 25 January, 2019.
  - Prize for oral presentation: National Conference on Cellular and Molecular Basis of Cancer: Molecules to Mechanism, Department of Biotechnology, S.P. Pune University, Pune, India, 7 - 9 February, 2019.
- **Pankaj Kumar Madheshiya** (Dr. R. Chauhan's group): David Blow Bursary Award at the DLS-CCP4 workshop, London UK, November 2018.
- **Prachi Kapse** (Dr. G. C. Kundu's group): First Prize - Poster Presentation, 5th International Conference on Angiogenesis Research, Kolhapur, India, 26 -27 October 2018.
- **Pranay Ramteke** (Dr. M.K. Bhat's group): DST travel award for presenting a poster at the 25th Biennial Congress of the European Association for Cancer research (EACR-25), Amsterdam, The Netherlands, 30 June-03 July, 2018.
- **Priyanka Dutta** (Dr. R. Chauhan's group): EMBO short-term fellowship award 2018 to visit a lab in Grenoble, France.
- **Rahul Bodkhe** (Dr. Y. Shouche's group): Fulbright Nehru fellowship - to carry out research as a resident fellow at the Mayo Clinic, USA, for 9 months in 2018-19.
- **Rajashri Shende** (Dr. A. Sahu's group):
  First Prize - Oral presentation: National Symposium on Recent Advances in Modern Biology and Biotechnology

2019 (RAMBB 2019), Dr. D.Y. Patil Bioinformatics and Biotechnology Institute. Tathwade, Pune; 14-16 March, 2019.

- **Rajesh Vinnakota** (Dr. J, Kumar's group): EMBO-short term fellowship.
- **Renuka Nawadkar** (Dr. A. Sahu's group):
  - Best poster award: Biological Engineering Society India Annual Meeting and Conference 2018, 26-27 October

2018, IIT Bombay.

- **Richa Pant** (Dr. S. Chattopadhyay's group): Best poster paper presentation, awarded by the 'Indian Society of Cell

Biology' at the XLII All India Cell Biology Conference, BITS Pilani, Goa, 21-23 December, 2018.

- **Rutuja Kuhikar** (Dr. L.S. Limaye's group): First prize for poster presentation, 4th Mini-symposium on Cell Biology, National Centre for Cell Science, Pune, India; 18, 19 July, 2018.
- **Sagar Varankar** (Dr. S. Bapat's group): Poster Award, Indo-Australian Symposium on Epithelial - Mesenchymal Transition, NCCS, Pune, India, 24 October, 2018.
- **Sahabram Dewala** (Dr. Y. Shouche's group):
  - ISME Early Career Travel Award for the "National conference on Microbiome Research: Understanding the diversity to improve plant, animal, human and environmental health", Gujarat, India (Mar, 2019).
  - Best Oral Presentation Award - 2nd Position at "National conference on Microbiome Research: Understanding the diversity to improve plant, animal, human and environmental health", Bhakta institute of Biotechnology, Uka Tarsadia University, Bardoli, Gujrat, India (Mar, 2019).
- **Sehbanul Islam** (Dr. M. Santra's group): Travel grant (Dec 2018) from CSIR to attend an international conference on cancer, 'Tracking Cancer: Detection and Monitoring, from Diagnosis to Therapy', Barcelona, Spain; 4 - 6 February 2019.
- **Upasana Kapoor** (DST-NPDF in Dr. N. Lenka's group): JNS-2018 Travel Award & abstract selected for Oral Presentation, 41st Annual Meeting of the Japan Neuroscience Society, Kobe, Japan; July 25-29, 2018.
- **Venkatesh Chanukuppa** (Dr. S. Rapole's group): Best poster award: International Conference on Proteomics for Cell Biology and Molecular Medicine, National Centre for Cell Science, Pune, India; 12-14 December, 2018.
- **Vikas Ghattargi** (Dr. Y. Shouche's group):
  - Best Poster Presentation Award - Computational Microbiome Section at 'International Conference on Microbiome Research (ICMR 2018)' organized by NCMR-NCCS at Hyatt Regency Pune from 19-22nd Nov 2018.
  - Best Poster Presentation Award - at '9th Probiotic Symposium - Probiotics through the lifespan' organized by Probiotic Association of India & Gut Microbiome at Amity University, Kolkata from 24-25th 2018.
- **Yashika Agrawal** (Dr. M. Santra's group): First Prize in Elevator Pitch: 4th Mini Symposium on Cell Biology, NCCS, Pune, India; 18, 19 July, 2018.
- **The Biotechnology Entrepreneurship Students' Team** from NCCS- Was among the top 20 teams shortlisted (from >85 entries) for the annual competition organized by the Association of Biotechnology Led Entrepreneurs (ABLE), India, and the Department of Biotechnology, Govt. of India.
  Team members: Sumit Das (Dr. G. C. Kundu's group), Ganesh Kumar Barik (Dr. M. K. Santra's group), Palak Agrawal (Dr. A. Sahu's group), Jatin Behari and Shehnaz Bano (Dr. V. Seshadri's group).
  Mentor: Dr. G.C. Kundu.

The Biotechnology Entrepreneurship Students' Team.

EXTRAMURAL FUNDING

Extramurally-Funded Projects / Fellowships of NCCS Faculty

No.	PI	Title	Start Date	End Date	Collaborator(s)	Funding agency	Country
1	Dr. Amitabha Majumdar	Studying the translational homeostasis landscape in Drosophila Fragile-X syndrome model.	27.02.2017	26.02.2020	Nil	DST	India
2	Dr. Janesh Kumar	Molecular mechanisms for Ionotropic glutamate receptors by their Auxiliary Subunits.	10.01.2014	09.01.2019 Extension 09.03.2020	Nil	Wellcome Trust/DBT	India
3	Dr. Sharmila A. Bapat	Development of a predictive algorithm for precision medicine in ovarian Cancer.	07.07.2017	06.07.2020	Nil	DBT	India
4	Dr. Bhaskar Saha	INLEISH: Immunometabolic Networks in the Regulation of Visceral Leishmaniasis.	26.05.2017	25.05.2020	Dr. Arup Sarkar TACT, Odisha; Dr. Ricardo Silvertre, University of Minho; Prof. Tamas Laskay, University of Lubeck, Germany; Dr. Jerome Estaquier, University CNRS, Paris	DBT	India
5	Dr. Bhaskar Saha	JC BOSE Fellowship	06.08.2018	05.08.2023	Nil	DST	India
6	Bhaskar Saha	Mode of CD40 clustering dictates its functional duality.	23.06.2017	22.06.2020	Dr. Christoph G. Baumann, Dept. of Biology, University of York, UK	DST INT/UK	India
7	Dr. Deepa Subramanyam	Dissecting the individual roles of Clta and Cltb in early mammalian development through selective CRISPR - Cas9-based knockout and knockin models.	27.03.2018	26.03.2021	Nil	DBT	India
8	Dr. Gaurav Das	Neurobiology of food choice driven by nutrient specific memories and diet.	13.02.2018	12.02.2023	Nil	DST	India
9	Dr. Lalita Limaye	Identification of aging-induced epigenetic changes causing hematopoietic stem cell dysfunction: Rescue using *in vitro* niche (IVN)- technology.	08.02.2017	07.02.2020	Nil	DBT	India
10	Dr. Gopal C. Kundu	Multi-omics analysis to decipher mechanisms of hormone resistance in breast cancer.	04.01.2017	03.01.2022	Dr. Sudeep Gupta, Cancer Research Institute,Tata Memorial Hospital, Mumbai; Dr. Amit Dutt, ACTREC, Mumbai; Dr. Akhilesh Pandey, Institute of	DBT	India

					Bioinformatics, Bangalore; Dr.Partha P. Majumdar, National Inst. of Biomedical Genomics, WB; Dr. Shona Nag, Jehangir Clinical Development Centre, Pune		
11	Dr. Gopal C. Kundu	Multilayer Nano - capsules and Targeted DNA Vaccines for Immunotherapy of cancer.	29.09.2016	28.09.2019	Dr. Siegfried Weiss, Helmholtz University, Germany; Dr. Suresh Gosavi, Dept. of Physics S.P. Pune University	DST	India
12	Dr. Girdhari Lal	Role of gamma-delta (y) T cells in the generation and maintenance of transplntation tolerance.	19.12.2016	18.12.2019	Nil	DBT	India
13	Dr. Girdhari Lal	Understanding the anti-tumor activity of natural killer (NK) and improving its adoptive cellular therapy potential to control tumor growth.	25.06.2018	24.06.2021	Nil	DST	India
14	Dr. Girdhari Lal	Antigen specific regulatory CD8 T cell vaccination to control food allergy and establishment of oral tolerance.	25.07.2017	24.07.2020	Nil	DST	India
15	Dr. Lalita Limaye	Molecular analyses of extra-cellular vesicles isolated from bone marrow-derived mesenchymal stromal cells treared with specific signaling modifiers and assessment of their effects on the fate of hematopoietic stem cells.	26.03.2018	25.03.2020	Nil	DBT	India
16	Dr. Shekhar Mande	Centre of Excellance in Biomolecular Structure and Function on Host-Pathogens Interactions (Structural Perspective of Molecular Interactions in Pathogenicity: Role of Regulatory Proteins of HIV-1 and Heat Shock Proteins of M. tuberculosis)	28.12.2016	27.12.2021	Dr. Sharmistha Banerjee, Dr. Krishnaveni Mishra, Department of Biochemistry, University of Hyderabad	DBT	India
17	Dr. Gopal C. Kundu	Establishment of A Pune Biotech Cluster, ''Model Organism to Human Disease."	29.06.2018	28.06.2021	Dr. Jayant Udgaonkar, IISER, Pune	DBT	India
18	Dr. Shekhar C. Mande	Assessment of antimicrobial and plant growth promoting potential of Indigenous Endophytic Bacterial Strains of Manipur	11.09.2018	10.09.2021	Dr. Debananda S Ningthoujam, Department of Biochemistry, Manipur University	DBT	India
19	Dr. Debashis Mitra	Centre of Excellence in Biomolecular Structure and	28.12.2016	27.12.2021	Nil	DBT	India

		Function on Host-Pathogens Interactions (Cellular Stress Proteins in HIV Infection: Biochemical and Functional Characterization).					
20	Dr. Yogesh S. Shouche	Identification of microbes in an activated sludge of BOT treatment plant.	17.11.2017	16.11.2018 Extension 15.11.2019	Dr. Supriya Sarkar, Head, Environmental Reseach, Tata Steel Limited	Tata Steel Limited	India
21	Dr. Radha Chauhan	Centre of Excellence in Biomolecular Structure and Function on Host-Pathogens Interactions (Structural & functional role of Nuclear Envelope in HIV infection.)	.28.12.2016	27.12.2021	Nil	DBT	India
22	Dr. Radha Chauhan	Establishing the Structural and functional role of Nup155 and Nup35 in Nup93 subcomplex of the nuclearpore Complex.	11.10.2018	10.10.2021	Nil	DBT	India
23	Dr. Sandhya Sitaswad	Therapeutic implication in ratio resistance mechanism of breast cancer stem cells (BCSC).	05.07.2018	04.07.2019	Nil	DAE	India
24	Dr. Manas Santra	Identification of ring-finger E 3 ubiquitin ligases involved in NF-B pathway activation and decipher the molecular mechanism.	23.03.2017	22.03.2020	Nil	DST	India
25	Dr. Manas Santra	Quest for Cancer Drugs: Screening and Bioassay guided phytochemical Investigation of selected endemic medicinal plants of Eastern Himalaya	18.09.2018	17.09.2021	Dr. Dwipen Kakati, Dept. of Chemistry, Rajiv Gandhi University, Itanagar; Dr. Ashish K Bhattacharya, Div. of Organic Chemistry, NCL, Pune; Dr. Temin Payum, Dept of Botany, Jawaharlal Nehru College, Pasighat; Dr. Jogendra Chandra Kalita, Dept of Zoology; Dr. Kandarpa K Saikia, Dept of Bioengineering & Technology, Gauhati University.	DBT	India
26	Dr. Shailza Singh	Understanding the mechanism sequestering proteins: structure based novel drug development of ABC-type metal against human pathogens.	20.01.2017	19.01.2020	Dr. Shankar Prasad Kanaujia & Dr. Vikash Dubey, Dept. of Biosciences & Bioengineering,IIT, Guwahati, Assam	DBT (Twinning program-me for the NE)	India
27	Dr. Vasudevan Sheshadri	Development of a stable and inducible CRISPR-Cas9 system					

		for high throughput site specific genome editing in plasmodium falciparum.	03.10.2018	02.10.2021	Nil	DBT	India
28 ,	Dr. Anjali Shiras	Altered microRNA and its targets in Glioblastoma cell lines.	01.01.201631.	12.2018 Extension 30.06.2019	Dr. Ravi Sirdeshmukh nstitute of Bioinformatics, Bangaluru	DBT	India
29	Dr. Anjali Shiras	Developing bank of hunam induced pluripotent stem cell for drug screening. Disease modelling and understanding disease biology.	26.05.2017	25.05.2020	Nil	DST	India
30	Dr. Anjali Shiras	Derivation of functional hepatocytes from human induced pluripotent stem cells.	01.03.2017	28.02.2020	Nil	ICMR	India
31	Dr. Anjali Shiras	Investigating the role of RNA binding proteins in pluripotency and differentiation of induced pluripotent stem cell.	21.06.2017	20.05.2020	Nil	DBT	India
32	Dr. Yogesh Shouche	To set up Maharashtra Gene Bank in Maharashtra State.	02.01.2014	01.01.2019 Extension	Dr. Milind Watve, IISER, Pune	RGSTC	India
33	Dr. Yogesh Shouche	Establishment of Center of Excellence for "National Center for Microbial Resorce (NCMR)".	30.03.2017	29.03.2020	Nil	DBT	India
34	Dr. Srikanth Rapole	Acquisition of Modern Orbitrap mass spectrometer for establishing state of the art proteomics facility at National Centre for Cell Science.	12.07.2016	11.07.2021	Nil	DBT	India
35	Dr. Srikanth Rapole	Exploring the volatome of noncommunicable diseases as a promising, innovative and integrating approach for its rapid diagnostics. The case study of cancer and neurodegenerative diseases.	29.09.2016	28.09.2019	Dr Vincent Rotello, University of Massachusetts; Jochen Schubert, Univesity of Rostock, Germany; Dr.Jose Sousa Camara, Chemistry Dept. Universiy of Madeira; Dr.H.A. Nagarajaram CDFD, Hyderabad	DST	India
36	Dr. Vidisha Tripathi	Investing the role of long noncoding RNAs in mammalian gene expression regulation.	01.04.2015	31.03.2020	Nil	DBT	India
37	Dr. Vidisha Tripathi	Understanding the role of mammalian long noncoding RNAs [lnc RNAs] in regulating cellular quiescence''.	08.08.2016	07.08.2019	Nil	DST	India
38	Dr. Mohan R. Wani	Regulation of development of pathogenic T - helper 17 cells in collagen induced arthritis.	08.10.2018	07.10.2021	Nil	DST	India
39	Dr. Mohan R. Wani	To evaluate the translational potential of IL - 3 for the treatment of osteoporosis and osteoarthritis.	29.06.2018	28.06.2021	Nil	DBT	India
40	Dr. Amitabha Majumdar	Understanding the mechanism of persistence of memory.	01.02.2014	30.01.2020	Dr. Hua Li, Stowers Institute of Medical Research, USA	Wellcome Trust/DBT	India

