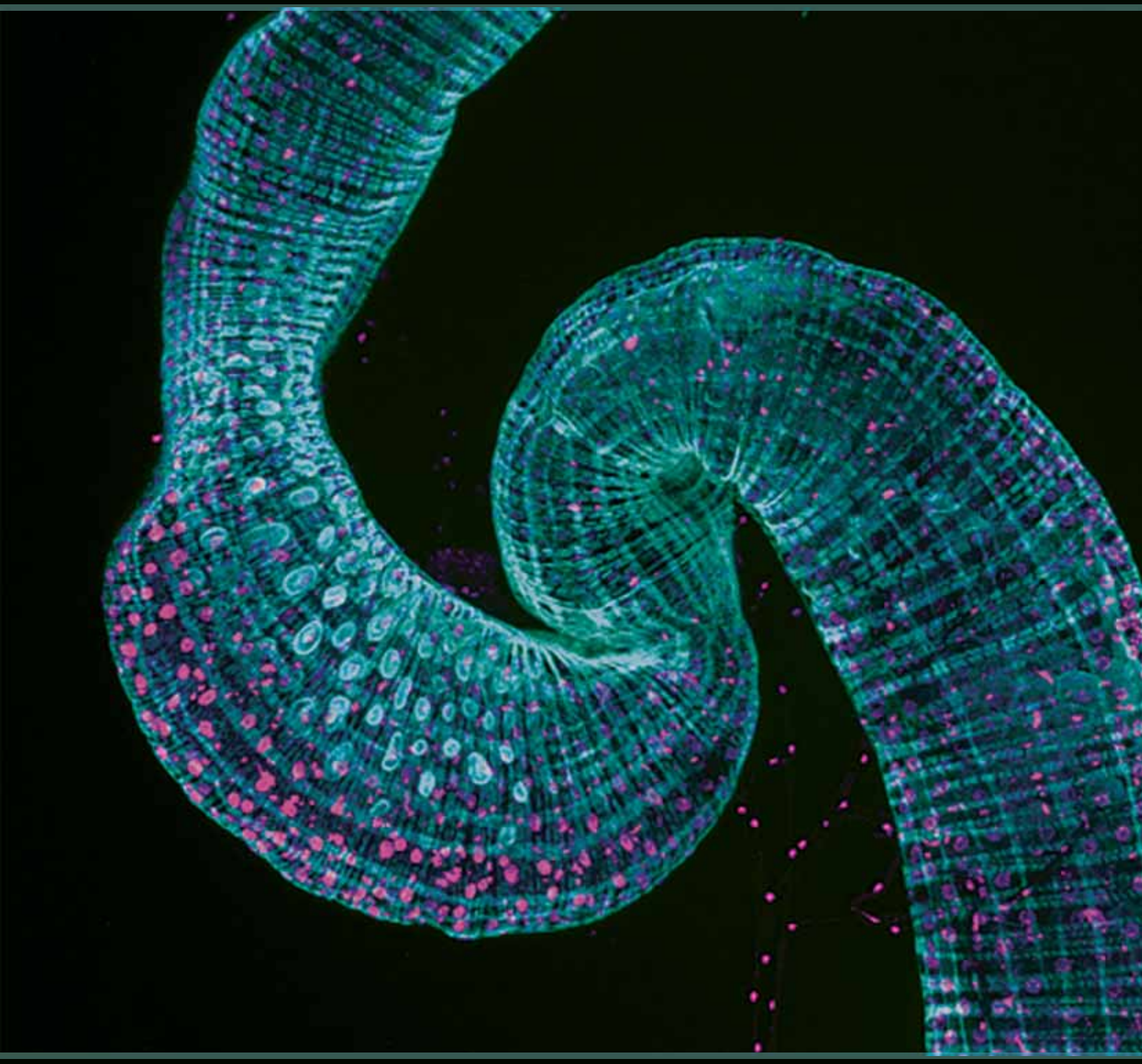
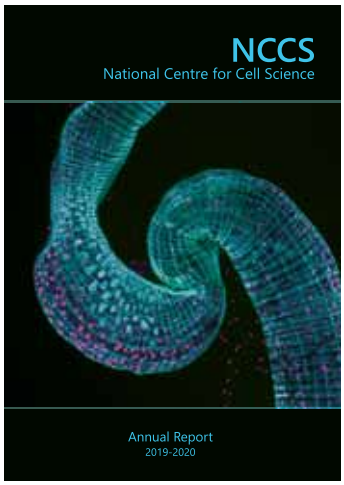
NCCS

National Centre for Cell Science



Annual Report

2019-2020

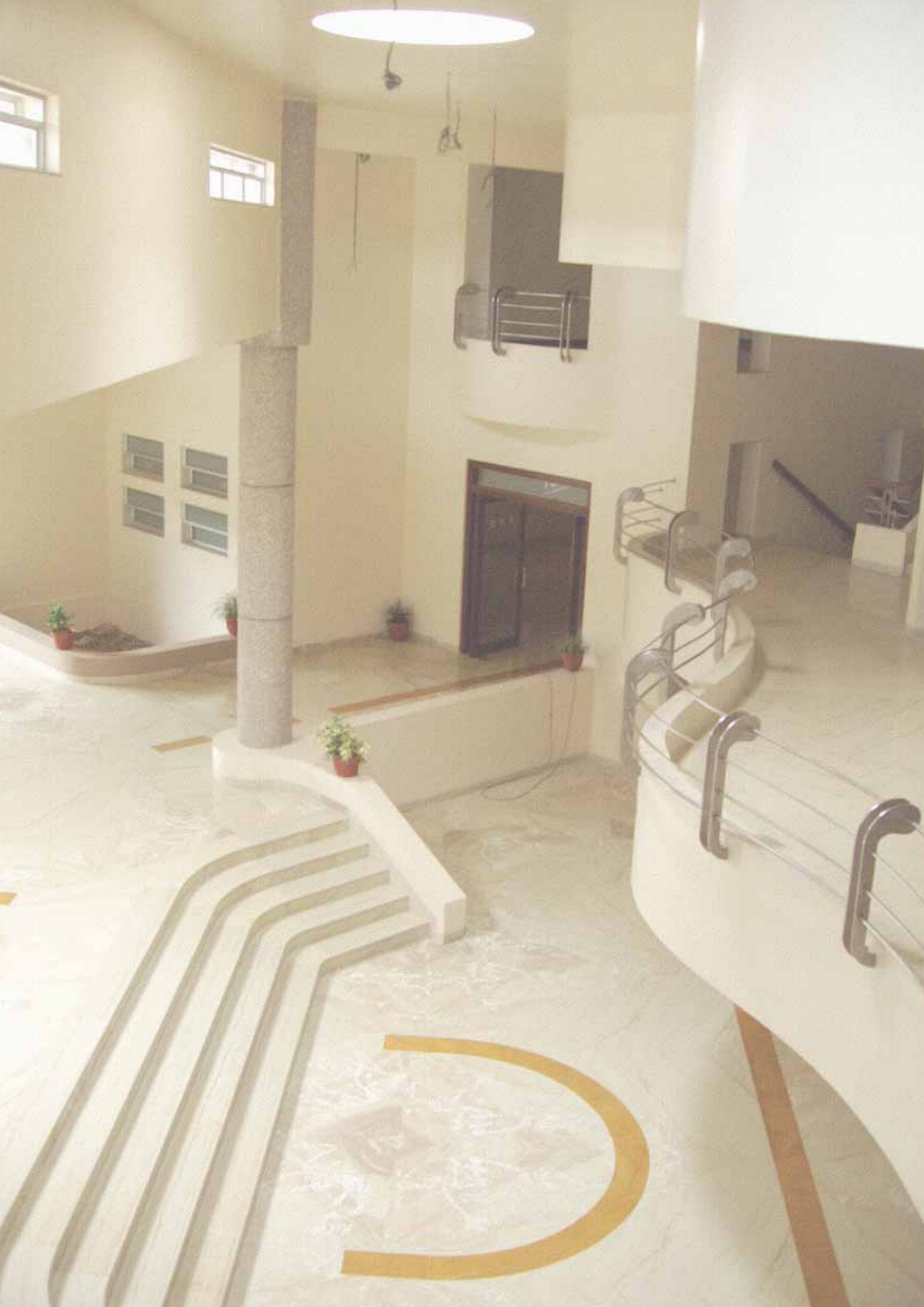


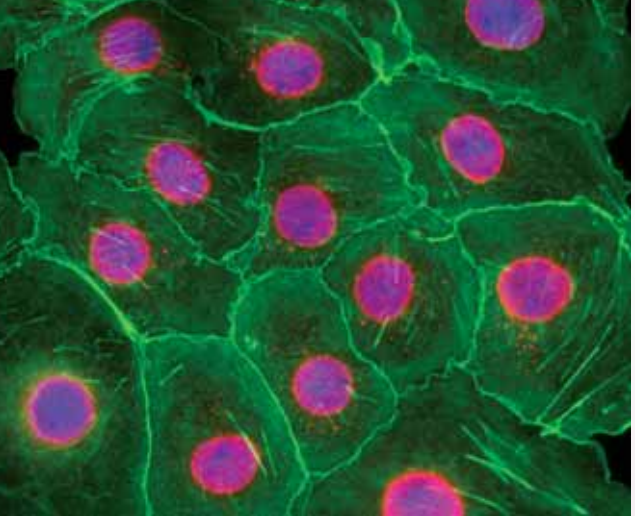
Cover page image:

Midgut of an adult fruit fly stained with DAPI (purple) and Phalloidin FITC (cyan)
(Image courtesy of Gaurav Das, Rusha Chakraborty and the NCCS bio-imaging facility)

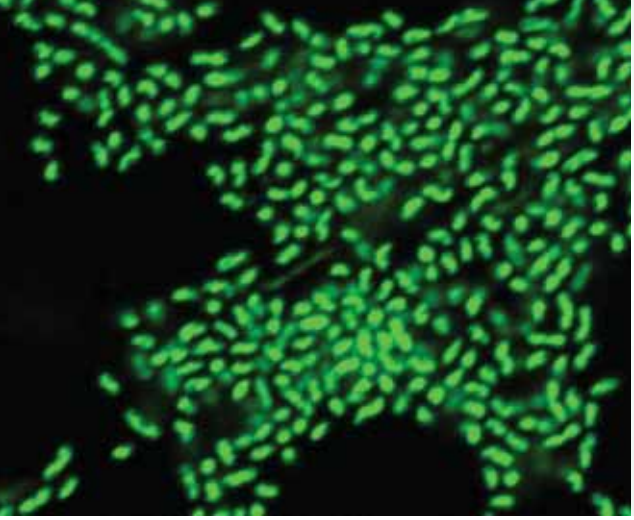
National Centre for Cell Science

Annual Report 2019 - 2020





Contents



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.

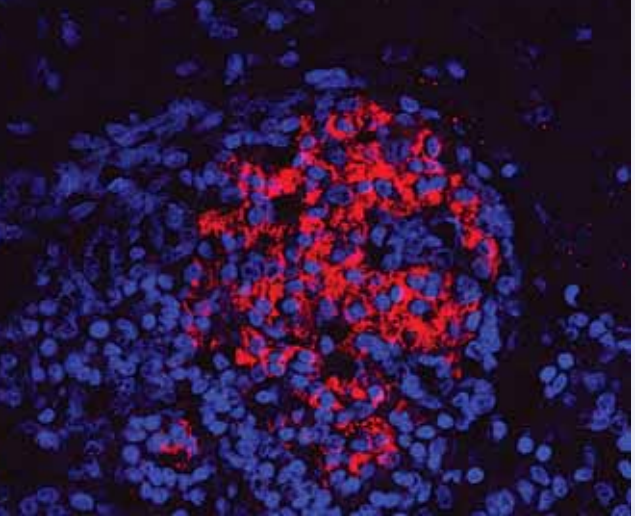
- To establish and conduct postgraduate courses, workshops, seminars, symposia and training programs in the related fields.

- 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 successful efforts in this direction. 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 NCCS Centre of Excellence, National Centre for Microbial Resource (NCMR), 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 NCMR is the largest individual collection of microorganisms in the world and is instrumental in India being internationally ranked among the top few countries with the largest collections 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, NCMR 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', was initiated by NCCS as an extramural teaching programme wherein the scientists teach fundamental concepts of science through lectures & hands-on activities to students and faculty 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 approaches and tools used in biology, which 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 Science Academies' Summer Research Fellows) and project trainees (from various academic institutions).

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

From the Director's Desk

It is my pleasure to present my first Annual Report as Director of the National Centre for Cell Science (NCCS), Pune, for the financial year 2019-20. I would like to take this opportunity to reflect on our progress over the last year and to envision our contribution to the scientific future of India.

Initially established as a National Cell Repository, NCCS serves the nation by maintaining and distributing a large number of animal cell cutures to various colleges, universities and research institutions in India. By doing so, we encourage the pursuit of cell biology in a large number of institutions. We have also created a state-of-the-art infrastructure for the characterization and authentication of cell lines. We take pride in providing this national service, and are continuously working towards upgrading our services.

NCCS has also established the Centre of Excellence, National Centre for Microbial Resources (NCMR), with a special mandate from the Department of Biotechnology (DBT), for the collection, identification, preservation and distribution of microbial cultures from various ecological niches across India. NCCS-NCMR is the the largest individual culture collection in the world, and has been instrumental in facilitating research in microbial ecology in India.

As one of India's leading research institutions, our primary focus is on addressing the current and emerging public health needs, along with striving to provide a better understanding of basic cell biological processes. Over a period, we have expanded our scientific base to research areas that focus on structural and computational biology, proteomics and neurobiology.-. These areas complement and strengthen the previously existing areas of research within NCCS, which focus on understanding the basis of development and progression of cancer, cellular metabolism and intracellular transport, and infectious diseases such as leishmaniasis, AIDS, tuberculosis and malaria. The research activities in the institute are augmented by an excellent experimental animal facility that procures and maintains animals, and provides technical support to the scientists. Other core facilities like the FACS, proteomics, bioimaging, XRD and bioinformatics facilities play an equally important role in facilitating NCCS to be at the leading-edge of research.

Our scientific productivity is reflected in numerous publications in prestigious international journals. In addition to institutional research funds, NCCS scientists have also been successful in obtaining numerous peer-reviewed competitive grants from various national and international agencies. NCCS scientists and students also share their research widely with peers through participation in national and international scientific conferences organized at NCCS and across the globe. We provide an encouraging environment to nurture the scientific curiosity and talent of graduate students, which facilitates them to shine and be among the best in the country. We also provide them with a platform to hone their skills through rigorous coursework, engaging research, and work seminars to showcase and discuss their work.

It is my pleasure to document here some of our recent major programmes. NCCS has initiated steps towards establishing a GMP-compliant National Repository for banking, safe deposit and supply of characterized mammalian cells for use in biopharma, under the aegis of the National Biopharma Mission. Another mega project involves studying the human microbiome of select endogamous populations of India. NCCS is also involved, along with IISER-Pune, and Persistent Systems Ltd., in spearheading the MANAV Human Atlas programme initiated by DBT to generate a Human Atlas by integrating the knowledge available in the scientific literature. The programme is expected to train large numbers of students to interpret,

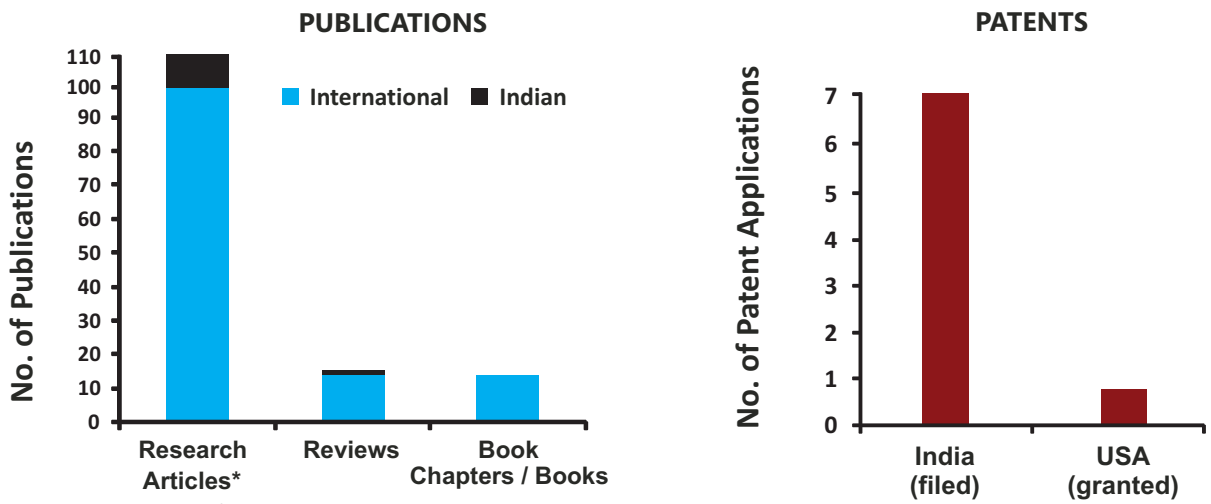
anayze and annotate data from the scientific literature, using an annotation platform created for this purpose. These major initiatives bear witness to the commitment of NCCS to support the scientific community and society, and to develop public-private partnerships and human resource. NCCS, in coordination with IISER-Pune, has been instrumental in setting up the Pune Biotech Cluster, an initiative by the DBT, to cater to the research needs of academic institutions and private companies in and around Pune.

Moving forward, NCCS will continue to focus on pertinent queries relevant to human health, while adopting cutting-edge technologies such as high throughput screening, cryo-electron tomography and single cell sequencing, for developing a better understanding about, and potential therapeutic leads for diseases.

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

Dr. Manoj Kumar Bhat
Director

Major Highlights (2019-20)

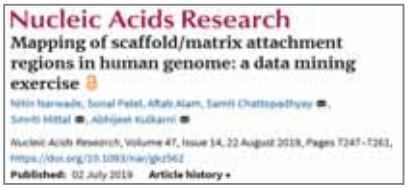


* Total citations = 347 *(from Google Scholar, as on 20 Aug, 2020)*

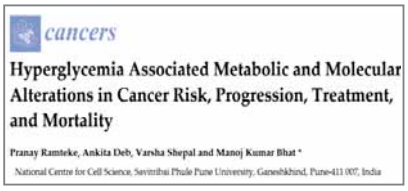
MAJOR SCIENTIFIC CONTRIBUTIONS


PNAS

Molecular engineering of an efficient four-domain DAF-MCP chimera reveals the presence of functional modularity in RCA proteins


Nucleic Acids Research

Mapping of scaffold/matrix attachment regions in human genome: a data mining exercise


cancers

Hyperglycemia Associated Metabolic and Molecular Alterations in Cancer Risk, Progression, Treatment, and Mortality

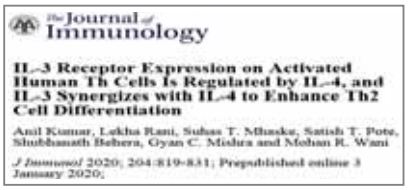
Pranay Ramteke, Ankita Deb, Varsha Shepal and Manoj Kumar Bhat *

National Centre for Cell Science, Savitribai Phule Pune University, Ganeshkhind, Pune-411 007, India


JBC

October 11, 2019

The tumor suppressor FBXO31 preserves genomic integrity by regulating DNA replication and segregation through precise control of cyclin A levels


The Journal of Immunology

IL-3 Receptor Expression on Activated Human Th Cells Is Regulated by IL-4, and IL-3 Synergizes with IL-4 to Enhance Th2 Cell Differentiation

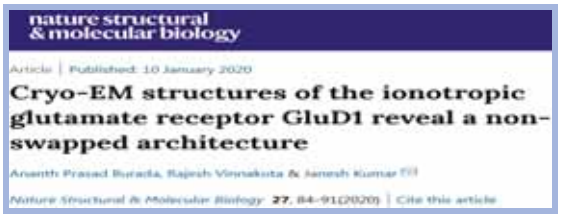
Anil Kumar, Lakha Rani, Suhas T. Mhaske, Satish T. Pote, Shubhanath Behera, Gyan C. Mishra and Mohan R. Wani

J Immunol 2020; 204:819-831; Prepublished online 3 January 2020;


European Journal of Immunology

CCR9 signaling in dendritic cells drives the differentiation of Foxp3+ Tregs and suppresses the allergic IgE response in the gut

3D molecular structure of a key brain receptor protein, GluD1, deciphered


nature structural & molecular biology

Article | Published: 10 January 2020

Cryo-EM structures of the ionotropic glutamate receptor GluD1 reveal a non-swapped architecture

Nature Structural & Molecular Biology 27, 84–91(2020) | Cite this article


Original Article | Published: 03 December 2019

A role of cellular translation regulation associated with toxic Huntingtin protein

Hiranmay Joag, Vighnesh Ghatpande, Meghal Desai, Maitheli Sarkar, Anshu Raina, Mrunalini Shinde, Ruta Chitale, Ankita Deo, Tania Bose & Amitabha Majumdar

Cellular and Molecular Life Sciences (2019) | Cite this article

A key cellular mechanism involved in Huntington's disease unravelled

A new microbial species from the Sambhar salt lake named after Dr. Renu Swarup, Secretary, DBT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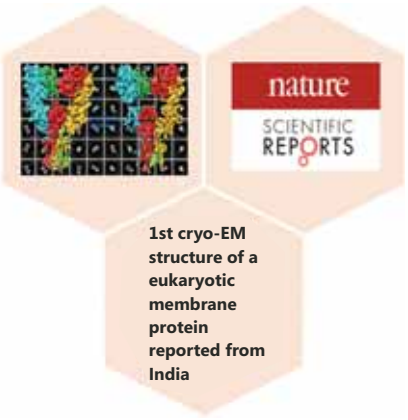
Research Article | Subscribed

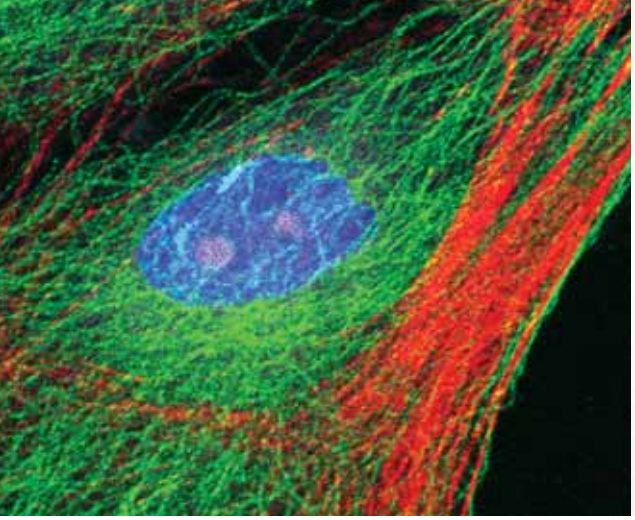
***Natrialba swarupiae* sp. nov., a halophilic archaeon isolated from a hypersaline lake in India**

Swapnil Kajale[1,2], Neelima Deshpande[2], Snigdha Pali[3], Yogesh Shouche[1], Avinash Sharma[1]



BENEFICIARIES OF THE ACADEMIC PROGRAMMES

Students awarded with a Ph.D. degree	22
Science Academies' Summer Research Fellows & Project Trainees	64
Students enrolled in the S.P. Pune University Biotechnology PhD coursework at NCCS	48



Human Resource Development

The beneficiaries of the NCCS academic programmes during the year 2019-20 are as follows:

Twenty-six Research Fellows joined NCCS, and twenty-six research scholars registered for a Ph.D. with the University during this year, taking the total number of registered Ph.D. students to a hundred and seven, as on 31st March, 2020. Twenty-one students submitted their theses to the University for evaluation, and twenty-two students were awarded with a Ph.D. degree during the said year.

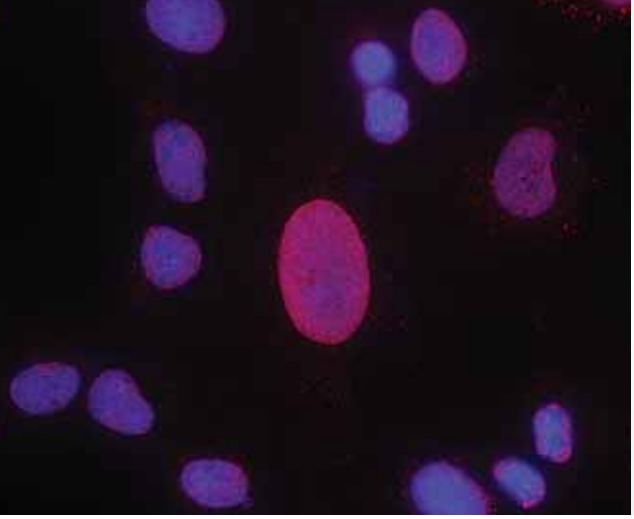
NCCS also conducts training programmes for students every year, as given below:

a) Project training is imparted either over 6-months' twice a year (during January-June and July-December), or over one year.

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 2019-20 is as follows:

Project Trainees: 38
Summer Trainees: 26



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 B*
Mr. Nitin Sonawane, *Technician C*
Mr. Bhimashankar Utage, *Technical Officer A*
Mr. Vikas Mallav, *Technician C*
Mr. Yogesh Kumbhar, *Assistant Technician*

NCCS has been long serving as a National Cell Repository for cell lines in India. The cell repository manages the expansion, cryopreservation and distribution of cell lines to researchers in academia and government as well as private research institutions and industry in India. In the year 2019-20, three thousand four hundred and thirty cell cultures have been provided to 2010 users in the country, spread across five hundred and four organizations. The repository has also supplied one hundred and eighty six cell cultures to scientists in NCCS. Furthermore, the repository caters towards providing a variety of cell culture media to in-house scientists, and has supplied almost 700 litres in the year 2019-20. Additionally, cell line authentication by Short Tandem Repeat (STR) analysis and Mycoplasma testing services provided by the repository are also used by both in-house scientists and external users.

The repository team initiated mechanisms for the addition of cell lines to its exiting collection. A Material Transfer Agreement was signed with the National Cancer Institute, National Institutes of Health, USA, Frederick, USA. 72 cell lines were obtained under this MTA for research purposes, to be used by the scientists of NCCS. Efforts were undertaken to encourage scientists from NCCS and other organizations to deposit their indigenously developed or modified cell lines in cell repository.

Two National hands-on training workshops on "Basic Cell Culture Technology" were organized from May 6th-9th, 2019 and October 22nd-25th, 2019. Training for important cell culture practices related to cell line maintenance, expansion, cryopreservation, revival and other specialized techniques were included in the workshop. Early career researchers including doctoral students, young faculty and technical staff from academic and non-academic institutions from all over the country were selected and imparted training. A total of 42 participants from 36 institutes across the nation have been imparted training.

The repository team participated in the Open Day organized as a prelude to India International Science Festival (IISF), 2019 on October 23rd, 2019, and subsequently participated in the 'Mega Science, Technology & Industry Expo' at IISF 2019, Kolkata from November 5th-8th, 2019 for popularization of science especially amongst students. The research activities of NCCS were highlighted, and various types of cell lines were displayed. The visitors to the NCCS booth were made aware of the importance of cell lines, cell repository and services offered. The repository personnel also participated in the Global Bio-India 2019

Training Program

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

6-9 May, 2019

No. of Participants trained

- Faculty: 4
- Ph.D Scholars: 16
- Technical: 2

Training Program

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

22-25 Oct. , 2019

No. of Participants trained

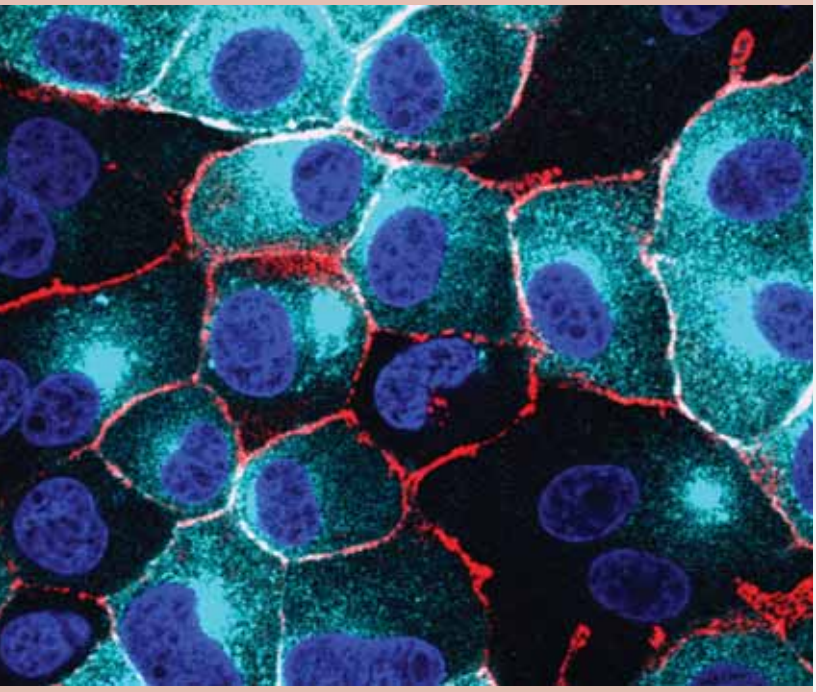
- Faculty: 7
- Ph.D Scholars: 12
- Technical: 1

from November 21st-23rd Nov, 2019, at New Delhi, where the services and initiatives of the cell repository that have relevance to the industry were exhibited. The repository team also actively participated in other out-reach events such as the healthcare exhibition, "Kutuhal", organized by Vidnyan Bharati, at Pune from February 7th-10th, 2020 and the National Science Day Open Day on February 28th, 2020. Various types of cell lines were displayed, and information about their importance and usage in research, and about the services of the cell repository was also disseminatied.

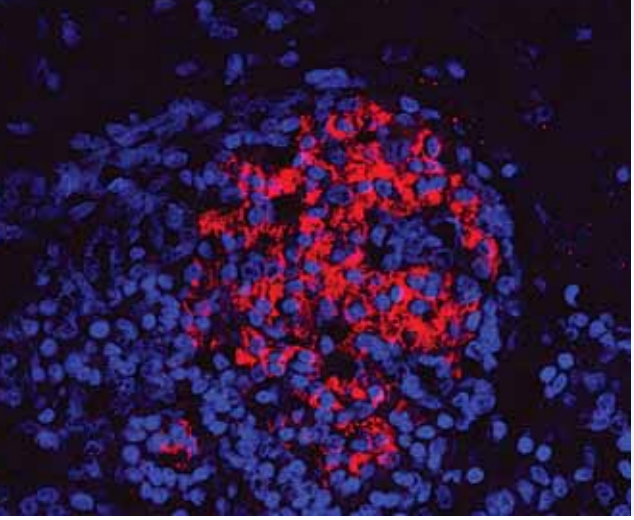
External Scientists Trained

- Institutes (Name, City, Country)
  - Punjabi University Patiala, Punjab
  - Gauhati University, Guwahati, Assam
  - Savitribai Phule Pune University, Pune
  - Uka Tarsadia University, Surat
  - CSIR- Central Leather Research Institute, Chennai
  - CSIR - National Chemical Laboratory, Pune
  - MAEER's Maharashtra Institute of Pharmacy, Pune
  - Manipal College of Pharmaceutical Sciences, Manipal
  - Veer Narmad South Gujarat University, Surat
  - Indian Institute of Technology, Indore
  - Amrita Institute of Medical Science and Research Centre, Kochi
  - St. Aloysius College, Mangalore
  - Mangalore University, Kodagu
  - Cotton University, Guwahati
  - Government College of Pharmacy, Amravati
  - Saurashtra University, Rajkot
  - Government Higher Secondary School, Nalli
  - Vector Control Research Centre, Pondicherry
  - National Centre for Cell Science, Pune

- Institutes (Name, City, Country)
  - Veer Narmad South Gujarat University, Surat
  - Savitribai Phule Pune University, Pune
  - Manipal College of Pharmaceutical Sciences, Manipal
  - Gauhati University, Guwahati
  - Indian Institute of Technology, Roorkee
  - Cotton University, Guwahati, Assam
  - Institute of Bioresources & Sustainable Development, Imphal
  - Davangere University, Davangere
  - All India Institute of Medical Science, Raipur
  - Vellore Institute of Technology, Vellore
  - Avinashilingam Institute for Home Science & Higher Education for Women, Coimbatore
  - Utkal University Bhubaneswar
  - CSIR-Central Food Technological Research Institute, Mysore
  - Abeda Inamdar Senior College, Pune
  - Rama University, Kanpur
  - Institute of Veterinary Biological Products, Pune
  - Homi Bhabha Cancer Hospital & Research Centre, Vishakhapatnam



Research Reports



Index of Research Reports

Sharmila Bapat

sabapat@nccs.res.in

Quantitative Evaluation of Modalities of Cell Migration

Objectives of the study

- Resolution and quantification of the differential modalities of cell migration *vis-a-vis* cooperative cell migration (CCM) vs. epithelial to mesenchymal transition (EMT) during wound healing using TLM imaging in a panel of ovarian cancer cell lines.

Summary

Background

Metastasis represents an array of entropic events that facilitate disintegration of tissue architecture via acquisition of migratory-invasive properties. We have earlier identified tumor groups based on distinct migratory behavior, either collective cell migration (CCM), or individual cell migration through epithelial to mesenchymal transition (EMT). Most studies on cell migration em ploy wound healing endpoint assays wherein data is acquired after a certain time interval to ascertain migration. This inadvertently, associate EMT to be the dominant (and often the only) process associated with metastasis, besides failing to capture dynamics of migratory mode switching in response to extrinsic cues. Application of time lapse microscopy (TLM) to traditional wound closure assays can effectively quantify and generate metrics to address theseissue; in this study, we TLM used to dyanamically quantify differences between CCM and EMT in ovarian cancer cells.