41	Dr. Yogesh Shouche	Development of efficient and lowcost biotechnology for colour removal of biomethanated spentwash from distillery.	22.06.2017	21.06.2020	Nil	DBT	India
42	Dr. Debashis Mitra	Synthesis and development of novel HSP90 inhibitors as potential anti - HIV candidate molecules and elucidation of their mechanism of inhibition.	03.10.2018	02.10.2021	Nil	DST	India
43	Dr. Nibedita Lenka	Generation of transgene-free human induced pluripotent stem cells using non-genetic approaches for cell therapeutic applications.	09.11.2016	08.11.2019	Dr. Rajkumar P. Thummer, Dr. Shirish Nagotu, Dept.of Biotechnology IIT, Guwahati	DBT DBT Twinning Programme	India
44	Dr. Manas Santra	Development of Novel Inhibitors of AKT: An Unothodox approach Targeting the pleckstrin homology Domain.	12.01.2017	11.01.2020	Dr. Debasis Manna, Department of Chemistry, IIT, Guwahati	DBT	India
45	Dr. Lalita Limaye	Studies on generation of induced pluripotent stem cells from umbilical cord tissue derived adult stem cells''.	09.02.2017	08.02.2020	Nil	DBT	India
46	Dr. Anjali Shiras	Cis-acting pair of novel non-coding RNAs- Ginir & Giniras in cell growth regulation & Transformation of mouse & human cells''.	11.06.2015	10.06.2018 Extension 10.12.2018	Nil	DBT	India
47	Dr. Manoj K. Bhat	Scaling up of proprietary lab scale Fenugreekseed extract production for management of obesity.	22.03.2019	21.09.2020	Dr. Ankur Kumar, Basic Ayurveda Ltd.	BIRAC	India
48	Dr. Gopal C. Kundu	MANAV Human Atlas Initiative	27.02.2019	26.02.2022	Dr. N. Balasubramanyam, IISER, Pune; Dr.Anamika Krishanpal, Persistent Systems Limited.	DBT	India
49	Dr. Amitabha Majumdar	Generation of knockout and Gal4 collection using CRISPR and recombineering for studying the in vivo function and DnaJ domain containing protein in Drosophila *melanogaster.*	05.03.2019	04.03.2022	Nil	DBT	India
50	Dr. Yogesh Shouche	Understanding the transmission of antibiotic resistance between hospitals and environment.	25.01.2019	24.07.2020	Nil	BIRAC	India
51	Dr. Jomon Joseph	Characterization of acute necrotizing encephalopathy 1 (AEN-1)- associated mutations in Nup358.	07.03.2019	06.03.2022	Nil	DBT	India
52	Dr. Arvind Sahu	Role of anaphlyotoxins C3a, C4a and C5a generated	12.03.2019	11.03.2022	Nil	DBT	India

		intracellularly in the infection locale in providing protection against viral infection.					
53	Dr. Gopal C. Kundu	Deciphering Osteopontin Driven Regulator(s) of metastasis in Triple Negative breast Cancer using dead Cas-based tools	07.02.2019	06.02.2022	Nil	DBT	India
54	Dr. Giridhari Lal	To Evalute the effect of Yakult on the immune system of late middle-aged Indian adults	27.04.2019	26.04.2022	Dr. Ashish Bavdekar, Department of Pediatrics, KEM Hospital, Pune; Dr. Anand Kawade, Pediatric Research, KEMHRC-VADU; Dr. Sanjay Juvekar, Officer Incharge VADU-KEMHRC	NCCS	India
55	Dr. Lalita Limaye	To establish 3D human skin equivalents for their future use in toxicity testing	30.05.2018	30.05.2019 Extension 30.11.2019	Dr. Abhay Deshpande, Jai Research Foundation, Gujarat	Jai Research Foundation	India
56	Dr. Deepa Subramanyum	The role of endocytosis in regulation of stem cell functions and cell fate decisions during early development.	01.05.2013	30.04.2018 Extension 30.04.2020	Nil	Wellcome Trust/DBT	India
57	Dr. Gopal C. Kundu	Chitosan nanoparticle mediated Andrographolide & / or Raloxifene delivery in Breast Cancer and its Impications in Multi-targetec Therapy	14.01.2016	13.01.2019	Nil	DBT	India
58	Dr. Gopal C. Kundu	Translational Development of Protein namomedicine and multifunctional hydroxyapatite nano-contrast agent	18.03.2016	17.03.2019	Dr. Anusha Ashokan, Dr. Shantikumar Vasudevan Nair & Dr.Manzoor Koyakutty Amrti Centre for Nanosciences & Molecular Medicine, Kolam & Kochi, Kerala. Dr. M Samson Molecular Oncology Cancer Institute (WIA) Adyar Cancer Institute, Chennai, Tamilnadu	DBT	India
59	Dr. Samit Chattopadhyay	JC BOSE Fellowship - Understanding of Cancer Cell metastasis and epigenegenics.	17.06.2013	16.06.2018	Nil	DST	India
60	Dr. Manas Santra	Understanding the role of intervention from herbal extracts/ Naturals in regulating tissue level quorum sensing in hair follicles.	01.08.2016	31.07.2018	Dr. Vijay Gadgil- Unilever Industries Pvt Ltd, Bangalore	Unilever	India
61	Dr. Shailza Singh	Molecular Motors as Nanocircuits in Leishmaniasis: System cues guiding Synthetic Biology Device Construction.	18.05.2016	17.05.2019	Nil	DBT	India

62	Dr. Vasudevan Seshadri	Post-transcriptional regulation of gene expression in Plasmodium falciparum.	04.12.2015	03.12.2018	Nil	DST	India
63	Dr. Anjali Shiras	Studies on exosome mediated regulation of angiogesis in glioblastoma.	22.09.2015	21.09.2018	Nil	DBT	India
64	Dr. Anjali Shiras	Examine cross-talk between epidermal and dermal skin cells through in vitro models in order to regulate hyper pigmentation.	01.12.2016	30.11.20018	Dr. Anita Damodaran and Ms. Nirmala Nair-Unilever Industries Pvt Ltd, Bangalore	Unilever	India
65	Dr. Jomon Joseph	Role of Nup358 in the regulation of cytoplasmic mRNP granules.	12.01.2016	11.01.2019	Nil	DST	India
66	Dr. Deepa Subramanyam	The role of emdocytosis in regulation of stem cell functions and cell fate decisions during early development	01.05.2013	30.04.2020	Nil	Wellcome Trust/DBT	UK and India
67	Dr. Manas Santra	Understanding the role of Post translational modification (s) on apoptotic activity of PUMA.	05.06.2015	31.03.2019	Nil	CSIR	India
68	Dr. Samit Chattopadhyay	Metabolic stress induced epigenetic changes in the transcriptional regulator gene SMAR1	2017	2020		DBTI	ndia

Other Major Projects

- Pune Biotech Cluster

  • The Pune Bio-Cluster, is a 3-year collaborative project between NCCS, Pune and IISER, Pune, funded by the Department of Biotechnology, Government of India, which was initiated in June, 2018. The project aims at creating opportunities for members of the cluster to take advantage of each other's expertise in using high-end facilities developed as a part of the cluster, such as a cryo electron microscope facility, and to nucleate available resources for better utilization by members and start ups, thus encouraging sharing of national resources. The project is expected to provide high end facilities like whole animal imaging to help develop animal models for tacking human disease, which is one of the key objectives.

Research Fellows awarded with Ph. D. Degrees

(01.04.2018 – 31.03.2019)

No.	Research Scholar	Title of the Thesis	Date of award of Ph.D.	Research Guide
1	Santosh Kumar Yadav	Regulation of PKCzeta Function by SUMO modification	04 April, 2018	Dr. Jomon Joseph
2	Vishal Dandewad	Identification of post transcriptional gene regulatory mechanism in *Plasmodium falciparum*	30 May, 2018	Dr. Vasudevan Seshadri
3	Suchismita Panda	Understanding mechanisms of long non-coding RNA - GINIR in cell transformation and tumorigenicity of mouse cells	01 June, 2018	Dr. Anjali Shiras
4	Ashish Kamble	Studies on mechanism of complement-mediated neutralization of vaccinia virus and its rescue by the virus encoded complement regulator VCP	04 June, 2018	Dr. Arvind Sahu
5	Akshada Gajbhiye	Identification and Characterization of Novel potential Biomarkers for Breast Cancer using Mass Spectrometry based Proteomics approaches and Bioinformatics Tools.	07 June, 2018	Dr. Srikanth Rapole
6	Aftab Alam	Proteomic profiling of SMAR1 regulated genes that orchestrate immune evasion and survival of cancer cells.	18 June, 2018	Dr. Samit Chattopadhyay
7	Aritra Das	Metabolic regulation of epigenetic changes in the tumour suppressor gene SMAR1	18 June, 2018	Dr. Samit Chattopadhyay
8	Snahlata Singh	Resistin & leptin: Their role in colon cancer	02 July, 2018	Dr. Manoj K. Bhat
9	Pruthviraj Bejugam	Autoregulatory RNA elements in *Leishmania* : Probing with small molecule inhibitors	12 July, 2018	Dr. Shailza Singh
10	Jitendra Kumar	Molecular characterization of vaccinia virus complement control protein, an immune evasion protein of vaccinia virus	13 July, 2018	Dr. Arvind Sahu
11	Aditi Singh	Mechanistic insight into the role of Nup358 in neuronal polarization	20 July, 2018	Dr. Jomon Joseph
12	Deepali Bobade	Modulatory effects of *Plasmodium falciparum* pigment, Hemozoin (Hz) on human monocytes	26 July, 2018	Dr. Prakash Deshpande
13	Sheetal Kadam	Role and mechanism of cell death cascade regulators in the rescue of diabetes-induced EPS dysfunction	09 August, 2018	Dr. Vaijayanti P. Kale
14	Rajeshkumar Manne	Understanding the role of RING-finger E3 ubiquit in ligasesin AKT signaling	20 August, 2018	Dr. Manas Santra
15	Divanshu Shukla	Role of Toll-Like receptors In *Leishmania* infection:Spatio-temporal Regulation of TLR Expression and function.	25 September, 2018	Dr. Bhaskar Saha
16	Tushar More	Metabolomics and lipidomics approaches towards the identification of potential targets for breast cancer	26 October, 2018	Dr. Srikanth Rapole
17	Sonal Patel	Maintenance of cellular homeostasis through transcriptional regulation of MAR binding protein SMAR1 and its role in embryonic development.	30 October, 2018	Dr. Samit Chattopadhyay

No.	Research Scholar	Title of the Thesis	Date of award of Ph.D.	Research Guide
18	Ankita Srivastava	TLR2 differentially modulates Ras isoforms expression	21 December, 2018	Dr. Bhaskar Saha
19	Shikha Nag	Investigation of Rv1694/TlyA mediated alternative model for *Mycobacterium tuberculosis* infections: Role in survival and antibiotic resistance.	30 January, 2019	Dr. M. V. Krishnasastry
20	Shruti V. Joshi	Stabilization of SMAR1 and its effect on anticancer activity through alternative splicing of CD44	06 February, 2019	Dr. Samit Chattopadhyay
21	Debasish Paul	Identification and elucidation of the role of Protein phosphatase 1 regulatory subunits in cancer	06 February, 2019	Dr. Manas Santra
22	Srinadh Choppara	Understanding the regulation of FBXO 31 in cell cycle.	14 February, 2019	Dr. Manas Santra
23	Indrasen Magre	Characterization of non-canonical functions of Nup358 in zebrafish epithelial tissues	22 March, 2019	Dr. Jomon Joseph

Teaching, Training and Outreach

Talks delivered at schools / colleges by NCCS scientists

Scientist	Topic / Symposium	Class / Department	Institution	Date
	FOR SCHOOL STUDENTS			
Deepa Subramanyam	Basic research –whats so exciting about it	Class X, XI, XII	DPS School, Pune	06/09/2018
Deepa Subramanyam	The exciting life of a stem cell	Class 8, 9	Dr. Kalmadi Shamarao high school, Pune	26/02/2019
Sharmila Bapat	Title - Cancer Stem Cells (at a half-day symposium on " Incredible Science – Star Gazing to Sustainibility)	8th – 10th Std.	Delhi Public School, Pune	18/08/2018
Shrikant Pawar	'Wonders of Microbiology'	7th and 8th standards	St. Ursulas School, Pune	14/12/2018
	FOR COLLEGE STUDENTS			
Akanksha Chaturvedi	Immune responses to viruses	MSc and PhD Virology Course, Discipline of Biosciences and Biomedical Engineering	IIT Indore	25/03/2019 26/03/2019 28/03/2019
Akanksha Chaturvedi	Spatial regulation of the B Cell Receptor and Toll Like Receptor signaling In B Cells	Discipline of Biosciences and Biomedical Engineering	IIT Indore	27/03/2019
Deepa Subramanyam	Traffic control in embryonic stem cells	BSc and MSc – 200 students	Nirmala college, Coimbatore	20/09/2018
Deepa Subramanyam	Traffic control in embryonic stem cells	MSc – 25 students	Department of Biotechnology, S.P. Pune University	12/01/2019
Girdhari Lal	Biology of T cells: A historical and current perspective.	M.Sc., Biotechnology	Pondicherry University, Pondicherry	04/04/2018
Girdhari Lal	Transmigration of CD4 T cells across the blood-brain barrier during neuroinflammation and autoimmunity.	Masters students	Pasteur Institute, Lille, France	22/05/2018
Gopal C. Kundu	Biotechnolgy, Cancer awareness in India	T.Y. BSc	Madhusudan College, Durgapur, West Bengal	30/11/2018
Gopal C. Kundu	CME Lecture series	MBBS	SRM University, Chennai	05/03/2019
Jomon Joseph	Annulate Lamellae: An obscure organelle with new functions	M.Sc. Biotechnology	Mount Carmel College, Bengaluru	18/02/2019
Nibedita Lenka	Expert in Thematic lecture series entitled 'Stem Cell and Regenerative Medicine'	M.Sc. (Biotech)	Dept. of Biotechnology, S.P. Pune University, Pune	16/03/2019
Neetha Joseph	National Conference on Biological Science Emerging Challenges and Issues	B. Sc.	Sri Ramakrishna College of Arts & Science for Women	16-02-2019
Praveen Rahi	The world of microbiology and basics of hygiene	9th and 10th Standards	Kendriya Vidyalaya, Aizawl	10/05/2018
Praveen Rahi	Advancements in the microbiome research with specialemphasis on phyto-microbiome	Refresher Course in Life Science (College teachers)	Sant Gadge Baba, Amravati University, Amravati	04/09/2018
Praveen Rahi	MALDI TOF MS based microbial identification	Refresher Course in Life Science (College teachers)	Sant Gadge Baba, Amravati University, Amravati	04/09/2018
Praveen Rahi	Addressed students on the development of scientific temper during the 'Centenary Ceremony' of the Shri Shankarrao Education Society	5th to 12th Standard (300 students)	Shri Shankarrao Education Society, Karajgaon, Amravati, Maharashtra.	23/01/2019
Praveen Rahi	How To Propose A Good Scientific Question	M.Sc. and research scholars	Savitribai Phule Pune University	05/02/2019
Praveen Rahi	Omics approaches in Microbial Ecology: Metaproteomics and Culturomics	M.Sc.	Savitribai Phule Pune University	22/02/2019

Scientist	Topic / Symposium	Class / Department	Institution	DateRohit
Rohit Sharma	Morphological Characterization of Mycrorriza (Teaching learning skills in Taxonomy, Biodiversity and Bioprospecting of Fungi)	M.Sc. & Ph.D. students	Department of Botany, Savitribai Phule Pune University, Pune	20/12/2018
Shrikant Pawar	'Marine Sponges: The hidden microbial diversity with in'	MSc	Vidya Pratishthans School of Biotechnology,Baramati	11/08/2018
Shrikant Pawar	'Maharashtra Gene Bank'	B.Tech. Biotechnology	Basveshwar Engineering College, Bagalkot. Karnataka	18/09/2018
Shrikant Pawar	DNA-Blue print of life	MSc Microbiology	Sinhagad college of Science, Pune	07/02/2019

Classes taught by NCCS scientists for the Ph.D. course work (2018)

(for Ph.D. students registered with the S.P. Pune University, Department of Biotechnology)

Scientist	Topic / Module
Dr. Arunkarthick S.	Cell Biology
Dr. Arunkarthick S.	Quantitative methods
Dr. Bankar R. M.	Biology & Husbandry Of lab animals (Animal Ethics)
Dr. Bhat Manoj K.	Cancer Therapy
Dr. Chauhan Radha (coordinator: Structural Biology course)	Structural Biology
Dr. Chauhan Radha	Quantitative methods
Dr. Das Gaurav (coordinator: Molecular Biology course)	Molecular Biology (An introduction to molecular mapping; Genetic tools to manipulate cells: design, function and utility)
Dr. Dhiraj Paul	Biodiversity
Dr. Dhotre Dhiraj	Molecular phylogenetics concepts Bootsrap MSA etc.
Dr. Dhotre Dhiraj	Phylogenetic Methods & Analysis
Dr. Janesh Kumar	Structural Biology; Membrane Proteins
Dr. Janesh Kumar	Quantitative methods
Dr. Joseph Jomon	Advanced Cell Biology
Dr. Joshi Amaraja	Microbial Systematics, Nomenclature, Classification and Identification
Dr. Kundu G. C.	Cancer Biology
Dr. Lal Girdhari	Transplantation Immunology
Dr. Lal Girdhari	Tumor Immunology
Dr. Lenka Nibedita	Ethics in Research (Mammalian Cloning: Pros – Cons and Ethics)
Dr. Majumdar Amitabha	Stem cell and neurobiology
Dr. Mande S. C.	Structural Biology
Dr. Mande S. C.	Immunology
Dr. Mande S. C.	Protein: Nucleic acid interactions
Dr. Pillai Ajay	Ethics in Research
Dr. Ramanmurthy B.	Laboratory Animal experimentation and ethics
Dr. Rapole Srikant	Quantitative methods (Proteomics basics and applications; Mass spectrometry Instrumentation MALDI-MS, ESI-MS, GC-MS; Quantitative Proteomics DIGE, iTRAQ, SILAC, Label Free etc.)
Dr. Sahu Arvind	Immunology; Complement System
Dr. Sahu Arvind	Complement System
Dr. Santra Manas Kumar	Cancer Biology
Dr. Santra Manas Kumar	Molecular Biology
Dr. Seshadri V.	Molecular Biology (Translation and control; Qunatitative PCR)

Classes taught by NCCS scientists for the Ph.D. course work (2018)

(for Ph.D. students registered with the S.P. Pune University, Department of Biotechnology)

Scientist	Topic / Module
Dr. Seshadri V. / Dr. Joseph Jomon / Dr. Pillai Ajay	Review Writing
Dr. Seshadri V./ Dr. Das Gaurav/ Dr. Joseph Jomon	Science Communication
Dr. Seshadri V./ Dr. Joseph Jomon	Course II
Dr. Sharma Om Prakash	Biodiversity – Microbial Diversity
Dr. Sharma Rohit	Microbial Ecology / Species Concept in Microbes
Dr. Singh Jyoti	NGS and Microarray
Dr. Singh Shailza	Computer Applications and Bioinformatics
Dr. Singhal Nishant	Pluripotency / Reprogramming
Dr. Sitasawad Sandhya	Ethics in Research; Biosafety
Dr. Subramanyam Deepa	Stem cells, development and neurobiology
Dr. Wani Mohan	Ethics in Research
Dr. Yadav Amit	Biodiversity - Tools and techniques in Microbial ecology

Talks Delivered by NCCS Faculty

Sharmila Bapat

- Invited talk: 'Novel Transcripts and Proteins in Tumors', Cancer Meeting on Mechanisms of Neoplasia and Precision Medicine in Oncology, National Centre for Biological Sciences, Bengaluru, India, 4 May, 2018.
- Invited talk: 'Concept of Cancer Stem Cells' and 'CSCs and drug resistance' UKIERI-UGC seminar on 'Tumor Microenvironment in Cancer Research', University of Hyderabad; India, 13 November, 2018.
- Invited talk: 'Drug recalcitrance and cancer stem cells', 14th Indo-Australian Biotechnology Conference on 'Emerging modalities to improve cancer outcomes', ACTREC - Tata Memorial Centre, Navi Mumbai, India, 22-23 October 2018.
- Invited talk: 'Development and Application of a Targeted Database for detection of Chimeric Peptides in Ovarian Cancer'; Invited speaker; Indo-US workshop on 'Understanding Cell Biology through Proteomics and Metabolomics' followed by 10th Annual Meeting of the Proteomics Society, India (PSI) & International Conference on 'Proteomics for Cell Biology and Molecular Medicine', National Centre for Cell Science (NCCS), Pune, India,10 - 14 December, 2018.
- Invited talk: 'Drug recalcitrance and cancer stem cells'; Symposium on 'Stem Cells & Cancer – India 2018', Somaiya Vidyavihar Campus, Mumbai, India, 1 February, 2019.
- Invited talk: 'Drug recalcitrance and cancer stem cells', National conference on 'Cellular and Molecular Basis of Cancer: Molecules to mechanisms'; Department of Biotechnology, Savitribai Phule Pune University, India, 7 - 9 February 2019.
- Invited talk: 'Drug recalcitrance and cancer stem cells', National symposium on 'Recent trends in Biology'; Department of Zoology, Savitribai Phule Pune University, India, 8 - 9 March, 2019.

Manoj K. Bhat

- Invited talk: 'Metabolic Impairments: Implications in Cancer and Chemotherapy', 45th National Conference of Association of Clinical Biochemists of India (ACBICON 2018), Kala Academy, Goa, 24-27 October, 2018.
- Invited talk: 'Hyperglycemia and Cancer: Implications in Cancer and Chemotherapy', 4th International Conference on Translational Research: Recent Developments and Innovations in Human Health and Agricultural Research, Goa, 11-13 October, 2018.
- Invited talk: 'OBESITY and CANCER: In- Vitro Cell Based and In-Vivo Experimentations', National Workshop on Animal Cell Culture, conducted at the Faculty Development Centre (UGC-Human Resource Development Centre (HRDC), Guru Nanak Dev University, Amritsar, 8-14 May, 2018.

Samit Chattopadhyay

- Tumor suppressor SMAR1 and its role in cancer stem cells', 20th transcription assembly meeting, Centre for DNA fingerprinting and diagnostics (CDFD), Hyderabad, India, 26 July 2018.

- To be or not to be: Recent perspectives on transformation of a cancer', Dr. J N Boruah Memorial Lecture, Agricultural University, Jorhat, India, 30 Aug 2018.
- Regulation of MHC-I presentation in cancer cells: Possible role of tumor suppressor SMAR1', invited lecture; XLII All India Cell Biology Conference & 2nd International Conference on Trend in Cell and molecular biology, BITS Pilani, KK Birla Goa Campus, Goa, India, 22 December 2018.
- Recent Perspectives and future goal in doing science in India', Young Investigators' Meet, Guwahati, India, 6-10 March 2019.
- Invited talk: 'Chromatin remodeling protein: Transcription factor that functions as an important tumor suppressor', Symposium on Emerging Trends in Biological Sciences Research, Institute of Life Sciences (ILS), Bhubaneswar, India, 19 March 2019.

Radha Chauhan

- Understanding the role of Nup93 subcomplex in nuclear pore complex assemblies and functions', NCCS work in progress talk series, NCCS, Pune, India, 27 July, 2018.
- Giardia: An anigmatic protozoan', NCCS retreat, Lonavla India, 26 September, 2018.

Jomon Joseph

- Invited talk: 'Annulate Lamellae: Getting to know more about an obscure organelle', Multiomic applications in medicinal plant research, held at Trans-disciplinary University, Bengaluru, India, 18 February, 2019.

M. V. Krishnasastry

- Invited talk: 'Single molecule image analysis and dynamics', National Level Workshp on Microscopy Image Analysis; Pune, India, 8 March, 2019.

Janesh Kumar

- Invited talk: 'Structural Insights into GluK3 receptor Functions', M4I, Masstricht University, Masstricht, The Netherlands, October 2018.
- Invited talk: 'Vitrification of Neuronal Ion-channels at Resting Membrane Potential for Cryo-EM' M4I, Masstricht University; Masstricht, The Netherlands, October 2018.
- Invited talk: 'N-glycans modulate GluK3-kainate receptor functions', 7th International Conference on Molecular Signaling; Pune, India, January 2019.
- Invited talk: 'Exciting your Neurons: Structure Function and Regulation of Glutamate Receptor Ion Channels', Recent Trends in Biology; S. P. Pune University, Pune, India, March 2019.

Gopal C. Kundu

- Invited Talk: Murdoch University, Perth, Australia, 9th April, 2018.
- Talk delivered at the Mini symposium on Cancer Stem Cell, Curtin University, Perth, Australia, 11th April, 2018.
- Talk delivered at the Science on the Swan Conference, Perth, Australia, 1st May, 2018.
- Invited Talk: National Institute of Science Education and Research (NISER), Bhubaneshwar, India, 14th May, 2018.
- Invited Talk: Jai Research Foundation (JRF), Vapi, India, 21st May, 2018.
- Talk delivered at the Transcription Assembly Meeting, CDFD, Hyderabad, India, 26th July, 2018.
- Invited Talk: Nutraceutical Society of India, Rishikesh, India, 15th September, 2018.
- Invited Talk: International Conference on Immunology, SRM Institute of Science and Technology, Chennai, India, 26th September, 2018.
- Inaugural Talk: 4th International Conference on Translational Research, Goa, India, 11th October, 2018.
- Plenary Talk: 5th International Angiogenesis Conference, Kolhapur, India, 26th October, 2018.

Girdhari Lal

- Invited talk: 'Mechanism of entry of pathogenic CD4 T cells in the central nervous system and its interaction with neurons', XLII All India Cell Biology Conference, The Cell in Action: Trends in Cell and Molecular Biology, Department of Biological Sciences, BITS Pilani, Goa, India; 21-23 December.
- Chemokine receptor CCR6 signaling perturbs cellular and metabolism in CD4 T cells and promotes a pathogenic response in gut autoimmunity', Indo-US workshop on Understanding cell biology through proteomics and metabolomics, NCCS, Pune, India; 10-11 December, 2018.

- Invited talk: 'The non-chemotactic function of CCR6 controls the plasticity of Th17 and Tregs', 45th Annual Conference of the Indian Immunology Society (IIS), IMMUNOCON 2018, Faridabad, Gurgaon, India; 1-3 November, 2018.
- Invited talk: 'Neuro-immune communication in inflammation and autoimmunity', CME programme organized by Society of Inflammation Research, Bangalore, India; 18 July, 2018.
- Invited talk: 'Tumor microenvironment drive how we treat cancers in future', IMsummit-2: Current Debates in Immuno-Oncology, Mumbai, India; 30 June, 2018.
- Invited talk: 'The role of inflammatory signals on transmigration of Th1 and Th17 cells across the BBB in neuronal autoimmunity', Bangalore NeuroImmunology Update 2018, Bangalore; 22-24 June, 2018.
- The non-chemotactic function of CCR6 promotes differentiation of pathogenic Th17 cells during gut inflammation and autoimmunity' (Kulkarni N, Meitei HT, Sharma PK, Mujeeb VR, Srivastava S, Lal G), 11th International Congress of Autoimmunity, Lisbon, Portugal; 16-20 May, 2018.

Nibedita Lenka

- Invited talk: 'Exploration of pluripotent embryonic stem cells in development and therapy', 3rd ISCSG's (Indian Stem Cells Study group's) International Conference on Stem Cells and Regenerative Medicine, D.Y. Patil Vidyapeeth, Pune, India; 29-31 March, 2019.
- Organ, Organoids and Bioimplants': Invited Course Resource Person for the AICTE-approved QIP Workshop on "Recent trends in Biotechnology Related to Tissue Engineering", IITM, Chennai, India; 7-11 January, 2019.

Lalita S. Limaye

- Invited talk: 'Cell therapeutic applications of Haematopoietic(HSCs),Mesenchymal (MSCs) and induced pluripotent stem cells (iPSCs) derived from cord tissues', MIT school of Bioengineering sciences and research, Loni Kalbhor, India; 31 October, 2018.

Amitabha Majumdar

- Lecture delivered at the Wellcome Trust-DBT IA annual fellows meeting, 2018.
- Lecture delivered at the India EMBO symposium, 'From synapses to memory: RNA based regulatory mechanisms', 2018.

Debashis Mitra

- Cellular stress proteins as potential targets for HIV-1 infection', International Symposium on Infectious Diseases, Regional Centre for Biotechnology, Faridabad, India; 12 -14 November, 2018.
- Cellular Heat Shock Proteins in HIV-1 Infection', XLII All India Cell Biology Conference, BITS Pilani, Goa Campus, India; 21 - 23 December, 2018.
- Cellular proteins as potential targets and repurposing of drugs in the fight against HIV/AIDS', International Conference On Biology and Therapeutics of HIV & Associated Infections' University of Hyderabad, Hyderabad, India; 19 - 21 January 2019.
- Stress proteins as potential targets and repurposing of drugs in the fight against HIV/AIDS', 6th Molecular Virology Meeting 2019, School mof Bioscience, IIT, Kharagpur, India; 28 Feb - 02 March, 2019.
- Cyclin F regulates HIV-1 infectivity by proteasomal degradation of viral Infectivity factor (Vif)', International Conference on Microbial Pathogenesis and New Frontiers, Institute of Microbial Technology, Chandigarh, India; 23 - 25 March 2019.

Srikanth Rapole

- Invited talk: 'Identification of Candidate Cancer Biomarkers/Targets using Proteomic and Metabolomic Approaches', Dr. D Y Patil Biotechnology & Bioinformatics Institute, Pune; 23 April, 2018.
- Invited talk: 'Quantitative proteomics and metabolomics towards candidate markers for Breast Cancer', National seminar on emerging trends in analytical sciences ETAS-2018 organized by Indian Institute of Chemical Technology IICT, Hyderabad, India; July 30-31, 2018.
- Invited talk: 'Identification of Candidate Cancer Biomarkers/Targets using Proteomic and Metabolomic Approaches', 4th International Conference on Translational Research: Recent Developments and Innovations in Human Health and Agriculture Research, organized by the Indian Society of Translational Research at the International Centre, Dona Paula, Goa, India; 11-13 October, 2018.
- Invited talk: 'Proteomic analysis of multiple myeloma towards new targets and chemoresistance markers', Cancer Proteogenomics-2018, IIT-Bombay, Mumbai, India; December 6-11, 2018.
- Invited talk: 'Metabolomics – Introduction and Basics', Metabolomics workshop, NCCS, Pune; December 9-10, 2018.

- Invited talk: 'Identification of Candidate Cancer Biomarkers/Targets using Proteomic and Metabolomic Approaches', Indo-US workshop on 'Understanding Cell Biology through Proteomics and Metabolomics', NCCS, Pune; December 10-11, 2018.
- Invited talk: 'Multipronged proteomic analysis of multiple myeloma towards new targets and chemoresistance markers', 10th Annual Meeting of Proteomics Society, India (PSI) & International Conference on 'Proteomics for Cell Biology and Molecular Medicine', NCCS, Pune; December 12-14, 2018.
- Invited talk: 'Identification of Candidate Cancer Biomarkers/Targets using Proteomic and Metabolomic Approaches', National Conference on Cellular and Molecular Basis of Cancer: Molecule to Mechanisms organized by S.P. Pun University, India; February 7-9, 2019.

Arvind Sahu

- Invited talk: 'Role of complement during pandemic influenza A(H1N1)2009 virus infection', EU-India Call on Next Generation Influenza Vaccine, NCCS Pune, India; 28 September, 2018.
- Invited talk: 'Species specificity of vaccinia virus complement control protein towards bovine classical pathway', International Symposium on Infectious Disease, Regional Centre for Biotechnology, New Delhi and Jamia Hamdard, New Delhi, India; 12 November, 2018.
- Understanding complement-mediated modulation of macrophage polarization', Indo-US Workshop on Understanding Cell Biology through Proteomics & Metabolomics, NCCS, Pune, India; 30 November, 2018.
- Invited talk: 'Role of complement during the pandemic influenza A(H1N1) 2009 virus infection', DAE-BRNS Life Science Symposium – 2019 (LSS-2019), Bhabha Atomic Research Centre, Mumbai, India; March 29, 2019.

Manas Kumar Santra

- Invited talk: 'F-box protein FBXO31: a novel stress responder during cancer therapy', DAE-BRNS Life Science Symposium -2019 (LSS-2019), BARC, Mumbai, India; March 30, 2019.
- Invited talk: 'Tumor suppressor F-box protein FBXO31: an important gatekeeper to prevents oncogenic transformation', Conference on 'Cellular and Molecular Basis of Cancer: Molecule to Mechanisms', S.P. Pune University, Pune, India; 9 February, 2019.
- Invited plenary talk: 'F-box only protein FBXO31: an important gatekeeper tumor suppressor controls the genome integrity', International Conference on Immunology - Major breakthroughs and advances in immunology for human diseases (26-28 Sep, 2018), SRM Institute of Science and Technology, Kattankulathur, Tamil Nadu; 28 September, 2018.
- Invited Keynote Address: 'Tumor suppressor F-box protein FBXO31: an important gatekeeper protein for maintaining the genomic integrity', Indo-European Partnership Symposium Emerging Trends in Cancer Research and Therapeutics, IIT Hyderabad, India, 12 September, 2018,

Vasudevan Seshadri

- Development of insulin resistance animal models to understand diabetes', 3rd International Diabetes Summit 2019, Pune (the presentation received a special recognition award).
- Invited speaker for the workshop cum training program on 'Preparatory Workshop on Competitive Exam-2018', organized by the Dr. D Y Patil Biotechnology and Bioinformatics Institute, Tathwade, Pune.

Anjali Shiras

- Invited talk: 'Mechanistic Insight into Linc RNA functions mediated via protein interactors', RNA Biology Meeting, Trivandrum, India; 2 - 4 May, 2019.
- Invited talk: 'Transformation of Neural Stem Cells To Tumor Stem Cells: The Ways To Assay Them!', Indian Society of Neuro-oncology (ISNOCON) meeting; Bhopal, India; 4 - 8 April, 2019.
- Invited talk: 'Unravelling potential of long noncoding RNAs in cell growth, transformation and cancer', Indian Association of Cancer Research (IACR) 2019; Chandigarh, India-April 1 - 3 April, 2019.
- Invited talk: 'Understanding Mechanisms of Action of Long Non-coding RNAs in Tumor Progression and Cancer', Trends in Biology; SP Pune University Campus, Pune, India; 8 March, 2019.
- Invited talk: 'Studies on long noncoding RNA-Ginir in mouse cells', National Conference on Cellular and Molecular Basis of Cancer: Molecule to Mechanisms (CMBC 2019); Department of Biotechnology, Savitribai Phule Pune University, Pune, India; 7-9 February, 2019.
- Invited talk: 'Identification of protein interactors for a novel linc RNA and elucidating their role in regulation of mitosis and stemness', ISSCR 2018 Annual Meeting Melbourne Convention and Exhibition Centre. Melbourne, Australia; 20 - 23 June, 2018.