Work Done

Our earlier correlation analysis identified a heterogeneity of phenotypic markers in HGSC which could be indicative of existing diverse phenotypes.

Lab Members

Sagar Varankar, *SRF*
Madhuri More, *SRF*
Snehal Nimdeokar, *SRF*
Ankita More, *JRF*
Amruta Jadhav, *JRF*
Aravindan Narayanan, *JRF*
Komal Patil, *Project JRF*
Sunita Krishnan, *Project Trainee*
Avinash Mali, *Technical Officer A*

Collaborator(s) - National

Dr. Mohit Kumar Jolly, *IISc, Bengaluru*

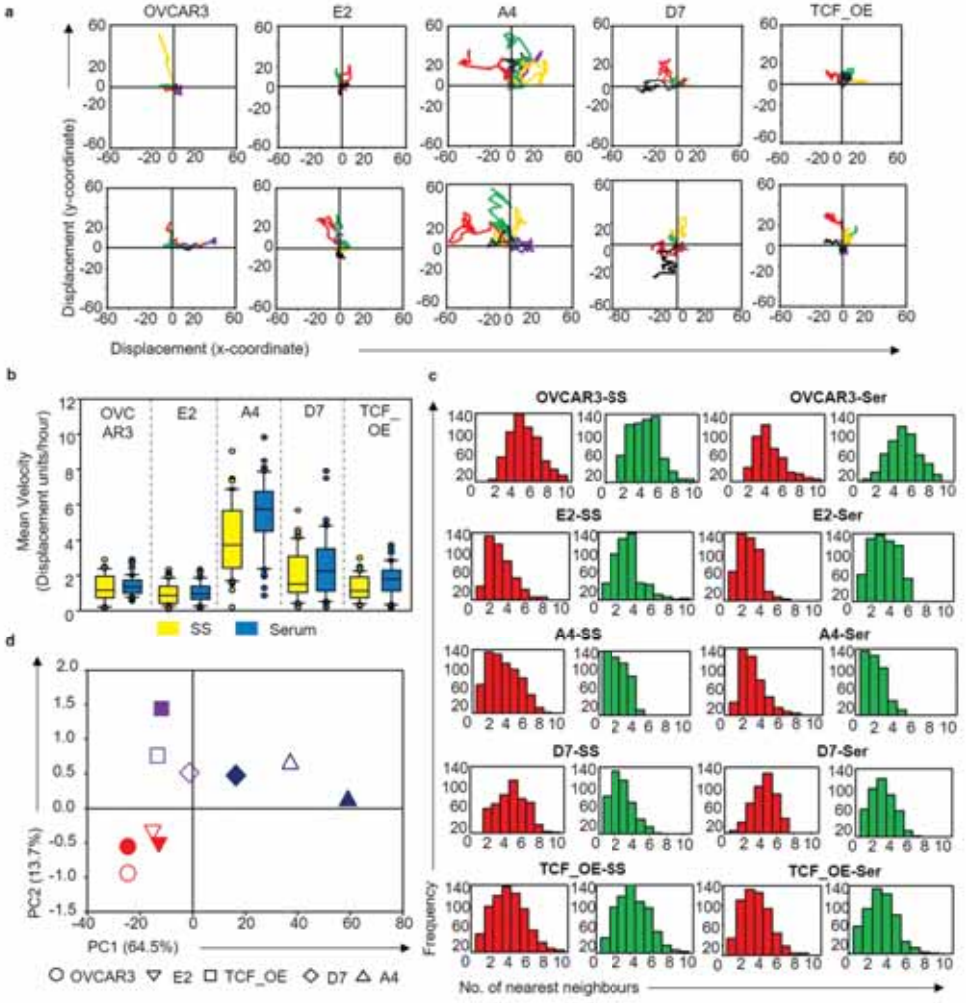


Fig. 1. Quantitative metrics for resolution of migratory modalities. a. Trajectories depicting migration directionality for parental cell lines (OVCAR3 / Tcf21^{native}, A4 / Slug^{native}) and respective derivatives (E2 / Tcf21$^{K/O}$, D7 / Slug$^{K/O}$ and TCF_OE / Slug$^{K/O}$Tcf21^{OE}). Plots represent trajectories of 5 randomly selected cells; b. Representative plots depicting mean migratory velocity of parental (OVCAR3, A4) and derivative cells (E2, D7, TCF_OE). Displacement and velocity were derived from 'x' and 'y' positional co-ordinates detected over a 16 hour duration; c. Frequency of nearest neighbours for parental cell lines (OVCAR3, A4) and derivative clones (E2, D7, TCF_OE) at 0 hr (red) and 16 hr (green) time points Distribution graphs depict Nn data for 750 cells . Experiments were performed in the absence / presence of serum. All cells identified in the microscopic field as particles were analyzed for displacement, velocity and Nn. However, only data points inclusive of the 'X', 'Y' co-ordinates and Nn over the entire duration of 16 hours were used for data representation and interpretation; d. Principle component (PC) analysis of time-lapse imaging-based migration data of parental (OVCAR3, A4) and derivative cells (E2, D7, TCF_OE), PC1 - variance between displacement (Final Y) and velocity vs. nearest neighbours, PC2 - variance between displacement and velocity; color gradient depicts migratory modes, blue-EMT, purple-aCCM, red-pCCM; filled and empty shapes indicate presence and absence of serum respectively.

Hierarchical clustering of known epithelial and mesenchymal TFs in this data yielded five distinct tumor groups including,

(i) exclusively epithelial (E) that expressed characteristically epithelial markes along with TCF21,

(ii) exclusively mesenchymal (M) that expressed vimentin with EMT-Transcription Factors (EMT-TFs) Slug, Snail, Twist1,

(iii) a hybrid E-M by virtue of a heterogeneous double-positive signature,

(iv) intermediate E (iE) which expressed E markers and low EMT-TFs but lacked Tcf21, and

(v) intermediate M (iM) exhibited EMT-TF expression.

Thereby, the entire range of phenotypic plasticity was identified across a panel of ovarian cancer cell lines as an interplay of E & M markers, TCF21 and EMT-TFs. The first impact of TLM imaging on assessing the modalities on the background of this plasticity in the in vitro wound healing assay was enhanced visualiztion of

the process of migration. Three migratory metrics viz., mean square displacement, velocity and number of nearest neighbors (Nn) were applied to TLM imaging in quantifying the process and identify effects of media components, additives, small molecules and chemotherapeutic agents on migration modes. OVCAR3 and E2 cells exhibited proliferation-driven CCM (pCCM) - this may well be the first time that imaging of CCM has been achieved. A4 cells mediated rapid wound healing through a combination of single cell and active CCM (EMT and aCCM, respectively) while its derivatives D7, (SlugK/OTcf21OE) exhibited aCCM exclusively. Cell position coordinates during wound closure allowed quantification of these processes by virtue of migration trajectories, mean cell velocity and Nn (Video available at Carcinogenesis Online; https://oup.silverchair-cdn.com/oup/backfile/Content_public/Journal/carcin/41/4/10.1093_carcin_bgz119/1/bgz119_suppl_supplementar y_video_s1.mp4). pCCM driven wound closure was associated with minimal cell displacement, low migratory velocity and a high Nn; aCCM was defined by moderate displacement and velocity and high Nn while EMT cells exhibited high displacement and velocity with low Nn (Figs. 1a-c). Serum addition enhanced displacement, velocity and reduced Nn in aCCM and EMT phenotypes while pCCM cells increased Nn by virtue of extensive cell proliferation. Presence of mitomycin C, a proliferation inhibitor, in the absence of serum distinguished cell displacement attributed by active migration (aCCM/EMT) as opposed to cell division driven passive movement (pCCM). Principal component analysis performed with these datasets supported differential migratory modes wherein PC1 (variance between velocity and displacement versus Nn) and PC2 (variance between displacement versus velocity) effectively resolved cell lines associated with pCCM, aCCM and EMT-aCCM modes of migration while capturing serum induced shifts in respective modalities (Fig.1d). Differential Nn frequencies between A4 and D7 proved a useful metric for distinguishing EMT from aCCM apart from the visualization in real time imaging.

The present study achieved an application and quantitation of time-lapse microscopy of the *in vitro* scratch assay. While visual outputs affirmed the distinct migratory modes in the derivative clones, principal component analysis permitted an unbiased segregation of these modalities as a function of TF expression. This gradient of migration modalities effectively agrees with the phenotypic spectrum ranging from an Epithelial to Mesenchymal cell morphology as defined earlier by us. Effectively, this emphasize rigidity of the E phenotype, a hybrid E/M phenotype and absence of biphasic phenotypic switches during EMT.

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Cancer, Chemotherapy and Metabolic disorders

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Objectives of the study

- To study the correlation between leptin and TNFα signaling in colon cancer progression under obese phenotype.
- To understand the molecular aspects of Leptin and TNFα signaling cascades in colon cancer progression under obese phenotype

Summary

Background

Obesity is a metabolic disease characterized by excessive deposition of fat in adipose depots. The WHO lists obesity as one of the top 10 global health problems. Several other diseases, including certain types of cancers have also been linked to obesity. Various studies suggest a plausible link between obesity, risk and progression of many cancers. Furthermore, obesity has been associated with nearly 20% of all cancers related deaths in women and 14% in men. Development of a low-grade, chronic inflammatory state due to increased adipose tissue mass in obese individuals causes increased secretion of growth factors and cytokines/ adipokines and link obesity with subsequent cancer risk. Some of the adipokines such as leptin and insulin-like growth factor-1 (IGF-1) play important roles in maintaining normal metabolism of the body and parallel have been shown to act as mitogens for cancer cells. Obesity causes increased secretion of hormones like leptin and resistin etc. in addition to several inflammatory cytokines which have been reported to facilitate the progression and metastasis of various cancers.

Worldwide, colorectal cancer (CRC) is second most diagnosed cancer in females and third most in males with 1.4 million new cases in 2012. Obesity is

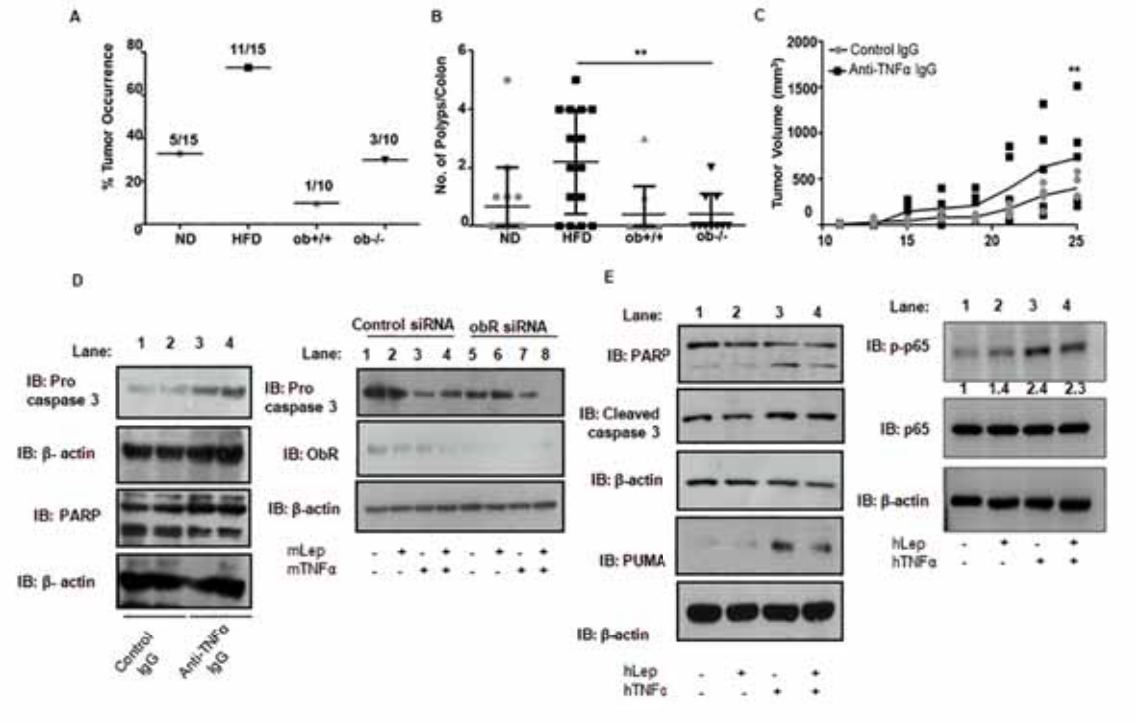

Fig. 1: Decreased tumor incidence regression in the absence of leptin is a consequence of increased apoptosisdue to TNFα action. A) Number of mice in each group which developed tumors is represented as percent tumor occurrence. B) Number of polyps obtained per colon was counted for each group. Colon from HFD mice had more number of polyps compared to ob-/- (*** p < .001). C) Rate of tumor progression was faster in mice injected with anti-TNFα IgG antibody compared to tumor progression in mice injected with control IgG (**p < .01). Data presented here shows tumor progression in five animals from each group. D) Control IgG injected mice showed cleavage of PARP and lower expression of procaspase 3 compared to anti-TNFα IgG injected mice (two tumor samples from each group, experiment was performed once). siRNA mediated knockdown of ObR prevents leptin mediated rescue of procaspase-3 cleavage induced upon TNFα treatment, in CT26 cells, Experiment was performed once. E) Western blot analysis of hLep and hTNFα treated cells subjected to SDS-PAGE and probed for levels of PARP, cleaved caspase-3, PUMA and pP65. All western blots were performed twice except cleaved caspase-3 (performed once). The results are given as mean ± standard deviation of an experiment in three separate wells ***, p < .001.

now recognised as a major risk factor besides other risk factors such as germline mutation, use of tobacco and alcohol. Epidemiological studies have shown that adiposity, especially visceral adipose tissue mass is directly correlated with the risk of colon adenoma and cancer. The multifunctional role of adipose tissue is disrupted in obese phenotype that causes inflammation and altered secretion of pro and anti- inflammatory cytokines.

Amongst adipokines, leptin is an important regulator of food intake. Humans or mice with congenital deficiency of leptin exhibit hyperphagia and are morbidly obese. Leptin has been shown to have mitogenic activity on colonic tumors subsequent to initiation. Increased level of leptin in human serum has been related with enhanced risk of colon, breast and thyroid cancers. In particular, leptin enhances the risk of colon cancer through up regulation of β- catenin.

TNFα is an adipokine with a molecular weight of 25.5 KDa. Its serum levels are elevated in various experimental models of obesity and obese humans. Multiple reports suggest that TNFα induces cancer cell death and inhibits cancer progression. TNFα binding to its receptor can induce the expression of p53 up regulated mediator of apoptosis (PUMA) in a p53 dependent or independent manner thereby triggering the cleavage of procaspase-3, 8 and 9.

The level of adipokines, particularly leptin and TNFα are significantly higher in obese phenotype, however the functionality of these two adipokines towards cancer progression is diverse. Interestingly, it has also been shown that leptin abrogates the functions of TNFα in cardiomyocytes and also ob-/- mice possess weaker cardiac muscles than normal

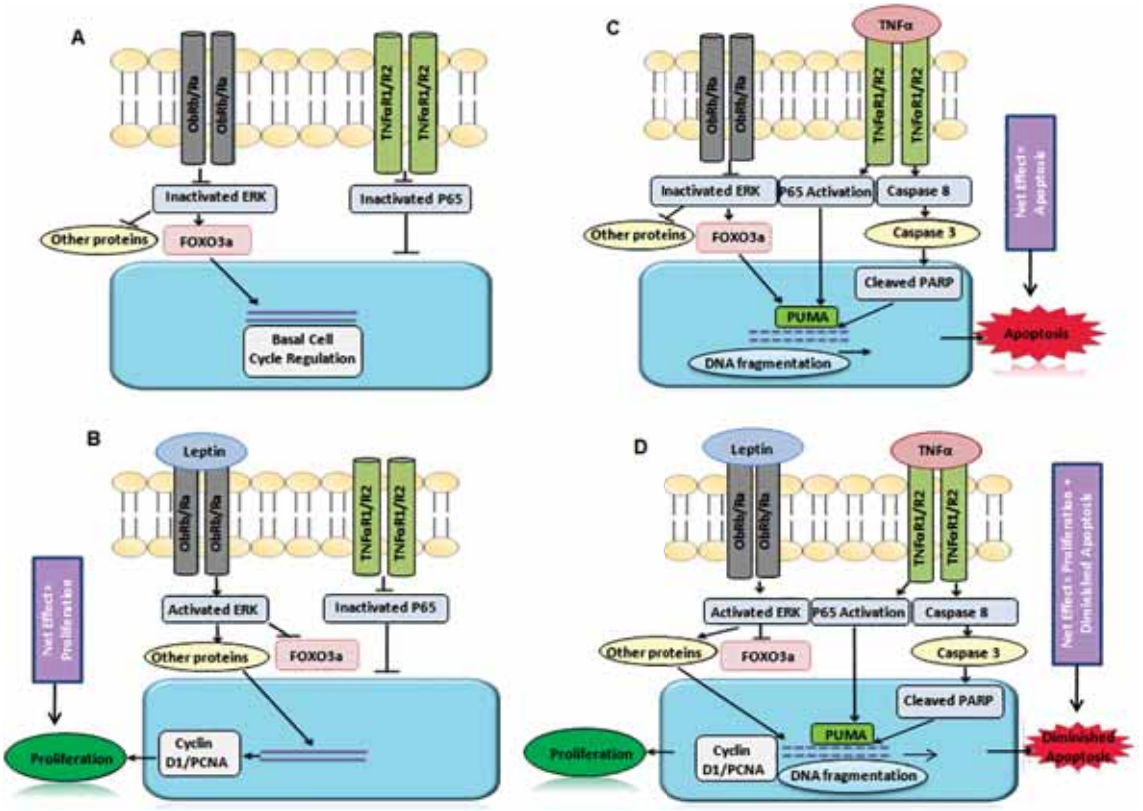

Fig. 2. Schematic representation of the proposed model. A) Under normal physiological condition a controlled cell cycle is maintained. B) In a situation where balance is skewed towards leptin, it induces the activation of ERK and subsequent degradation of FOXO3a. Upregulation of Cyclin D1 and PCNA assist in rapid cell proliferation. C) Under situations where balance is skewed towards TNFα, it is likely that TNFα will potently exhibit apoptotic function. In this condition, PUMA is upregulated through activation of transcription factors such as pP65 and FOXO3a. D) In a condition where leptin and TNFα both are elevated, leptin induced ERK degrades FOXO3a, leaving pP65 alone to act as a transcription factor for PUMA.

mice. These reports are suggestive of a protective role of leptin against TNFα induced cell death. Hence in the light of available literature, we hypothesised that presence or absence of functional leptin may affect the pro-apoptotic effect of TNFα on colon cancer cell proliferation and tumor progression.

Findings of the study

1. Leptin deficiency in the serum of genetically obese animals hampers tumor growth and AOM/DSS induced polyp formation is lesser in these animals as compared to high fat diet induced obese animals with high leptin.

2. We observed that tumor regression or decreased incidence, in the absence of leptin is a consequence of increased apoptosis, primarily because of TNFα action. Depletion of TNFα in mice reduces apoptosis and therefore does not restrict tumor growth. Our findings indicate that leptin abrogates TNFα induced apoptosis in cancer cells.

3. TNFα induces p53 independent cell death through upregulation of p53 upregulated modulator of apoptosis (PUMA). TNFα induced PUMA was inhibited upon preexposureof cells to leptin, prior to TNFα treatment. Collectively these results indicate that obesity due to leptin non functionality facilitates TNFα induced colon cancer cell death

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Deciphering the role of chromatin remodeling protein SMAR1 in PKM alternative splicing

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Objectives of the study

- Role of SMAR1 in regulation of PKM alternative splicing.
- Role of SMAR1 in regulation of Warburg effect in breast cancer cells.

Background

Chromatin mainly comprises of nucleic acids and proteins that interacts with various accessory proteins so as to perform numerous 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 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 negatively regulate alternative splicing by modulating the acetylation status of Sam68 by recruiting HDAC6 (Nakka et al. 2015 PNAS). Amongst many different functions of SMAR1, one such study involving the role of SMAR1 in inhibition of Warburg effect via regulation of PKM alternative splicing has been discussed below.

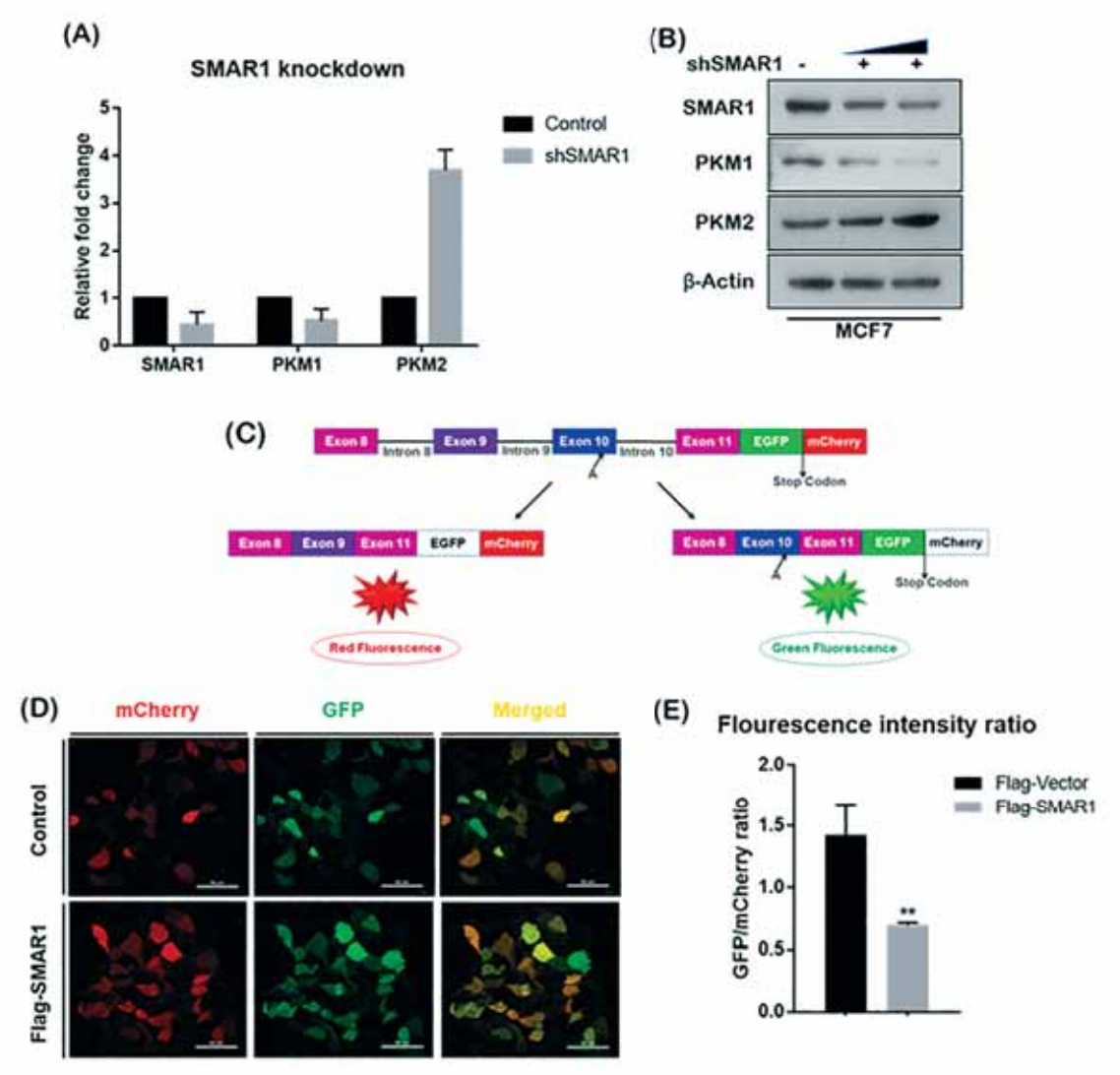

Fig. 1: SMAR1 regulates PKM alternative splicing: (A) Upon SMAR1 knockdown there is upregulation in PKM2 and down regulation in PKM1 at mRNA level in MCF7. (B) Upon SMAR1 knockdown there is upregulation in PKM2 and down regulation in PKM1 at protein level in MCF7. (C) schematic representation of dual chromatic PKM minigene system. (D) Confocal imaging of PKM minigene system upon SMAR1 overexpression in MCF7. (E) GFP/mCherry ratio gets reduced upon overexpression of SMAR1 along with Dual chromatic PKM minigene system in MCF7.

Summary

Cancer cells utilize more glucose and produce more lactate independent of oxygen availability. This phenomenon is known as aerobic glycolysis or Warburg effect. Cancer cells achieve this by upregulating the embryonic isoform of pyruvate kinase enzyme; PKM2. PKM1 and PKM2 are two isoforms of pyruvate kinase which are regulated by mutually exclusive alternative splicing, reflecting inclusion of either exon 9 (PKM1) or exon 10 (PKM2). SMAR1 being a tumor suppressor reduces rate of glycolysis and promotes mitochondrial biogenesis. Moreover, SMAR1 is known to regulate alternative splicing of CD44 variants, FAS and DNMT3. This suggests that SMAR1 might be involved in regulation of alternative splicing of other cancer associated genes such as PKM. To check regulation of PKM alternative spicing by SMAR1, PKM isoforms expression was checked upon SMAR1 over-expression and knockdown. This study suggests that SMAR1 promotes expression of PKM1 and suppresses PKM2. To further validate role of SMAR1 in PKM alternative splicing regulation we cloned exon 8 - exon 11 of PKM gene along with introns in the dual reporter system. Upon incorporation of exon 9 it gives red color and upon incorporation of exon 10 it gives green color. We over-expressed SMAR1 along with PKM minigene and checked for fluorescence intensity by confocal imaging. GFP/mCherry ratio for SMAR1 overexpression was reduced compared to vector

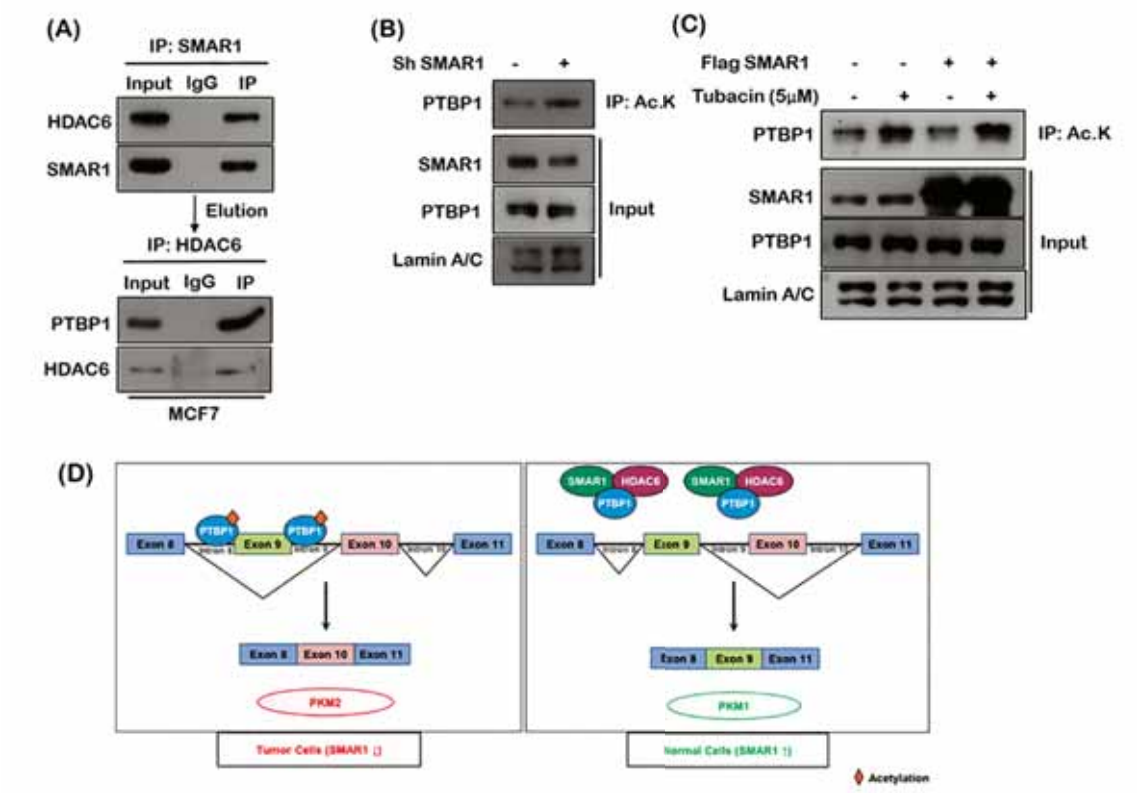

Fig. 2: SMAR1 deacetylates PTBP1 via recruitment of HDAC6: (A) SMAR1-HDAC6 makes a triple complex with PTBP1. (B) Acetylation status of PTBP1 increases upon SMAR1 knockdown. (C) SMAR1 deacetylates PTBP1 in HDAC6 dependent manner. (D) Proposed model. In normal cells or in ectopic SMAR1 expression (High SMAR1 condition): SMAR1-HDAC6 makes triple complex with PTBP1 and deacetylates it. Deacetylated PTBP1 has low affinity for PKM pre-mRNA and leads to incorporation of exon 9 and exclusion of exon 10 which results into higher expression of PKM1 compared to PKM2. In cancer cells (Low SMAR1 condition): PTBP1 stays in acetylated condition and binds to PKM pre-mRNA and leads to exclusion of exon 9 and incorporation of exon 10 which results into higher expression of PKM2 compared to PKM1.

control. This validates role of SMAR1 in PKM alternative splicing regulation. SMAR1 regulates PKM alternative splicing via HDAC6 mediated deacetylation of PTBP1. Moreover, SMAR1 inhibits Warburg effect by promoting expression of PKM1 over PKM2. Our study suggests that tumor suppressor protein SMAR1 plays an important role in regulation of tumor metabolism via modulation of PKM alternative splicing. Therapeutic strategies targeting tumor metabolism and stabilization of SMAR1 expression might prove to be an effective approach to eradicate cancer.

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

Objectives of the study

- To understand how TLRs modulate B cell responses
- To understand BCR and TLR crosstalk in autoimmunity

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 antigen 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 are also trying to determine 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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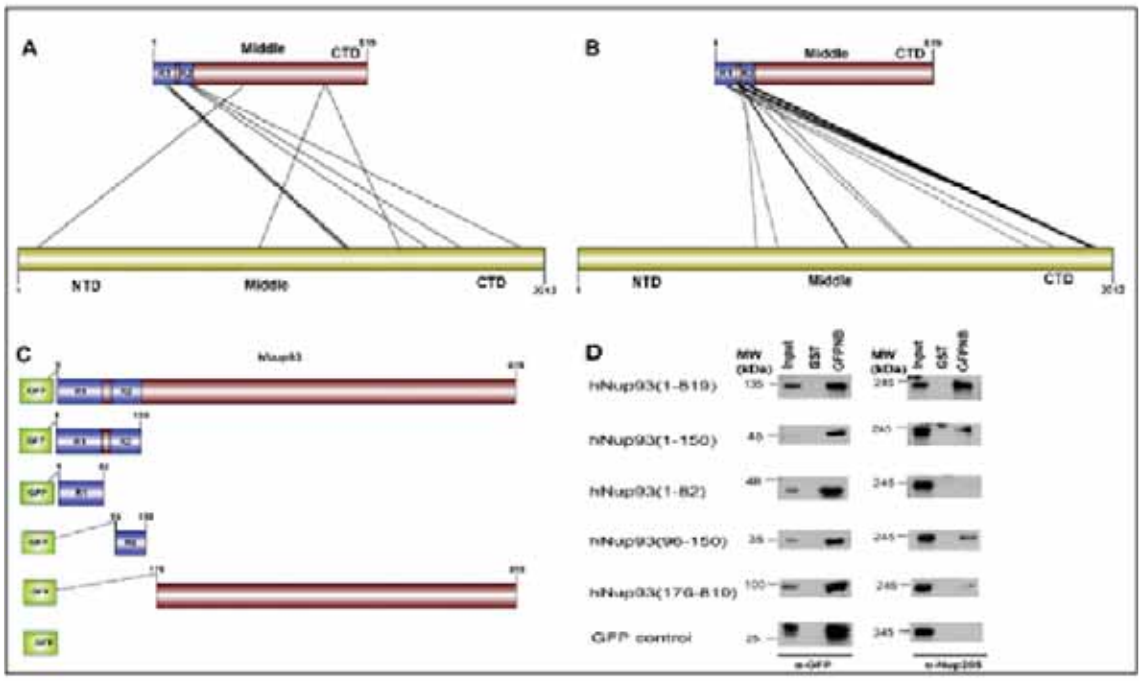

Fig. 1: Prediction and validation of interface regions for Nup93-Nup205 A. Cross-linking based mass spectrometry defined proximity regions between Nup93-Nup205 (adapted from Jan Kosinski, et.al, Science, 2016). B. Top 10% regions predicted by CoRNeA. Edges in bold depict three most significant regions (N-terminal of Nup93 with C-terminal of Nup205). C. GFP-fused deletion constructs for Nup93 for validating the predictions. D. Immunoprecipitation results depicting N-terminal region (1-150) and R2 regions (96-150) of Nup93 specifically interact with endogenous Nup205. GFPNB: GST-anti-GFP-nanobody

Very recently we attempted to decipher protein-protein interactions of NPC by using computational tools and since no such method was available earlier, my group generated a novel 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.

To test the applicability of the pipeline on the dataset without known structural information, hNup93-hNup205 interaction interface was explored. Nup93 is a linker protein of the Nup93-subcomplex of the NPC. It is known to connect the adaptor/inner ring of the spoke region with the central channel pore of the NPC. The adaptor region consists of the four proteins viz., Nup188, Nup205, Nup35, and Nup155. In terms of the known interactions of the specific domains of the Nup93, its R1 region which spans the first 82 amino acids is known to interact with the Nup62 of the central channel. Nup93 is specifically known to form mutually exclusive complexes with either Nup188 or Nup205 of the adapter ring. The interaction interface information for these pair of proteins is not known specifically from mammalian origin owing to difficulties in biochemical reconstitution of these complexes. However, for hNup93-hNup205, proximity information for this pair of proteins is known through crosslinking based mass spectrometry analysis. The cross-linking data suggests three different regions of Nup93 to be in proximity of Nup205 (i.e. N-terminal, middle and C-terminal) but the most prominent hits are seen between the R2 (96-150) region at the N-terminal of Nup93 with the C-terminal of Nup205 (Figure 1A).

CoRNeA was employed to identify the interaction interface of Nup93-Nup205 complex by utilizing full length sequence information of both the proteins (Nup93: 819 amino acids and Nup205: 2012 amino acids). Since, the secondary structure prediction of both these proteins depicts ?- helices, hence the 3*3 kernel matrix derived random forest model was utilized to predict the interface pairs. The resultant high scoring pairs, which pertained to specifically the R2 region of Nup93 (96-150) with the C-terminal region of Nup205 obtained from CoRNeA (Figure 1B), are in consensus with cross-linking mass

spectrometry analysis (Figure 1B). However various low scoring pairs were also identified for Nup93 middle and C-terminal region but they did not span more than three continuous pairs (such as 89-91 of Nup93 with 1201-1205 of Nup205) between the two proteins. Further, validation of the interacting interface between Nup93 and Nup205 predicted with CoRNeA analysis was done by in-vitro pull-down experiment using Nup93 deletion constructs (Figure 1C). Upon pull down with GST tagged anti-GFP nanobody, N-terminal region of Nup93 (1-150) was able to pull endogenous Nup205 efficiently. Further mapping the minimal interaction region, R2 fragment of Nup93 (96-150) was found to interact with endogenous Nup205 thus validating the in-silico prediction by CoRNeA. A diminished interaction of the Nup93 region (176-819) was also observed through this pull-down experiment (Figure 1D), which is also consistent with the identification of low scoring regions identified by CoRNeA. This experimental validation depicts that CoRNeA is able to predict the short stretches of interaction hotspots between known pair of interacting proteins from only their sequence information and hence can be used to decipher the minimal interacting regions of pair of large proteins. Thus, aiding in their biochemical reconstitution followed by structural elucidation

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Neurobiology of Nutrient Specific Memories and Feeding Behaviour in *Drosophila*

Objectives of the study

- To find neural circuitry underlying protein and lipid reinforced memories
- To understand how post-ingestive nutrient perception occurs in the gut

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 component from a food source is encoded in the brain and remembered. We have developed novel behavior paradigms to assay for protein or lipid feeding reinforced learning and memory expression. We will use these assays to understand the neural circuit basis of forming, storing and recalling nutrient specific information.

Nutrients, like sugar, have distinct taste and nutritional (post-ingestive) components. We intend to study the perception of purely the post-ingestive nutrient component in isolation from the taste of a nutrient. This is hard to achieve, without complicated and most often incomplete ablation of peripheral taste neurons. We have solved this problem by feeding flies acid-sensitive liposome/mesoporous silica nanoparticle encapsulated nutrients. We have shown that this approach works in flies and encapsulated cargo dye is released directly into the acidic fly midgut. Our first paper detailing our approach was published recently.

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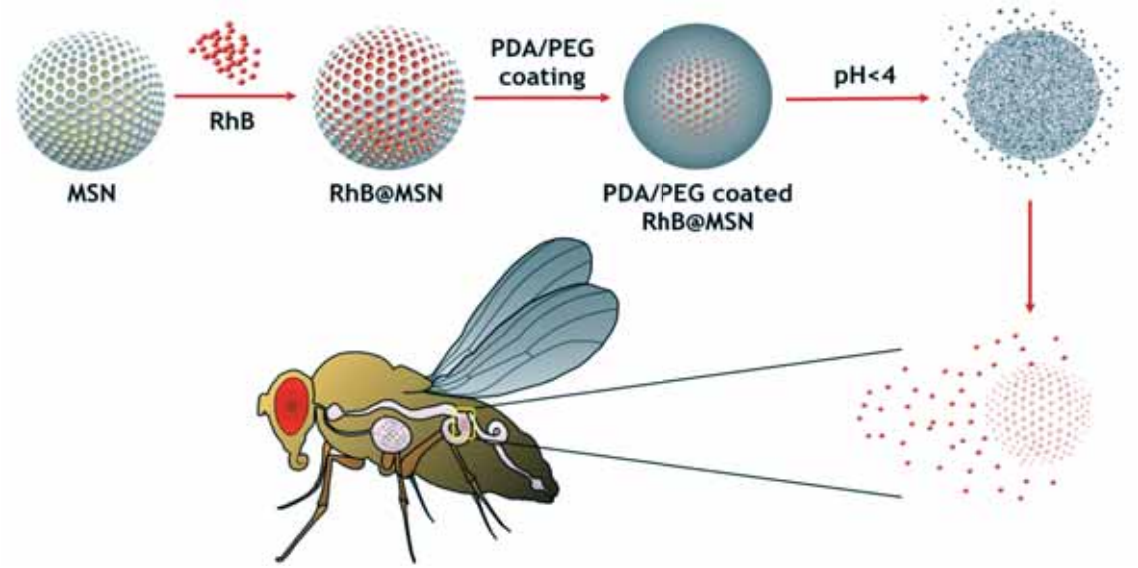

Fig. 1: Schematic representation of our approach to deliver cargo directly to the acidic fly midgut. All peripheral detection is bypassed.

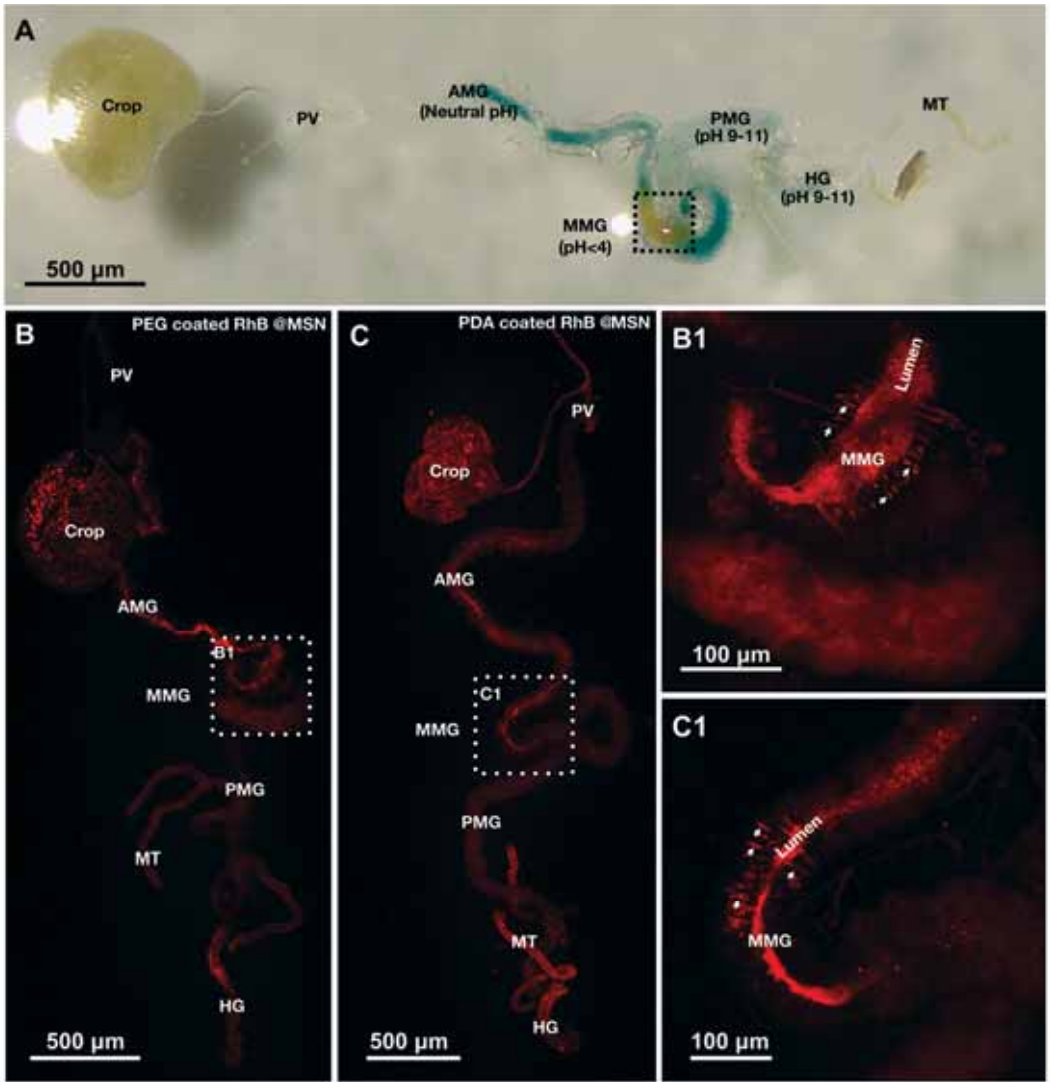

Fig. 2: (A) pH profile of a 4-5 days old CS-Q female fly gut fed with standard cornmeal medium with bromothymol blue for two hours after 24 hrs of starvation period, (B) in vivo particle distribution of 0.1 mg/ml PEG coated RhB@MSN and (C) 0.02 mg/ml PDA coated RhB@MSN fed CS-Q adult female. (B1) Middle midgut pH responsive release of PEG coated RhB@MSN and (C1) PDA coated RhB@MSN. Small white arrows in B1 and C1 indicate paracellular transport of RhB in between the middle midgut (MMG) epithelial cells. Note: PV=Proventriculus, AMG=Anterior midgut, MMG=Middle midgut, PMG=Posterior midgut, MT=Malpighian tubules and HG=Hindgut. Figure from Sapre and Chakraborty et al. in RSC RSC Adv. 2020;10: 11716-11726

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Nup358 Regulates Microridge Length by Controlling the SUMOylation-dependent Activity of aPKC in Zebrafish Epidermis

Objectives of the study

- Studying the role of Nup358 during early zebrafish development.
- Investigating the effect of Nup358 on the aPKC-Lgl-dependent microridge formation on peridermal cells.
- Understanding the mechanism for Nup358-dependent regulation of microridges.

Summary

The Par polarity complex, consisting of Par3, Par6 and atypical protein kinase C (aPKC), plays a crucial role in the establishment and maintenance of cell polarity. Although activation of aPKC is critical for polarity, how this is achieved is unclear. The developing zebrafish epidermis, along with its apical actin-based projections, called microridges (Fig.1), offers a genetically tractable system for unraveling the mechanisms of the cell polarity control. The zebrafish aPKC regulates elongation of microridges by controlling levels of apical Lgl, which acts as a pro-elongation factor. Here, we show that the nucleoporin Nup358 (also known as RanBP2) - a component of the nuclear pore complex and a part of cytoplasmic annulate lamellae (AL) - SUMOylates zebrafish aPKC. Nup358-mediated SUMOylation controls aPKC activity to regulate Lgl-dependent microridge elongation (Fig.1). Our data further suggest that cytoplasmic AL structures are the possible sites for Nup358-mediated aPKC SUMOylation (Fig. 2). We have unraveled a hitherto unappreciated contribution of Nup358-mediated aPKC SUMOylation in cell polarity regulation.

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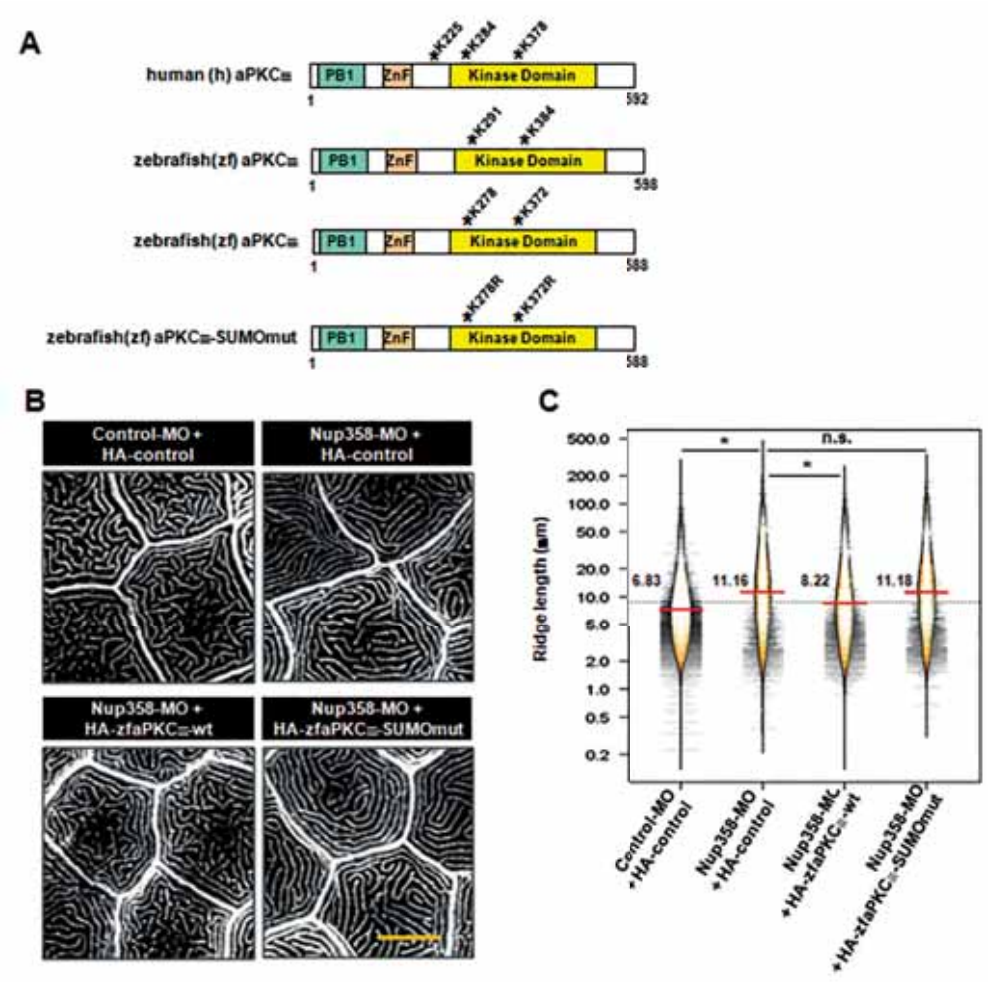

Fig. 1: Nup358 mediated regulation of microridges is aPKC dependent (A) Schematic representation of the conserved SUMOylation sites in human aPKCζ (h, zebrafish (zf) aPKCζ and zfaPKCζ. Both the conserved SUMOylation sites, K278 and K372, were mutated to R to generate zebrafish (zf) aPKCζ-SUMOmut. PB1, Phox and Bem1 domain; ZnF, Zinc finger domain. (B) Apical confocal sections of control-MO + GFP-HA RNA, Nup358-MO + GFP-HA RNA, Nup358 MO + HA-zf-aPKCζ or Nup358 MO + HA-zf-aPKCζ-SUMOmut injected embryos at 33 hpf stained with phalloidin to visualize the microridges (white). Fifty micro-molar concentration of MO was used for injection. Scale bar = 10 μm. (C) Bean plots representing the distribution of microridge lengths in the respective groups. Quantitation of microridge lengths was done using ImageJ. Ridge length data of all the groups were analyzed using Kruskal-Wallis test, and pairwise comparison between two groups was made by the Dunn's method.

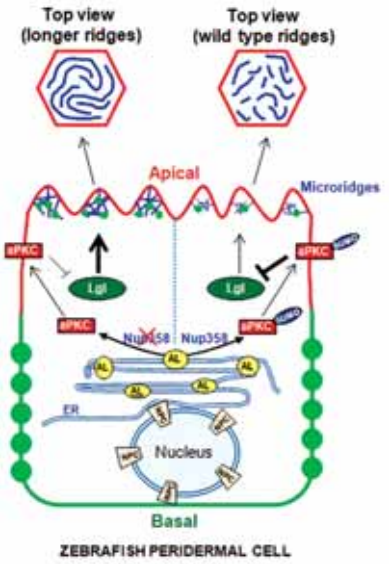

Fig. 2: Proposed working model for the mechanism of Nup358-mediated regulation of microridges
In zebrafish peridermal cells, AL-associated Nup358 SUMOylates and activates aPKC, which in turn phosphorylates and inhibits Lgl, and thereby restricting the microridge formation.

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Evolution of Cooperation by Mycobacteria: Importance of Defection Paths

Objectives of the study

- To trace the path the populations followed during the selection route by examining resultant population at 'select' selection step. The path the WT populations tend to choose to gain resistance, when triggered by sub-lethal concentration of an antibiotic agent.

Background

Replicating life forms are an interesting phenomenon in that they have evolved to deal with the environment as it comes since evolution does not invest in future! All the adaptive responses, with reference to the environment, can be broadly grouped into three distinct possibilities; get into a cocoon (retraction into a shell of safety), deal with its ability which may be risky to its survival and win it over the situation to forge ahead. The evolution of antibiotic resistance by many pathogenic bacteria can also be viewed through the same prism that gives us an overall picture of the organisms' ability to deal with its prevailing environment. The illustration, shown in Fig. 1, is gross representation of evolution of antibiotic resistance. The illustration demonstrates as the bacterium's ability to deal with the external environment that contains an antibiotic agent that can be causal factor to its survival.

Our laboratory has engaged in understanding the evolution of cooperation in bacteria following the thought process of social dilemma games viz. Prisoners Dilemma game, which has been the benchmark for evolution of cooperation. Here, cooperative forms of the bacterium are nothing but the preservation of pathways that can help in establishment of pathogenesis. We have recently

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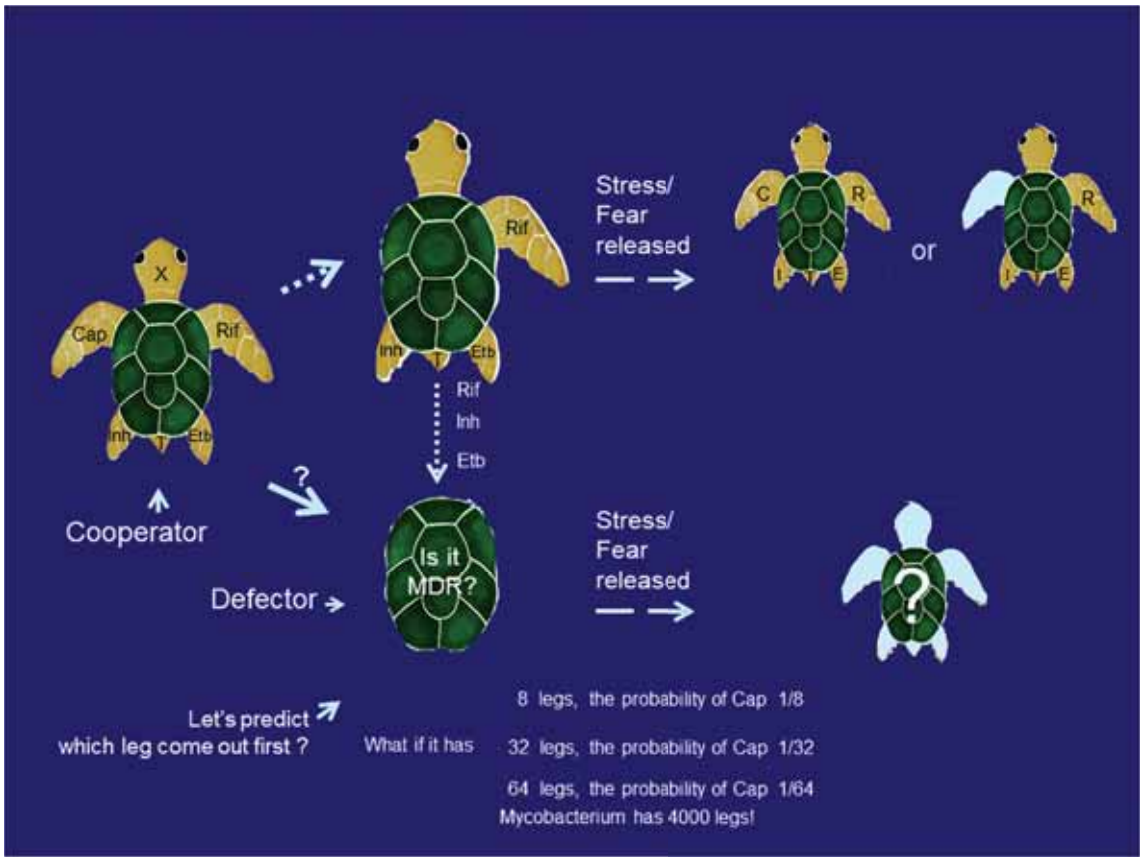

Fig. 1: The illustration in Fig.1 depicts an analogy between turtle and a bacterium. The responses of a turtle when hit its leg with a stick (an antibiotic) may result in retraction of that leg into its shell. This can be said to be evolution of resistance to that antibiotic. Post striking of the leg, the turtle's each of the other legs can also be hit successively (dotted arrow path), with another antibiotic and so on till of all its legs are retracted along with head and tail into a shell, an equivalent form of Multi-Drug Resistance of a pathogen. However, a danger signal to one of its legs is also a danger signal to all of its extended parts and hence, it can retract all of its extended parts into the shell at once (the solid arrow) to arrive at the same MDR form! Here, upon withdrawal of fear factor or antibiotic stress (the dashed arrow) can result in that leg or an alternative coming out of its shell. For the same of imagination, if the turtle has many legs, can a new leg occupy that place enabling the turtle to get on with its living? This is much like an alternate pathway helping the pathogen for its growth and/or survival while maintaining the resistance to that antibiotic. It is important to note that as the number of legs (alternate pathways in a bacterium) increases, the probability of that leg coming-out (making the bacterium susceptible again) decreases!

shown that bacteria must keep its cooperative population intact in order to establish the infection, while retracting to a shell like or least cooperative forms can be termed as defectors that can be, in principle, resistant to many situations/environments, such as MDR.

The goal of the project is to understand the pathways that result in emergence of MDR form of the pathogen, through defection, using antibiotic selection process and compare them with in vivo observed populations as far as possible. It is pertinent to note that sequencing of many clinical isolates, ranging from 10-25% of isolates, did not have any mutants or otherwise explainable for the resistance property exhibited by these strains. This clearly indicates that alternate pathways exist in the pathogen that results in evolution of drug resistance.

Summary

- The *M. marinum* population grown over Ethambutol (ETB, 2µg/ml) showed extended lag phase during the selection process and the growth kinetics of selected population over pyrazinamide was same as wild type *M. marinum* population.

- The ETB selected population does not acquire any cross resistance over capreomycin and other antibiotics tested.
- ETB selected population showed delayed and reduced virulent potential when compared to wild type *M. marinum* infection.
- C57BL/6 Mouse tail infections of *M. marinum* population exposed to ETB (2µg/ml) showed delayed and reduced virulent potential when compared to wild type *M. marinum* infection.
- Expression of TlyA protein on wild type *M. marinum* was observed by immunostaining with confocal microscopy.

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Structure-Function and Regulation of Ionotropic Glutamate Receptors

Objectives of the study

- Cloning, expression and purification of orphan glutamate delta receptors (GluD1 and GluD2).
- Structure determination of GluD1 and GluD2 receptors by single-particle cryo-EM.
- Electrophysiology based functional assays on GluD receptors.

Summary

Delta receptors belong to the ionotropic glutamate receptor (iGluR) family along with α-amino-3-hydroxy-5-methyl-4-isoxazole propionic acid (AMPA), kainate (KA) and N-methyl-D-aspartate (NMDA) receptors. This enigmatic class of iGluRs is referred to as "orphan" because they are not activated by endogenous ligands. The family consists of two members, GluD1 and GluD2, that are expressed in multiple regions of the brain with GluD1 predominantly expressed in the inner ear and GluD2 in cerebellar Purkinje cells (PC). The two subtypes share ~50 % sequence similarity with each other and around 20-30 % with other iGluRs. While multiple structures of the intact iGluRs have been reported for AMPA, KA and NMDA receptors, structural insights into a full-length Delta receptor is still lacking.

While crystal structures of isolated amino-terminal domains (ATD), ligand-binding domains (LBD) and the intact extracellular region (ATD-LBD) have been reported for GluD receptors, the full-length structure of either member of this family is still elusive. In order to address this and to gain structural insight into the function of these orphan receptors, we have determined the structure of homotetrameric rat GluD1 receptors using single-particle cryo-electron

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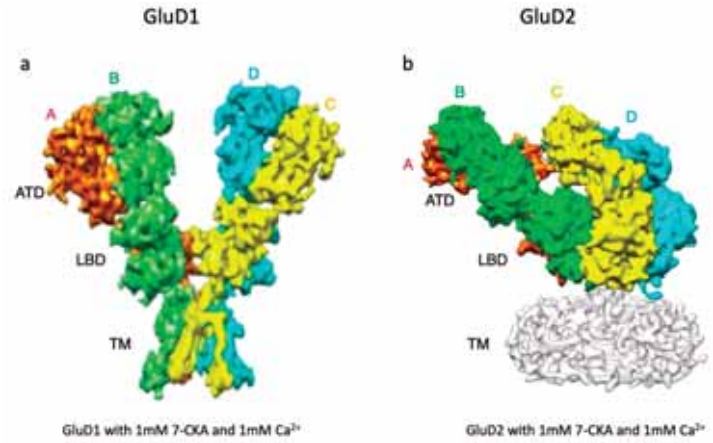

Fig. 1: GluD1 and GluD2 structures in presence of calcium ions and 7-CKA. GluD1 (PDB ID: 7KSP) (a) and GluD2 (6LUP) (b) are shown with the broadest view parallel to the membrane highlighting the arrangement of the extracellular domains.

microscopy (cryo-EM). The structure reveals a distinct architecture when compared to other iGluRs. We validated the observed receptor assembly via cysteine crosslinking experiments and whole-cell patch-clamp electrophysiology. Our results provide insights into architecture and assembly of orphan delta receptors and provide molecular blueprints for understanding their functions.

Our cryo-EM analysis revealed a Y-shaped GluD1 receptor tetramer with a three-layered arrangement of the ATD, LBD, and TM domains. The ATD and LBD are arranged in a 2-fold symmetric dimer-of-dimers configuration as observed for other iGluRs. However, remarkably, domain swapping is not observed at the ATD-LBD layer **(Fig. 1)** between the proximal and distal subunits. It is noteworthy that all ionotropic glutamate receptor structures reported till-date for N-methyl-D-aspartate (NMDA), AMPA, and KA receptors exhibit domain swapping at the LBD layer.

Due to this non-swapped architecture of GluD1 receptors, the two arms of the receptor tetramer are formed by subunits AB and DC with the domains of same subunits forming 2-fold symmetric dimers at the ATD and LBD layers **(Fig. 2 a, g, h)**. Thus the conformations of subunits BD, proximal to the axis of tetramerization and subunits AC, that are distal to the axis of tetramerization are similar. Our electrophysiology experiments demonstrate that CT-deletion necessary for overexpression and purification of GluD does not affect receptors assembly **(Fig. 3 a-b)**.

Using a minimally modified construct, we have purified and determined the structure of detergent-solubilized GluD1 and GluD2 receptors in-solution. Owing to the conformational heterogeneity of GluD1, the resolution of our EM maps is limited to ~8Å. However, by fitting crystal structures and models of various domains into the constraints of EM density map, we provide the first insight into the subunit arrangement for a homo-tetrameric GluD1 and GluD2 receptors. While all the previous models for GluD receptors depict domain swapping at the ATD-LBD interface, our study shows a unique non-swapped architecture for this enigmatic class of receptors. However, whether this non-crossover is the sole cause for the inactive ion channel needs to be addressed in the future.

Due to non-crossover, the two extracellular arms of the receptor seem to have a broader range of movement resulting in conformations where the receptor could adopt a "splayed" conformation. Another important feature of the GluD1 receptor is the close packing of ATD and LBD domains. While, it's not clear currently if this is driven by the shorter ATD-LBD linker when compared to other iGluRs, it has been reported that mutation of the linkers leads to loss of function in GluD2 receptors. Pertaining to this, D-serine application induced Parallel Fibre-long term depression (PF-LTD) in cerebellar slices in Purkinje cells (PCs) expressing wild-type receptors while it failed to do so in PCs expressing GluD2 in which a glycosylated linker was inserted between the two domains. This could result likely from the uncoupling of the ATD-LBD interactions, which might lead to reduced transduction of forces generated by ligand binding to the transmembrane domains. This along with other recent pieces of evidence suggest that not just the short linkers, but the ATD-LBD interface interactions, and contribution of the hinge region of the GluD2-LBD in the weak ligand affinity among other things might contribute to the inactivity of the GluD receptors. In overview, our results provide a molecular framework to design future studies directed towards resolving the long-standing questions concerning this family of receptors. These results suggest that orphan delta receptors of the iGluR family likely have a different mode of assembly and provide a foundation for future studies directed towards understanding the functions of these receptors in light of this structural information.

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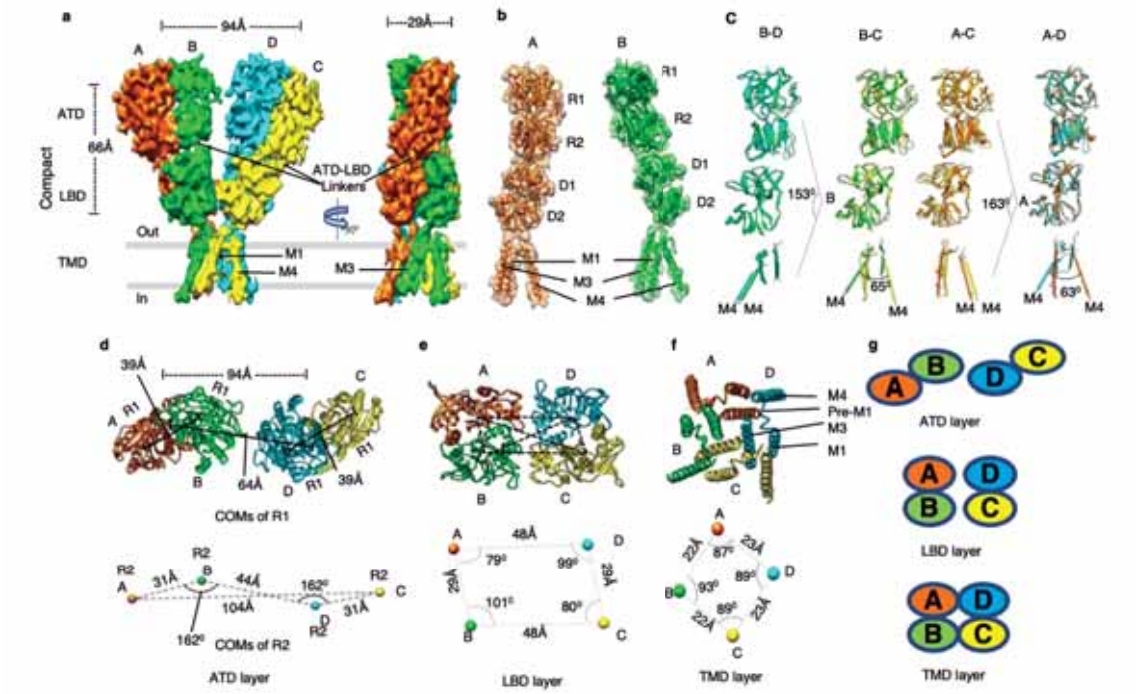

Fig. 2: GluD1 has an unprecedented non-swapped architecture. Panels a-g show the architecture of compact conformation of GluD1 receptors in complex with 7-CKA and calcium. a, Side view highlighting the broadest face of the Y- shaped receptor and 90° rotated views of the sharpened 3D density map is shown. Each subunit is depicted in a different color. The EM reconstructions clearly show the non-swapped arrangement of the ATD and LBD layers. The distances between the centroids (R1-R1 of ATD domains) for AB and CD dimer pairs are shown above the model. The vertical separation between the COMs of ATD dimers and LBD dimers are also shown. Panel b shows the segmented density map for subunits A and B fitted with protein co-ordinates. c, Superimposition of subunits B/D, B/C, A/D and A/C are shown highlighting similar AB and BC conformations. Helices and sheets are represented as pipes and planks, respectively. Top views of ATD (d), LBD (e) and TM domains (f) are shown. The distances and the angles subtended between the COM (Centre of Mass) of various subunits were measured and are indicated below the top views. Panel g shows the schematic of the domain arrangement for the ATD, LBD, and TM layer.