- Invited talk: 'Understanding biological function of noncoding RNA-Ginir in mouse cells', Society for Biological Chemists (SBC 2018); 26 - 28 November, 2018.

Yogesh Shouche

- 26 talks delivered at Universities and colleges - S. P. Pune University (Dept. of Microbiology, Bioinformatics Centre); HPT Arts & RYK Science College Nashik; KTHM College Nashik; SGB Amaravati University; Ramkrishna More College (Akurdi), Pune; Modern College, Pune; Sastra University, Tamil Nad; Shivaji University, Kolhapur; AFMC, Pune; MIT ADT University, Pune; Cochin University of Science and Technology, Kerala; Sardar Patel University, Gujrat; IIIT Hinjewadi Pune; D.Y. Patil college Pune; Jaypee Institute, Noida; National Law University, Bangalore; University of Mysore; CFTRI Mysore; Uka University, Bardoli, Gujarat; University of Rajasthan.
- 10 talks delivered at other organizations, conferences, workshops, etc. - Merck India Limited, Mumbai; 3rd Rashtriya Adhiveshan of Vijnana Bharati, Bangalore; Genomics Workshop, New Delhi; Vakshmitra, Pune; International Conference on Microbiome Research (ICMR 2018); 9th Probiotic Symposium, Amity University, Kolkata; Genomics India 2019 conference, Bengaluru; Dr. Madhav Gajanan Deo - Pune International Centre; National Space Science Symposium, S.P. Pune University; Association of Biotechnology Led Enterprises (ABLE) Bangalore.

Shailza Singh

- Invited talk: 'Engineering Synthetic Regulatory Circuits in Infectious Disease', The UGC Refresher Course): Interdisciplinary approach to Science Research and Innovation, Department of Botany, SPPU, Pune, 28th August 2018.
- Invited talk: 'Deciphering lipid metabolism in leishmaniasis using systems and synthetic perspective'; The UGC Refresher Course): Interdisciplinary approach to Science Research and Innovation, Department of Botany, SPPU, Pune, 29th August 2018.
- Invited talk: 'Systems driven Synthetic Immunology in Leishmaniasis', NGBT 2018, Nextgen Genomics, Biology, Bioinformatics and Technologies Conference, Hotel Fairmont, Jaipur, 30th September 2018.
- Keynote lecture: 'Health- Prediction of Infectious Disease System Dynamics using Machine Learning and Mathematics'; International Conference on Data Science 2018, National Institute of Genetics (NIG), Japan and Research Organization of Information and Systems (ROIS), Japan, 12th-15th November 2018.
- Invited talk: 'Synthetic based Molecular Nanodevice in Leishmaniasis' (Invited talk), ISNSCON, 6th World Congress on Nanomedical Sciences, Vigyan Bhawan, New Delhi, 7th-9th January 2019.
- Invited talk: 'Systems driven synthetic bio therapeutics device in leishmaniasis', International Conference on Advances in Materials Science & Applied Biology (AMSAB), SVKM's NMIMS (Deemed-to-be University), Mumbai, 10th January 2019.
- Invited talk: 'Synthetic based Structural RNA architectures in Infectious Disease: Design, Construction and Validation', 11th National Symposium cum Workshop on "Recent Trends in Structural Bioinformatics and Computer Aided Drug Design", Alagappa University, Karaikudi from 12th-15th February 2019.
- Invited tall: 'Computational Immunology in Designing Synthetic Device for Immunotherapy'; Recent Advancements in Biochemical Engineering and Biotechnology, IIT BHU, Varanasi, 15th-16th March 2019.

Nishant Singhal

- Invited Talk: 'Recreating Neurological Disorder in a Dish'; A System Approach to Pre-Clinical Studies, Pune, India, January 2019.

Deepa Subramanyam

- Invited talk: 'Regulation of embryonic stem cell pluripotency by intracellular trafficking', International Conference on Molecular Signaling, Pune, Jan 2019.
- Invited talk: 'Regulation of embryonic stem cell pluripotency by intracellular trafficking', 'Recent Advances in Modern Biology and Biotechnology, Pune, March 2019.

Vidisha Tripathi

- Understanding the role of long noncoding RNAs in mammalian gene expression regulation': 8th Ramalingaswami Conclave, NIPGR, New Delhi, 2018.

Mohan Wani

- Migration potentials of mesenchymal stem cells': School of Regenerative Medicine, Bangalore, June 22, 2018.
- Immunomodulatory role of IL-3 in rheumatoid arthritis': CME of Society of Inflammation Research (SIRCON 2018) meeting, Bangalore, August 19, 2018.

- Stem cell therapy in animal models of rheumatoid arthritis and osteoarthritis': 2nd National Congress on Osteoarthritis (OACON) and 1st Annual State Rheumatology Meeting (MRACON), Pune, August 31-September 2, 2018.
- IL-3 inhibits osteoclastogenesis by upregulating the cytoprotective enzymes and diverts the cells toward M2 macrophages': Research paper presented at the Annual Meeting of the American Society for Bone and Mineral Research, Montreal, Canada, 28 September - 01 October, 2018.
- Pathophysiology of bone and cartilage remodeling in musculoskeletal disorders', Modern College, Pune, February 13, 2019.
- T lymphocytes derived molecules regulates biology and pathophysiology of bone cells', Centre for Cellular and Molecular Biology, Hyderabad, February 15, 2019.
- Recent developments in mesenchymal stem cell biology and regenerative medicine', Department of Biotechnology, S. P. Pune University, Pune, February 16, 2019.
- Plenary Talk: 'Cytokines regulated migration and bone regenerative potential of mesenchymal stem cells'; Current Trends in Drug Discovery Review-2019 meeting at CSIR-Central Drug Research Institute, Lucknow, February 20-23, 2019.
- Immunotherapy in Rheumatoid Arthritis', Conference on Emerging Trends in Disease Model Systems, National Centre for Cell Science, Pune March 25-26, 2019.

Talks Delivered by NCMR Scientists

Abhay Bajaj:

- DNA sequencing: Method and Troubleshooting', Workshop on Microbial preservation and identification, Pune, India, 7-12 January, 2019.
- Invited Lecture at a seminar on "National Biodiversity Act and its Implications in Biodiversity Research" Organised by AMI Pune Unit at Modern College, Pune on October 5, 2018.

Amit Yadav

- Invited talk: 'Association of multi-species phytoplasmas with mango malformation disease, putatively transmitted by multiple polyphagous insect vectors', National Symposium on 'Recent Challenges and Opportunities in Sustainable Plant Health Management' at the Department of Mycology and Plant Pathology, Institute of Agricultural Sciences, Banaras Hindu University, Varanasi, Utter Pradesh, India; 26-29 February, 2019.
- Invited talk: 'Unexplored Diversity of Mollicutes (Phylum *Tenericutes*)', 59th Annual Conference of Association of Microbiologist of India (AMI) and International Symposium on Host-Pathogen Interactions, University of Hyderabad, Telangana; 09-12 December, 2018.

Avinash Sharma

- Invited talk: 'Impact of mass gatheirngs events on human health', at the International Conference on Microbiome Research, Pune, India; 19-22, November, 2018.
- Invited talk: 'NCMR, a microbial reservoir at NCCS, Pune', at the International Symposium on Biodiversity and Biobanking; Indian Institute of Technology, Guwahati, India; 27-29, January, 2018.

Dhiraj Dhotre

- Invited as a resource person to conduct a two-day workshop on 'Advanced metagenomic analysis' at Institute of Advanced Study in Science and Technology (IASST), Guwahati on 21st and 22nd March 2018.
- Invited as a speaker at the '1st International Workshop on Systems Biology for Human and Plant Nutrition'; International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Hyderabad; 22-24th March 2018.
- Invited talk: 'Microbiome in Health and Diseases', Symbiosis School of Biological Sciences, Pune; organized jointly by Indian Academy of Biomedical Sciences (IABS) as IABS Pune chapter; 28th September 2018.

Om Prakash Sharma

- Invited talk: 'Optimization of Protein Extraction Method for Human-gut Proteomics', at ICERB-2018, Guru-Ghasidas Central University Bilaspur; 27 - 31 October, 2018.
- Invited talk: 'Assessment of Protein Extraction Methods for Gut-Proteomics', Indian Society for Soil Contamination meeting 2018 at KIIT-Bhuvneshawar.
- Invited talk: 'Newer Technology for QuickerDiagnosis / identification of Anaerobes', Microbiology Department of Krishna Institute of Medical Science, Karad, 2018.

- मानवी आंत्र मेटाप्रोटियोमिक्सः मानवी आंत्र माइक्रोबायोटा के क्रियात्मकता के अध्ययन की एक उभरती विधा। (पेपर प्रस्तुतकर्ता- डॉ. ओमप्रकाश शर्मा, राष्ट्रीय कोशिका विज्ञान केन्द्र, पुणे).

Pravin Rahi

- Invited talk: 'Population structure of rhizobia and rhizosphere microbial communities associated with pea cultivated in different agro-climatic regions of India', 4th National Conference on Plant Growth Promoting Rhizobacteria for Sustainbility in Agriculture held at Mizoram University, Aizawl, India, on 11-12 May 2018.
- Invited talk: 'Pea plant shapes its microbiome in the stressed ecosystems of the North-Eastern regions of India', 10th DAE-BRNS Life Science Symposium held at Mumbai, India, 28-30 March 2019.

Rohit Sharma

- Invited talk: 'Molecular Characterization of ECM Mushrooms', Workshop; Pune, India, December 2018.

Other Outreach

1] National Science Day at NCCS

a) Premier screening of 'Cellular Insights' *(documentary about NCCS to commemorate 30 successful years)*

Inauguration by Prof. Nitin Karmalkar (Vice Chancellor, S.P. Pune University)

Screening of 'Cellular Insights'

Mr. Nandan Kudhyadi (Director, 'Cellular Insights')

The film production team

b) Open day - Displays and visits to the laboratories and central facilities












c) *Open Day at the NCMR*

- Public Talk, 'Life under a microscope', followed by lab visits - 120 students (8th, 9th & 11th standards) from the DSK School, Ryan International School, City Pride Junior College and Kalmadi Shamrao School visited NCMR - 26 February, 2019
- Public talk in Marathi, 'Drushti aad Srushti', followed by lab visits - 100 school students (8th & 9th standars) from the Seva Sadan School, Madhyamik Vidyalaya, Sutarwadi & Zilla Parishad School, Pashan, visited NCMR - 26 February, 2019.

Other Public Talks & Open Days

- What Causes Cancer; why knowing more is also less': Public talk delivered in Marathi by Dr. Anjali Shiras, at a session organized by the Marathi Vidyan Parishad at the Indian Institute of Education, Pune; 24 January, 2019.
- Biology of cancer cells': Public talk delivered by Dr. Anjali Shiras for the Cancer Support Group, Institute for Psychological Health, Pune; 13 March, 2019.
- Anjali Shiras interacted with tribal students of standards VII - IX, and delivered a talk in Marathi on 'Making of a Scientist, and Opportunities in Biotechnology' at the Eklavaya ScienceCon–2019, organized by Ekalavya Schools, at the Shree Chhatrapati Shivaji Sports Complex, Balewadi, Pune. 28-30 January, 2019.
- Basic research – whats so exciting about it': Public talk delivered by Deepa Subramanyam for students of Class XI, XII, at LearnAc, Pune; 18 November, 2018.
- The exciting life of a stem cell': Public talk delivered by Deepa Subramanyam for students of Class 7 - 12, at the Exciting science forum; 24 February, 2019.
- Amitabha Majumdar: Delivered two talks for school students at the 'Summer Science Workshop' organized by the Muktangan Exploratory Science Centre, Pune, in April, 2018.
- Public talk delivered by Dr. Yogesh Shouche at the Muktangan Exploratory Science Centre, Pune, 25 March, 2019.
- Cryo-Electron Microscopy Revolution and Biology': Public talk delivered by Janesh Kumar at the National Students seminar, 'Frontiers in Physics XII' in the area of Biophysics, Fergusson college, Pune, 02 February, 2019. (200 B.Sc. &, M.Sc. students from multiple colleges from India attended).
- Invited Talk by Dr. Gopal Kundu at the Young Investigator Meet (YIM) organized for Post-doctoral Fellows, Guwahati, India, 10 March, 2019.
- Open day involving demonstration of embryonic stem cells - 20 students of MSc. Zoology, 2nd year, Govt. Science College, Bangalore, visited NCCS. 24 January, 2019.
- Over two hundred students from various colleges across India visited NCCS over several open days organized during the period of this report. The students were informed about the activities, facilities and services of the NCCS, and were shown and explained the high-end technologies used in research

Public talks delivered at NCMR / Students' visits to NCMR

- Visit to NCMR by 20 Professionals and PhD Scholars from the UDA summer school, where they learnt about NCMR and its activities: 22 June, 2018.
- Public talk cum students' visit to NCMR: 20 High school students from the Ryan International School participated. 10 August, 2018.
- Public talk cum students' visit to NCMR: 300 high school students form the Global Indian International School participated. 27-31 August, 2018.
- Public talk on 'Advances in Sequencing Technologies', cum students' visit to NCMR: 48 MSc students from Modern College, Ganeshkhind, Pune, participated. 10 September, 2018.
- Talk on NCMR and its activities cum visit to NCMR by 19 MSc students: 30 January, 2019.
- Public talk on 'Advances in sequencing technologies', cum students' visit to NCMR by 48 MSc students: 20 February, 2019
- Talk on NCMR and its activities cum visit to NCMR by 35 BSc students from the Dayanand College, Solapur: 22 February, 2019.

Pre-Orientation Workshop of NBOs in Maharashtra for NSOIM-IISF-2018 11 September, 2018

(co-organized with Vibha Vani Maharashtra Chapter)

IISF-2018 Outreach Programme: Open Day at NCCS 21 September 2018

An open day was organized at NCCS to create awareness among the general public about the activities of NCCS and about IISF-2018.

India International Science Festival (IISF 2018), Lucknow 5 - 8 October 2018

NCCS exhibited displays at the 4th India International Science Festival (IISF) at Lucknow, which was organized by the Ministry of Science & Technology and the Ministry of Earth Sciences, Government of India, in association with Vijnana Bharati (VIBHA).

Edu-Bridge

This is an ongoing programme where the faculty members of NCCS visit the the Jankidevi Bajaj College of Science (JBCS), Wardha, to teach the fundamental concepts of science through lectures & hands-on activities to students. The NCCS scientists visited JBCS on 14, 15, 22 and 23 February, 2019 to conduct training for BSc and MSc students and faculty. 7 faculty members of JBCS visited NCCS and were trained in various projects: 20 May - 15th June 2018.

Dr. Arunkarthick conducting workshop on 'Quantitative Microscopy Image Analysis'

Dr. Gaurav Das conducting a workshop on 'Fly Behavioural Genetics'

The Foldscope Project

- 'Exposure tour' under the aegis of the foldscope project - 15 Xth standard students and 2 teachers from the MeECL Secondary School, Umiam, Meghalaya, and 2 project staff from ICAR visited the facilities and laboratories at NCCS & NCMR : 8-16 November, 2018.

Training program	Date	Participants
Foldscope Workshop at NCMR-NCCS	25 July 2018	Students and teachers from: Schools : DSK School, St. Ussula High School, Loyala High School, Sunflower high School, Bharat English School, New English School, Maan and City Pride School. NGOs : Being Jigyasu, Marunjii and Urmee.
Workshop on applications of foldscope at NCMR-NCCS	12-15 Nov. 2018	Students and teachers from: MeECL Secondary School, Umiam, Meghalaya, participated. (organized under the NE student exchange program)
Foldscope Workshop	19 Dec. 2018	Students and teachers from: City Middle School, Poonch, J&K
Foldscope Workshop	21 Dec. 2018	Students and teachers from: High School, Palma, J&K
Foldscope Workshop	22 Dec. 2018	Students and teachers from: High School, Sankari No. 1, J&K
Foldscope Workshop	24 Dec. 2018	Students and teachers from: High Secondary School, SAAJ, J&K
Hands-on training on 'Legume-Rhizobia Symbiosis'	26 Oct. 2018	MSc. Students from HPT RYK College, Nasik, Maharashtra.
Demonstration-cum-training workshop on the utility of the foldscope in agriculture	29 Jan. 2019	20 Local farmers from Village Mynsain, District Ri Bhoi, Meghalaya
Learning Backyard Biodiversity through Foldscope: Hands-on training	19 Sep. 2018	7-10 Std. and XI, XII Std. students from: Government Raghav Krishi Higher Secondary School, Bohani, Tehsil- Gadarwara, District- Narsinghpur, M.P.
Learning Backyard Biodiversity through Foldscope: Hands-on training	20 Sep. 2018	7-10 Std. and XI, XII Std. students from Government Higher Secondary School, Sihora (Bohani), Tehsil- Gadarwara, District- Narsinghpur, M.P.
Learning Backyard Biodiversity through Foldscope: Hands-on training	22 Sep. 2018	7-10 Std and XI, XII Std. students from: Government Girls Higher Secondary School Gadarawara, District- Narsinghpur, M.P.