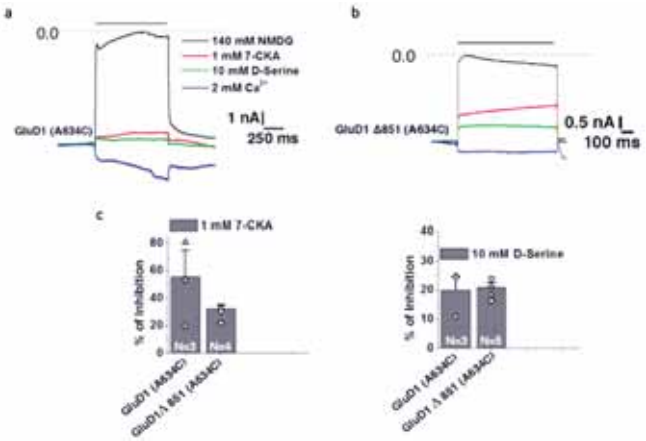

Fig. 3: a, Representative traces for show whole-cell patch clamp recordings (holding potential = -60 mV) from constitutively active GluD1 A634C point mutant receptors. The seal resistance before entering into the whole-cell configuration was always at least 1 GΩ. Panels a and b show overlay of representative traces showing application of either NMDG solution or 1 mM 7-CKA (red), 10 mM D-Ser (green) or 2 mM $CaCl_2$ (blue). Dashed line indicates zero current level achieved by application of impermeant NMDG which blocks the constitutive inward currents for both GluD1 A634C (a) and GluD1 Δ851-A634C receptors (b). The constitutive currents are also modestly inhibited by D-Ser or 7-CKA application and potentiated by Ca^{2+} for both the full-length and CT truncated GluD1 receptors. c, shows percent inhibition of spontaneous currents by 7-CKA and D-Ser calculated with respect to NMDG inhibition.

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Role of Hypoxia and Osteopontin in Regulating Cancer Stemness and Metabolic Rewiring in Breast Cancer

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Objectives of the study

- To understand how hypoxia regulates cancer stemness in breast cancer.
- To examine how osteopontin regulates metabolic adaptations in breast cancer.

Summary

In recent years, the major focus of our laboratory has been shifted to delineate the role of hypoxia and altered glucose metabolism in breast cancer progression. Hypoxic regions tend to develop in the solid tumor microenvironment owing to differential availability of oxygen. Cancer cells residing in these regions exhibit altered signaling networks and metabolic attributes. Cancer stem cells (CSCs) which are different from the bulk tumor cells by virtue of chemoresistance, radioresistance and self-renewal, form a niche in these hypoxic areas. CSCs have enhanced potential for contributing to angiogenesis and metastasis of primary tumors. Acquisition of the CSC phenotype has also been associated with the phenomenon called epithelial-to-mesenchymal transition (EMT). Breast cancer specific CSCs can be identified by means of surface expression of markers like cluster of differentiation 44 (CD44), EpCAM, ganglioside 2 (GD2), activity of enzymes like aldehyde dehydrogenase (ALDH) or absence of expression of CD24. Cancers cells in solid tumors exhibit a phenomenon called Warburg effect whereby they shunt most of the pyruvate produced to lactate rather than utilizing for ATP production. Although energetically inefficient, this phenomenon confers growth advantages to the cancer cells as glycolytic intermediates are used for production of nucleotides, amino acids, and lipids. Pyruvate kinase (PK) is a glycolytic enzyme and it

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catalyzes the conversion of phosphoenolpyruvate to pyruvate. Pyruvate kinase has four isozymes, PKL, PKR, PKM1, and PKM2. PKM1 and PKM2 are alternative splicing products of the primary transcript encoded by the PKM gene. As PKM2 is less efficient than PKM1 in catalyzing conversion of phosphoenolpyruvate, cancer cells having more PKM2 than PKM1 pile up glycolytic intermediates and produce more lactate. Lactate acidifies the tumor microenvironment and the latter is conducive for spreading of primary tumor cells to secondary organs. These Warburg-type cancer cells are enriched in the hypoxic regions of a solid breast tumor. 6-Phosphofructo-2-kinase/fructose-2,6-bisphosphatase-3 (PFKFB3) regulates level of fructose-2,6-bisphosphate. Fructose-2,6-bisphosphate is an allosteric regulator of another rate limiting enzyme of glycolytic pathway phosphofructokinase 1 (PFK1).

In this report, using in vitro and in vivo breast cancer models, we have been developed to study the intricate interplay of hypoxia and estrogen receptor alpha (ERα) in the context of cancer stemness and EMT. It could be established that hypoxia downregulates ERα at the level of transcription and that suffices enrichment of CSCs. Moreover using in vitro and chemical carcinogen induced murine breast cancer models, role of osteopontin (OPN), a chemokine like protein in adapting to metabolic needs of cancer cells could be illustrated.

Work done
Hypoxia enriches cancer stem cell population defined by the surface marker GD2 in ERα positive breast cancer cells. Hypoxia increases invasive properties of these cells by initiating EMT. Hypoxia upregulates expression of mesenchymal markers like N-cadherin, Vimentin, Twist, Slug concomitantly downregulating epithelial marker E-cadherin (Figure 1). Hypoxia stabilizes a master transcription factor called hypoxia inducible factor 1 alpha (HIF1α). The latter binds the promoter of ERα and downregulates its expression. Downregulation of ERα expression is sufficient for induction of EMT and enrichment of the stem cell pool. Treatment with selective estrogen receptor modulators (SERMs) enriches CSCs in xenograft mammary tumors.

The study establishes a link between OPN and glucose metabolism in breast cancer cells. OPN enhances glucose uptake and lactate release by breast cancer cells. OPN increases expression of PKM2. OPN stabilizes HIF1α under normoxic condition by signaling through its receptors CD44 and integrin

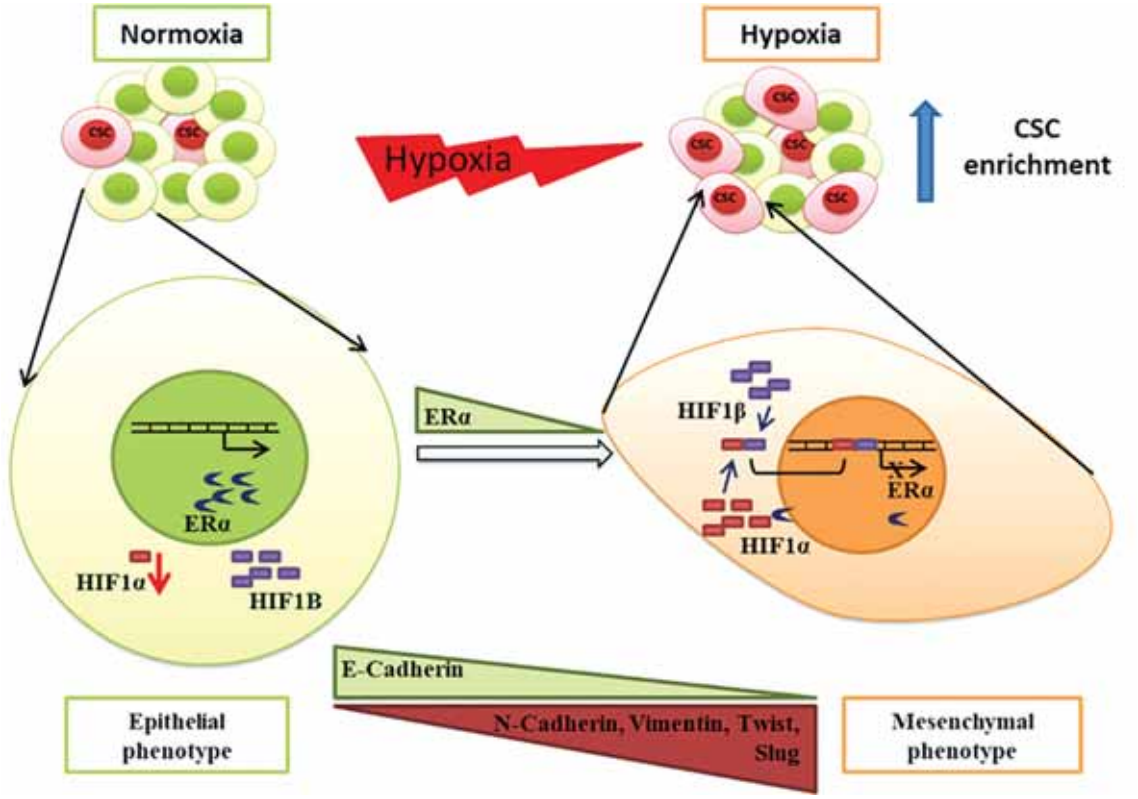

Figure 1. Schematic illustrating mechanisms underlying enrichment of cancer stem cells under hypoxic conditions in breast tumors

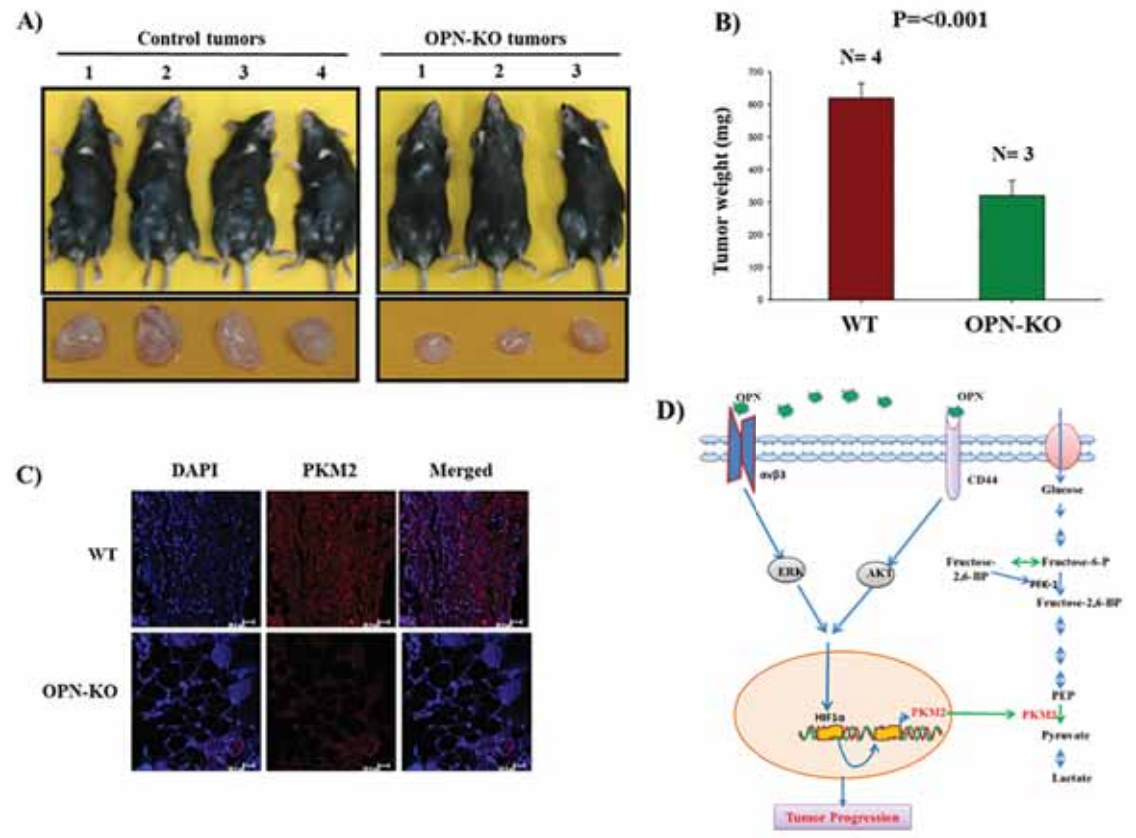

Figure 2. (A) Representative images of chemical carcinogen (pristane) induced OPN Wild type (WT, control) and OPN-knockout (OPN-KO) murine mammary tumor models; (B) bar graph representing weight of control (WT) and OPN-KO tumors; representative confocal micrograph showing immunofluorescence staining of PKM2 (C) in control (WT) and OPN-KO tumor sections. (D) Schematic representation of OPN-regulated metabolic adaptation in breast cancer.

$\alpha_v\beta_3$ in breast tumors. HIF1α in turn binds to the promoter of PKM2 and increases its expression. Pristane, a chemical carcinogen induced murine mammary tumors exhibit lower level of PKM2 in OPN knockout (OPN KO) mice and showed reduced tumor growth in these mice as compared to OPN wild type mice (Figure 2).

The study reveals mechanisms whereby hypoxic microenvireonment and oncogenic protein OPN modulates transcription machinery and cellular metabolism of breast cancer cells (Figures 1 & 2).

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Role of Chemokine Receptor CCR9 in Controlling Inflammation and Autoimmunity

Objectives of the study

- To determine how the chemokine receptor CCR9 controls the differentiation and function of mucosal inflammation.
- To determine the role of $CCR9^+$ dendritic cells in controlling the differentiation of effector and regulatory immune response in gut.

Summary

Chemokine (C-C motif) receptor 9 (CCR9) is expressed on IgA-producing B cells, $CD8^+$ T cell, $CD4^+$ T cells, γδ T cells and dendritic cells (DCs), and drives the migration to its only known chemokine ligand CCL25, which is constitutively expressed on small intestinal epithelial cells and thymic epithelial cells in mice and human. Intestinal epithelial cells during gut inflammation or in the inflammatory bowel disease (IBD) produce several folds higher CCL25 and drive the recruitment of $CCR9^+$ immune cells. Due to its gut tropism activity, CCR9 and CCL25 are suggested as a potential therapeutic target. A phase 2 study using a CCR9 antagonist (vercirnon or GSK1605786A also known as CCX282-B) showed clinical remission in moderate to severe Crohn's disease (CD), but subsequent phase 3 study failed to improve clinical response and remission. Moreover, CCR9 antagonist treatment showed a dose-dependent adverse reaction in almost all the patients. We investigated the functional role of $CCR9^+$ DCs in the presence of CCL25 in the differentiation of regulatory $CD4^+$ T cells (Treg) or Th17 cells. Our results showed that $CCR9^+$ DCs mainly $CD11b^-$ $CD103^+$ DCs recruited to the gut and gut-associated lymphoid tissues during gut inflammation. $CCR9^+$ DCs induces Treg differentiation in the presence of CCL25 (Figure 1). Further, we demonstrate that thymic stromal lymphopoietin (TSLP) produced by $CCR9^+$ DCs but not IL-10 promotes the differentiation of Treg. $CCR9^+$ DCs in the GALT show an immature and regulatory phenotype and suppressed the cholera toxin and ovalbumin-induced gut allergic response in mice.

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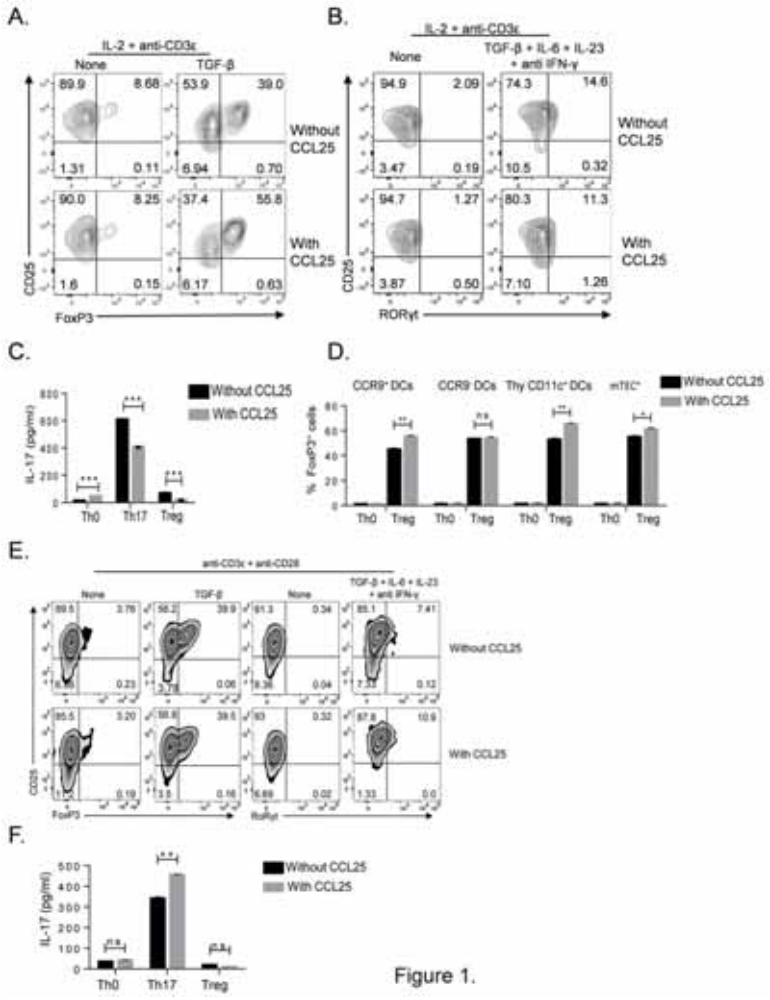

Figure 1: CCR9$^+$ DCs promote Foxp3$^+$ Tregs and inhibit Th17 cells differentiation. Naïve CD4$^+$ T cells (CD4$^+$CD25$^-$CD44$^-$ cells) were cultured with purified CCR9$^+$CD11c$^+$ DCs in presence or absence of CCL25 under Treg or Th17 differentiation conditions for four days. After four days, cells were surface stained for CD4, CD25, and intracellular Foxp3 and RORγt. **(A)** Expression of Foxp3 was analyzed after gating CD4$^+$ cells. **(B)** Expression of RORγt was analyzed after gating on CD4$^+$ cells. The numbers in the contour plots show the percentage of cells in the marked quadrants **(A, B).** Data shown are representative of one of the three experiments **(A, B). (C)** After four days of culture, the supernatant was collected, and the secretion of IL-17 was measured by ELISA. Error bars indicate the mean ±SEM. n = 2 experiments. ***P <0.001 **(D)** Naive CD4$^+$ T cells were cultured with peripheral CD11c$^+$CCR9$^+$ DCs, CD11c$^+$CCR9$^-$ DCs, thymic CD11c$^+$ DCs and thymic medullary epithelial cells (mTEC$^+$ cells) in presence of CCL25 under Treg differentiation condition. Error bars indicate the mean ±SEM. n = 2 experiments. *P < 0.05, **P < 0.01 and ns, not significant **(E)** Naïve CD4$^+$ T cells were cultured in anti-CD3ε mAb-coated 96 well plates in the presence of soluble anti-CD28 mAb along with Th17 and Treg differentiating condition in the absence of DCs. After four days of cultures, Foxp3 and RORγt expression were analyzed using flow cytometry. Data shown are representative of one of the three independent experiments. The numbers in the contour plot show the percentage of cells in the marked quadrants. **(F)** Secretion of IL-17A in culture supernatant from E was measured by ELISA and plotted. Error bars indicate mean ±SEM. n = 2 experiments. **P < 0.001; ns, not significant.

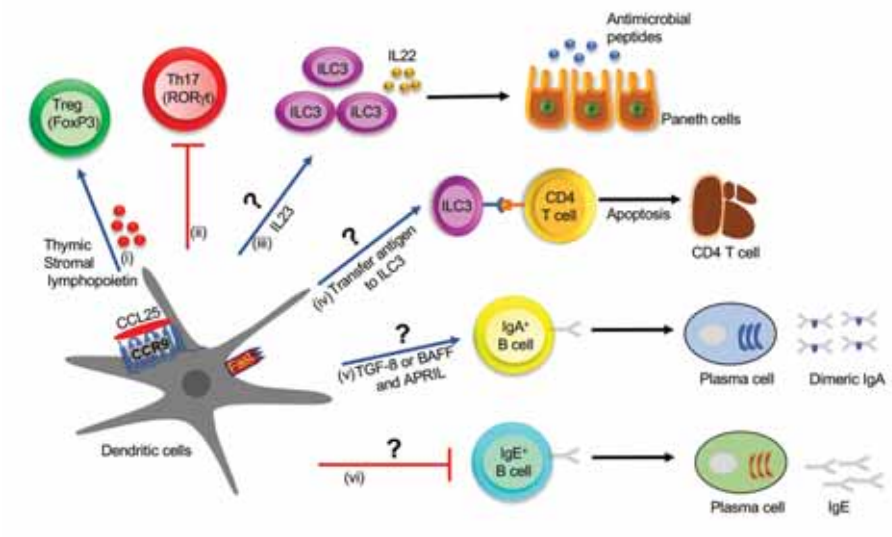

Figure 2. Role of CCR9$^+$ DC in the regulation of innate and adaptive immune cell function in the intestine during homeostasis: (i) CCL25-CCR9 interaction on DC increases the production of thymic stromal lymphopoietin (TSLP) and expression of FasL and latency-associated peptide (LAP) which promotes Treg differentiation. (ii) CCR9$^+$ DCs inhibits Th17 differentiation by an unknown mechanism. (iii) CCR9$^+$ DCs might regulate the ILC3 function by regulating IL-22 production by secreting IL-23 cytokine. IL-22 augments the production of AMP and helps in maintaining epithelial cell integrity. (iv) Innate lymphoid cell 3 (ILC3) may acquire antigen from CCR9$^+$ DCs and eliminate commensal-reactive CD4$^+$T cells by activating the apoptotic pathway. (v) CCR9$^+$ DCs may regulate IgA$^+$ B cell class switching by activating the TGF-β pathway or increasing expression of B-cell activating factor (BAFF) or a proliferation-inducing ligand (APRIL) and generate high-affinity IgA antibodies. TSLP provides an autocrine effect on DCs and increases expression of BAFF or APRIL, which is required for IgA class switching (vi) CCR9$^+$ DCs may inhibit IgE class switching by an unknown mechanism.

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Fabrication and Characterization of Bioactive and Biocompatible Scaffolds and Their Usage for Various Tissue-Engineering Applications Using Stem Cells

Objectives of the study

- Fabrication and characterization of Bioactive and Biocompatible scaffolds and assessing their efficacy in bone tissue engineering using MSCs as the cellular source.

Summary

Tissue engineering offers an interdisciplinary avenue that has gained immense interest among the investigators worldwide. The recent surge in exploring various biomaterials for fabricating tissue engineered implants does put emphasis on the scaffold environment mimicking the cellular niche, as well as in selecting the ideal cellular source for the same. We have used mesenchymal stem cells (MSCs) derived from various sources and also embryonic stem cells (ESCs) as the source materials for assessing the safety and efficacy of various fabricated scaffold materials with/without surface modifications in supporting growth and differentiation of stated stem cells. Moreover, the ultimate target has been to use those as biomaterials for various tissue engineering applications especially to neural, cardiac and osteogenic ones.

Biomaterials with better osteogenic capacity, rapid osteo-integration and higher mechanical strength are undoubtedly preferred for successful bone implant development. Accordingly, we have successfully developed various formulations of nano-HAp Collagen and characterized for their functional group, microstructural and elemental analyses, mechanical strength, degradation kinetics etc. Subsequent to verification of bioactivity, the fabricated scaffolds have been tested for biocompatibility using MSCs as the cellular

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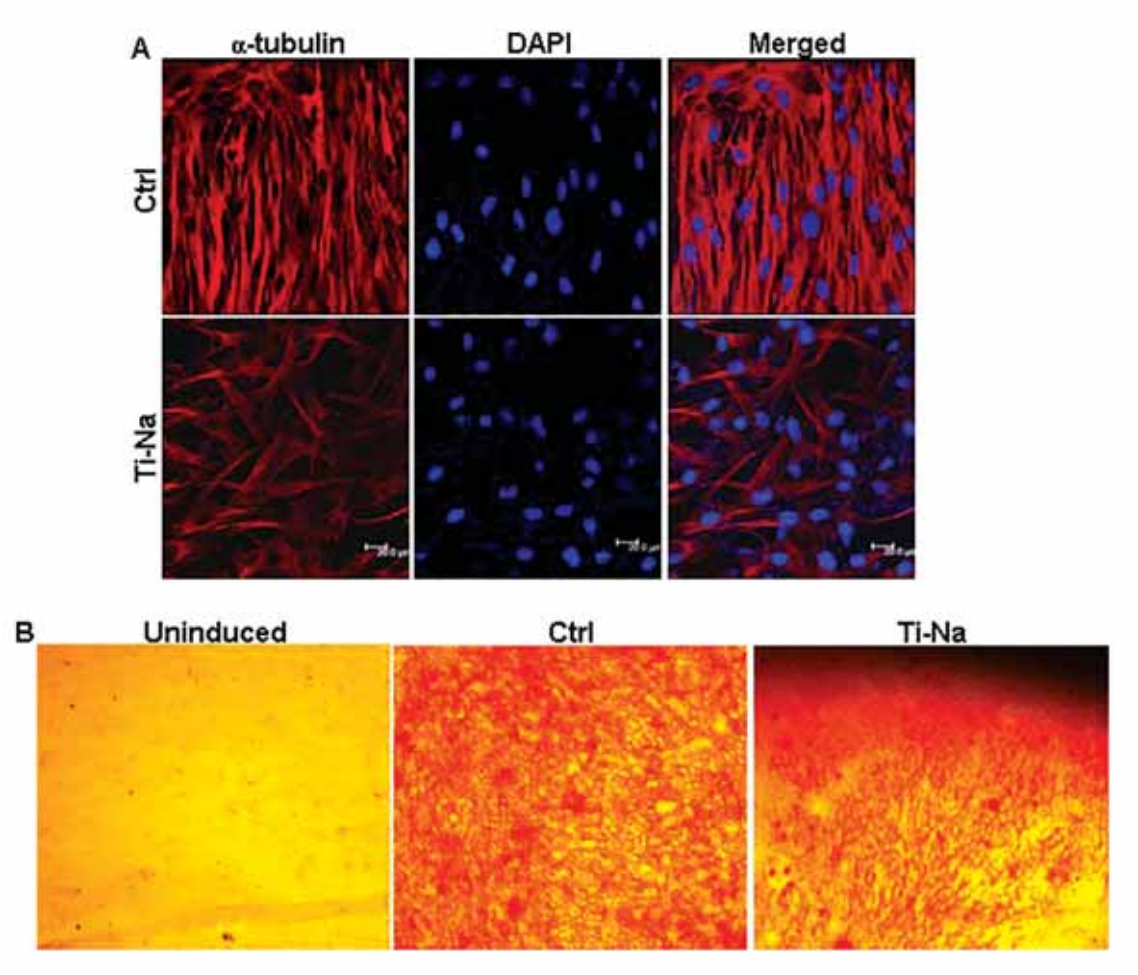

Fig. 1: (A) MSCs cultured on the surface modified Ti-sheets show adhesion and growth of cells expressing cytoskeletal marker, α-tubulin and with Dapi, staining the mucleus. (B) Calcium deposits seen upon osteogenic differenation of MSCs cultured on surface modified Ti-for 3w followed by Alizarin Red staining.

source. Further, we have demonstrated successful integration of MSCs into the scaffold, their adhesion and subsequent differentiation into osteogenic lineage. Similarly, in a collaborative pursuit, we have used surface modified Titanium as a mean for conferring better mechanical strength for osteogenic implant development. Treatment of Ti- metal with NAOH could convert it to porous sodium hydrogen titanate that further got converted to sodium titanate having either anatase or rutile TiO2 phase depending on the temperature used for heat treatment. While the former displayed elongated rod like structure, the latter one had distracted network morphology. Our study could successfully demonstrate the efficacy of anatase TiO2 to be bioactive by being capable of forming bonelike apatite in simulated body fluid, rather than the rutile form. The stated TiO2 was further proven to be biocompatible upon being laden with MSCs. Moreover, MSCs could successfully adhere to the surface modified titania layer (Fig. 1A) and upon induction could exhibit extensive osteogenic differentiation (Fig. 1B). Collectiverly our data suggested the fabricated porous scaffolds as ideally suited materials for bioimplant development in bone tissue engineering.

Future Research Plans - Assessing the *in vivo* efficacy of fabricated bioimplants and their integration into host using animal models with bone defect.

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Understanding the Role of Cellular Translation Regulation Associated with Toxic Huntingtin Protein

Objectives of the study

- Understanding the effect of Pathogenic Huntingtin on protein synthesis.
- Understading the crosstalk between pathogenic Huntingtin and Orb2.

Summary

Huntington's disease is caused due to expansion of poly Q repeats on Huntingtin gene. This expansion causes the protein to aggregate and such aggregates can disturb several cellular processes including axonal transport, transcription, etc. What we observed is pathogenic Huntingtin protein causes a reduction in protein synthesis in cells. One possible mechanism we find is the Huntingtin aggregates sequester another protein involved in translation called Orb2. Orb2 was earlier identified as a physiologically benificial prion like protein which is crucial for maintenance of memory in fruit flies. By sequestering Orb2, Huntingtin changes the dynamic nature associated with Orb2 and possibly its function associated with translation. We further reasoned if sequestration of Orb2 is associated with toxicity of Huntingtin then overexpression of Orb2 can rescue the toxicity associated with Huntingtin. In a fly model we find the same. Using biochemical assay we find the rescue is not due to a decrease in the aggregate load but through increasing the translation in the cells. We further find the human homologues of Orb2, the CPEB family of proteins also get sequestered by Huntingtin aggregates suggesting our findings with translation and Orb2 in the fruitfly model can be relevant for the human disease condition.

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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 hallmark of the disease is gradual depletion in the number of $CD4^+$ T cells leading to the onset of opportunistic infections. The therapeutic regimen being used at present can reduce the viral load significantly but is not the ultimate answer to AIDS patients as a treatment 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 still remains to be clearly understood. We have reported earlier that cellular Hsp40 and HSF-1 proteins interact with viral Nef

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protein and positively regulate HIV-1 replication. Although involvement of different heat shock protein family members in viral pathogenesis has been 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 including their isoforms. 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. We have shown earlier that silencing of selected Hsp40 isoforms either reduced or enhanced LTR promoter activity significantly. These results were further confirmed by over expression study as well. Furthermore, among the selected isoforms, we have now observed that DNAJB8 seems to have a role in HIV-1 virion infectivity. We have also checked the expression of Hsp70 isoforms at the mRNA level and found that known heat inducible isoforms get highly upregulated during HIV-1 infection as well. Further, we are trying to study the localisation of cellular Hsp70 isoforms into the HIV-1 virions. We are also trying to understand the interaction of these cellular HSP70 isoforms with viral proteins. GST pull down studies have shown that Nef interacts with HSPA8, HSPA9 and HSPA5. We have been also studying the role of HSP70 binding protein; HspBP1, a co-chaperone molecule of Hsp70. We have also observed that HIV-1 down-modulates the expression of this nucleotide exchange factor, HspBP1. We have now observed that the virus downregulates HspBP1 promoter activity. Further, we have tested different viral proteins for their effect on the promoter activity and found that Tat causes downregulation of HspBP1. We are now trying to further elucidate the mechanism through which Tat acts on the HspBP1 promoter. Heat shock protein 90 (Hsp90) is also an important cellular factor necessary for the completion of HIV-1 life cycle. Inhibition of Hsp90 leads to decreased HIV replication as well as reactivation of the virus from latency. Hsp90 having differently compartmentalized isoforms in eukaryotic cells might have some different roles apart from acting as a chaperone in life cycle of the virus. As Hsp90 inhibitors available till date are mostly pan-isoform inhibitors, it is still unclear that inhibition of which isoform is majorly affecting the virus life cycle. To explain the differential pattern of expression of these isoforms during HIV-1 infection, we are also studying the expression of the Heat Shock Factor 1 (HSF1), the major transcription factor of the heat shock proteins reported in other stress conditions. In addition, role of the Hsp90 isoforms in HIV-1 replication is being evaluated to find their functional relevance in HIV-1 pathogenesis. Furthermore, we are also trying to elucidate the molecular mechanism through which the selected isoform acts on HIV-1 life-cycle.

Studies done till date to elucidate the pathways involved in HIV-1 induced T cell depletion has revealed that apoptosis underlie the etiology; however, a clear molecular understanding of HIV-1 induced cell death has remained elusive. In this context, we are currently 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*. We have also observed that autophagy is down-modulated in presence of Nef whereas it is up-regulated in absence of Nef during HIV-1 infection. The role of DAPK/ZIPK in HIV-1 induced cell death is being studied further. 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 tried to identify deregulated miRNAs through bioinformatic analysis of existing data in GEO database, which has led to identification of several differentially expreseed miRNAs in HIV-1 infection. These miRNA expression changes have ben further validated in HIV-1 infected PBMCs. We have taken forward one such upregulated miRNA for further characterization. This study provides an interesting lead to unfold the mystery as to how these small non-coding RNAs govern the activity of the virus inside the host. Finally, we have also initiated studies on cellular stress response during HIV-1 infection. Endoplasmic reticulum (ER) dysfunction due to various physiological and pathological conditions lead to an evolutionarily conserved cell stress response, the Unfolded Protein Response (UPR). Pathogenic exposures including virus infection leads to production of large quantity of viral proteins causing ER stress. The host UPR modulation by HIV-1 has not been studied well and the detailed mechanism remains to be characterized. To monitor the UPR activation during HIV-1 infection, different markers of UPR were investigated first. It was found that HIV-1 induces the IRE1 dependent pathway of UPR which is also marked by increased phosphorylation of IRE1α followed by induced splicing of XBP1, an important participant of UPR activation. When another branch of UPR, which is mediated by PERK was analyzed, it was found that there is an increased phosphorylation of eIF2α depicting increased translational attenuation during the course of HIV-1 infection. These results provide an interesting aspect to investigate further and derive the mechanism responsible for this activity.

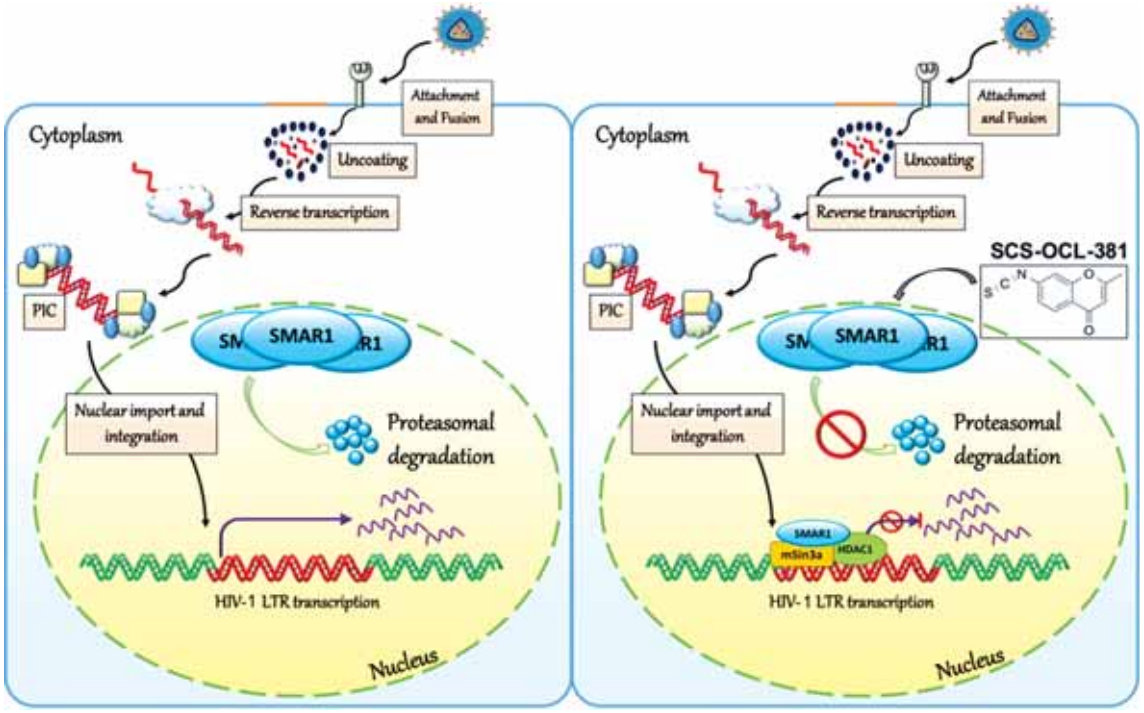

Figure - 1: Schematic representation of the mechanism of SCS-OCL-381 mediated anti-HIV activity. HIV-1 infection results in proteasomal degradation of SMAR1 in T-cells (Left panel). This supports the active transcription mediated by HIV-1 LTR and thus viral replication. SCS-OCL-381 treatment results in stabilization of SMAR1 (Right panel). This results in the formation of repressor complex on HIV-1 LTR that inhibits LTR mediated transcription and thus viral replication.

Finally, we have been also involved in identification of novel anti-HIV molecules and study of their potential use as microbicides. The current therapeutic strategy involving the use of anti-retrovirals in combination (HAART) has proven to be useful in controlling the virus but is not sufficient to eradicate the virus from the patients. Extensive work is being done throughout the globe to identify new ant-HIV therapeutic strategies. 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 elucidating the role of Hsp90 in HIV-1 replication and exploiting it as a potential therapeutic target. For this, in collaboration with BIT, Mesra, we have designed and synthesized 15 novel Hsp90 inhibitors based on the isoxazole scaffold found in some second generation Hsp90 inhibitors. These molecules have conserved anti-HIV activity across virus isolates and cell types. Mechanistically, these novel molecules were observed to interact with crucial amino acids situated in the N-terminal ATP-binding pocket of Hsp90. Further systemic studies of these novel Hsp90 inhibitors in combination with currently used ART regimen are in progress.

Synthetic as well as natural Isothiocyanate (ITCs) group of chemicals (-N=C=S) are found in some of the most common dietary sources such as various cruciferous vegetables including broccoli and cauliflower. ITCs have occupied a prominent place in biomedical science for their dynamic properties including cell cycle arrest, anticancer activity, antimicrobial, antifungal and antiviral activities. In a recent multi-institutional collaborative study, we have reported potential anti-HIV activity of several novel synthetic ITC derivatives with known SMAR-1 stabilizing activity, a nuclear matrix binding protein. The essential role of SMAR1 reported earlier in HIV-1 LTR driven gene expression suggests SMAR1 as an HIV dependency factor (HDF). We have now reported anti-HIV activity of 8 novel isothiocyanate (ITC) derivatives that differentially stabilise SMAR1. Out of 8 novel ITC derivatives, SCS-OCL-381 was observed to inhibit HIV-1 replication most significantly in a reporter T-cell line, CEM-GFP. Furthermore, the highly conserved anti-HIV activity of SCS-OCL-381 is a cell type, virus isolate and viral load independent phenomena and is approximately three-fold more effective than the representative ITC, Sulforaphane (SFN). Further, SCS-OCL-381 does not inhibit the activity of viral enzymes reverse

transcriptase, integrase and protease. Mechanistically, SCS-OCL-381 stabilises SMAR1 which, otherwise undergoes proteasomal degradation upon HIV-1 infection in T-cells. This stabilisation results in the recruitment of repressor complex on HIV-1 LTR resulting in repression of LTR mediated transcription and gene expression leading to inhibition of viral replication (Fig-1). Taken together, our results suggest that ITC derivatives including SCS-OCL-381 should further be considered for *in vivo* characterisation of its anti-HIV potential.

Future Research Plans

We will continue to elucidate the role of individual heat shock protein isoforms in HIV-1 replication and pathogenesis, with specific reference to Hsp40, Hsp70 and Hsp90 isoforms. We will continue the characterization of novel Nef interacting host cell proteins identified previously like ZIPK, for their functional relevance in HIV life cycle, cell death and autophagy. We intend to continue our studies to understand the role of microRNAs and ER stress in HIV pathogenesis. Finally, studies to identify novel anti-HIV molecules will be continued with the objective to identify novel lead molecules with cellular targets like Hsp90 and molecules with potential for use as anti-HIV microbicides.

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Identification of Potential Targets and Biomarkers for Multiple Myeloma Using Quantitative Proteomics and Molecular Approaches

Objectives of the study

- Identification and validation of potential biomarkers for Multiple Myeloma using bone marrow mono nuclear cells (BM MNCs).
- Investigation of marginal zone B and B1 cell specific protein (MZB1) as a candidate marker of multiple myeloma using molecular approaches.

Summary

Multiple myeloma (MM) is a plasma cell cancer that accounts for nearly 13% 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 malignancies 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.

Bone marrow mononuclear cells (MNCs) are the actual affected cells in MM. MNCs may serve as the most appropriate site for identification of dysregulated protein signature for MM that can be useful for designing novel theranostic interventions for MM. Surprisingly, MNCs have not been explored till date

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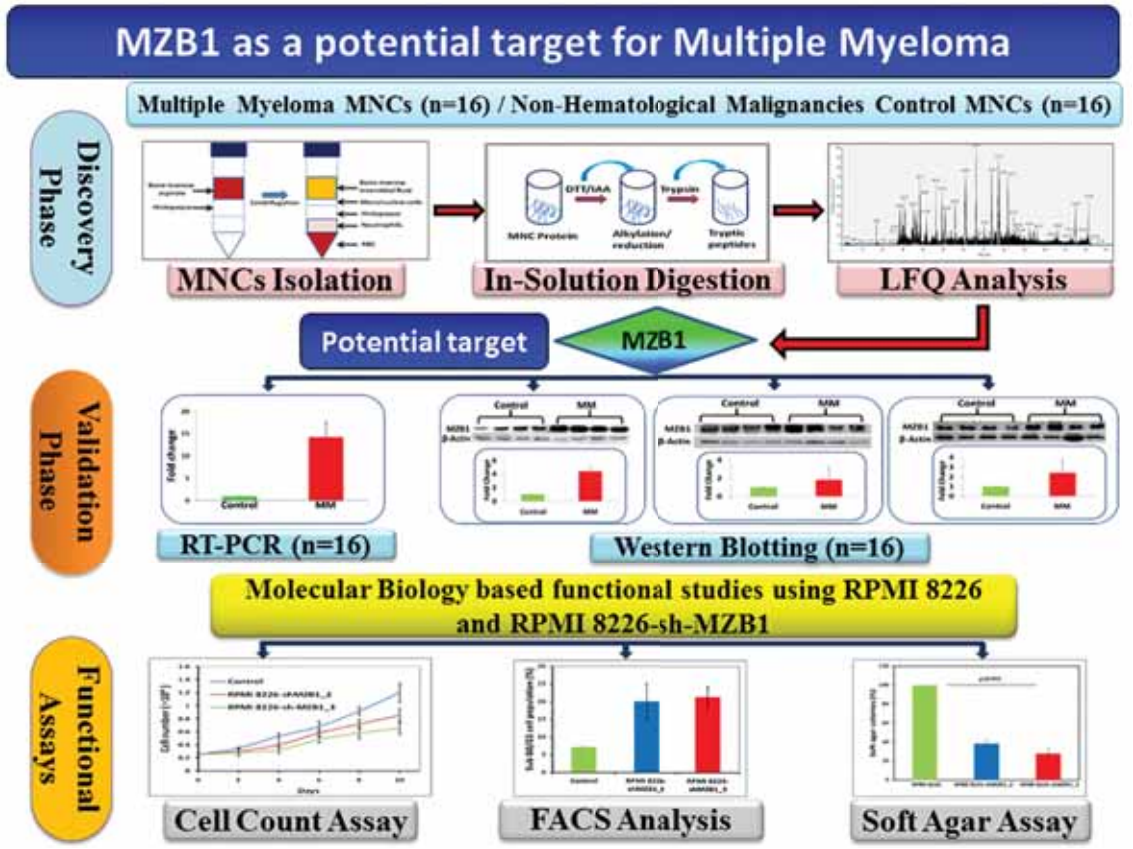

Fig. 1: A flowchart depicting experimental design and overall results obtained for Multiple myeloma MNCs proteomics analysis. In the discovery phase, 192 differentially expressed proteins were identified using LFQ based proteomics analysis. MZB1 was selected for validation and functional studies based on functions of MZB1 are quite related to characteristic features of MM such as calcium homeostasis, immunoglobulin production and cell replication. Cell count assay, FACS analysis and soft agar assay suggest that elevated level of the MZB1 play a crucial role in MM disease progression.

towards the identification of proteome alterations for this disease. In this study, we hypothesized that proteomic alterations in MM MNCs may play a crucial role in disease occurrence and progression. In order to identify the differentially regulated proteins in MNCs from MM compared to the MNCs of non-hematological malignancies, label free quantitation (LFQ) based proteomic analysis was performed using Orbitrap Fusion mass spectrometer. Proteomic analysis identified 715 common proteins from the total dataset, out of which 192 proteins were differentially regulated. Among these differentially regulated proteins, the expression of 79 proteins was upregulated and 113 proteins showed a downregulated pattern. Using different bioinformatic tools like IPA, DAVID and PANTHER, we identified the molecular functions, biological processes, protein classes and pathways that were altered in MM MNCs. Among the statistically significant proteins, marginal zone B and B1 cell specific protein (MZB1) [log2 FC = 3.4] was selected for further functional studies using MM cell line model as this protein turned out to be one of the significantly altered proteins and it also has significant role in cell proliferation as well as immunoglobulin synthesis. Furthermore, functions of MZB1 are quite related to characteristic features of MM such as calcium homeostasis, immunoglobulin production and cell replication. Western blotting analysis also showed that expression levels of MZB1 are markedly increased in MM MNCs as compared to the control samples. In order to further confirm our observation, we examined the expression level of the MZB1 levels in the MM patient's serum and BMIF samples. We found a distinct upregulation of MZB1 in the MM patients compared to the respective controls.

To investigate the role of MZB1 in MM progression, we stably depleted MZB1 in RPMI 8226 cells (MM cell line) using lentivirus short hairpin RNA interference in RPMI 8226 cells. We then investigated the proliferation of RPMI 8226 cells stably expressing shRNA against MZB1. Cell count results clearly showed that the depletion of MZB1 results in a slower proliferation of RPMI 8226 cells. To examine how depletion of

MZB1 led to retardation of RPMI 8226 cell proliferation, we performed flow cytometry to examine the population of apoptotic cells. Results showed that the knockdown of MZB1 significantly increased the sub-G1 cell population i.e. apoptotic cells.

Cancer cells grow in an anchorage-independent manner. RPMI 8226 being a suspension cell type, we examined whether MZB1 has any role in anchorage-independent growth of RPMI 8226 cells. To address this, we also performed soft agar colony formation assays. We found that the depletion of MZB1 resulted in inhibition of anchorage-independent growth of the RPMI 8226 cells indicating that MZB1 might regulate growth proliferation-associated proteins. We, therefore, investigated the proteins associated with the cell cycle progression in the wild type and MZB1 depleted cells. Immunoblotting results revealed that the expression of many proteins associated with promoting cell cycle progression was reduced in MZB1 depleted RPMI 8226 cells. For instance, AKT and MAPK kinase pathways were markedly inhibited. Similarly, cyclins involved in G1 phase (cyclin D1), S phase (cyclin A) and G2/M phase (cyclin A and cyclin B) were significantly declined in MZB1 depleted RPMI 8226 cells suggesting that MZB1 is important for proliferation of MM. Collectively, our results suggested that the elevated level of the MZB1 plays a crucial role in MM disease (Fig. 1). Therefore, MZB1 could function as a putative oncogene in MM pathogenesis and might be a potential marker.

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Role of T cells and non-T cells in Leishmania infection and in tumor

Summary

Leishmania is a protozoan parasite that inflicts a complex of diseases called leishmaniasis in 88 countries affecting 320 millions of people. However, it remains a neglected tropical disease, as neither a non-toxic drug nor a vaccine is available. Because the alarmingly small repertoire of drugs is turned effectively smaller due to emergence of resistance against antimony and miltefosine, vaccines remain the only ray of hope in controlling this disease. However, three generations of vaccines have consistently failed in clinical trials [1]. Therefore, we continued our efforts to develop two vaccine strains of the parasite, which are now the only characterized strains in the world [2], and, in collaboration, to develop an immunotherapy against the drug-resistant parasites [3]. The only part that remains to be verified whether there can be recombination, albeit a highly improbable sequence of events, to regenerate virulent parasites in the vector. Besides the development of vaccine strains of *Leishmania*, we have also had preclinical trials in experimental mouse models with the antigens rationally chosen from the comparison between the virulent and the avirulent strains or with an antigen that might have implication in the parasite survival [4-6].

We experimented with modulation of thymic T cell population as an anti-leishmanial therapy; however, that could not be performed here. Therefore, we performed it in a tumor model in collaboration and have worked out a novel principle of immune plasticity whereby the maturing thymocytes are differentiated into a particular subset of dendritic cells that regulate the anti-tumor immune response [7]. The tumor antigens-pulsed, TLR2 ligand-treated dendritic cells provided full resistance to repeated challenges with the tumor leading to the only model for testing tumor recurrence in a therapeutic or

prophylactic model of cancer treatment [8] or for immunomodulation using nanoparticles [9]. As preventing tumor relapse is a key to long-lasting anti-tumor surveillance, this is a key development for turning experimental models into a resounding success in clinical trials. The TLR2 targeting is another facet of the TLR2 functional duality that we reported six years ago [Pandey SP et al. 2014. J. Immunol.193: 3632-43] Recently, a structural model has been built and forwarded as a plausible molecular explanation for this duality at the level of the receptors structure [10]. However, for wider application of this TLR2 functional duality- for example, in viral infection [11], a consolidated working hypothesis has been reported [12]. Similarly, a working hypothesis on the IL-27 functional duality has also been constructed [13].

The above observations indicate that membrane receptors are key biological response controllers. As a first deviation from the conventional concepts of cell signaling, we uncovered the reciprocal CD40 signaling and proposed the first framework for duality in membrane receptor signaling [Awasthi A et al. 2003. J. Exp Med. 197:1037-1043; Mathur RK et al. 2004. Nat Med. 10:540-544]. We have reviewed and framed how perception of cell signaling has evolved over the last few decades [14]. The CD40 functional duality may originate at the membrane [Rub A et al. 2009. Nat Immunol. 10:273-280] and sustain through the reciprocal signaling, as Ras isoforms play an important role in the process [Chakraborty S et al. 2015. J. Immunol. 194: 3852-60. 2015]. Despite Ras isoforms' strong implications in oncogenesis and embryogenesis, the signaling specificity of Ras isoforms remained unknown. The signaling and functional specificities of Ras isoforms remain the crux of the problem in Ras-targeted therapy, as a pan-Ras blocker inhibits most cellular functions leading to huge cytotoxic effects. Therefore, in order to reinforce the drugability of Ras inhibitors, uncovering the Ras isoform-specific signaling and functions was essential. We showed the first fractals of Ras isoforms and the first level of Ras isoform-specific signaling mechanism and Immune functions using three classes of hapten-carrier conjugates and *Leishmania* infection as a model disease [15, 16]. The role of Ras isoforms in the modulation of *Leishmania*-infected host macrophage metabolism [17, 18] remains to be discovered. Ras isoforms' functional specificity may indeed turn out to be the key factor in CD40 functional duality.

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In silico Annotation of Complement Regulatory RCA Proteins and Their Experimental Validation

Objectives of the study

- In silico identification of motifs that are unique to complement-regulatory domains in RCA proteins.
- Experimental validation of the participation of computationally predicted motifs in complement regulation.

Summary

Background

The complement system is a key constituent of innate immunity, which is believed to have appeared in evolution at least 600 million years ago. It functions as a surveillance system in the body - facilitates pathogen elimination directly via lysis, and indirectly via enhancing phagocytosis and contributing to activation of adaptive immunity. Triggering of complement occurs via three major pathways, namely classical, alternative and lectin pathways, which converge with the formation of C3-cleaving enzymes C3 convertases (C4b2a and C3bBb) on the pathogen surface. Protection of host cells from complement is largely mediated by a family of proteins termed regulators of complement activation (RCA), which target C3 convertases. It is, therefore, not surprising that mutations and polymorphisms in RCA proteins are linked to various diseases such as age-related macular degeneration, atypical hemolytic uremic syndrome and dense deposit disease.

The RCA family proteins are formed by tandemly repeating complement control protein (CCP) domains. Functional annotation of these proteins, however, is challenging as contiguous CCP domains are found in proteins with

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varied functions such as cell adhesion, coagulation, neurotransmission, cytokine signalling and blood clotting. An apparent conundrum, therefore is, what common attributes annotate a string of CCP domains in an RCA protein as complement-regulatory domains? Knowing this is crucial as it can be employed to classify unannotated regulatory RCA proteins and locate regulatory domains within them..

Complement regulatory CCP domains harbour a signature motif pattern

Identification of motif(s) that discriminate between complement regulatory and non-regulatory CCP domains demanded a large input dataset comprising of regulator-like sequences. Although genome sequencing of various animals and viruses have generated an enormous amount of sequence data of CCP containing proteins, only a few sequences have been annotated to have complement regulatory activities. Thus, the first step was to create a dataset of regulator-like RCA sequences and select sequences that showed evolutionary coupling with functionally characterized complement regulatory proteins. We generated such a dataset and then examined if the dataset sequences encompass any motifs that are associated with complement regulatory CCP domains. RCA proteins interact with multiple proteins to impart regulatory activities. It was thus expected that regulatory sequences encompass multiple motifs. Consequently, we chose to employ Multiple Em for Motif Elicitation (MEME) for detection of motifs. Optimization of various input parameters resulted in the identification of five conserved motifs viz., M1, M2, M3, M4 and M5. These motifs showed the occurrences of many residues with high probability. Importantly, an examination of the existing mutagenesis data on RCA proteins revealed that multiple motif residues with high probability are indeed critical for the regulatory activities of these proteins. The MAST scanning showed that the five motifs we identified were present in complement regulatory as well as non-regulatory CCP sequences, but the presence of all the motifs in a specific order (M5-M3-M1-M2-M4) was found only in regulatory sequences **(Fig. 1).**

Experimental validation of the participation of computationally predicted motifs in complement regulation

Among the human complement regulators, CR1 is the only regulator that encompasses three distinct regulatory sites - one in each of its three out of four long homologous repeats (LHRs). The fourth LHR or LHR-D, however, lacks the regulatory site and the reason for this was not known. Our examination of the LHRs for the presence of 5 motif pattern showed the absence of motif 4 (M4) in LHR-D as opposed to LHR-A, -B and -C. We thus asked if the lack of activity in LHR-D is owing to the absence of M4. Substitution of M4 at the collinear site in LHR-D indeed resulted in gain-of-function, suggesting the involvement of these motifs in the regulatory function.

The success of identification of motif patterns led us to the exciting possibility of identifying novel complement regulators in humans. We, therefore, performed MAST scanning of human protein database (NCBI proteome ID:UP000005640) using motifs. The search revealed the signature motifs in two novel proteins to our knowledge apart from the well-known complement regulators: a) β2-glycoprotein I, and b) polydom/Svep1. Interestingly, both the proteins had the first 4 motifs (M5-M3-M1-M2) and the fifth motif (M4) was replaced by M1, which is most similar to M4 (60% similarity); the MAST search prefers a replacement of motifs that are >60% similar to each other. This, therefore, suggested that both these proteins are likely to have the complement regulatory activities. β2-glycoprotein I (Apolipoprotein H) has recently been demonstrated as complement regulator. Interestingly, the regulatory activity was shown to reside precisely where the motif pattern resides (i.e., CCP1-3). Polydom (also known as SVEP1; Sushi, von Willebrand factor type A, EGF and pentraxin domain-containing protein 1) on the other hand is a member of the pentraxin family and is not yet associated with any specific function. It is a large protein (387 kDa) with a unique blend of domains including 34 CCP domains. Expression analysis of polydom showed that it is strongly expressed in human and mouse placenta and in adult bone-associated skeletal tissues, mesenchymal stromal cells, and pre-osteoblastic cells. To determine whether polydom indeed has complement regulatory activities, we tested its ability to function as a complement regulator. As the motif pattern was found only in CCP12-14, we expressed this region of polydom, along with the accompanying C-terminal domain (CCP15), because in many human RCA proteins, the C-terminal domain assists in binding to C3b/C4b. The expressed protein displayed a regulatory activity. These findings thus reiterate that the presence of a signature motif pattern in complement regulators indicates the presence of binding sites for complement components and regulatory activities.

Importance of the motifs in protein-protein interaction

The RCA proteins impart their C3-convertase (C3bBb and C4b2a) regulatory activities - cofactor activity and decay-accelerating activity - owing to the formation of trimolecular

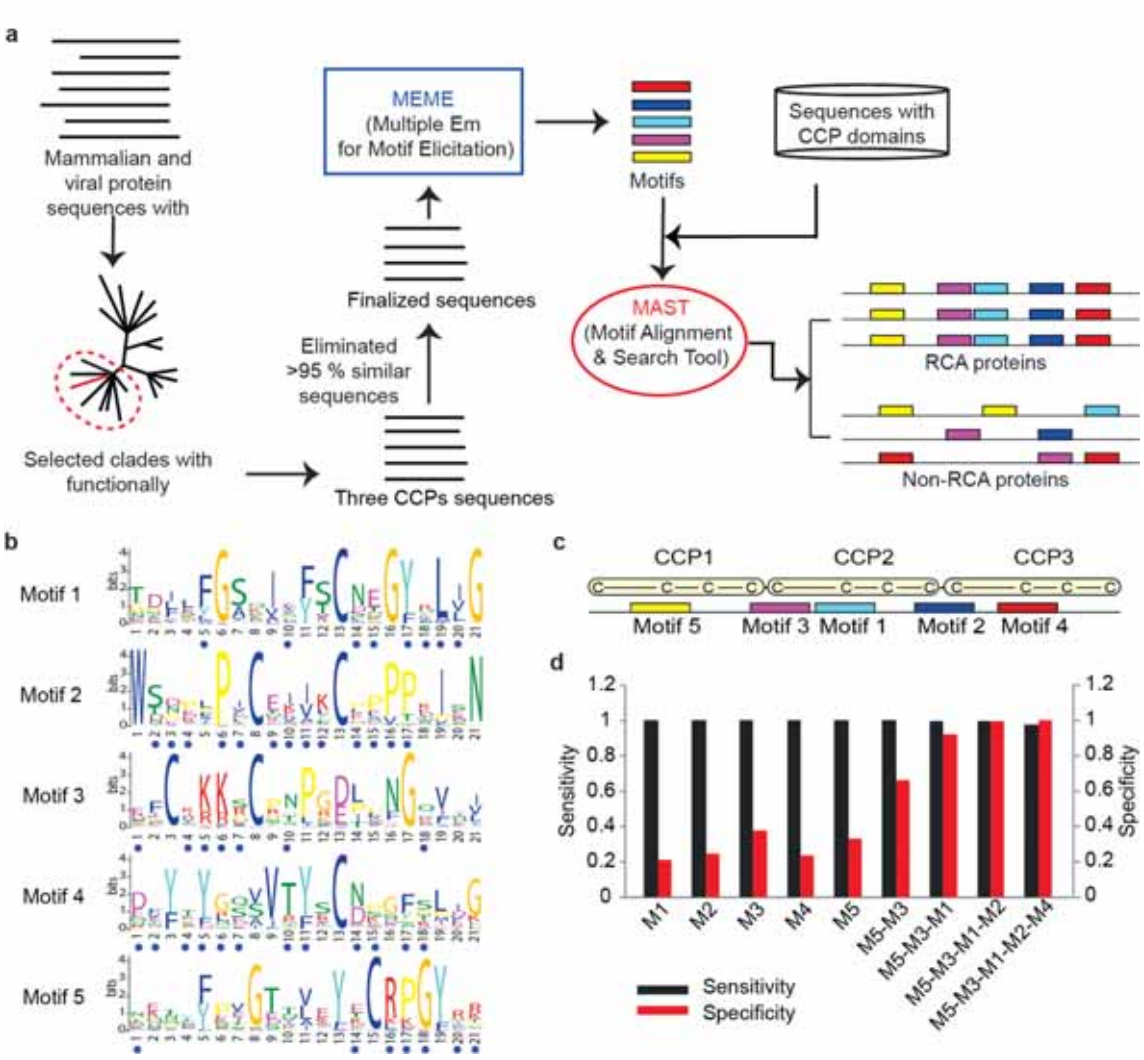

Fig. 1: A specific pattern of motifs annotate complement regulatory CCP domains. a. Schematic workflow for motif recognition and annotation of complement regulatory CCPs. The putative complement regulatory mammalian and viral RCA protein sequences were shortlisted by phylogenetic tree construction of CCP domain sequences and selection of clade(s) harbouring at least one functionally characterized RCA protein; <95% similar RCA sequences were considered for identification of motifs with MEME. The MAST-mediated motif scanning using 5 motifs was employed to identify signature motif patterns in complement regulatory CCPs versus non-complement regulatory CCPs. b. Motifs (M1-M5) generated by MEME. The height of each letter represents the probability of amino acids at the respective position. The blue dot represents the crucial position in regulators according to the mutagenesis data. c. Order and position of the five motifs as numbered by their E-value in a minimal functional unit of three CCPs. The motifs occur in the sequence of Motif 5 (M5 -yellow; E-value: 2.3e-706), Motif 3 (M3 -pink; E-value: 2.1e-743), Motif 1 (M1 -sky blue; E-value: 2.6e-887), Motif 2 (M2 -blue; 1.6e-825) and Motif 4 (M4 -red; 3.8e-735). d. Sensitivity and specificity of individual motifs and signature motif patterns.

complexes. During cofactor activity, the RCA protein interacts with C3b/C4b and factor I (a protease that cleaves C3b/C4b), while during decay-accelerating activity the RCA protein interacts with C3b/C4b and Bb/C2a (the subunits of the convertases). It is, therefore, plausible that the motifs associated with the regulators are a part of the interfaces between RCA and its interacting partners. We thus mapped the motifs onto the available experimentally solved structure of complexes.

To understand the importance of motifs in the cofactor activity, we mapped the motifs onto the recently solved crystal structure factor H (FH) complexed with C3b and factor I (FI) (C3b-FH-FI

complex; PDB ID: 5O35). Interestingly, these motifs cover a large portion of the interfaces between RCA protein and its interacting partners such as C3b/C4b and FI. Next, to understand the contribution of motifs in decay-accelerating activity, we looked into the available mutagenesis data as the structure of RCA with C3 convertase (C3bBb or C4b2a) is not available. We observed that majorly mutations in M5 are linked with loss in decay-accelerating activity without any loss in binding to C3b/C4b, suggesting that M5 is likely involved in the interaction with Bb/C2a.

Owing to the importance of the motifs identified in our study, in predicting regulatory RCA proteins, we have developed an in silico regulatory RCA prediction tool CoReDo (Complement regulatory domains; http://coredo.nccs.res.in/meme-5.0.3/CoReDo/home.html) that allows scanning of the unannotated proteins for the presence of the regulatory motifs.

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F-box Protein FBXO31 Functions as a Tumor Suppressor by Regulating Cell Cycle

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Objectives of the study

- To understand the role of FBXO31 in cell cycle progression.
- To decipher the molecular mechanism of cell cycle regulation by FBXO31.

Summary

Human genome encodes genes for 69 F-box family proteins. Each member of this family has conserved F-box motif typically at the N-terminal domain. 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 investigated the role of FBXO31, an F-box protein, cell cycle progression and elucidated the molecular mechanism. Our study showed that FBXO31 plays an essential role in progression of and G1 and S phase progression through limiting the expression levels of cycle A and maintains the genome integrity through precise controlling the licencing the origin of replication.

Major findings

Aim 1: To understand the role of FBXO31 in cell cycle progression

We have investigated the role of FBXO31 in cell cycle progression following an effective and stable depletion of FBXO31 in MCF7 cell lines using shRNAs against FBXO31. Scrambled shRNA was used as a non-specific (NS) control to rule out the off-target effects. In order to investigate the contribution of FBXO31

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in cell cycle regulation, we monitored cell cycle profile of these cells by synchronizing them at the prometaphase using nocodazole for 16 h and then release to progress into different phases of cell cycle. It was observed that FBXO31 depleted (FBXO31KD) cells showed an early progression into S-phase. In particular, at 12 h post-release from nocodazole when only 25% of NS cells could mark their entry into S-phase, around 35% of FBXO31KD cells have already entered to S-phase. Hence, compared to NS, around 40% more of FBXO31KD cells progressed to the S-phase . In order to further validate the early commitment of FBXO31KD cells to DNA replication, we performed BrdU incorporation assay. Interestingly, we found a noticeable increase in BrdU incorporation in FBXO31KD cells when compared to the NS cells, clearly suggesting an early S-phase entry of FBXO31KD cells. These observations suggest that FBXO31 may play a crucial role in regulating G1 to S phase transition during cell cycle progression.

Cells having inherent defects arising during replication are sensitive towards replication stress inducers. So, we postulated that FBXO31KD cells might have increased propensity towards inherent replicative stress which makes them sensitive towards replication stress inducers. To address this, cell were synchronized with hydroxyurea (HU). BrdU incorporation studies clearly showed that a significant population of FBXO31KD cells was halted in S-phase and show delay in transition from S to G2/M phase. We observed that in comparison to NS, around 30% of FBXO31KD cells were slower in the transition from S to G2/M phase.