Microbial Science Outreach Initiative (MSOI)

(Screening of documentaries and public talks, followed by 'Chai Pe Charcha' sessions, organized by members of Dr. Y. Shouche's group regularly at the NCMR, for students and the public)

- Documentaries Screened -
  - Virus Evolution (25/05/2018);
  - Vaccines – Calling the Shots (22/06/2018)
  - Attenborough and the Empire of Ants (10/08/2018)
  - Western Ghats – Monsoon Mountains (08/06/2018)
  - The Power of Plants-Photosynthesis (13/07/2018)

- Talks
  - Dr. Aparna Watve – 'Biodiversity and ecology of Indian Rock Outcrops'; 24th August 2018.

55 MSc (Microbiology) students from 4 colleges in Pune (Abasaheb Garware College, Fergusson College, Modern College, Ganeshkhind and Shivajinagar) attended the talk.

- Dr. Yogesh Shouche - 'Penicillin- Celebrating 90 years of discovery of Penicillin'; 26th Oct 2018.

Radio Programs

a) Public awareness campaign on Nipah virus

NCCS partnered with the ICMR-NIV and All India Radio, Pune, to spread awareness about the Nipah virus in Marathis snd English.
Participants: Drs. Kavita Lole & Atanu Basu from NIV, and Drs. Shekhar Mande, Arvind Sahu, Yogesh Shouche & Jyoti Rao (coordinator) from NCCS.
Broadcast details - Discussion in Marathi: 10 June, 2018; Discussion in English: 13 June, 2018.

b) Radioscope

A conversation between Dr. Shekhar Mande and Dr. Yogesh Shouche on 'The Human Microbiome' was recorded for 'Radioscope', a national science magazine broadcast by the All India Radio, New Delhi, to educate the general public about diverse topics in science. The programme was broadcast on 13 July, 2018, on the Rajdhani Channel of the AIR.

Nipah virus awareness

Radioscope

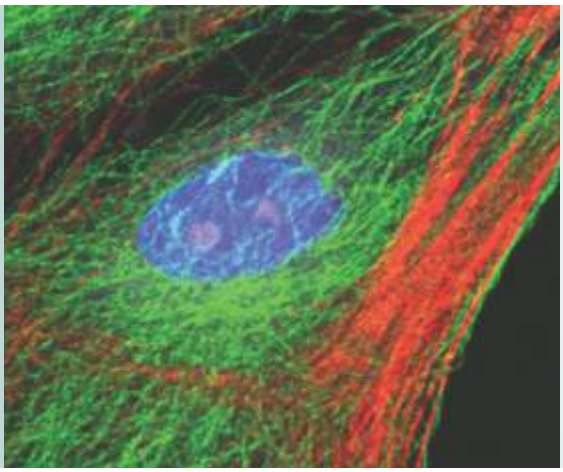
Research training provided at NCCS to extramural students and faculty

(in addition to the IAS Summer Training Fellows, Project Trainees, and students of the Ph.D. course work)

- Mr. Sujit Shah, Ph.D. Scholar from the Central Department of Botany, Tribhuvan University, Kathmandu, Nepal, who was awarded the India Science and Research Fellowship for the year 2017-18, received 6 months' research training under the guidance of Dr. Yogesh Shouche. He arrived at NCCS on 7th June, 2019.
- One B. Tech. 2nd year student from IIT, Madras and one MSc. Biotechnology 2nd year student from the Center for Human Genetics, Bangalore received 2 months' research training under the guidance of Dr. Deepa Subramanyam.
- One student who completed her 12th standard and was on a gap year, received 10 months' research training under the guidance of Dr. Deepa Subramanyam.
- Dr. Gopal Kundu trained two faculty members from colleges under the DBT STAR College Programme, F C College, Pune, and the J B College of Science, Wardha, August 2018

Other activities with societal relevance

- A laboratory was constructed under the aegis of the Foldscope Project funded by the DBT, for students (IX to XII standards) from the Government Raghav Krishi Higher Secondary School (Hindi medium), Narsinghpur, M.P. - 19 September, 2018.
- A session on 'Importance of cleanliness but not overdoing it' was conducted in Marathi for students of the Marathi medium schools (VI to X standards) at post Galandwadi, Taluka Daund, Pune District.
  26 January, 2019.



Conferences / Workshops / Other Events

Participation by the NCCS Faculty

Sandhya Sitaswad

- 5th International conference on "Angiogenesis Research: Targeted anti-angiogenic therapy" (Angio-2018); D.Y. Patil Medical College, Kolhapur; 27, 28 October, 2018.
- International Symposium on Tumor Microenvironment and Cancer Prevention & Therapeutics; SLS, JNU, New Delhi; 8, 9 February, 2019.
- International Conference on 'Translational Research in Cardiovascular Sciences' (IACS 2019); NIMHANS Convention Center, Lakkasandra, Bangalore; 15-17 February, 2019.

Mohan Wani

- 3rd Annual Symposium on "Cell and Gene Therapy" at Christian Medical College (CMC), Vellore, September 6-7, 2019.
- Guha Research Conference (GRC) 2018 meeting, Santineketan, West Bengal, November 30-December 4, 2018.
- Molecular Immunology Forum (MIF) 2019, Centre for DNA Fingerprinting and Diagnostics, Hydreabad, February 7-9, 2019.

Participation by Other Scientists, Students and Staff of NCCS

- **Abhay Bajaj** (Dr. Y. Shouche's group): Oral Presentation on "Genome Based Analysis of Carotenoid Synthesis in *Paracoccus* sp. Strain AK26" in INSCR International Conference, KIIT, Bhubaneshwar, India, 26-27 September, -2018.
- **Abhijit Kulkarni** (Dr. Y. Shouche's group): 'A comprehensive microbiome analysis of *Rongmei* tribal community from North-East India' (Kulkarni AS, Dhotre D, Devi I, Sahoo D and Shouche YS) - Poster presented at the International Conference on Microbiome Research (ICMR2018), Pune, 19-22 November 2018.
- **Abhijeet Singh** (Dr. M.K. Bhat's group): 'Glucose Induced Redox State Regulates Metabolic Switch In Cancer Cells' (Chaube B, Singh A and Bhat MK), XLII All India Cell Biology Conference and 2nd International Conference of Trends in Cell and Molecular Biology, BITS Pilani, Goa, India, 21-23 December 2018.
- **Adrita Guha** (Dr. M. Wani's group): XLII All India Cell Biology Conference and 2nd International Conference on Trends in Cell and Molecular, BITS Pilani, Goa, December 21-23, 2018.
- **Alapani Mitra** (Dr. D. Mitra's group):
  - 'Heat shock protein-90 isoforms in regulation of HIV-1 infection' (Alapani Mitra, Debashis Mitra), 4th Mini Symposium in Cell Biology, National Centre for Cell Science, Pune, India; 2018.
  - 'Isoform specific role of Hsp90 in regulation of HIV-1 infection' (Alapani Mitra, Debasish Mitra), 6th Molecular Virology Meeting, Indian Institute of Technology, Kharagpur, India; 28th Feb-2nd March, 2019.
- **Amit Singh Yadav** (Dr. G. C. Kundu's group): 'pH sensitive peptide conjugated chitosan nanoparticle for andrographolide delivery in breast cancer; (Amit Singh Yaday, NNV Radharani, Mahadeo Gorain, Anuradha Bulbule and Gopal C. Kundu), 4th International Conference on Translational Research, Goa, India, 11-13 October 2018. (Oral Presentation).
- **Amit Yadav** (Dr. Y. Shouche's group):
  - 'DNA Barcoding of Phytoplasma Strains of 16SrV (Elm Yellows) Group and their Putative Insect Vectors' (Amit Yadav, Vipool Thorat and Kiran Kirdat), Oral Presentation in Technical Session VIII: Etiology and Microbial

Taxonomy. At National Symposium Plant Health Management Embracing eco-Sustainable Paradigm during 70th Annual Meeting of Indian Phytopathological Society, New Delhi. February 15-17, 2018. Jorhat, Assam, INDIA.

- 'The MLSA of group 16SrII Phytoplasmas Associated with Phyllody Diseases of Pulse Crops, Weeds and Insects vectors in India; (Kiran Kirdat, Vipool Thorat and Amit Yadav), Poster Presentation in Technical Session VIII: Etiology and Microbial Taxonomy. At National Symposium Plant Health Management Embracing eco-Sustainable Paradigm during 70th Annual Meeting of Indian Phytopathological Society, New Delhi. February 15-17, 2018; Jorhat, Assam, India.

- **Amrita Mishra & Namrita Haldar** (Dr. G. Lal's group): 'Role of neurotransmitters in modulating the immune cell functions' (Mishra A, Haldar N and Lal G), NCCS Retreat, 26 September, 2018. (Best Poster award).
- **Ananth P. Burada** (Dr. J. Kumar's grup): NSC 46: Structural Insights into Orphan Ionotropic Glutamate Receptors, NIMHANS, Bangalore, India, 27-29 June 2018.
- **Anil Kumar** (Dr. M. Wani's group): Presented a poster entitled "Regulation of interleukin-3 receptor expression on human T helper cells" at XLII All India Cell Biology Conference and 2nd International Conference on Trends in Cell and Molecular Biology, BITS Pilani, Goa, December 21-23, 2018.
- **Anindita Dasgupta** (Dr. D. Mitra's group):
  - 'Differential expression of miRNAs during HIV-1 infection and their possible role in viral replication and infectivity' (Anindita Dasgupta, Payel Ghosh, Debashis Mitra), 6th Molecular Virology Meeting, Indian Institute of Technology, Kharagpur, India; 28th Feb-2nd March, 2019.
  - 'Differentially expressed cellular microRNAs during HIV-1 infection and their possible role in viral replication and infectivity' (Anindita Dasgupta, Payel Ghosh, Debashis Mitra), 4th Mini Symposium in Cell Biology, National Centre for Cell Science, Pune, India; 2018.
- **Anjali Tripathi** (Dr. D. Mitra's group):
  - 'Unfolded Protein Response: Regulation and function during HIV-1 infection' (Anjali Tripathi and Debashis Mitra). 4th Mini Symposium on Cell Biology, National Centre for Cell Science, Pune, India; 2018.
  - 'Unfolded Protein Response: Cytoprotective or destructive response during HIV-1 infection' (Anjali Tripathi and Debashis Mitra), 6th Molecular Virology Meeting. School of Bioscience, Indian Institute of Technology, Kharagpur, India; 28th Feb-2nd March, 2019.
- **Ankita Deb** (Dr. M.K. Bhat's group): 'Mechanistic insight into the role of resistin in breast cancer progression: a mouse model study' (Deb A and Bhat MK), 4th Mini Symposium in Cell Biology, National Centre for Cell Science, Pune, India, 18, 19 July, 2018.
- **Anshul Assaiya** (Dr. J. Kumar's grup):
  - GIAN Course 2018: Recent Advancements in Biophysical Techniques and Virology at IIT Roorkee, Roorkee, India, 15-21 April 2018.
  - Cryo-EM workshop: Hands on training in cryo-EM sample preparation at NCBS, Bangalore, India, 12-16 July 2018.
- **Anuradha Bulbule** (Dr. G. C. Kundu's group): 'The Extract of Tridax procumbens Exhibits Potent Anticancer Activity by Modulating Apoptosis and ERK1/2 Signaling in Melanoma and Breast Cancer Models' (Anuradha Bulbule, Ramesh Butti, Gaurab Roy, Dhiraj Kumar and Gopal C. Kundu), 4th International Conference on Translational Research, Goa, India, 11-13 October 2018. (Poster Presentation).
- **Anurag Kumar** (Dr. S. Singh's group): 'Systems Metabolic Engineering of Trypanothione Reductase in *Leishmania:* Crosstalk and Functionality' (Anurag Kumar and Shailza Singh); Recent Advancements in Biochemical Engineering and Biotechnology, IIT BHU, Varanasi, 15, 16 March 2019. (Poster).
- **Apoorva Parulekar** (Dr. S. Chattopadhyay's group): 'SMAR1 transcriptionally repress hTERT and alters the stem cell population in colorectal cancer cells' (Apoorva Parulekar and Samit Chattopadhyay), 25 th Biennial Congress of the European Association for Cancer Research (EACR25), Amsterdam, The Netherlands, 30 June - 03 July 2018.
- **Ashwani Kumar** (Dr. S. Mande's group): International Conference on "Proteomics for Cell Biology and Molecular Medicine, Protein Society of India (ICPMM-PSI-2018), NCCS Pune, India; 12th -14th December, 2018.
- **Avinash Sharma** (Dr. Y. Shouche's group):
  - 'Displacement of Autochthonous Microbial Communities of Godavari River During World's Largest Mass Bathing Event' (Avinash Sharma, K Jani, D Dhotre, Y Shouche), ISME International conference, Leipzig, Germany, 12-17 August, 2018.
  - Attended the 2nd WIPO Meeting of Representatives of International Depositary Authoritie under the Budapest Treaty on the International Recognition of the Deposit of

Microorganisms for the Purposes of Patent Procedure at Tepatitlán de Morelos, Jalisco, Mexico, September 4, 5, 2018.

- **Bhavana Deshmukh** (Dr. M.K. Bhat's group): 'Serum factors of obese mice induce proliferation and alter DNA damage response in cancerous and non-cancerous cells' (Deshmukh B, Bhat MK), 4th Mini Symposium in Cell Biology, National Centre for Cell Science, Pune, India, 18, 19 July, 2018.
- **Bithika Chatterjee** (Dr. S. Mande's group): GIAN workshop, "Systems Biology for Drug Discovery and Personalized Medicine", School of Life Sciences, University of Hyderabad, India; 2 - 14 July, 2018.
- **Debasish Paul** (Dr. M. Santra's group): 106th Indian Science Congress, Jalandhar, India, 7th January, 2019.
- **Deepti Tomar** (Dr. G. C. Kundu's group):
  - 'Differential expression of miR-424 and miR-505 under hypoxia regulates angiogenesis and tumor growth in breast cancer' (Deepti Tomar, Anuradha Bulbule, Ramakrishna Nimma, Mahadeo Gorain and Gopal C. Kundu), 4th International Conference on Translational Research, Goa, India, 11-13 October 2018. (Oral Presentation).
- **Dinisha Kamble** (Dr. S. Sitasawad's group): Presented a paper, 'Role of Nrf2 in breast cancer stem cells radio-resistance and tumour recurrence' (Dinisha Kamble, Dr. Sandhya Sitaswad); 25th Biennial Congress of the European Association for Cancer Research; Amsterdam, The Netherlands; 30 June - 3 July, 2018.
- **Diptaraj Chaudhari** (Dr. Y. Shouche's group):
  - International Society for Microbial Ecology-17 (ISME 17) Conference, Leipzig, Germany, 11-17 August 2018.
  - Poster presented at the International Conference on Microbiome Research (ICMR2018), Pune, 19-22 November 2018.
- **Fahima Munavar** (Dr. N. Lenka's group): 9th Bangalore-Benny Shilo Course on Developmental Biology, NCBS, Bangalore; 1-11 January, 2019.
- **Garima Pandey** (Dr. M. Wani's group):
  - 2nd National Congress on Osteoarthritis (OACON) and 1st Annual State Rheumatology Meeting (MRACON), Pune, August 31-September 2, 2018.
  - XLII All India Cell Biology Conference and 2nd International Conference on Trends in Cell and Molecular, BITS Pilani, Goa, December 21-23, 2018.
- **Heikrujam Thoihen Meitei** (Dr. G. Lal's group):
  - 'Molecular interaction of T cell receptor and chemokine receptor CCR6 signaling in the differentiation of pathogenic Th17 cells in autoimmunity' (Meitei HT, Shirolkar A, Rapole S and Lal G), 2nd Society of Inflammation Research Conference, Bangalore; 19 August 2018. (Oral Presentation, Best oral presentation award).
  - 'Chemokine receptor CCR6 signaling promotes differentiation of inflammatory Th17 cells' (Meitei HT and Lal G), NCCS Mini-symposium in Cell Biology, NCCS, Pune, India; 18, 19 July, 2018. (Poster presentation).
  - 'Chemokine receptor CCR6 signaling alters several important physiological and metabolic pathways in the Th17 cells' (Meitei HT, Kulkarni N, Shirolkar A, Rapole S and Lal G), 10th Annual meeting of Proteomics Society, India and International Conference on Proteomics for Cell Biology and Molecular Medicine, NCCS, Pune, India; 12-14th December, 2018. (Poster presentation).
- **Himanshi** (Dr. M.K. Bhat's group):
  - 'The therapeutic effect of antimetabolic drug combination in colon and breast cancer cells' (Himanshi and Bhat MK), Cellular and molecular basis of cancer: molecules to mechanisms, Department of biotechnology, S.P. Pune University, Pune, India, 7-9 February, 2019.
  - Himanshi attended Federation of Clinical Immunology Societies (FOCIS): Asian advanced course in basic and clinical immunology, Jaipur, India, 26-29 March, 2019.
- **Jay Trivedi** (Dr. D. Mitra's group): 'Novel HSP90 inhibitors as anti-HIV drug candidates' (Jay Trivedi and Debashis Mitra), International Conference on Biology and Therapeutics of HIV and Associated Infections, University of Hyderabad, Hyderabad, India; 19-21st January 2019.
- **Juilee Karhade** (Dr. M. Wani's group):
  - 2nd National Congress on Osteoarthritis (OACON) and 1st Annual State Rheumatology Meeting (MRACON), Pune, August 31-September 2, 2018.
  - XLII All India Cell Biology Conference and 2nd International Conference on Trends in Cell and Molecular, BITS Pilani, Goa, December 21-23, 2018.
- **Kailash Gupta** (Dr. D. Mitra's group): 'Heat shock protein 40 isoforms: differential regulation during HIV-1 infection and their possible role' (Kailash Gupta and Debashis Mitra), International Conference on Biology and Therapeutics of

HIV and Associated Infections, University of Hyderabad, Hyderabad, India; 19-21st January 2019.