Aim 2: To decipher the molecular mechanism of cell cycle regulation by FBXO31

The phenotypic defect of hastened S-phase entry and defective mitosis that we observed upon FBXO31 depletion has been attributed majorly to altered levels of cyclin A. Importantly, cyclin A-CDK complex is the rate-limiting factor for G1 to S transition and is required till prometaphase. So, any error in cyclin A regulation may create a havoc in cell cycle and compromised genomic integrity. So, we anticipated that depletion of FBXO31 may alter cyclin A stability resulting in genomic instability. Interestingly, knockdown of FBXO31 using two independent shRNAs showed stabilization of cyclin A at the protein level. A prominent accumulation of cyclin A indicates of high cyclin A-CDK activity (Fig. 2B). Further we found that FBXO31 interacts with cyclin A to promote its K-48 linked polyubiquitination

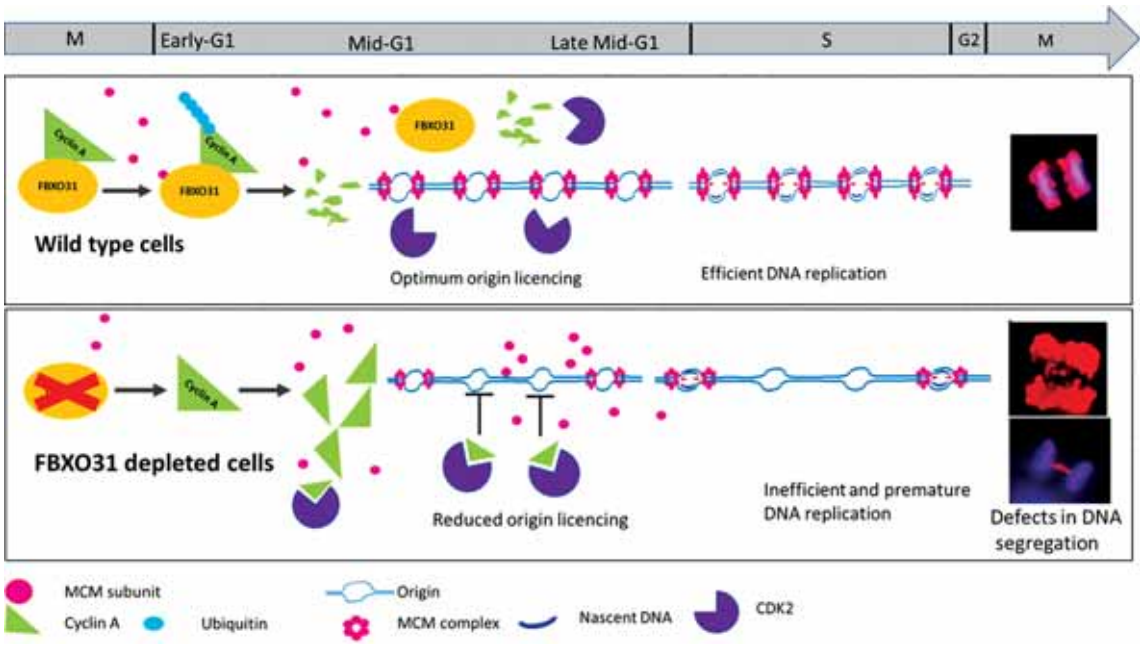

Fig. 1: Proposed model depicts the role of FBXO31 in coordinated cell-cycle progression. Polyubiquitination of cyclin A by FBXO31 facilitates its degradation during mitosis and G1 phase thus maintaining low cyclin A-CDK activity during G1. This environment is favorable for MCM complex loading and licensing of origins and efficient DNA replication. Cells lacking FBXO31 accumulate cyclin A during mitosis and throughout G1 phase resulting in high cyclin A-CDK activity, which promotes dissociation of MCM complex from origins and hence hampers origin licensing. High level of cyclin A being a rate-limiting factor for S-phase progression stimulates S-phase progression with reduced number of licensed origins resulting in inefficient DNA replication and DNA damage. Segregation of damaged DNA during mitosis results in genomic instability in the form of lagging and bridging chromosomes.

proteasomal degradation. Therefore, FBXO31 knockdown results in accumulation of cyclin A in the G1 phase leading to compromised chromatin loading of MCM4. This observation suggests that the absence of FBXO31 results in the unscheduled activity of cyclin A in G1 cells which interfere with the loading of MCM complex onto the chromatin resulting in defective DNA replication. Thus, FBXO31 knockdown leads to premature S-phase entry, reduced DNA replication accompanied by increased DNA damage (Figure 1)

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Role of RNA-Protein Interactions in *Plasmodium falciparum* Infection

Objectives of the study

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

Summary

It is believed that the main role of PIP4K2A is in regulating the levels of PI5P in mammalian cell. PIP4K2A is predominantly a cytoplasmic protein, however its substrate is membrane bound. Phospho inositides and their kinases also play an important role in the growth of *P. falciparum*. Parasite export several proteins to the erythrocytes that require the interaction of these proteins to lipid associated Phosphatidyl Inositol 3 Phosphate in the parasite endoplasmic reticulum. Proteins regulating these have been identified as specific target for drugs against malaria. We have shown that one member of this pathway, PIP4K2A, is imported into the parasite from the host where it associates with specific parasite RNA. The exact mechanism of how PIP4K2A is imported into the parasite is still unclear. Although we show that PIP4K2A interact with few specific RNA, it is possible that it may bind to other targets in both host and parasite. In case of PIP4K2A, the relationship between the RNA binding activity and the kinase activity seems to be independent, however it is possible that the RNA binding may regulate its interaction with other proteins and may affect the localization. RNA binding activity of PIP4K2A may be an important function of PIP4K2A apart from its role in phospho inositides metabolism.

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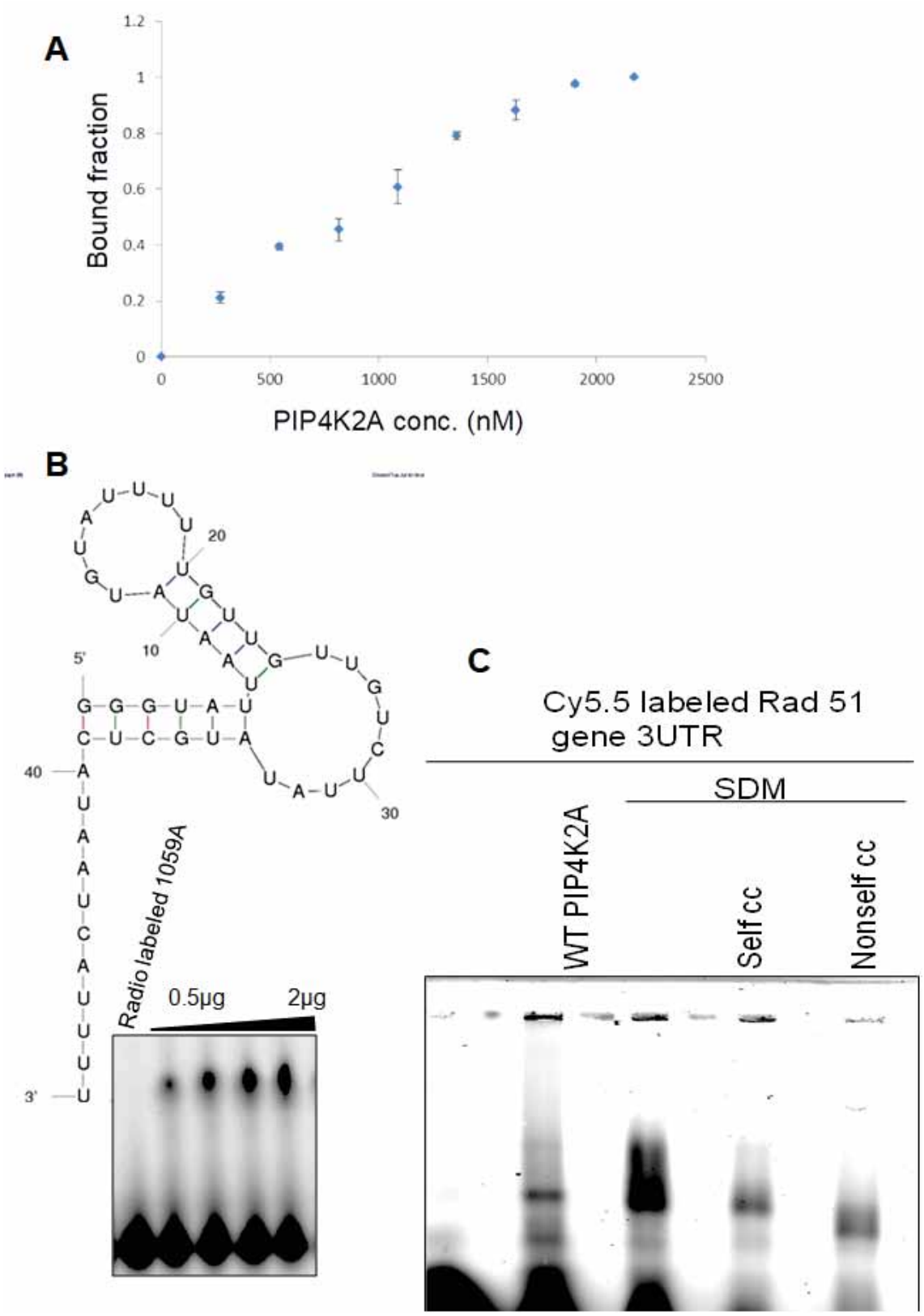

Fig 1. Wildtype and Kinase mutant PIP4K2A binds to RNA (A) Purified recombinant PIP4K2A was used for performing gelshift experiments with labeled RNA. Amount of RNA bound fraction was plotted for varying concentration of PIP4K2A and the dissociation constant was calculated to around 750 nM. (B) predicted secondary stucture of the RAD51 UTR RNA that can bind to PIP4K2A (top panel). 1-35 region that forms the stem loop structure was synthesized and was labeled and incubated with increasing amount of recombinant PIP4K2A in gel shift experiment (lower panel). The lanes are indicated. (C) Recombinant His tagged PIP4K2A WT and kinase mutant (G131L, Y138F) was incubated with Cy5.5 labelled *P. berghei* RAD51 transcript 3'UTR fragment (1059a). RNA along with self- cold competitor (self cc-1059a) (lane 4) and non-specific (PC 1/3 RNAs) (lane 5)

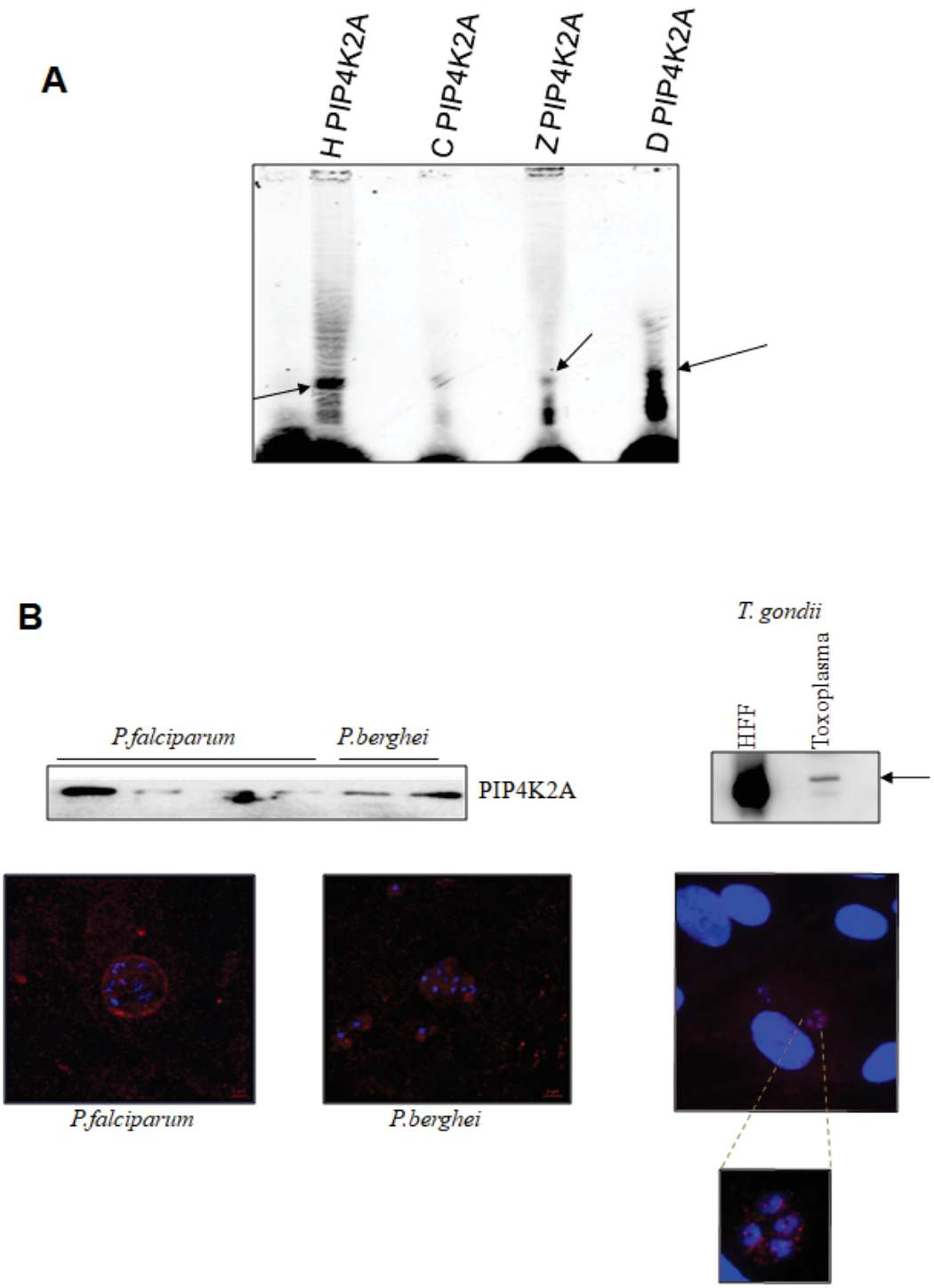

Fig 2. Conserved RNA binding activity and Import of PIP4K2A from host Apicomplexan parasites (A) Recombinant PIP4K2A of human, C. elegans, Drosophila and zebra fish origin were purifed and used in RNA EMSA studies with labelled RNA. 200 ng of purified protein was incubated with Cy5 labelled 1059a RNA. The RNA-protein complex was analysed by native PAGE followed by fluorescent scanning in phosphor imager. The recombinant protein in each lane is indicated. (B) Presence of host PIP4K2A was analysed by western blotting (top panel) or immunofluorscence (lower panel). *Plasmodium falciparum* and *Plasmodium berghei* was purified from infected human and mouse RBC respectivelyby saponin lysis. Human foreskin fibroblast cells were infected with toxoplasma and the parasite were isolated from culture supernatent after gentle agitation. 10 microgram of total lysate was analysed by western blot using anti human PIP4K2A antibody. Paraformaldehyde fixed parsite infected host cells were immunostained for PIP4K2A. DAPI (blue) was used to stain nucleus and alexaflour 595 (red) labeled secondary antibody was used to visualize PIP4K2A. Four cell stage infection of *Toxoplasma* is shown as magnified image in the bottom right panel.

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Investigating the Role of RNA Binding Proteins in Pluripotency and Differentiation

Objectives of the study

- To identify the pluripotency-related candidate RNA binding protein/s (RBP) in mouse ES cells.
- To elucidate pivotal candidate RNA binding protein- RNA networks and determine their significance in regulating pluripotency and differentiation.

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Summary

This study is aimed at understanding the significance of a RNA binding protein Rbm47 in early mammalian development. RNA binding motif 47 (Rbm47) is a vertebrate-specific, 64 kDa RNA binding protein whose significance in mammalian development is poorly understood. Rbm47 homozygous knock out mice generated showed embryonic lethality at mid-gestation indicating that this protein was important in early mammalian development (Fossat et al., 2016). Due to the lack of mechanistic data about the role and function of Rbm47 during mammalian development, we have chosen Rbm47 for our studies. To study its role in early mammalian development *in vitro*, we used mouse embryonic stem cell-line AB2.2 as our prototype ESC line. Expression studies indicated that Rbm47 was abundantly expressed both at the transcript and protein levels in mESCs compared to differentiated cells such as mouse embryonic fibroblasts (MEF) (Figure 1A and 1B). Sub-cellular localization studies indicated that Rbm47 protein was enriched in the nuclear fraction (Figure 1C) suggesting that Rbm47 could be involved in regulating pre-mRNA processing and epigenetic landscape of pluripotent stem cells (PSCs). Interestingly, the Rbm47 knockdown did not affect the undifferentiated state and cell cycle profile of mESCs. To further gain insight into its function, stable ESC lines expressing Rbm47 shRNA were generated by lentivirus infection

followed by puromycin selection. These stable ESC knock-down lines were used for alkaline phosphatase (ALP) staining (Figure 1D) immunofluorescence and real-time qPCR experiments. shRNA construct #1 gave maximum knockdown efficiency of ~80% at mRNA level and ~50% at the protein level (Figure 1E and 1G). Control ESCs and Rbm47 knockdown ESCs showed a marginal morphological difference in the appearance and alkaline phosphatase (ALP) staining. The cells showed diffused boundaries that made them appear slightly irregular in shape as compared to control colonies which showed clear boundaries and a regular shape (Figure 1D top). Further, ALP staining showed a marginally weaker color development in Rbm47 knock-down ESCs (Figure 1D bottom). This suggested that there could be a change in cellular signalling related to cell adhesion in Rbm47 knockdown cells. Next, cell cycle analysis showed that Rbm47 knockdown ESCs possessed almost similar profiles to that of control ESCs indicating that Rbm47 depletion did not affect cell cycle progression (Figure 1F). To evaluate, whether Rbm47 depletion affected any core pluripotency genes, we performed real-time qPCR and assayed for various pluripotency and lineage-specific markers. There was a similar pattern of mRNA expression and the observed changes were non-significant indicating that core pluripotency was not affected upon Rbm47 knockdown (Figure 1G). Similarly, to determine the differential expression of lineage markers, we performed real-time qPCR for various marker genes from three germ layers. We found that upon Rbm47 depletion, Neurod1 (Neuronal marker) and Gata6 (primitive endoderm and extra-embryonic marker) were upregulated significantly whereas Pax6 (Neural progenitor marker) and Gata4 (endodermal and known cardiac marker) were significantly downregulated (Figure 1H, 1I and 1J). Further, to support the RT-qPCR data, we performed immunostaining for Nanog, SSEA1, and Pax6. We found strong corroboration of Nanog and Pax6 protein levels with transcript levels in control and knockdown cells. However, immunostaining of SSEA1, a known surface marker of mESCs resulted in a weaker signal in Rbm47 knockdown cells as compared to control mESCs (Figure 1K). Altogether, the data indicated that neuronal progenitor marker Pax6 was significantly downregulated in Rbm47 KD cells suggesting that it could contribute towards perturbation of neural differentiation of ESCs.

Since Rbm47 knockdown had no effect on the growth and maintenance of undifferentiated mESCs and caused the deregulation of few key lineage-specific molecules, we performed an in vitro differentiation assay to explore its role in differentiation. We used FBS to differentiate the ESCs spontaneously to all lineages and RA for differentiation towards neural lineage (Figure 2A). In FBS treated Rbm47 knockdown cells, there was upregulation of ectoderm and endoderm markers and compromised expression of mesoderm markers as compared to control cells. This suggested that Rbm47 might play a key role in fine-tuning lineage specification (Figure 2B and 2C). After 6 days of RA induced differentiation, knockdown cells showed a significant change in morphology as compared to control cells. Control cells were able to form organized rosette-like structures that were absent in Rbm47 knockdown cells. Rbm47 knockdown cells mostly showed neuronal morphology (Figure 2D). Real-time qPCR analysis of Rbm47 depleted mESCs upon RA treatment showed a significant reduction in neural progenitor markers such as Nestin, Pax6, Sox2 and upregulation of Tubb3 which encodes ß-III-tubulin (Figure 2E). Immunostaining for the above-mentioned markers distinguished anomalous differentiation in knockdown cells. Knockdown cells expressed a higher number of ß-III-tubulin and Sox2 double-positive cells indicating the formation of immature neurons as compared to control. Knockdown cells also lacked Pax6+ and Sox2+ neural progenitors as compared to control ESCs (Figure 2F).

Next, we performed promoter studies for Rbm47. Our data indicated that *Rbm47* was regulated both at the transcript and protein levels during the differentiation of mESCs. We designed experiments to determine the potential transcription factors (TFs) involved in the regulation of *Rbm47* transcription. For this, we amplified various genomic regions upstream to *Rbm47* TSS and cloned them in pGL3 basic vector. Dual-luciferase assay was performed in HEK 293T and mESCs to assess the potential transcriptional activity of various fragments. We found that the region between -250 bp and -10 bp possessed core promoter elements necessary for transcription. We found a variant of the TATA box called 'ATA box' positioned between -180 to -185. The promoter fragment without the ATA box showed a very minimal luciferase activity indicating the presence of one of the core DNA elements to initiate transcription. The region between -450 bp and -1000 bp possessed proximal promoter elements which may have binding sites for various TFs. Computational prediction of TF binding sites revealed many mammalian development-related TFs such as FoxA1, FoxA2, MyoD, Myogenin, HoxA5, Yy1 which might be the potential regulators of Rbm47 transcription. A screening experiment based on luciferase constructs with mutated/deleted binding sites of the above-mentioned TFs is necessary to achieve more insight into Rbm47 transcriptional.

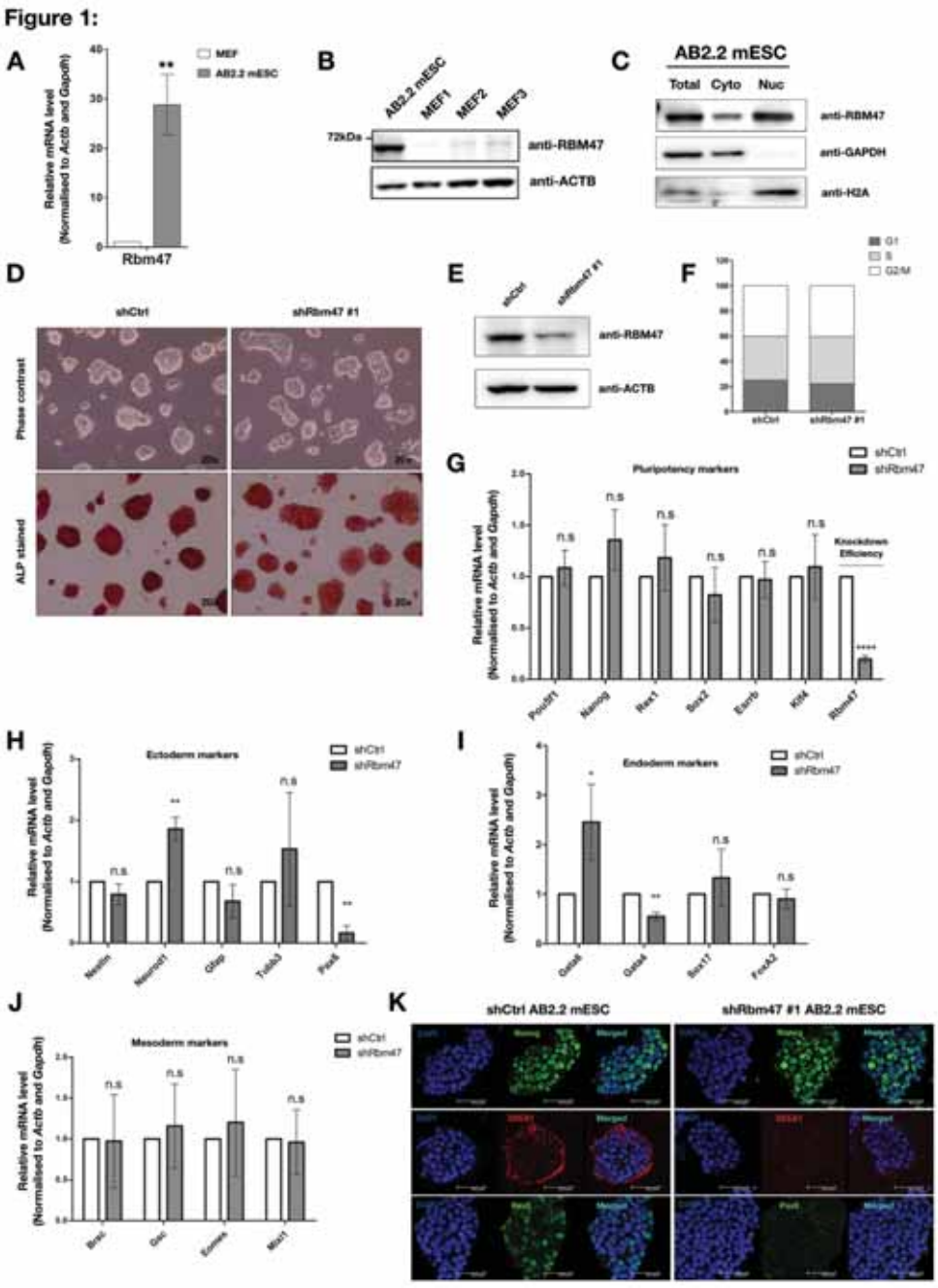

Figure 1: A: Real-time qPCR measurement of Rbm47 mRNA normalized to Actb and Gapdh expression indicated cell types (MEF-mouse embryonic fibroblast; AB2.2- mouse embryonic stem cells). Error bar represents the standard deviation from three biological replicates, n=3 (*p<0.05; **p<0.01; ***p<0.001).

B: Western blot analysis of Rbm47 in mentioned cell types. b-Actin (ACTB) was used as loading control.

C: Nuclear (Nuc) and cytoplasmic (Cyto) fractionation followed by western blot analysis of Rbm47. GAPDH was used as a cytoplasmic marker and Histone 2A (H2A) was used as a nuclear marker.

D: Phase-contrast images of mESC stably expressing non-targeting control shRNA (LacZ) and Rbm47 targeting shRNA (Top). Cells were fixed and stained for alkaline phosphatase (ALP) activity (bottom).

E: Western blot analysis for determining the knockdown efficiency of shRNA targeting Rbm47.

F: Cell cycle structure of shCtrl ESC and shRbm47 ESC analyzed by DNA content.

G to J: Real-time qPCR measurement of various pluripotency and differentiation markers in shCtrl and shRbm47 ESC normalized to Actb and Gapdh expression. These values were plotted by assaying three biological replicates (n=3). Error bars indicate standard deviation from three assays (*p<0.05; **p<0.01; ***p<0.001; n.s- non-significant).

K: Confocal micrographs of shCtrl and shRbm47 ESC immunostained with Nanog, SSEA1and Pax6 specific antibodies.

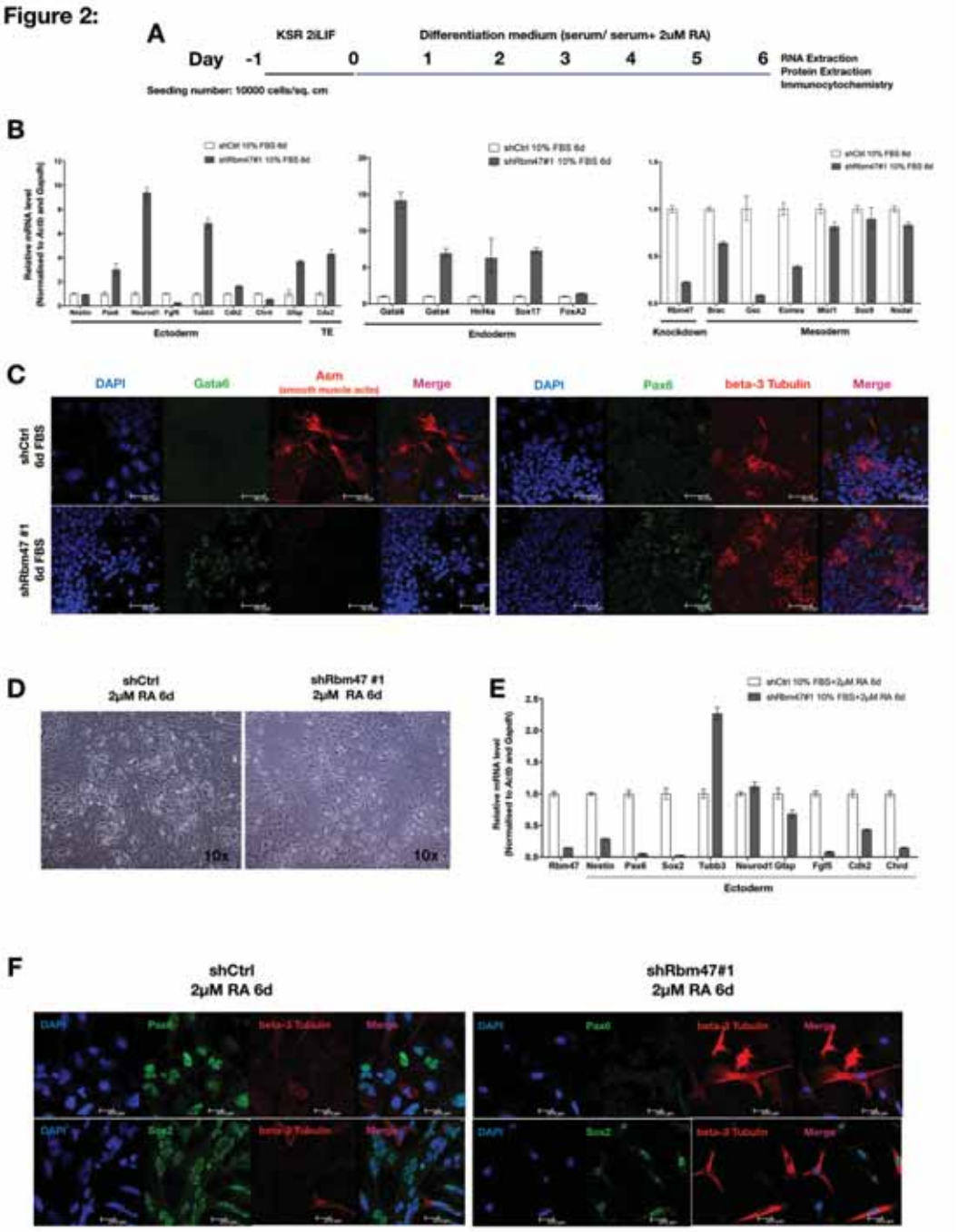

Figure 2:

A: Schematic representation of ESC differentiation assay. The differentiation medium contained 10% FBS or 10% FBS with 2 M Retinoic acid (RA).

B: Real-time qPCR measurement of various differentiation markers in shCtrl and shRbm47 ESC normalized to Actb and Gapdh expression. Error bars indicate standard deviation from one biological replicate and a triplicate assay.

C: Confocal micrographs of differentiated shCtrl and shRbm47 ESC immunostained with Gata6, Sma (smooth muscle actin), Pax6, and beta-III-tubulin specific antibodies.

D: Phase-contrast images of control ESC and Rbm47 knockdown ESC differentiated with 2 M RA for 6 days.

E: Real-time qPCR measurement of various ectoderm related genes in shCtrl and shRbm47 ESC differentiated with 2 M RA for 6 days. Actb and Gapdh expression were used for normalization. Error bars indicate standard deviation from one biological replicate and a triplicate assay.

F: Confocal micrographs of differentiated shCtrl and shRbm47 ESC immunostained with Pax6, Sox2, and b-III-tubulin specific antibodies.

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Indian Human Microbiome - Perspectives from breast milk microbiome, select Indian tribal populations and meta-analysis of Indian communities with other global tribal populations

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Objectives of the study

- Characterization of the diversity of the microbiota of colostrum and mature milk samples collected from healthy Indian mothers.
- Meta-analysis: testing association of diet and lifestyle with microbiome profile.
- Identification of Indian tribal populations based on their unique dietary habits and lifestyle & determining the gut and oral microbial diversity and its function potential using 16S rRNA gene targeted amplicon sequencing and shotgun metagenomics.

Summary

Next-generation sequencing technologies have significantly advanced our understanding of the complexity and diversity of the microbial communities associated with humans. Understanding the Human Microbiome now involves looking at mother-infant microbiota transfer, gut and oral microbial diversity & function in healthy individuals and understanding the evolution of microbiome across lifestyles and urbanization gradient.

- Breast Milk Microbiome

Till date, we have successfully collected, characterized and analyzed the microbiota of the 39 breast milk samples of healthy Indian mothers. The microbial diversity analysis revealed the most abundant bacterial phyla in the breast milk of healthy Indian mothers to be Firmicutes followed by

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Proteobacteria and Actinobacteria. While at the genus level Megasphaera is the most abundant genus contributing 40.28% of the total bacterial community in the breast milk. The core milk microbiota consists of genera like Megasphaera, Streptococcus, Staphylococcus, Bacillus and Williamsia at a detection level of 0.01%. We compared the microbial diversity of 30 breast milk samples collected from 15 healthy mothers. Despite the previous reports in other populations, we have found no differences were detected in microbial profiles based on the lactation period, using both weighted and unweighted UniFrac distances (Fig.1). The NMDS profile of microbial diversity shows that there is no distinct clustering in colostrum and mature milk samples but mature milk samples appear to be more dispersed as compared to colostrum milk samples. When plotted at genus level both colostrum and mature milk samples showed a nearly equal distribution of genera like *Megasphaera*, *Staphylococcus*, *Streptococcus*, *Bacillus*, *Acinetobacter* and *Williamsia* in all samples (Fig.2).

- Meta-analysis with other global populations

In the present study, we have selected human microbiome data available in public domain from the Indian tribal, urban and rural populations. Additionally, microbiome data of the African hunter-gathers and agriculturist population, healthy human microbiome data of American population, as compared with the Indian population. However, the shifts in lifestyles and associated influence on gut microbiomes in tribal, rural, and urban (preindustrial to industrial) populations remain poorly understood. In order to explore how a gradient of traditional lifestyles and diet together affect the human gut microbiome, in the present study, we compared the gut microbiome data of endogamous agriculturist Indian (EAI) sub-population with other ethnic groups such as the urban, rural and tribal population of India, Hadza and BaAka hunter-gatherers from Africa, Bantu agriculturist from Africa and urban population from the USA.