- **Kruthika Iyer** (Dr. D. Mitra's group): 'Promoter characterization and transcriptional regulation of HSPBP1 promoter during HIV-1 infection' (Kruthika Iyer, Priyanka Chaudhary and Debashis Mitra), International Conference on Biology and Therapeutics of HIV and Associated Infections, University of Hyderabad, Hyderabad, India; 19-21st January 2019.
- **Kusum Dhakad** (Dr. Y. Shouche's group): International Society for Microbial Ecology-17 (ISME 17) Conference, Leipzig, Germany, 11-17 August 2018.
- **Lekha Rani** (DST Woman Scientist in Dr. M. Wani's group): 2nd National Congress on Osteoarthritis: Update & Research Society for Osteoarthritis Research, organized by Arthritis Research and Care Foundation, Center for Rheumatic Diseases, Pune, August 31- September 02, 2018.
- **Madhav Sridharan** (Dr. G. Das's group): 3 days Intensive Workshop on Advanced Arduino, 11/12/2018- -13/12/2018, December, 2018, Pune, India.
- **Madhuri More** (Dr. S. Bapat's group):
  - 'Understanding cellular, molecular attributes and tumor cell dormancy during growth of solid tumors in ovarian cancer' (More MH, Bapat SA), Symposium on 'Stem Cells & Cancer - India 2019', Somaiya Vidyavihar, Mumbai, India, 1stFeb 2019. (Oral Presentation Award).
  - 'Study of tumor progression in ovarian cancer' (More MH, Bapat SA), 4th Mini-Symposium on Cell Biology, Pune, India, 18 - 19 July, 2018.
  - 'Epithelial to mesenchymal transition during tumor progression in ovarian cancer' (More MH, Bapat SA), Indo-Australia Symposium on Epithelial – Mesenchymal Transition, 24th October 2018, Pune, India.
- **Madhvi Mandhania** (Dr. M.S. Patole's group): Microbial diversity dynamics of the fermentation of idli batter (Mandhania Madhvi, Sharma Lokesh, Paul Dhiraj, Suryawanshi Mangesh, Shouche Yogesh, Patole Milind), International Conference on Microbiome Research, Pune, India; 19 - 22 November, 2018.
- **Mahadeo Gorain** (Dr. G. C. Kundu's group): 'Gated nanomechine for cancer theranostics' (Mahadeo Gorain, Rajendra Prasad, Deepak S. Chauhan, Amit S Yadav, Janhavi Devrukhkara, Ram Krishn Gupta, Rohit Srivastava and Gopal C. Kundu), 4th International Conference on Translational Research, Goa, India, 11-13 October 2018. (Poster Presentation).
- **Manjushree Bahir** (DST, WoSA Fellow in Dr. N. Lenka's group): '*In vitro* biological assessment of synthetic porous 3D graft for bone tissue engineering. 3rd ISCSG's' (M. Bahir, N. Lenka.), Indian stem cells Study group's International Conference on Stem Cells and Regenerative Medicine, D.Y. Patil Vidyapeeth, Pune, India; 29-31 March, 2019, (Oral presentation).
- **Mohd Yousuf Ansari** (Dr. S. Mande's group): National workshop on "Small angle and wide angle X-ray scattering (SWAXS)-2018", Defence Institute of Advanced Technology, Pune, India; 12, 13 December, 2018.
- **Mohsina Khan** (D. A. Shiras's group): 'Attenuation of tumor suppressive function of FBXO16 ubiquitin ligase activates Wnt signaling in Glioblastoma'; 4th Mini-symposium in Cell Biology, Pune, India; 19 July, 2018.
- **Mohsina Khan, Samruddhi Zende, Rasika Avatade** (D. A. Shiras's group): 'Let the blood be a Guinea pig to save lives; peripheral blood derived hepatic organoids, an alternative for liver transplantation'; 4th Mini-symposium in Cell Biology, Pune, India; 19 July, 2018.
- **Muneesh Kumar Burman** (Dr. D. Mitra's group): 'Studies on the role of Nef interacting cell death regulatory protein ZIP Kinase during HIV-1 infection' (Muneesh Kumar Burman and Debashis Mitra), 4th Mini Symposium on Cell Biology, National Centre for Cell Science, Pune, India; 2018.
- **Namrita Haldar** (Dr. G. Lal's group): 'Role of acetylcholine receptors in the modulation of immune response in inflammation and autoimmunity' (Haldar N, and Lal G), Asian Advanced Course in Basic and Clinical Immunology organized by Federation of Clinical Immunology Societies (FOCIS), Jaipur, Rajasthan, India; 26-29 March, 2019. (Poster presentation).
- **Nawadkar R.** (Dr. A. Sahu's group): 'Role of complement anaphylatoxins C3a and C5a generated in the infection locale protect from viral infection' (Nawadkar R, Kamble A, Mullick J, Lal G, Sahu A), Annual meeting of Biological Engineering Society of India (BESCON), IIT Bombay, Mumbai, India; 26, 27 October, 2018. (Best poster award).
- **Navvya Premraj** (Dr. J. Kumar's grup): GIAN Course 2018: Recent Advancements in Biophysical Techniques and Virology at IIT Roorkee, Roorkee, India, 15-21 April 2018.
- **Nimma Ramakrishna** (Dr. G. C. Kundu's group): 'A Study on Role of Osteopontin in Metabolic Reprogramming Leading to Breast Cancer Progression' (Ramakrishna Nimma, Ramesh Butti and Gopal C Kundu), 4th International Conference on Translational Research, Goa, India, 11-13 October 2018. (3rd Prize - Poster Presentation).

- **NNV Radharani** (Dr. G. C. Kundu's group): 'Role of Tumor Associated Macrophages (TAMs) in regulation of Cancer Stem Cell (CSCs) enrichment in breast cancer' (N.N.V Radharani, Amit S.Yadav, T.V.S. Kumar, N. Ramakrishna, Anuradha Bulbule and Gopal C. Kundu), 4th International Conference on Translational Research, Goa, India, 11-13 October 2018. (2nd Prize - Poster Presentation).
- **Nutan Chauhan** (Dr. S. Singh's group): 'Understanding dynamic system models through structural modeling approach to investigate anti-leishmanial therapy' (Nutan Chauhan and Shailza Singh); National Conference on Emerging Trends in Disease Model Systems, NCCS-NASI Pune Chapter, 25-27 March 2019. (Best Poster Award by NCCS-NASI Pune Chapter 2019).
- **Om Prakash Sharma** (Dr. Y. Shouche's group):
  - 'Preservation of Intact Fecal Sample for Future Meta-metabolomic Analysis', International Conference on Microbiome Research (ICMR) 2018, Pune, India, 19-22 November 2018.
  - 'Assessment of the Role of Wastewater Treatment Plant in Spread of Antibiotic Resistance and Bacterial Pathogen', 2018 AMI–Meet organized by University of Hydrabad, India, (Poster presentation).
- **Osheen S.** (Dr. Rapole's group):
  - Presented a poster, 'New tricks for an old fox- Role of FBXO31 in DNA damage repair and genomic stability', International Conference on Proteomics for Cell Biology and Molecular Medicine, National Centre for Cell Science, Pune, India; December 12-14, 201. (Best poster award).
  - 7th International Conference on Molecular Signalling, National Centre for Cell Science, Pune, India. 23 - 25 January, 2019.
  - National Conference on Cellular and Molecular Basis of Cancer: Molecules to Mechanism, Department of Biotechnology, S.P. Pune University, Pune, India, 7 - 9 February, 2019.
- **Pankaj Kumar Madheshiya** (Dr. R. Chauhan's group): 'Role of Nup62 in Mammalian Nuclear Pore Complex (NPC) Assembly' (Pankaj Kumar Madheshiya, Parshuram Sonawane and Radha Chauhan), DLS-CCP4 workshop, London UK, 2-9 December, 2018.
- **Prachi Kapse** (Dr. G. C. Kundu's group): 'Role of hypoxia in regulation of cancer stem cell mediated breast tumor progression', (Totakura V.S. Kumar, Prachi Kapse, Radharani N.N.V., Venkatesh C.H., Dnyanada G., Srikanth G., G.F. Weber and G.C. Kundu), 5th International Conference on Angiogenesis Research, Kolhapur, India, 26 -27 October 2018. (1st Prize - Poster Presentation).
- **Prajakta Nimsarkar** (Dr. S. Singh's group): 'Systems study unravels the role of mir-146 in regulating host-pathogen interaction in leishamaniasis' (Prajakta Nimsarkar and Shailza Singh); Recent Advancements in Biochemical Engineering and Biotechnology, IIT BHU, Varanasi, 15, 16 March 2019. (Poster).
- **Pranay L. Ramteke** (Dr. M.K. Bhat's group): 'Metabolic and molecular reprogramming induced due to hyperglycemia in breast cancer' (Ramteke P. and Bhat MK), 25th Biennial Congress of the European Association for Cancer research (EACR25), RAI, Amsterdam, The Netherlands, 30 June - 03 July, 2018.
- **Pravin Rahi** (Dr. Y. Shouche's group): 'Genetic diversity of pea rhizobia in India and comparative genomics of Rhizobium leguminosarum genospecies', Satellite Meeting - Workshop on the Genomics of N-Fixing Organisms at Stockholm, Sweden, 18 August 2018.
- **Priyanka Padghan** (Dr. G. Lal's group):
  - 'B cell-intrinsic signaling controls Ig class-switch recombination during gut inflammation' (Padghan P, and Lal G), International Conference on Molecular Signaling (ICMS-2019), NCCS, Pune, India; 23-25 January, 2019. (Poster presentation).
  - 'CCR6 signaling modulates class switch recombination in B cells during gut inflammation' (Padghan P and Lal G), 45th Annual meeting of Indian Immunology Society, THSTI, Faridabad, 1-3 November, 2018. (Oral Presentation).
- **Radhika Mohandasan** (Dr. G. Das's group): One day workshop on spray drying and encapsulation (BUCHI INDIA), 29/6/2018, June 2018, Mumbai India.
- **Rajesh Vinnakota** (Dr. J. Kumar's grup): NSC 46: Probing Receptor Function with Chimeric Ionotropic Glutamate Receptors, NIMHANS, Bangalore, India, 27-29 June 2018.
- **Rajashri Shende** (Dr. A. Sahu's group): National Symposium on Recent Advances in Modern Biology and Biotechnology 2019 (RAMBB 2019), Dr. D.Y. Patil Bioinformatics and Biotechnology Institute. Tathwade, Pune; 14-16 March, 2019. (First Prize - Oral presentation).
- **Ramesh Butti** (Dr. G. C. Kundu's group): 'Reciprocal interaction between cancer cells and fibroblasts: OPN and SDF-1 are mediators (Ramesh Butti and Gopal C. Kundu), 4th International Conference on Translational Research, Goa, India, 11-13 October 2018. (Oral Presentation)

- National Workshop on Microscopy Image Analysis, Pune India, 6-8 March 2019.

- **Ravindra Taware** (Dr. S. Rapole's group): Presented a poster, 'Urinary and Salivary Volatomic investigation of head and neck cancer for identification of non-invasive putative diagnostic markers', 10th Annual Meeting of Proteomics Society, India and International Conference on Proteomics for Cell Biology and Molecular Medicine, National Centre for Cell Science, Pune, India; December 12-14, 2018.
- **Richa Pant** (Dr. S. Chattopadhyay's group): 'Role of nuclear matrix binding protein SMAR1 in adipogenesis' (Richa Pant, Aftab Alam, Samit Chattopadhyay), XLII All India Cell Biology Conference and 2nd International Conference on Trends in Cell and Molecular Biology, Goa, India, 21-23, December, 2018.
- **Rohit Sharma** (Dr. Y. Shouche's group): 'Isolation and Identification of Fungal Isolates and their Molecular Characterization' (Satish Pote, Mahesh Sonawane, Praveen Rahi, Milind Patole, Rohit Sharma, Sunil Shah, Madhuri Thakar), International Conference on Microbiome Research, 19-22, November, 2018, Pune, India.
- **Rutuja Kuhikar** (Dr. L.S. Limaye's group): 'In vitro generation of red blood cells and neutrophils from Hematopoietic stem cells', Poster presented at the 4th Mini-symposium on Cell Biology, National Centre for Cell Science, Pune, India; 18, 19 July, 2018. (First prize).
- **Sagar Varankar** (Dr. S. Bapat's group): 'Cellular and migratory plasticity in HGSC' (Varankar SS, Bapat SA), Indo-Australian Symposium on Epithelial – Mesenchymal Transition, NCCS, Pune, India, 24 October, 2018. (Poster Award).
- **Satish Pote** (Dr. M. Wani's group): Presented a poster "Isolation and identification of fungal isolates and their molecular characterization" at International Conference on Microbiome Research 2018, Pune, November 19 -22, 2018.
- **Sehbanul Islam** (Dr. M. Santra's group): An international conference on cancer, 'Tracking Cancer: Detection and Monitoring, from Diagnosis to Therapy', Barcelona, Spain; 4 - 6 February 2019.
- **Shubhanath Behera** (Dr. M. Wani's group): XLII All India Cell Biology Conference and 2nd International Conference on Trends in Cell and Molecular, BITS Pilani, Goa, December 21-23, 2018.
- **Shyamananda Singh Mayengbam** (Dr. M.K. Bhat's group):
  - 'Diet induced obesity enhances colorectal cancer tumor progession in mouse model: role of cholesterol', (Mayengbam SS, Bhat MK), XLII All India Cell Biology Conference and 2nd International Conference of Trends in Cell and Molecular Biology, BITS Pilani, Goa, India, 21-23 December, 2018.
  - 'Does accumulation of intracellular cholesterol influence colorectal cancer cell growth?' (Mayengbam SS, Bhat MK), 4th Mini Symposium in Cell Biology, National Centre for Cell Science, Pune, India, 18, 19 July, 2018.
- **Shreyas Kumbhare** (Dr. Y. Shouche's group): The Wellcome Trust/DBT India Alliance Science Communication Workshop (SciComm) in New Delhi, 24-25 September 2018.
- **Snehal Kulkarni, Deepak Khairnar, Akshay Gaike, Jyoti Priyadarshini, Vaishnavi Gurav, Siddhali Sawantdesai, Vikas Ghattargi, Gaikwad Meghana, Shrikant Pawar, Nidhi Shetty, Purva Dhepe, and Akshay Gaike** (Dr. Y. Shouche's group):
  - 'Exploration of halophilic archaea isolated from West Coast of India for production of exopolysaccharide' (Kulkarni Snehal O.; Khairnar Deepak V.; Gaike Akshay H.; Shouche Yogesh S.), International Conference on Microbiome Research (ICMR2018), Pune during 19-22 November 2018. (Poster presentation).
  - 'Study of halotolerant bacterial community from mangrove sediment of Shriwardhan, West Coast of Maharashtra, India' (Kulkarni Snehal O.; Khairnar Deepak V.; Priyadarshini Jyoti, Gurav Vaishnavi S.; Shouche Yogesh S.), International Conference on Microbiome Research (ICMR2018), Pune during 19-22 November 2018. (Poster presentation).
  - 'Study of halotolerant bacterial and haloarchaeal community isolated from marine sponges collected from West Coast of India' (Sawantdesai Siddhali P.; Kulkarni Snehal; Khairnar Deepak V.; Ghattargi Vikas C.; Meghana Gaikwad; Pawar Shrikant; Shouche Yogesh S.), International Conference on Microbiome Research (ICMR2018), Pune during 19-22 November 2018. (Poster presentation).
  - 'Study of exopolysaccharide producing halophilic bacteria isolated from saline environments' (Snehal O. Kulkarni, Deepak V. Khairnar, Nidhi Shetty, Purva Dhepe, Akshay Gaike and Yogesh S. Shouche), 59th Annual International Conference of Association of Microbiologists of India (AMI), School of Life Sciences, University of Hyderabad, 9-12 December 2018. (Poster presentation).
- **Suhas Mhaske** (Dr. M. Wani's group):
  - Presented a poster entitled "Interleukin-3 augments

osteogenesis by upregulation of β-catenin expression in preosteoblasts" at XLII All India Cell Biology Conference and 2nd International Conference on Trends in Cell and Molecular, BITS Pilani, Goa, December 21-23, 2018.