A meta-analysis of the human gut microbiome was done towards the understanding of diet and lifestyle associated relationships. Gut microbiome of the study population was compared with the available urban, rural and tribal population from India, Hadza and BaAka hunter-gatherers from Africa, Bantu agriculturist from Africa and urban population from USA. In addition to the gut microbiome data generated in the present study, a publicly available 16S rRNA gene amplicon sequencing

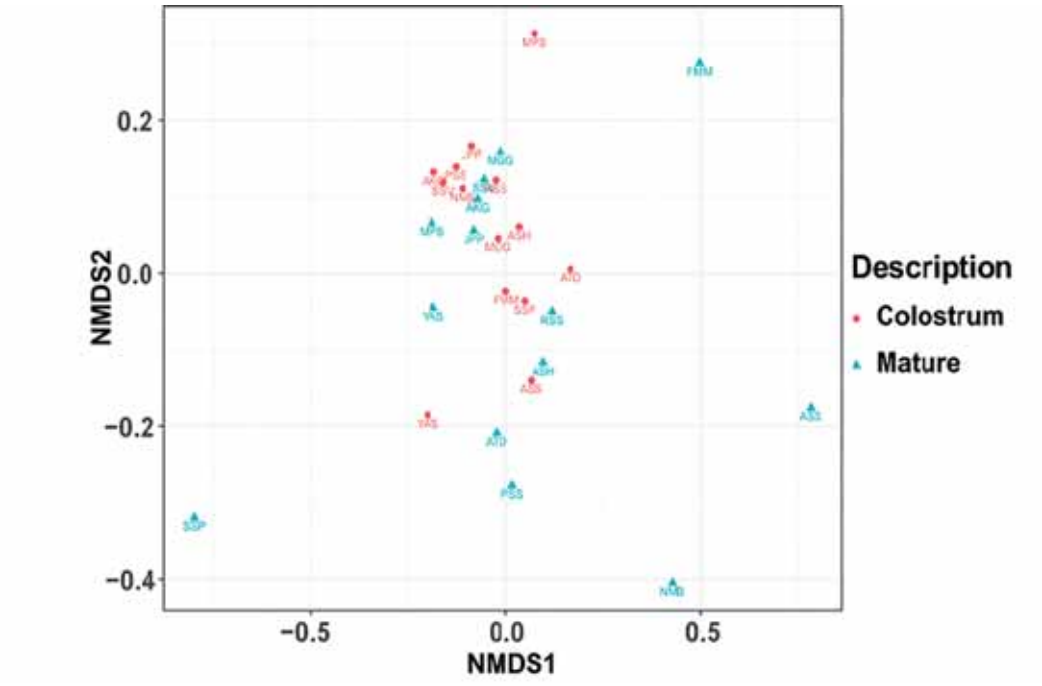

Figure 1: NMDS Plot for Mature and Colostrum Milk Samples from Healthy Indian Mother (n=15)

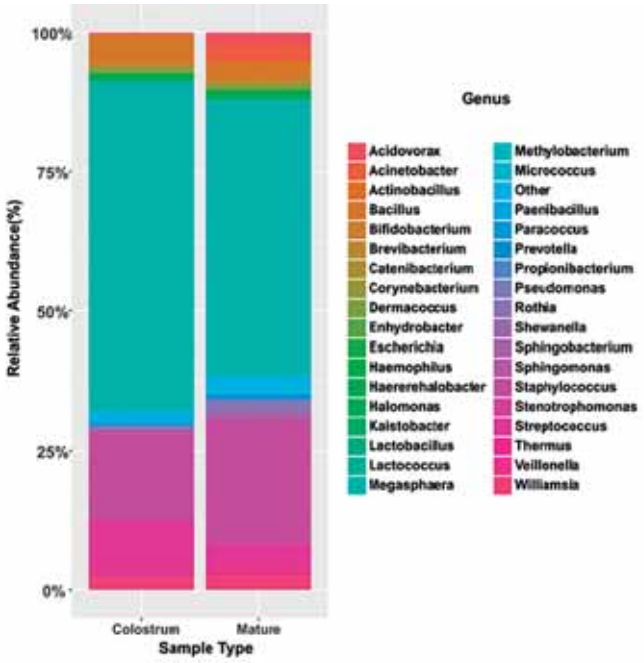

Figure 2: Bar plot showing Mean relative abundance at genus level in mature and colostrum milk samples

data from published literature were downloaded and analyzed. For comparability of the results, we reprocessed and analyzed the downloaded data using the same pipeline, which was used for Indian human subsets. Principal coordinate analysis (PCoA) based beta diversity on unweighted UniFrac distances between the samples showed that Indian, African and American samples segregate in distinct groups. However, EAI sub-population samples were closer to the Indian tribal samples in comparison to the north Indian rural and urban populations (Fig. 3).

Phylum level microbiome analysis revealed statistically significant differences (ANOVA, $p<0.05$ with Benjamini-Hochberg FDR corrections) in the relative abundance of bacterial phyla Bacteroidetes and Firmicutes between Indian, African, and American populations. These phyla constituted more than 80% of the gut microbiomes of these populations (Fig. 4). Phylum Bacteroidetes showed a gradient by a steady increase in its abundance from African hunter-gatherers to agriculturist and Indian tribal to rural populations while decrease

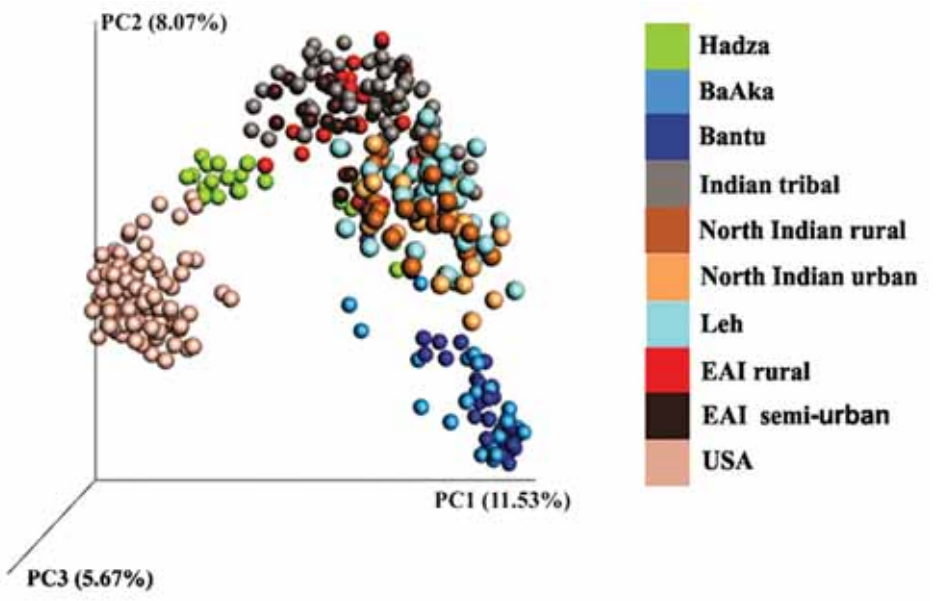

Figure 3: Principal coordinates analysis (PCoA) of unweighted UniFrac distance among the Indian, African, and American samples. Each circle (designated by the color) represents a sample of the respective population.

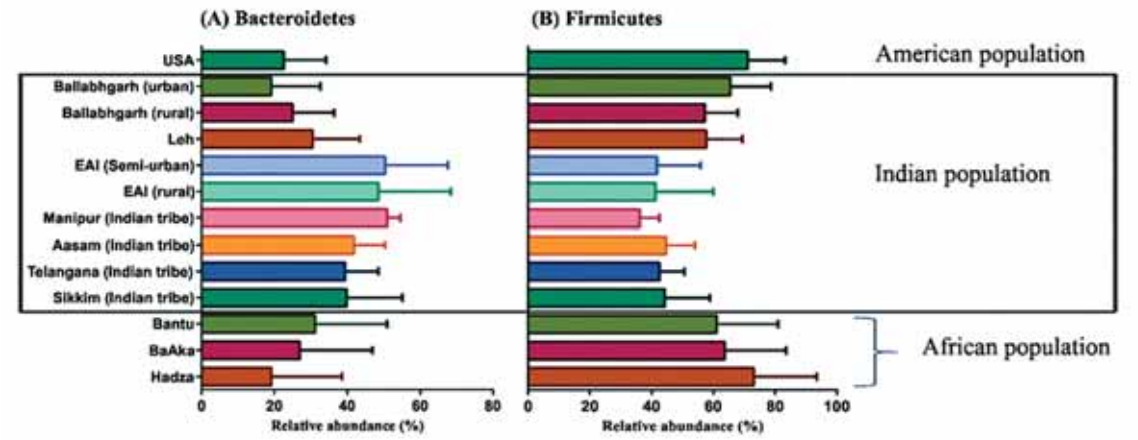

Figure 4: Bar chart depicting differentially abundant bacterial phyla Bacteroidetes (A), Firmicutes (B) across the Indian, American, and African populations (ANOVA, $p<0.05$ with Benjamini-Hochberg FDR corrections).

in Indian urban and American population. However, the inverse pattern was observed for Firmicutes. The abundance of Firmicutes was more in the American and African populations while the abundance of Bacteroidetes was more in the Indian population. A higher abundance of the genus Prevotella was recorded across the tribal, rural, and urban Indian populations as well as African tribal populations.

- Tribal Microbiome Sample collection

Microbiome sampling from 8 Indian tribal populations was successfully completed. These included the tribal populations of Rongmei from Manipur, Warli from coastal Maharashtra, Madia and Gond from central India and Purigpa, Balti, Brokpa and Boto from Kargil district. Samples collected included oral and fecal/stool samples (gut ecosystem) alongwith detailed dietary metadata. The dietary data includes 24-hour recall as well as Food Frequency Questionnaire and seasonal variation within the vegetables and items consumed. On-Field methods were also tested for suspending the sample under anoxic conditions for anaerobic cultivation of microbes present in the gut. The sampling also provided for a great exercise to optimize logistics, protocols and gain field experience about sample collection in remote areas. Community DNA extraction from fecal (representative of the gut) and oral-wash samples was done using QIAamp stool DNA mini kit and QIAamp DNA mini kit (Qiagen, USA) respectively. DNA extraction was performed according to the manufacturer's instruction with bead beating for 6 mintues. Metagenomic sequencing of V4 region of 16S rRNA gene is now planned.

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Drug Efflux Mechanism and Transport proteins in Leishmania: Translating Allosteric Machinery

Objectives of the study

- Molecular modelling of proteins involved in drug resistance, i.e., P-gp, P4ATPase and CDC50.
- Peptide designing against these proteins.
- In vitro testing of designed peptides with standard antileishmanial drug.
- In vivo validation of designed peptides with standard antileishmanial drug.

Summary

Background

This project aims at computationally designing small protein specific peptides that allosterically modulate the activities of Miltefosine transporter proteins (P-gp and P4ATPase-CDC50) of L. major in a manner that maximum amount of drug (Miltefosine, a phosphatidylcholine analog) retains inside parasite thereby reversing a Miltefosine resistant strain towards sensitive one. Computational approach was adopted to study the conservedness of these proteins and based on sequential conservedness parasite specific motifs were identified. 3D structure of transporter proteins was predicted and there stability in physiological conditions was tested through long scale membrane embedded molecular dynamics simulations. A small library of computationally designed peptides was created against parasite specific motifs. From the initial screening through protein-peptide docking, 8 peptides were shortlisted, which were further subjected for short scale molecular dynamics simulation in order to study their interactions. The 3 best peptides were selected and tested both in in vitro and in vivo, which gives sufficient impetus for being novel therapeutics to counteract the drug resistance phenotype in leishmania parasites.

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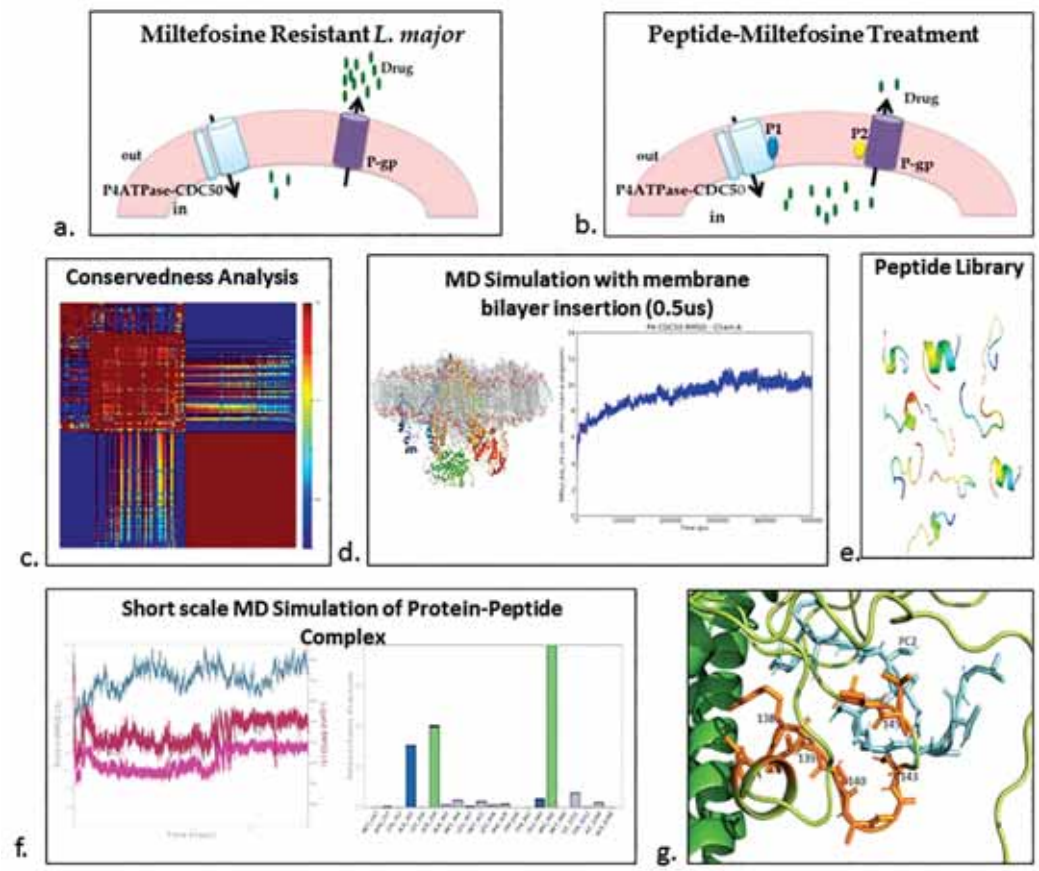

Fig. 1: In silico designing and screening of protein specific peptides against Miltefosine transporter proteins of L. major. (a) Miltefosine resistant condition: Less amount of drug accumulates inside the parasite and maximum amount is effluxed out due to decrease in P4ATPase-CDC50 complex activity and increase in P-gp activity. (b) Peptide-Miltefosine combination treatment condition: Maximum amount of drug retains inside the parasite and minimum amount is effluxed out on combinatorial treatment of the drug with small peptides. (c) Conservedness analysis through phylogenetic tree construction and Statistical Coupling Analysis. (d) Large scale molecular dynamics simulation with membrane bilayer insertion to check stability of predicted structures of Miltefosine transporters. (e) Peptide Library construction against parasite specific motifs. (f) Short scale molecular dynamics simulation of protein-peptide complex. (g) Interacting residues in protein-peptide complex.

Main Findings

This project aims at computationally designing small protein specific peptides that allosterically modulate the activities of Miltefosine transporter proteins (P-gp and P4ATPase-CDC50) of L. major in a manner that maximum amount of drug (Miltefosine, a phosphatidylcholine analog) retains inside parasite thereby reversing a resistant strain towards sensitive one. L. major is the causative agent of Cutaneous Leishmaniasis, a neglected tropical disease-causing sores and ulcers on the skin. Emergence of drug resistance is a major concern for combating against Cutaneous Leishmaniasis. P-gp and P4ATPase-CDC50 proteins are highly conserved at the amino acid sequence level as well as at their positional level. These proteins are an intrinsic part of the mechanism resulting in development of resistance in L. major against Miltefosine. The initial clues of conservedness analysis have helped in the identification of sequential motifs which might be relevant in conformational changes. We have undergone the detailed functional and conformational study of the transporter proteins affecting substrate specificity, their structural rearrangement results from the intra- and inter-molecular forces as well as effect of insertion of membrane that finally governs the substrate influx and efflux. This resulted in elucidating the structural information of these transporter proteins which encodes for functional differences accounting selectivity, sensitivity, specificity, response to substrates and the designed set of peptides serving as modulators. Allosteric conformational transitions as observed through extensive large scale molecular dynamic simulations with membrane bilayer insertion for P-gp

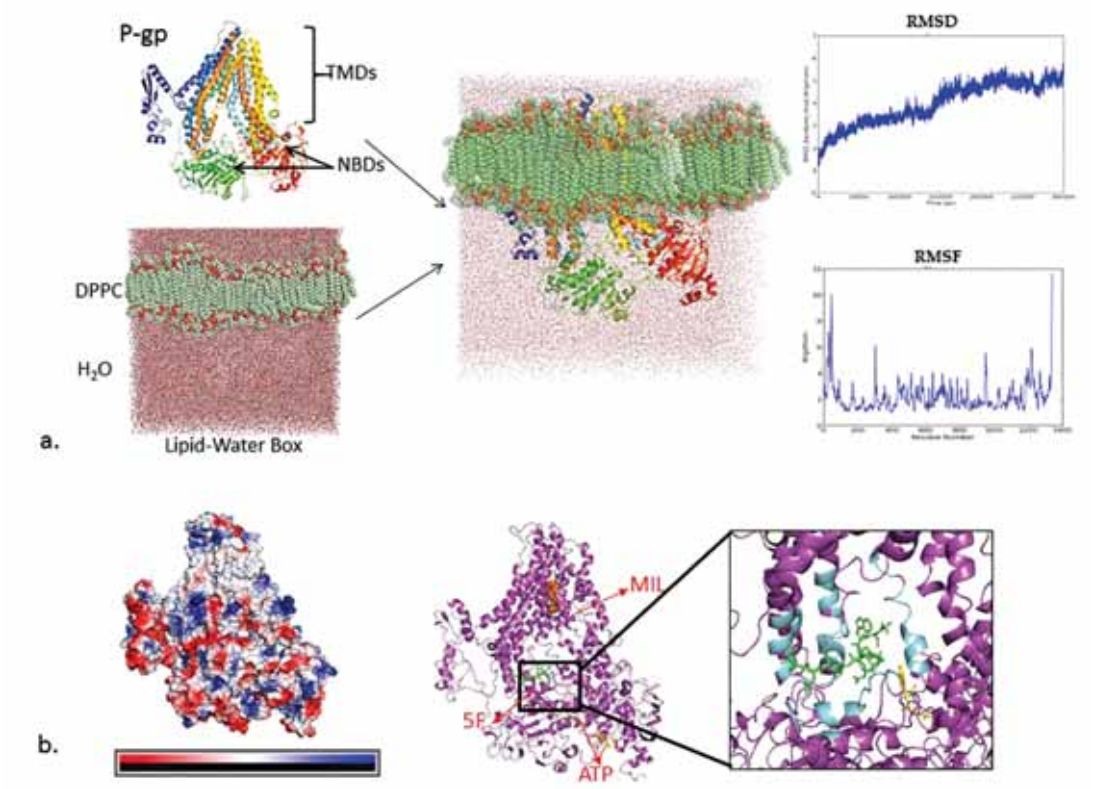

Fig. 2: Molecular Dynamics Simulation and docking of Protein-peptide Complex. (a.) Membrane Bilayer insertion and extensive long scale simulation of Miltefosine transporter proteins. (b.) Protein-peptide-Miltefosine-ATP complex docking and interacting residues.

and P4ATPase-CDC50 complex have helped in laying a framework to design and interpret the experimental results. In combination with the experimental approaches, in silico methodology adopted, have helped form a critical insight into the dynamicity and structural elements being determined individually. Furthermore the approach laid also envisages the study in combination with the peptides binding specificities and their associations with the lipid bilayer system.

For the conservedness analysis, 96, 207 and 189 sequences in total were extracted respectively for P-gp, P4ATPase and CDC50. The phylogenetic tree constructed and statistical analysis coupling done for studying the sequential and positional conservedness of amino acids respectively, revealed that these proteins are highly conserved. The 3-D structures of Miltefosine transporters were predicted either based on homology or abinitio. The predicted structure of P-gp consists of 2 transmembrane domains (TMDs) with 6 transmembrane helices in each domain and 2 nucleotide-binding domains (NBDs). The TMDs and NBDs are arranged in a head to tail fashion. The structure of P4ATPase has 10 transmembrane helices and 3 cytoplasmic domains (Actuator Domain; Phosphorylating Domain and Nucleotide Binding Domain). In the same way, 2 transmembrane helices and a large exo-cytoplasmic loop was seen in the predicted structure of CDC50. The stability of the predicted structures were validated by mimicking physiological conditions including membrane bilayer through extensive large scale molecular dynamics simulations. Based on the conservedness analysis and extensive molecular dynamic simulations, the parasite specific sequential motifs, capable of initiating conformational changes if interfered, were identified. These consensus motifs constitute a total 29, 30 and 19 motifs respectively in P-gp, P4ATPase and CDC50 proteins of L. major. Out of these obtained set of motifs, nine motifs were shortlisted based on their secondary structure, their domain location, least sequence similarity with respective human homologues as well as SCA sectors. Against these nine motifs, a library of 103 computationally designed synthetic peptides was created. These peptides were then screened against their respective proteins, i.e., P-gp and P4ATPase-CDC50 complex, for their specific binding, minimum energy conformations, their specific binding with proteins, number of interactions, stearic hindrance as well as reverse docking. Six peptides (Pg1A, Pg6A, Pg8A, Pg5F, Pg8F, and Pg10F) were shortlisted against P-gp and two peptides (PC1 and PC2) against P4ATPase-CDC50 complex. The short scale (20ns) MD

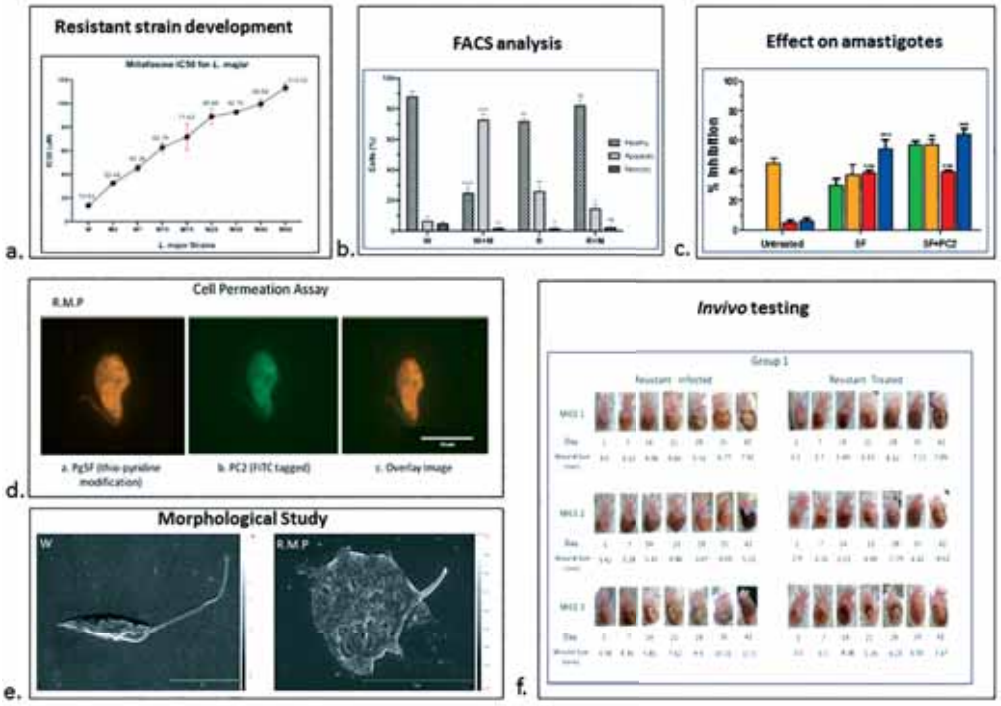

Fig. 3: In vitro and In vivo validation of computationally designed synthetic peptides. (a) Development of Miltefosine resistant L. major strain. (b) FACS analysis to confirm the nature of resistant strain as well as the effect of peptides on promastigotes in presence of Miltefosine. (c) Effect of peptides on macrophage infected amastigotes. (d) Cell Permeation Assay of fluorescence tagged peptides Pg5F and PC2. (e) Morphological assessment of L. major promastigotes. (f) Effect of peptides on Mice, Balb/c.

Simulation of protein-peptide complex with ATP and Miltefosine revealed that in presence of peptide Pg5F and Pg8F, P-gp-Miltefosine interactions have weakened suggesting that these peptides might have caused allosteric changes and thereby decrease in drug efflux. P-gp, an ABC transporter with 2 TMDs and 2 NBDs, drive the transport processes through binding and hydrolysis of ATP accounting for intra- and inter-domain interactions. MD simulations have provided an insight of maintaining the closed form of NBD dimer through ATP binding. In addition, the interaction between P-gp and Pg5F is subtle at the hinge of TMD1 and NBD1, which determines the overall conformational changes. Similarly, the exo-cytoplasmic loop of CDC50 in P4ATPase-CDC50 complex is being targeted by PC2 peptide. These observations obtained from our in silico analysis were in accordance with the results obtained from in vitro and in vivo testing. In in vitro, the peptides in absence and presence of Miltefosine were tested directly on Wildtype and Miltefosine resistant promastigotes as well as macrophage infected amastigotes. The peptides were found to be more effective on amastigote stage compared with promastigote stage. In amastigotes, concentration dependent inhibition was seen on Wildtype as well as Resistant strains with Pg5F in combination with PC2 and Miltefosine being the most effective with >60% inhibition. Morphological changes on wildtype and resistant promastigotes upon administration of Miltefosine at IC50 and peptide Pg5F (125µg/ml) and PC2 (50µg/ml) have been seen through Giemsa staining as well as scanning electron microscopy. Furthermore, FACS analysis showed significant increase in apoptotic deaths in Wildtype as well as Resistant promastigotes treated with peptide Pg5F (125µg/ml) and PC2 (50µg/ml) in presence of Miltefosine indicating towards reversal of resistant strain towards sensitive. The cell permeation assay done with fluorescence tagged peptides Pg5F and PC2 further confirms that both the peptides not only interacts with the cell membrane of parasites but penetrates the membrane also. This combination was found to lower the wound size to some extent and drastic decrease in parasite load (80-90% decrease) in Balb/c mice infected with either Wildtype or Resistant strains. The results in mice were comparable to those of Wildtype infected mice when treated with Miltefosine (~70% decrease in parasite load). In addition, these peptides were tested directly on macrophages also for their toxic effect and Pg8F with PC2 was found to be toxic at higher concentrations. These results suggest that the peptides in combination with Miltefosine were able to reverse the resistant strain into sensitive ones by allosterically modulating Miltefosine transporter proteins. The effect of peptides seen on Wildtype amastigotes and Wildtype infected Balb/c indicates the probability of these peptides behaving as synthetic AMPs.

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Role of novel human chromosome 21 gene HMGN1 in normal and Down syndrome neurogenesis

Objectives of the study

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

Summary

Down syndrome is one of the most common genetic causes of intellectual disability. Down syndrome is caused by the trisomy of chromosome 21 (HSA21; Homo Sapiens Autosome 21). 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, it is not known that which HSA21 genes cause reduced neurogenesis in Down syndrome.

To study the role of HSA21 genes in reduced neurogenesis, we have developed human iPSCs based model of neurogenesis. In this study we showed reduced neurogenesis in DS cells. It is consistent with DS fetal brain sections. In addition to cellular defects, global transcriptomic analysis using RNAseq of human iPSCs derived late-stage neural progenitors revealed upregulation of several pathways in DS cells e.g. S-phase promoting regulators, Notch pathway and REST that favor reduced neural differentiation. Additionally, components of chromatin remodeling complex including that of BAF chromatin remodeling complex were downregulated in DS neural progenitors. Consistently, neurogenic genes NFIB and POU3F4, genes activated by PAX6-BAF complex interaction, were downregulated. ChIPseq analysis of late-stage DS progenitors

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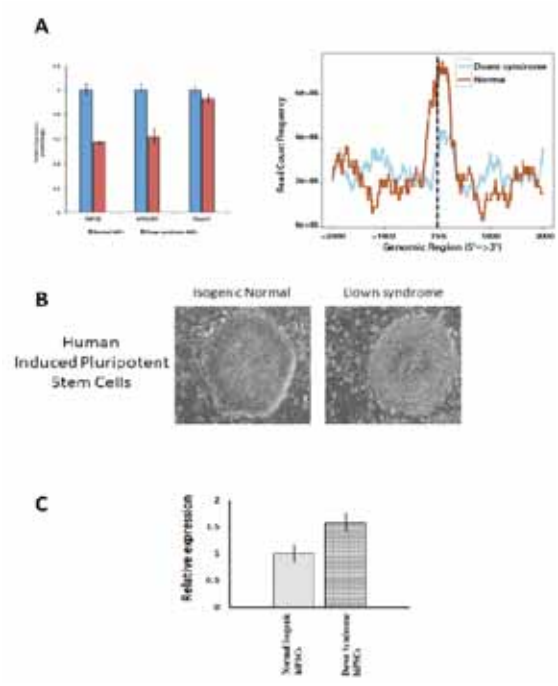

Fig. 1: Potential role of HMGN1 in Down syndrome reduced neurogenesis (A) hNF1B and hPOU3F4, genes downstream to PAX6- BAF neurogenic pathway were downregulated and PAX6 recruitment was aberrant in Down syndrome cells. (B) Representative images of isogenic normal and down syndrome human iPSCs. (C) Relative expression of HMGN1 in isogenic normal and Down syndrome human iPSCs.

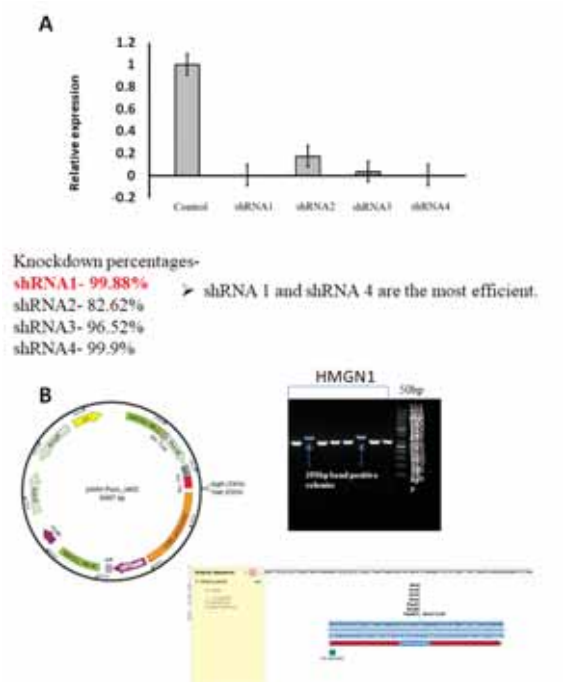

Fig. 2: Generation of inducible knockdown construct of HMGN1 (A) Four shRNAs were screened in human fibroblasts for their knockdown efficiency of HMGN1. shRNA1 shows best knockdown efficiency. (B) ShRNA was cloned and sequence verified into pAAV-puro-siKD vector.

found that overall PAX6 binding was increased but recruitment at transcription start site was reduced (Figure 1A), indicating abnormal chromatin packaging in DS progenitors

HMGN1 is a gene present on chromosome 21 and thus have three copies in Down syndrome cells. HMGN1 is involved in chromatin decompaction and tend to co-localize with DNA hypersensitive sites and fine-tune enhancer organization. HMGN1 and 2 have been shown to maintain cell identity. In DS, HMGN1 overexpression has been shown to cause aberrant transcription as well as B cell leukemogenesis. However, its role in neurogenesis is not clear. Given its role in chromatin decompaction and maintaining cell identity, I posit that HMGN1 overexpression in DS cells may cause defective recruitment of proneurogenic transcription factors such as PAX6 and contribute towards defective neurogenesis. Considering that the HMGN1 role is not known in normal neurogenesis, we are studying its role along with molecular mechanisms in normal and DS neurogenesis in a stage-specific manner.

Quantitative real time of isogenic normal and Down syndrome human iPSCs established in the lab (Figure 1B) found increase expression of HMGN1 in Down syndrome human iPSCs lines (Figure 1C) as expected. To generate a inducible knock down construct of HMGN1, four different shRNAs were cloned into pLKO vector and tested for their knockdown efficiency. All shRNA showed good knockdown efficiency with shRNA1 showing abve 99% knockdown efficiency (Figure 2A). This shRNA has been cloned into pAAV-puro-siKD vector to target it into the gene safe harbor AAVS1. Clones have been sequence verified (Figure 2B).

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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.
- Evaluation of ROS and DNA damage at different doses of radiation (single dose, fractionated doses and radio-resistance doses).
- Elucidation of the role of Nrf2 and its downstream regulators in radio-resistance of BCSCs.
- Understand 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 breast tumor.

Summary

Major obstacles of radiotherapy intervention are tumour resistance and recurrence. Growing evidence showed that the acquired resistance of tumour is due to a subset of the tumour population called cancer stem cells (CSCs). Spheroid culture renders microenvironment for enrichment of Breast cancer stem cells (BCSCs), which are chemo/radio-resistant in nature. The transcription factor NF-E2-related factor 2 (Nrf2), a master regulator of antioxidant genes and a key regulator of cellular redox homeostasis in the cells is linked to CSC chemo/radioresistance. Nrf2 is negatively regulated by KEAP1. The role of NRF2 in BCSC is not studied, hence we aimed to investigate the role and underlying mechanism of Nrf2 in radioresistance in mammospheres. Earlier we had shown that, fractionated doses of radiation induce BCSC population via Nrf2 activation in MCF-7 formed mammospheres and adherent cells.