- Presented a poster entitled "IL-3 inhibits osteoclast differentiation by scavenging reactive oxygen species" in 4th Biannual NCCS Retreat 2018, Lonavala, September 2018.

- **Sumit Das** (Dr. G. C. Kundu's group):
  - 'Role of Osteopontin Isoforms in Regulation of Breast Cancer Stem Cell Phenotypes' (Sumit Das, Venkatesh Chanukuppa, Khushman Taunk, Amey Shirolkar, Srikanth & Gopal Kundu), International Conference on Proteomics for Cell Biology and Molecular Medicine (of Proteomics Society of India), Pune, India, 12 -14 December 2018. (Poster Presentation)
  - 'Role of Osteopontin Isoforms in Regulation of Breast Cancer Stem Cell Phenotypes' (Sumit Das, Mahadeo Gorain, Anuradha Bulbule, Nimma Ramakrishna, Venkatesh Chanukuppa, Khushman Taunk, Amey Shirolkar, Srikanth & Gopal Kundu), 4th International Conference on Translational Research, Goa, India, 11-13 October 2018. (Poster Presentation).
- **Surya Bansi Singh** (Dr. D. Subramanyam's group): Understanding the effect of Huntingtin toxic aggregates on vesicular trafficking (Surya Bansi Singh, Amitabha Majumdar and Deepa Subramanyam), Biennial meeting of Indian Society of Developmental Biologists, 11-15 Dec, 2018.
- **Tushar Lodha** (Dr. Y. Shouche's group): 'Mining of bacteria for hopanoid biosynthesis and occurrence of the hopanoid biosynthetic pathway in microorganisms' (Tushar Lodha, Ch. Sasikala, Ch. Venkata Ramana), 59th Annual Conference of The Association of Microbiologists of India, Hyderabad, India, 8-12 December, 2018.
- **TV Santosh Kumar** (Dr. G. C. Kundu's group): 'Hypoxia Mediates Cancer Stem Cell (CSC) Enrichment Through Downregulatiobn of Estrogen Receptor Alpha (ERα) Expression in ER Positive Breast Cancer Cells' (Totakura V.S. Kumar, Radharani N.N.V., Venkatesh C.H., Dnyanada G., Srikanth G., G.F. Weber and G.C. Kundu), 4th International Conference on Translational Research, Goa, India, 11-13 October 2018. (Poster Presentation).
- **Upasana Kapoor** (Dr. N. Lenka's group):
  - 'Investigation of therapeutic potential of plumbagin, a napthoquinone, in human glioblastoma' (U. Kapoor, N. Lenka), National Conference on Emerging Trends in Disease Model Systems, NCCS, Pune, India; 26-27 March, 2019, (Poster Presentation).
  - 'Plumbagin: putative mechanisms of action mediating cells cycle, metabolism, and apoptosis in glioblastoma cells' (U. Kapoor, N. Lenka), 41st Annual Meeting of the Japan Neuroscience Society, Kobe, Japan; 25-29 July, 2018. (Oral Presentation).
- **Venkatesh Chanukuppa** (Dr. S. Rapole's group): Presented a poster, 'Multipronged proteomic analysis of multiplr myeloma towards new targets and chemoresistance markers', 10th Annual Meeting of Proteomics Society, India and International Conference on Proteomics for Cell Biology and Molecular Medicine, National Centre for Cell Science, Pune, India; December 12-14, 2018. (Best poster award).
- **Vibhuti Kumar Shah** (Dr. S. Chattopadhyay's group): 'Remodeling of chromatin by SMAR1 helps in CD4+ memory T cell differentaiation' (Vibhuti Kumar Shah and Samit Chattopadhyay), Asian Advanced Course in Basic and Clinical Immunology by FOCIS, Jaipur, India, 26-29, March, 2019.
- **Yashika Agrawal** (Dr. M. Santra's group): Presented an elevator pitch on, 'F-Box Protein FBXO41 and Cancer'; 4th Mini Symposium on Cell Biology, NCCS, Pune, India; 18, 19 July, 2018.

NCCS Foundation Day

(Celebrating 30 glorious years - 26th August, 2018)

Foundation Day Oration: 'From Incremental to Diusruptive Game Changing Innovation'

by Prof. Raghunath A. Mashelkar FRS




Felicitation of employees who have completed 20 years of service







Scientific Conference in Hindi 3, 4 April, 2018

(organized in association with ARI and CSIR-NCL, Pune)




Science Academies' Summer Research Fellows' Symposium 29 June, 2018

4th Mini-Symposium in Cell Biology 18, 19 July, 2018

EU-India call on Next Generation Influenza Vaccine to Protect Citizend Worldwide 28 Sep. 2018

(Information and preparatory session organized by NCCS for the DBT, in association with the Delegation from the European Union to India)

Indo-Australia Symposium on 'Epithelial- Mesenchymal Transition' 24 October 2018

Organized in association with the Queensland University of Technology (QUT), Brisbane, Australia, and the Institute for Bioinformatics (IOB), Bangalore, India; Funded by the from the Australia India Council.

(NCCS Organizing Committee Member: Dr. Bapat)

International Conference on Microbiome Research (ICMR 2018) 19 - 22 November 2018

Education day on 'Current Trends in Proteomics and Metabolomics' 11 December, 2018

More than 100 participants, including clinicians from the Armed forces Medical College, Pune, participated

International Conference on Proteomics for Cell Biology and Molecular Medicine & 10th Annual meeting of the Proteomics Society, India (PSI) 12-14 December, 2018




International Conference on Molecular Signaling (ICMS-2019) 23-25 January, 2019

(Organized by NCCS jointly with the Department of Zoology, S. P. Pune University & The Society for Molecular Signalling)




Strategies to facilitate technology innovations & scale up in academic institutions 23 February 2019




National Conference on 'Emerging Trends in Disease Model Systems' 25 - 27 March 2019

[Organised in association with the National Academy of Sciences, India (NASI)-Pune Chapter]




Extramural Events Organized

NCCS Retreat at Lonavala 26, 27 September, 2018




4th International Conference on Translational Research: Recent Developments and Innovations in Human Health and Agricultural Research 11 - 13 October 2018

Organized at Goa jointly by NCCS and the Indian Society of Translational Research (ISTR), New Delhi; National Cancer Institute (NCI) - AIIMS; Institute of Bioresources & Sustainable Development, Imphal; Institute of Advanced Study in Science and Technology, Guwahati. (Organizing Secretary: Dr.Gopal Kundu)

5th International Conference on Angiogenesis Research: Targeted anti-angiogenic therapy 26 - 27 October 2018

Organized at Kolhapur jointly by NCCS with the Dept. of Stem Cell & Regenerative Medicine, Centre for Interdisciplinary Research, Kolhapur. (NCCS Organizing Committee member: Dr. Gopal Kundu).

Symposium on 'Stem Cells and Cancer - India 2019' 01 February, 2019

(Organized at Mumbai jointly by NCCS, Somaiya Vidyavihar and Sathgen Biotech, Mumbai)

(NCCS Organizing Committee member: Dr. Sharmila Bapat)

Talks Delivered at NCCS by Invitees

- 'Scope and challenges in Integrative Research of Ayurved and Contemporary Medicine'
  Dr. Mukund Sabnis
  President, Jeevanrekha ayurved chikitsalaya
  and research center.
  2nd April, 2018

- 'Deciphering signaling pathways within host cells hijacked by pathogens'
  Dr. Vikash Singh
  Department of Pathology, University of Cambridge, UK
  12th April, 2018

- 'Enjoying a Three-way marriage between Maths, Biology and Medicine'
  Dr. Anurag Agrawal
  Director, CSIR-Institute of Genomics & Integrative Biology (IGIB), New Delhi.
  13th April, 2018

- 'Computational systems biology of cancer metastasis: can theory help understand cancer biology?'
  Mohit K. Jolly,
  Department of Bioengineering, Rice University, USA
  25th May, 2018

- 'Molecular Mechanisms of Metastasis'
  Prof. Georg F. Weber
  University of Cincinnati, Ohio, USA
  28th May, 2018

- 'Importance of cellular organelles in controlling the miRNA-mediated gene expression in mammalian cells'
  Dr. Suvendra Bhattacharyya
  Head, Molecular Genetics Division, CSIR-Indian Institute of Chemical Biology, Kolkata
  30th May, 2018

- 'RNA tunes the solubility and phase behaviour of prion-like RNA-binding proteins'
  Dr Shovamayee Maharana,
  Max Planck Institute of Molecular Cell Biology and Genetics, Germany.
  26th July, 2018

- 'Discovery of a novel form of developmental protein JARID2 and its implications to diseases'
  Dr. Aditi Kanhere
  School of Biosciences, University of Birmingham, UK
  10th August, 2018

- 'Tossing coins inside living cells'
  Prof. Roop Mallik
  Dept. of Biological Sciences, Tata Institute of Fundamental Research, Mumbai.
  27th August, 2018

- 'Mechanisms involved in regulation of hematopoietic stem cell function and fate decision'
  Dr. Ashwini Hinge
  Wellcome Trust-DBT Intermediate Fellow
  29th August, 2018

- 'Genetic and epigenetic control of antigen receptor gene assembly'
  Dr. Ranjan Sen
  NIH/National Institute on Aging, USA
  31st August, 2018

- 'Engineeering functional materials and soft-organic nanohybrids for cancer detection and bioimaging'
  Dr. Sivaramapanicker Sreejith
  Biomedical Institute for Global Health Research and Technology, National
  University of Singapore, Singapore.
  19th September, 2018

- 'Non canonical roles of BER enzymes in RNA processing: novel perspectives in cancer biology through the study of APE1 protein - and RNA-interactomes'
  Prof. Gianluca Tell
  The School of Medicine - University of Udine (UNIUD), Italy
  25th September, 2018

- 'Delinating the function of the messengers in *M. tuberculosis*'
  Dr. Vinay Kumar Nandicoori
  National Institute of Immunology, New Delhi, India
  9th October, 2018

- 'SWR1C: A nucleosome editing machine'
  Dr. Raushan Singh
  University of Massachusetts Medical School, USA
  15th October, 2018

- 'Anti-VEGF therapy: clinical conundrums and optimisms'
  Prof. Debabrata (Dev) Mukhopadhyay
  Mayo Clinic College of Medicine and Science, USA
  23rd October, 2018

- 'The TP53 gene: A tumor suppressor gene? An oncogene? Or both?'
  Dr. Susanta Roychoudhury
  Molecular Biology Research and Diagnostic Laboratory, Saroj Gupta Cancer Centre and Research Institute, Kolkata, India
  25th October, 2018

- 'Conversion of a staphylococcal pathogenicity island (SaPI) to an antibacterial drone (ABD)'
  Dr. Geeta Ram
  Regional Centre for Biotechnology, Faridabad, India
  15th November, 2018

- 'Explore molecular mechanism of non-coding RNA metabolism for symmetric mutation at IGH locus'
  Dr. Pankaj Kumar Giri
  Columbia University, New York, USA
  19th November, 2018

- T cell immune memory in infectious diseases: lessons from single-cell transcriptome analysis'
  Dr. Veena Patil
  La Jolla Institute for Allergy and Immunology, USA
  26th November, 2018

- 'Immune homeostasis by regulatory T cells and circulating immunoglobulins'
  Dr. Jagadeesh Bayry
  Director of Research, Inserm, Paris, France
  17th December, 2018

- 'Lipid droplet and peroxisome vesicle budding from the ER subdomains'
  University of North Carolina, Chapel Hill, USA
  Dr. Amit Joshi
  7th January, 2019

- 'Obesity: Liver dictates meta-inflammation via secretory hepatokine, dipeptidyl peptidase 4 (DPP4)'
  Dr. Dr. Devram Ghorpade
  Department of Medicine, Columbia University, New York, USA
  31st January, 2019

- 'The evolving landscape of translational cancer research & future challenges in India'
  Prof. G. K. Rath
  In-charge, National Cancer Institute-India & Chief, Institute Rotary Cancer Hospital, AIIMS, New Delhi.
  5th February, 2019

- 'Brainstem Control of Response to Pain and Itch'
  Dr. Arnab Barik
  National Center for Complementary and Integrative Health (NCCIH), National Institutes of Health (NIH), USA
  6th February, 2019

- Structure and Function of Epithelial Calcium Channel TRPV
  Dr. Appu Kumar Singh
  Department of Biochemistry and Molecular Biophysics, Columbia University, USA
  11th February, 2019

- 'Planarians as a model to study conserved gene regulatory mechanisms controlling adult stem cell dynamics'
  Dr. Prasad Abnave
  Department of Zoology, University of Oxford, UK
  14th February, 2019

- 'CRAC channels Ca2+ microdomains in NFAT activation and gene expression'
  Dr. Pulak Kar
  Department of Physiology, Anatomy and Genetics, University of Oxford, UK
  20th February, 2019

- 'Dual roles of Swi6 (Heterochromatin Protein 1) in controlling recombination around centromeres and segregation in meiosis'
  Dr. Mridula Nambiar
  Division of Basic Sciences, Fred Hutchinson Cancer Research

Center, USA
7th March, 2019

- 'Identifying mechanisms underlying formation of nuclear membraneless compartments and their role in neurodegenerative diseases'
  Dr. Shovamayee Maharana
  Max Planck Institute of Molecular Cell Biology and Genetics, Germany
  12th March, 2019

- 'Discovery & development of Badaquiline - A new drug for drug-resistant tuberculosis: Harnessing the value of innovation'
  Dr. Anil Koul
  Director, CSIR-Institute of Microbial Technology (IMTECH).
  15th March, 2019

- Information session on 'Funding Opportunities for carrying out Research in Germany'
  Devi Arand, Honorary Director, DAAD Information Centre, Pune
  15th March, 2019

- 'DEAD-box RNA helicases: A family affair in governing translational control of eukaryotic gene expression'
  Dr. Neelam Sen
  National Institute of Child Health and Human Development, NIH, USA
  26th March, 2019

Technical Seminars / Demonstrations

Technical seminars / demonstrations organized by the FACS facility

Sr. No.	Date	Details of the Seminars
1	21/05/2018	Presentation on 'Acoustic technology - Attune Nxt Flow cytometer' by Invitrogen. (Demonstration and workshop: 21-25 May, 2018)
2	12/11/2018	Introduction to Imaging Flow Cytometry (AMNIS)- by Merck Life Science Pvt. Ltd (13-20 Nov: Demonstration and hands-on workshop).
3	01/03/2019	Technical talk (and demonstration) by BD Life Sciences on "BD Rhapsody- Single cell multi-omics solution".

Technical seminars / demonstrations organized by the bio-imaging facility

Sr. No.	Date	Details of the Seminar
1	30/05/2018	Capabilities of Nikon High-end microscopes available at NCCS and its applications - by Nikon India Private Limited.
2	20/06/2018	Novel concepts in an in vivo imaging & Multiplex IHC - by PerkinElmer
3	26/06/2018	Insights into Cell Biology with Real-Time Quantitative Live-Cell Analysis - by Sartorius Bio analytics.
4	23/07/2018	The new age of SEMs for Life Sciences - by Carl Zeiss India Pvt. Ltd.,
5	27/07/2018	High Sensitive Spectral Multiphoton Microscope System – DIVE - by Leica Microsystems - a Div. of DHR Holding India Pvt. Ltd.
6	14/08/2018	High Sensitive Spectral Multiphoton & Confocal Microscope System - by Leica Microsystems - a Div. of DHR Holding India Pvt. Ltd.
7	20/08/2018	Recent developments in High speed confocal live cell imaging and High Speed deep tissue imaging techniques - by Olympus Corp.
8	04/09/2018	Nikon High End Microscopy Imaging Techniques: Brief Introduction and Recent developments. – by Nikon India Pvt. Ltd
9	17/09/2018	Lecture on FV3000 CLSM microscope system – by Olympus Corp. Lecture & demonstration (18-28 September 2018). (Demonstration: 17-28 Sep. 2018)
10	18/09/2018	High Content Imaging: Spinning-Disk Confocal Technology with Advanced Informatics. – by PerkinElmer Inc.,
11	19/09/2018	Cryo CLEM - The Combination of Cryo Fluorescence Microscopy &Cryo Electron Microscopy – by Leica Microsystems - a Division of DHR Holding India Pvt. Ltd.

Sr. No.	Date	Details of the Seminars
12	11/10/2018	Technical talk : High Content Analysis Instrument Invitrogen CellInsight HCS CX7 LED - by Invitrogen. (Demonstration: 11-19 Oct. 2018)
13	22/10/2018	Presentation on High Content Imaging and 3D Holo Tomographic Live cell Imaging. – by Biotron Healthcare (India) Pvt Ltd
14	25/10/2018	The ImageXpress Micro Confocal Platform - A complete solution for Automated Confocal Imaging and High Content Analysis". – by Spinco Biotech
15	25/10/2018	GE Healthcare: IN Cell Analyzer 6500HS: A Multi modal imaging solution for high content analysis. – by GE Healthcare.
16	13/11/2018	iQ Screener Plus The Intelligent Flow by IntelliCyt Corp. (A Sartorius Group) High Content imaging – by Sartorius
17	26/11/2018	Technical Seminar - Nikon A1R-HD Confocal Microscope. – by Nikon India Private Limited (Demonstration workshop: 26 Nov. - 7 Dec. 2018)
18	27/11/2018	Nikon High Content Imaging System Capabilities – by Nikon India Pvt Ltd
19	17/12/2018	ONI Nanoimager - Super resolution microscope - Oxford Nanoimaging Ltd. (Demonstration workshop: 17 Dec. 2018 – 5 Jan. 2019)

Other Technical Seminars / Demonstrations

- 'New technology in the area of Small Animal Live Imaging' - MARS Preclinical Spectral CT System'
  Prof. Anthony Butler - Director of Bioengineering; Head of Department of Radiology, University of Otago, New Zealand.
  10th April, 2018

- 'Multiplex fluorescence western blotting'
  Dr. Ben Wang - Global Product Manager and Field Application Scientist, Bio-Rad
  18th April, 2018

- 'Developing 3D cell culture within 1 hr / Importance of Primary cells & Techniques to Avoid *Mycoplasma* Infections'
  Divay Bagga - Marketing Manager, Lonza
  6th July 2018

- 'Droplet Digital PCR (ddPCR) Technology' - Workshop (lecture and demonstration)
  Dr. Abhijit Dixit - Bio-Rad
  30th July - 3rd August, 2018

- 'Digitizing your qPCR assays with Clarity System' (lecture & demonstration)
  Dr Ashutosh Upadhyay - Product Manager (Genomics), Premas Life Sciences
  17th - 19th October, 2018

- 'A Brief Overview of Instrumentation & Application Highlights Powered by TIMS TOF and PASEF Technology'
  Arghya Acharjee - Application Specialist, Bruker India Scientific Pvt. Ltd.
  4th February, 2019

- 'APEER - Open image analysis platform'
  Dr. Sreenivas Bhattiprolu - Director of Digital Solutions, Carl Zeiss Microscopy Inc, USA.
  21st February 2019

- 'Triple TOF and QTRAP: Next-Gen Proteomics Platform and Data Analysis system'
  Dr. Dipankar Malakar - Application Support Manager, Sciex, Gurgaon
  27th February, 2019

Other Workshops / Training Programmes Conducted

Hands-on Training Workshops on Basic Cell Culture Technology
Organized by the Cell Repository, for early career researchers from all over India



14 - 17 May, 2018 29 October - 01 November, 2018

Training Workshop on 'Light Microscopy' 7 - 9 August, 2018
(In-house training organized by the bio-imaging facility for PhD research scholars, post-docs and technicians, on the Zeiss LSM 510 Meta Confocal laser scanning microscope, the inverted microscope & the Apotome microscope)

Metabolomics - National Hands-on Workshop 9 - 10 December, 2018
(25 PhD students and post-doctoral scientists were trained)

Indo-US Bilateral Workshop on 'Understanding Cell Biology through Proteomics and Metabolomics' *(organized in association with IUSSTF)* 10-11 December 2018

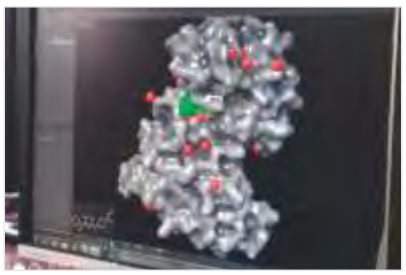



National Workshop on 'Microscopy Image Analysis' 6-8 March, 2019




Training on 'Confocal Fluorescence Microscope' 14 March, 2019
Organized for faculty from the D.Y. Patil University

National Workshop on 'Systems Biomedicine and Network Pharmacology' 27 March 2019
(Organised by the bioinformatics facility in association with NASI-Pune Chapter)



Attune Nxt Flow cytometer workshop 21-25 May 2018.
The FACS facility organized an in-house workshop

Proteomics workshops
In-house proteomics hands-on training workshops conducted by the proteomics facility for the students of NCCS - Sample preparation and Orbitrap mass spec analysis of the proteome.
18-22 June, 2018; 9-13 July, 2018; 6-10 August, 2018; 4-8 September, 2018.

FACS Canto-II training
The FACS facility organized an in-house training for students: 22-23 March 2018, 3-4 May 2018, 28-29 May 2018, 30-31 August 2018, 17-18 September 2018 and 15-16 November 2018.

Dr. Nibedita Lenka was an invited course resource person at the AICTE-approved QIP workshop on "Recent trends in Biotechnology Related to Tissue Engineering", organized for College Teachers around Chennai (~ 20), at IITM, Chennai, January 7-11, 2019.

Training Conducted by NCMR Scientists	Date
Workshop on Genome annotation *(for MSc. Students from Garware college)*	12 - 15 November, 2018
Workshop on Basic Molecular Biology Technique *(for MSc Zoology students of the Ramkrishna More Vidyalaya, Pune)*	21 December, 2018
Workshop on Microbial Identification and Preservation	07 - 12 January, 2019
Workshop on Microbial Genomics	14 - 19 January, 2019

Other Happenings at NCCS

1) Visit by the Hon'ble Parliamentary Standing Committee on Science & Technology, Environment & Forests *27 April, 2018*



2) MoU signed with Jai Research Foundation, Gujarat *30 May 2018*

(for collaborative work to generate, validate and characterize 3D human tissues)

International Day of Yoga *21st June, 2018*



'Public Health & Yoga' - by Dr. Avinash Patwardhan (Adjunct Assistant Professor in Global and Community Health)

Yoga session conducted by Mr. Sunil Kachare & Dr. Jyoti Singh

International Women's Day 8th March, 2019

'आनंदमयी शिक्षा की ओर'

Talk by **Shubhada Joshi** *(Founder of 'Khelghar')*

NCCS research highlighted in the media

- Media coverage of the research carried out by Dr. Anjali Shiras and her group, which was published in PLoS Biology (Panda *et al*, 2018 Oct 8; 16(10):e2004204).

- *Radio*

  * 26th Oct, 2018: Delhi Rainbow FM; * 17 Oct, 2018: AIR primary channel - Regional news

- *Television*

  * 18th Oct, 2019: Mumbai Doordarshan Kendra-DD News Live - 10 pm

  * 19th Oct, 2019, Mumbai, IBN Lokmat.

- *Articles in News papers / magazines*

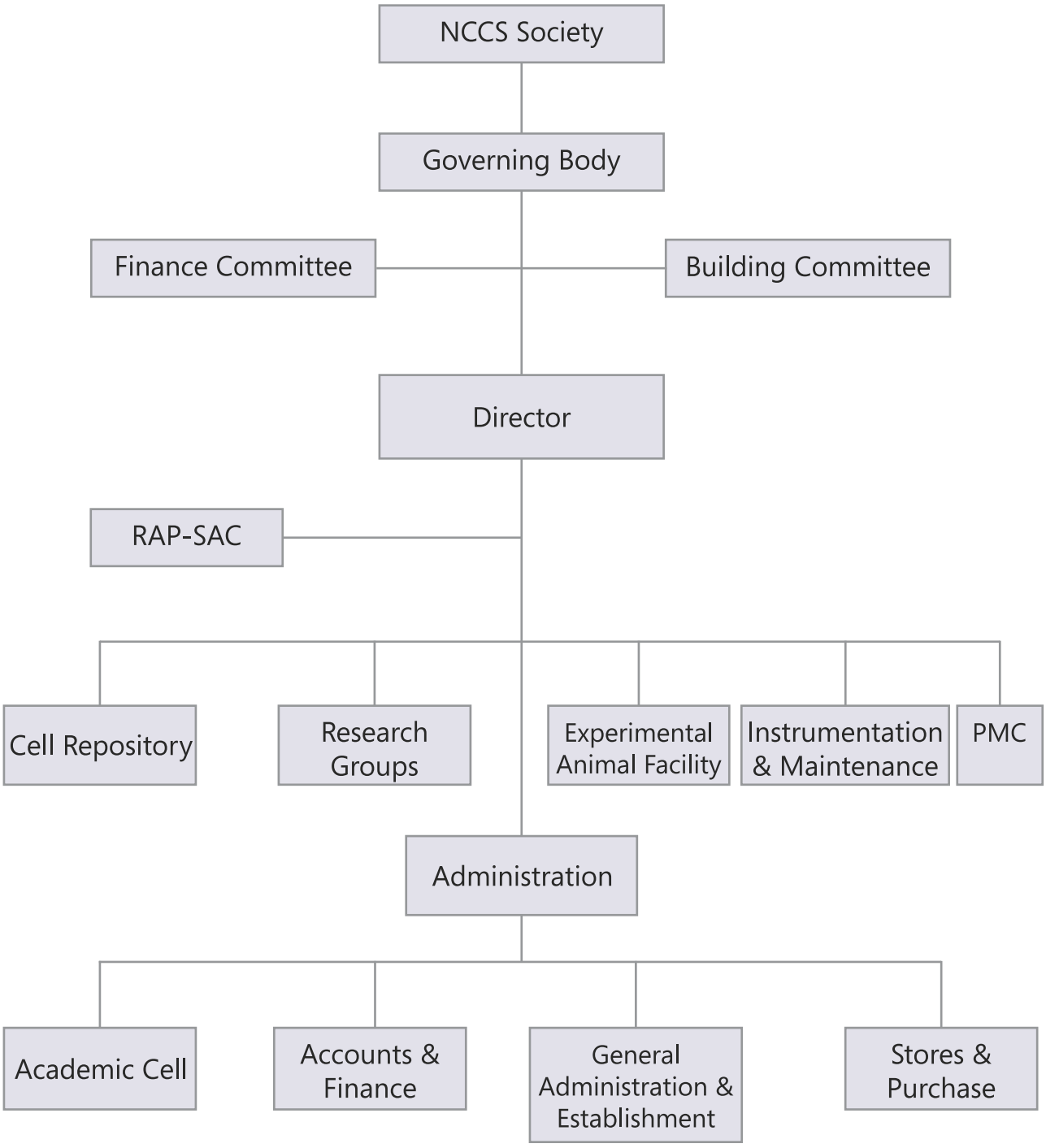
  * Researchers from NCCS Pune and KIIT Bhubaneswar decode one more factor that can cause cancer; Bhubaneswar Buzz; October 20,2018.

  * Pune scholars decode one more factor that can cause cancer; Hindustan Times; Oct 17,2018.

  * Team of researchers finds cancer-causing RNA strain; Times of India; October 17, 2018.

  * The carcinogenic role of untranslated RNAs; Research Matters, Pune, December 6th 2018.

NCCS Organization



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New Delhi 110 003, India

Administration

The NCCS Administration consists of the following sections: General Administration & Establishment, Civil Maintenance, Accounts & Finance, and Stores & Purchase. The centre also has an Instrumentation & Maintenance unit. All these sections provide support services to the main scientific activities of the centre.

The NCCS staff strength (as on 31st March, 2019):

Scientists	:	34
Administrative Staff	:	41
Technical Staff	:	74

Total	:	149

Reservation Policy

NCCS follows the Government of India orders on reservation matters. For direct recruitments, respective rosters are followed, with reservation as follows: 15% for SC, 7.5% for ST and 27% for OBC, on an All India Basis by Open Competition. Liaison officers have been nominated to ensure compliance with the reservation orders issued in favour of SC/ST/OBC. NCCS also follows the Government of India reservation policy for physically handicapped candidates.

Right to Information Act 2005

As per the requirement of the RTI Act 2005, NCCS has nominated Shri. V. S. Shinde, Officer 'C' (Administration) as the CPIO and Dr. Jomon Joseph, Scientist 'F', has been nominated as the First Appellate Authority.

Security

NCCS has engaged a private Security Agency for providing security services on a contractual basis. All important places in the complex have been manned by security personnel throughout 24 hours in a day. As on date, there is no security-related problem at the Centre.

Committees

The Centre has formed the following committees as required under various statutes and guidelines for smooth functioning of the institute:

1. Grievance Committee
2. Internal complaints committee (for the prevention of sexual harassment at the workplace)
3. Institutional Animal Ethics Committee (IAEC)
4. Institutional Biosafety Committee (IBSC)
5. Institutional Ethical Committee (IEC) and Institutional Committee for Stem Cell Research (IC-SCR)

Disciplinary Matters

The Centre follows CCS (CCA) rules 1965 and NCCS bye-laws for monitoring disciplinary matters at the Centre.

Vigilance Matters

The monthly and quarterly reports of all vigilance-related matters, including responses to departmental inquiries and complaints (if any), were regularly sent by the part-time Chief Vigilance Officer (CVO) of the NCCS to the CVO of the Department of Biotechnology, New Delhi.

NCCS also observed a 'Vigilance Awareness Week' during the time period, 29th October to 3rd November, 2018. The theme of this year as laid down by the CVC was "Eradicate Corruption – Build a New India". All the staff members, students and project fellows took the pledge of integrity on 31.10.2018 at 11:00 am. Banners with information to curb corruption were displayed near the NCCS gate and in the reception area as a reminder of the vigilance awareness week.

Implementation of the Official Language

The Director, NCCS, strongly supports the use of the Official Language in official work, and other related activities carried out at the Centre. NCCS has constituted an Official Language Implementation Committee to implement the orders of the

Government of India to use the Official Language in day-to-day official work.

A scientific conference was organised in Hindi on the 3rd & 4th of April, 2018, in association with two other organizations in Pune, the Agharkar Research Institute (ARI) and National Chemical Laboratory (CSIR-NCL), to promote the use of the official language in the field of science. Dr. Rishipal Dheeman ('Rishi'), scientist & writer from Ahmedabad, was invited as the Chief Guest. A total of 58 research papers were presented in Hindi during the conference. 125 participants from 17 different institutes across India participated in the conference. Shri. Jayant Sahastrabuddhe, Organising Secretary, Vijnana Bharati, chaired the valedictory session.

The Hindi fortnight was celebrated with much enthusiasm by holding various competitions for the staff & students of NCCS, including 'Hindi essay writing', 'Hindi Kavita Pathan', 'Hindi handwriting & dictation' 'Hindi Shabdagyan" and 'Hindi elocution'. Dr. Gorakh Thorat, Head of the Department of Hindi, Sir Parshurambhau College, Pune, graced the Hindi Day function held on 21st September, 2018, as the Chief Guest. On this day, the sixth issue of 'Meemansa' (Hindi Patrika) was released at the hands of Dr. Gorakh Thorat, Dr. G. C. Mishra (former Director of NCCS), Dr. Shekhar C. Mande (Director, NCCS) and Dr. Shailza Singh (Scientist & Chief Editor, Meemansa).

A workshop on the topic entitled 'हिन्दी के प्रगामी प्रयोग के संबंध मे राजभाषा नीतियों का अनुपालन और उसमे आने वाली बाधाएँ' was conducted on 25th May, 2018, by DBT Officials at NCCS. A lecture and hands on activity on the topic entitled 'राजभाषा, संपर्कभाषा तथा अंतर्राष्ट्रीय भाषा के रूप में हिंदी का महत्त्व' by Dr. (Mrs) Swati Chaddha, Hindi Officer, CSIR-NCL was organized during a Hindi Workshop held on 6th December, 2019. On the occasion of the International Women's Day, i.e. 8th March, 2019, Ms. Subhada Joshi (Founder of 'Khelghar') gave a talk in Hindi on 'आनंदमयी शिक्षा की ओर'

Release of the sixth issue of '**Meemansa**'
Dr. Gorakh Thorat, (HoD, Hindi Dept., S.P. College, Pune), Dr. G. C. Mishra (former Director of NCCS), Dr. Shekhar C. Mande (Director, NCCS) and Dr. Shailza Singh (Chief Editor-Meemansa) - 21st September, 2018

Hindi workshop 25 May, 2018

Hindi workshop 6th Dec., 2018

National Centre for Cell Science
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