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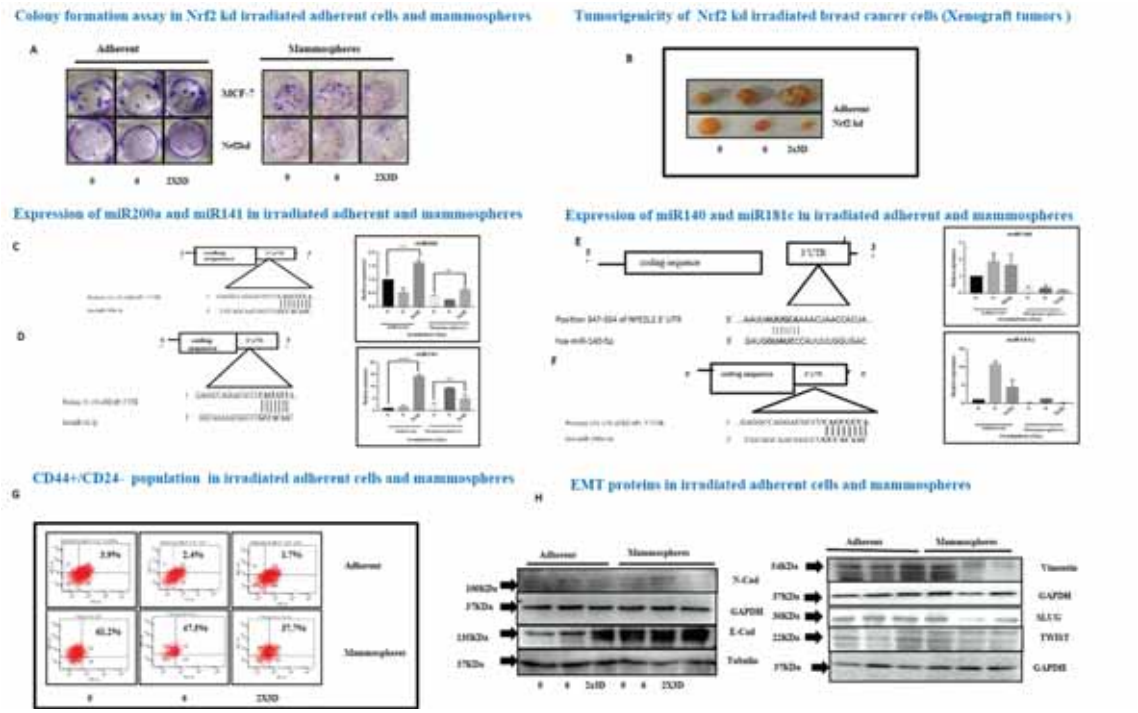

Fig. 1: **(A) Radioresistance in irradiated Nrf2 knockdown adherent cells and mammospheres:** Colony formation was carried out in Nrf2 knockdown mammospheres and adherent cells treated with acute dose and the fractionated dose of radiation. Colonies were stained with 0.2 % crystal violet for visualisation. **(B) Tumorigenesity of Nrf2 knockdown MCF7 cells:** Irradiated MCF- cells were implanted in SCID mice and tumour volume was measured. Representative pictures of solid tumours from irradiated MCF7 cells. **(C) Detection of Nrf2 and Keap1 regulating miRNAs in irradiated MCF7 adherent cells and mammospheres:** Keap1 and Nrf2 regulating miR200a **(D) miR141 (E) miR140 (F) miR181c** were determined by qPCR. The graphs represent the mean of the three identical experiments for the fold change in the expression of miRNAs. (Data represents in SEM, *P < 0.05; ***P < 0.001). **(G). $CD44^{+}/CD24^{-}$ population in irradiated adherent cells and mammospheres:** Dot plots represent $CD44^{+}/CD24^{-}$ population in MCF-7 adherent cells and mammospheres irradiated with fraction dose of 2GY for 3 and single dose of 6GY as compared to the sham irradiated cells. **(H) EMT markers in irradiated adherent cells and mammospheres:** EMT markers, E-cadherin, N-cadherin, vimentin, SLUG and TWIST were analysed by western blot. The intensity was normalized with GAPDH.

We identified that, fractionated doses of radiation elevated BCSC population in the CSC-enriched Mammospheres. Further, increased tumour growth was also observed in MCF-7 cells irradiated with fractionated doses of radiation in vivo. However, Nrf2 knockdown resulted in the reduction of $ALDH^{+}$ population and diminished SOX2, KLF4, NANOG expression and mammosphere formation efficiency. In line with these results, Nrf2 silencing displayed increased radiosensitivity in mammospheres and adherent cells during irradiation. Collectively, our results demonstrated that Nrf2 activation contributed to the acquired radioresistance of BCSC enriched mammospheres. These findings reveal that BCSC mediates radioresistance through stabilisation of Nrf2 via KEAP1 degradation. Fractionated doses of radiation induce epithelial-BCSCs expressing mesenchymal- epithelial transition (MET) markers and downregulate epithelial to mesenchymal transition (EMT) markers. These results suggested that radiation induces epithelial like BCSC population in mammospheres after treated with fractionated doses. Collectively, our findings revealed that radiation induced-Nrf2 activation contributes to the acquired radioresistance of BCSC enriched mammospheres by enhancing epithelial- BCSC population.

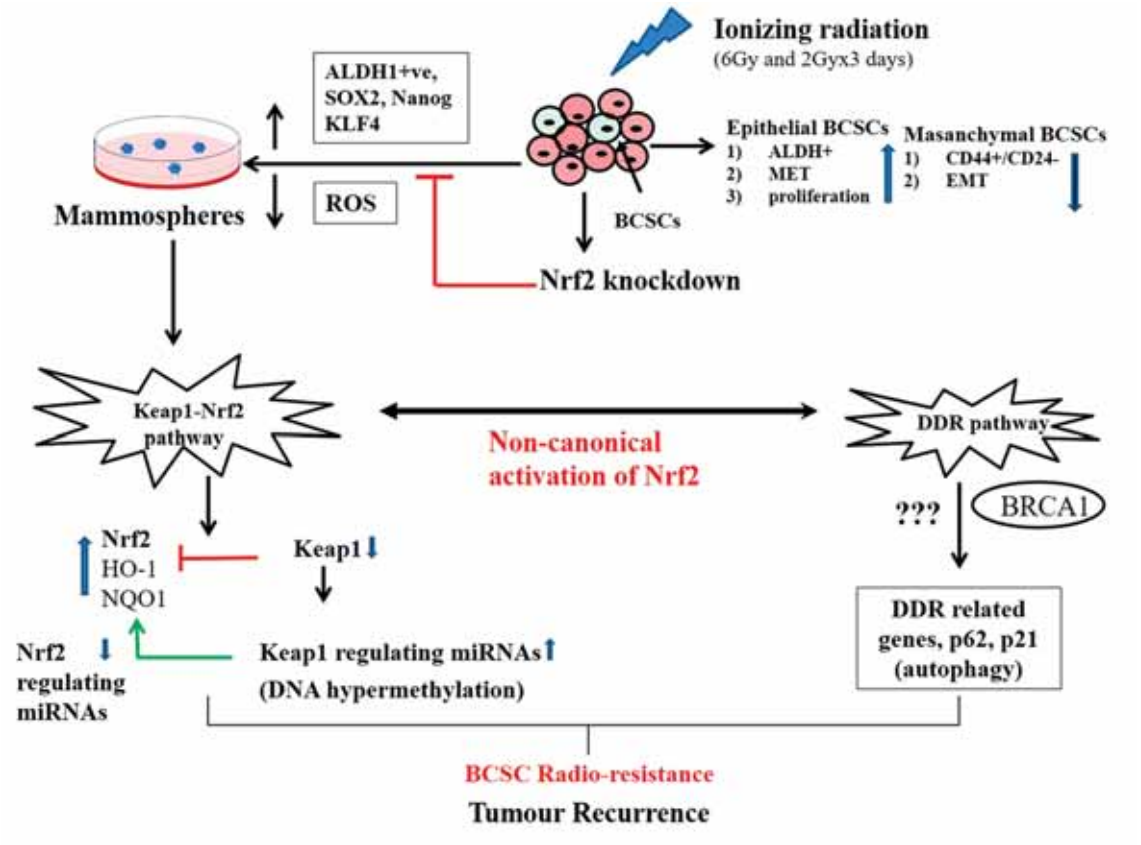

Fig. 2: Schematic representation of Nrf2 pathway in adherent and mammosphere radioresistance

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Understanding the Role of Clathrin-Mediated Endocytosis in Development and Disease

Objectives of the study

- To determine the role of clathrin-mediated endocytosis in embryonic stem cells, in lineage-specific differentiation and during development.
- To study the role of clathrin mediated endocytosis in disease, in the context of Huntington's disorder using *Drosophila melanogaster* as a model system.

Background

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

Embryonic stem cells lacking clathrin heavy chain display higher Young's modulus, which is due to reorganization of the actin cytoskeleton. These cells

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Collaborator(s) - National

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Shivaprasad Patil, *IISER Pune.*
Amitabha Majumdar, *NCCS, Pune.*

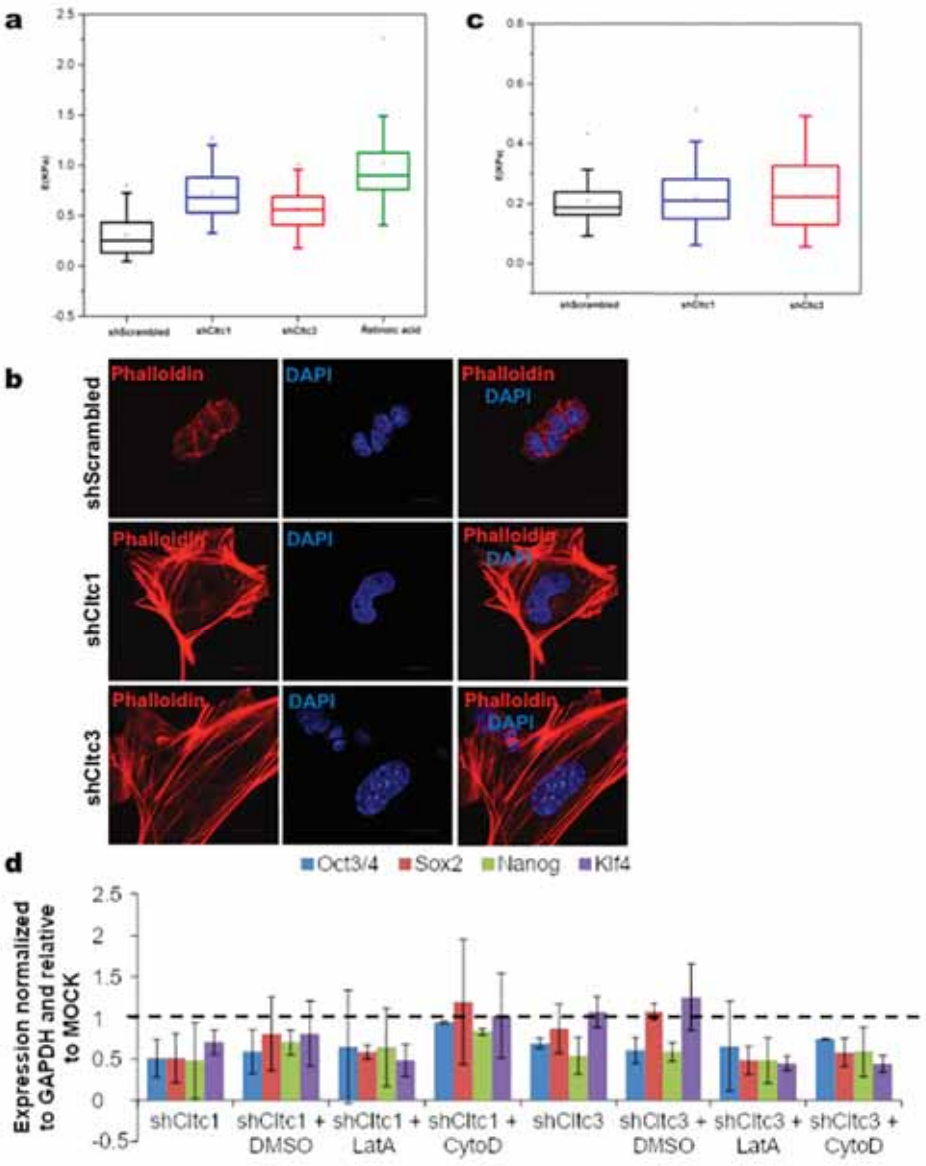

Fig. 1: a) Young's modulus (E) of shScrambled (embryonic stem cells treated with scrambled shRNA), shCltc1 (clathrin heavy chain knockdown using shRNA 1), shCltc3 (clathrin heavy chain knockdown using shRNA 1), and retinoic acid treated mESCs. b) Representative confocal micrographs showing actin filaments stained with Phalloidin in shScrambled, shCltc1, shCltc3 mESCs. The scale bar represents 10µm (N=15). c) Young's modulus (E) of shScrambled, shCltc1, shCltc3 treated mESCs treated with Latrunculin A (actin depolymerizing agent). d) RT-qPCR analysis of pluripotency markers in shScrambled, shCltc1 and shCltc3 mouse embryonic stem cells. Bar graph showing the expression of pluripotency markers in mESCs under indicated conditions relative to the relevant shScrambled control. Control is shown as a dotted line at 1. Error bars represent range for experiments in duplicate (N = 2).

also display reduced expression of pluripotency markers. While destabilization of the actin cytoskeleton results in reduction of stiffness, this does not result in a restoration of expression of pluripotency markers, indicating that active intracellular transport through the clathrin pathway may be a critical requirement in attaining pluripotency. An initiation of CME may be essential for the transport of molecules that ultimately regulate the pluripotency network of a stem cell. Our results also suggest that a rescue of mechanical properties need not necessarily always reflect a change in the transcriptional network of an mESC. Furthermore this may also suggest that an inherent hierarchy may exist with respect to specific events that dictate when a cell achieves pluripotency (Figure 1).

Regarding the role of clathrin-mediated endocytosis in the context of Huntington's disease, we are using hemocytes isolated from transgenic *Drosophila* lines that express either an aggregating or non-aggregating form of the Huntingtin protein. We are in the process of dissecting the role of various proteins involved in intracellular trafficking in the context of pathogenic forms of the Huntingtin protein.

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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 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 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-specific cellular information),

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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 thousands 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.

Quiescence is an important phenomenon exhibited by various cell types, including adult stem cells, fibroblasts, lymphocytes, progenitor cells, hepatocytes, some epithelial cells & cancer stem cells. The balance between quiescence and proliferation should be maintained for a proper tissue homeostasis. Any disturbance in this balance leads to various hyper- and hypo-proliferative diseases. Proliferation has been widely studied and the factors involved in proliferation regulation are well known. Whereas, an extensive research needs to be done in order to delineate quiescence regulation. LncRNAs have emerged as a class of important regulatory ncRNAs and are known to fine-tune numerous cellular processes such as cell cycle regulation, splicing, dosage compensation, development etc. Several lncRNAs such as MEG3, GAS5 have been reported in anti-proliferative roles. We aimed to understand the involvement of lncRNAs in quiescence regulation. The RNA- seq data from our studies revealed a unique set of quiescence specific lncRNAs showing higher fold expression levels in quiescent fibroblasts as compared to asynchronous fibroblasts. The quiescence specific candidate lncRNAs were validated by qPCR. The candidate lncRNAs- *LNC339*, *LNC607*, *LNC67L2*, *LNC1279* and *MIR503HG* were the top five quiescence specific lncRNAs. The functional studies revealed that the depletion of MIR503HG negatively affected quiescence induction but had no effect on cell cycle progression, suggesting their possible roles in quiescence attainment and maintenance. The proteomics screen identified downregulation of p38 pathway upon MIR503HG depletion, suggesting pro-proliferative state in MIR503HG depleted cells. The MIR503HG encoded miR-503 has already been reported to target cyclin D1 and CDC25a. We confirmed that the depletion of MIR503HG lead to increase in the levels of miR-503 targets- cyclin D1 and CDC25a, thus impairing the quiescence attainment. With the help of bioinformatics prediction tools, we found that MIR503HG has binding sites for miR-508-3p. We hypothesized that MIR503HG might act as a sponge for miR-508-3p, thus positively regulating the levels of miR-508 targets. Interestingly, we observed that MIR503HG depletion leads to drastic decrease in the levels of miR-508-3p targets- PTEN, INNP5J and INPP4A. Additionally, we also found that MIR503HG depletion lead to a significant reduction in PTEN protein levels with a concomitant increase in pAkt levels, suggesting that MIR503HG limit proliferation by negatively regulating miR-508. The direct interaction between MIR503HG and miR-508 was confirmed by Ago2 pulldown and luciferase reporter assay. We also observed that MIR503HG is transcriptionally regulated by FOXO3 in quiescent conditions. The overall results indicate that the FOXO3 regulated MIR503HG acts as a ceRNA for miR-508 by regulating the PTEN levels in quiescent condition.

We have also 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 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, U2OS). 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 approx. 733 lncRNAs that display a cell cycle regulated expression dynamic. 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.

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 role of IL-3 in regulating the pathogenic responses of Th17 cells

Objectives of the study

- To evaluate the role of IL-3 on differentiation of Th17 and Treg cells from IL-2 knockout mice.
- To investigate the in vivo role of IL-3 on development of Th17 and Treg cells and amelioration of CIA.
- To investigate the role of IL-3 on human Th17 cell differentiation.

Summary

Rheumatoid arthritis (RA) is an autoimmune disease characterized by synovitis that occur due to infiltration of leukocytes at affected joints and leads to destruction of cartilage and bone. IL-17 producing T helper 17 (Th17) cells plays a critical role in pathogenesis of RA and collagen-induced arthritis (CIA). The decreased incidence of CIA and collagen-specific autoreactive responses in IL-17 knockout mice also suggests the crucial involvement of Th17 cells in RA pathogenesis. In contrast, FOXP3-positive regulatory T (Treg) cells prevent autoimmunity by maintaining immune homeostasis. Aberrant immune activation due to imbalance between Th17 and Treg cells is associated with development of various autoimmune diseases. The enrichment of pathogenic Th17 cells in inflamed joints and their correlation with disease severity has been reported in many studies. Therefore, the molecules that will inhibit the development of Th17 cells or reduce their pathogenicity and induce tolerance is very important for prevention of RA.

IL-3, a cytokine secreted by Th cells stimulates the proliferation, survival and differentiation of hematopoietic cells. IL-3 has potent anti-inflammatory activity

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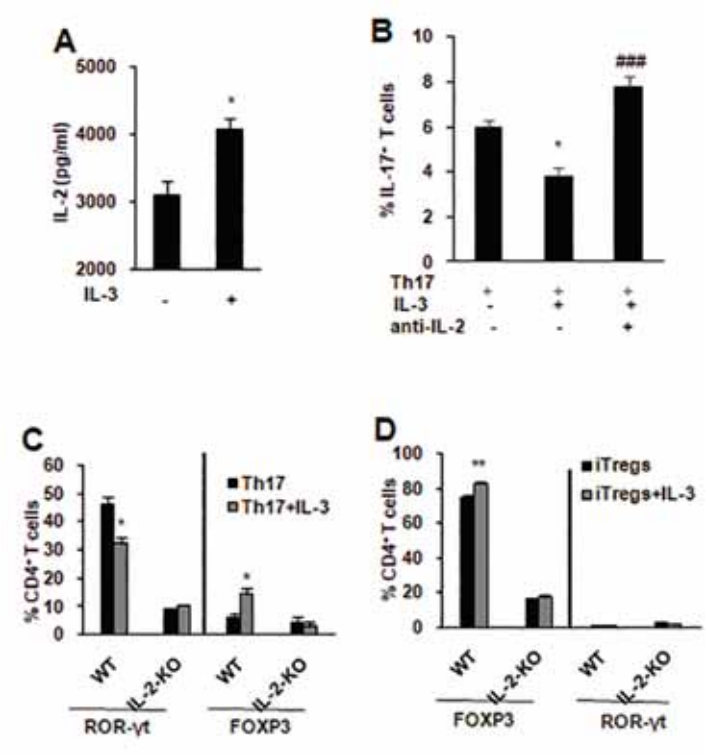


Fig. 1. IL-3 maintains Th17/Treg cell balance through IL-2. Naïve $CD4^+$ T cells were activated under Th17-polarizing conditions in presence of IL-3 with or without neutralizing IL-2 Ab (10 µg/ml). After 3 days, cells were analyzed for the percentage of $IL\text{-}17A^+$ T cells and secretion of IL-2. (A) IL-2 levels in culture supernatants. (B) $IL\text{-}17A^+$ T cells. p values were calculated using one-way ANOVA with Bonferroni's multiple comparison test. (C and D) Percentage of ROR-γt^+ and $FOXP3^+$ T cells after Th17 and iTreg cells differentiation of naïve $CD4^+$ T cells isolated from IL-2 wild type and knockout mice in the presence of IL-3. p values were calculated using unpaired t-test. Data are presented as mean ± SEM from three independent experiments. *$p < 0.05$; **$p < 0.01$ vs untreated Th17 or Tregs. ###$p < 0.05$ vs IL-3 treated Th17 cells.

and prevents pathological bone and cartilage loss in animal models of skeletal diseases. IL-3 also enhances the differentiation of Treg cells. However, the role of IL-3 in development of pathogenic Th17 cells and their effector responses; and Th17/Treg balance is not fully delineated. Recently, we have demonstrated that IL-3 inhibits the differentiation of Th17 cells and favors Treg cells. IL-3 also decreases the number of pathogenic Th17 cells by inhibiting the phosphorylation of STAT3. In further studies we investigated the role of IL-3 on differentiation of Th17/Treg cells from IL-2 knockout mice and disease pathogenesis in vivo in CIA mice.

We observed that IL-3 enhances the secretion of IL-2 under Th17-polarizing conditions (Fig. 1A). Also, anti-IL-2 antibody abrogated the suppressive effect of IL-3 on $IL\text{-}17^+$ T cells (Fig. 1B). To confirm the IL-2-mediated effect of IL-3 on Th17/Treg cells, we generated Th17 and iTreg cells from naïve $CD4^+$ T cells of wild type and IL-2 knockout mice. As expected, IL-3 showed no effect on number of Th17 or Treg cells generated from IL-2 deficient naïve $CD4^+$ T cells (Fig. 1C and D). Consistently, IL-3 decreased ROR-γt^+ Th17 cells and enhanced FOXP3 expressing cells generated from wild type $CD4^+$ T cells. Thus, our results suggest that IL-3 regulates Th17/Treg axis in IL-2-dependent manner.

Th17 cells are known to enhance bone destruction in arthritis by inducing osteoclast differentiation through IL-17 and RANKL. Therefore, the effect of IL-3 was evaluated on RANKL expression and Th17 cells-induced osteoclast differentiation. IL-3 significantly inhibited RANKL expression under Th17 conditions both at transcript and protein levels (data not shown). To evaluate the role of IL-3 on Th17 cells-induced osteoclastogenesis, mouse bone-marrow cells were co-cultured with IL-3 treated Th17 cells in presence of M-CSF and RANKL. We observed that IL-3 significantly reduced the osteoclastogenic ability of Th17 cells (data not shown).

To investigate the role of IL-3 on Th17 cells-mediated disease pathogenesis, we used CIA mice. IL-3 was injected into mice after secondary immunization. We observed that IL-3

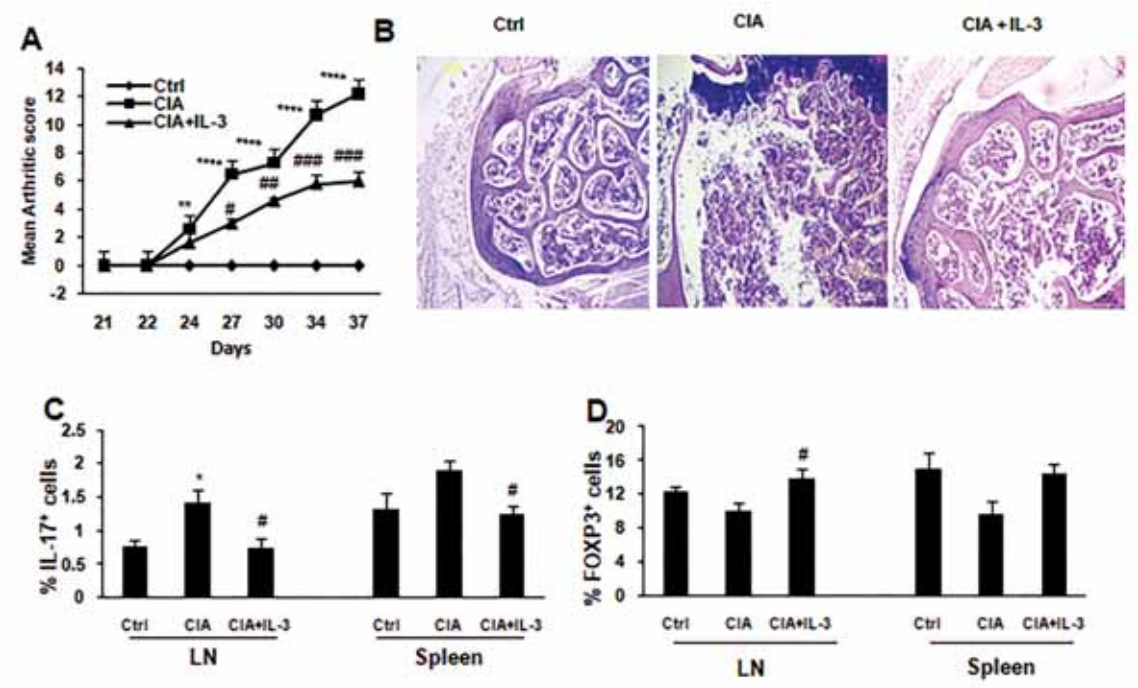


Fig. 2. IL-3 prevents development of Th17 cells and ameliorates CIA in mice. CIA was induced in DBA/1J mice. On day 22, mice were injected i.p. with 1 µg of IL-3 or PBS as a vehicle control. (A) Disease severity was assessed by calculating mean arthritic score per animal. (B) Histopathological analysis for cellular infiltration and degenerative changes in knee joints after H & E staining. Percentage of IL-17$^+$ (C) and FOXP3$^+$ (D) CD4$^+$ T cells from lymph nodes and spleen. Data are presented as mean ± SEM from two independent experiments (n = 10). p values were calculated using one-way ANOVA with Bonferroni's multiple comparison test. *p < 0.05, **p < 0.01, ****p < 0.0001 vs ctrl group. $^{\#}$p < 0.05; $^{\#\#}$p < 0.01; $^{\#\#\#}$p < 0.001 vs CIA.

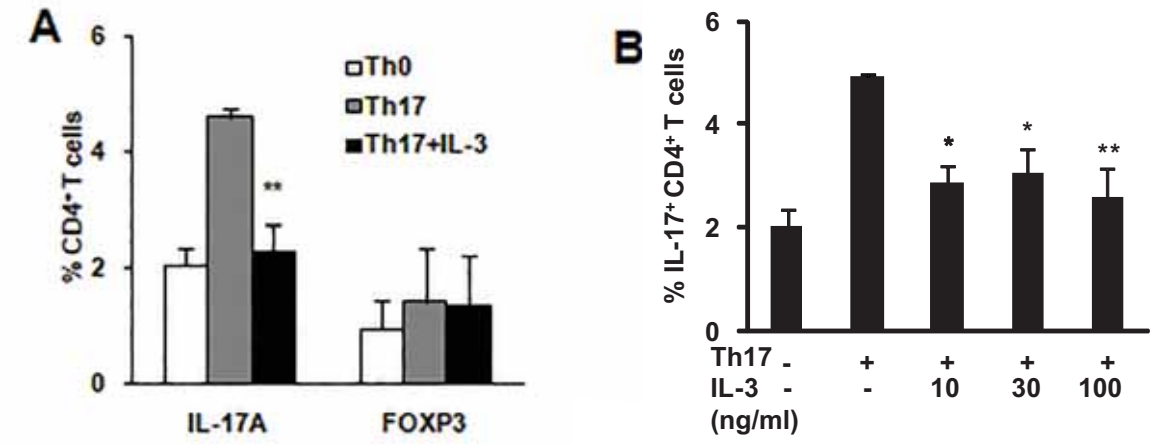


Fig. 3. IL-3 inhibits the development of human Th17 cells. Human naïve T cells were activated with plate bound anti-CD3ε (2 µg/ml) and soluble anti-CD28 (1 µg/ml) antibodies in presence of rhIL-1β and rhIL-23 with or without IL-3. On day 4, cells were stimulated with PMA/ionomycin and stained intracellularly for IL-17A and FOXP3 expression. (A) Percentage of IL-17A$^+$ and FOXP3$^+$CD4$^+$ T cells. (B) Effect of different concentrations of IL-3 on differentiation of human Th17 cells. Data are presented as mean ± SEM from two to three independent experiments. p values were calculated using one-way ANOVA. *p < 0.05; **p < 0.01 vs untreated Th17 cells.

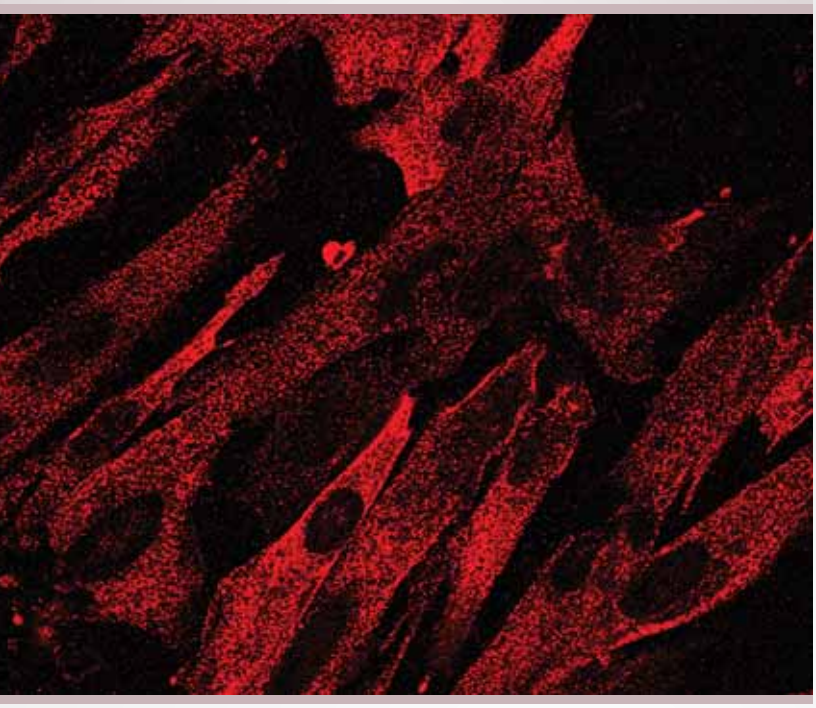
significantly reduced clinical score and disease severity in mice (Fig. 2A). Histopathological analysis of knee joint revealed significant reduction in cellular infiltration and degenerative changes by IL-3 (Fig. 2B). In consistent with in vitro findings, IL-3 decreased the number of IL-17$^+$CD4$^+$ T cells and increased FOXP3$^+$ Treg cells in both spleen and lymph nodes (Fig. 2C and D). IL-3 significantly decreased the number of pathogenic IL-17$^+$TNF-α$^+$ and IL-17$^+$IFN-γ$^+$ Th 17 cells in lymph nodes and IL-

17^+TNF-α^+ Th17 cells in spleen. However, IL-3 showed no effect on non-pathogenic IL-17^+IL-10^+ Th17 cells in both lymph nodes and spleen (data not shown). These results indicate that IL-3 is important regulator of Th17/Treg cell imbalance; and inhibits the Th17 cells-mediated immunopathology in CIA mice.

To determine whether the inhibitory effects of IL-3 on Th17 cells observed *in vitro* and in CIA mice also reproduce in human cells, we stimulated human peripheral blood-derived naïve $CD4^+$ T cells under Th17-polarizing conditions in presence of IL-3. After 72 h, cells were stimulated with PMA and ionomycin; and analyzed for IL-$17A^+$ and $FOXP3^+$ T cells. We observed that IL-3 significantly decreased the number of IL-17^+CD4^+ T cells, and showed no effect on $FOXP3^+$ $CD4^+$ T cells (Fig. 3A). The effect of IL-3 on inhibition of human Th17 cells was seen at different concentrations (Fig. 3B). These results suggest that IL-3 also inhibit development of human Th17 cells. In conclusion, our studies suggest the novel role of IL-3 in inhibiting pathogenic Th17 cells responses and maintenance of immune homeostasis in RA.

Future Research Plans

To investigate the role of IL-3 on Th17 and Treg cells isolated from RA patients.



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)

RATS: WISTAR

RABBITS: NEWZEALAND WHITE

* BALB/c with cataract mutation # Outbred

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

Standard Operating Procedures are in place for every activity that has a direct bearing on the management and husbandry of animals housed in the facility.

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 support and advice is extended as per demand to the Scientists and their group members for the conduct of experiments under IAEC approved projects.

The total number of mice strains, inbred, outbred, and mutant and hybrids, being maintained at the Experimental Animal Facility stands at 54. The foundation/nuclear colonies of mice are housed in Individually Ventilated Caging systems. Genetic monitoring using standard PCR 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 2019-20, a total of 31 fellows underwent the course which comprised of both theory and practical sessions.

As per the rules and regulations framed by the Committee for the Purpose of Control and Supervision of Experiments on Animals (CPCSEA) Govt. of India, the EAF provides the requisite oversight on the conduct of experiments on laboratory animals in the Institute.

The breeding of laboratory animals has been planned to meet the needs of Scientists / Research Scholars for various animal experiments.

Conference Organized:

The 9th International Conference of LASA India with the theme "Laboratory Animals in Biomedical Research-The Way Forward" was organized between November 21 to 23, 2019. The Conference was organized jointly by NCCS and IISER, Pune. Both IISER and NCCS were shared venues for the event. More than 300 national and international delegates participated in this conference.

Publications:

Vitexin alleviates non-alcoholic fatty liver disease by activating AMPK in high fat diet fed mice. Inamdar S, Joshi A, Malik S, Boppana R, Ghaskadbi S. Inamdar S, et al. Biochem Biophys Res Commun. 2019 Oct 29;519(1):106-112. doi: 10.1016/j.bbrc.2019.08.139. Epub 2019 Aug 29. Biochem Biophys Res Commun. 2019.PMID: 31472955

Proteomics Facility

Dr. Srikanth Rapole (Scientist In-Charge)
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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, which provides services for mass spectrometric analysis of biological samples. The various instruments available at this facility are listed below:

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 MSn 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 534 samples including 10 external samples from April-2019 to March-2020.

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 86 samples including 10 external samples from April-2019 to March-2020.

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 coupled to Eksigent Express Micro LC-Ultra System. The system is used for targeted proteomic applications, metabolomic applications and lipidomic applications.

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)

Pratibha Patil
Technical Staff

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.

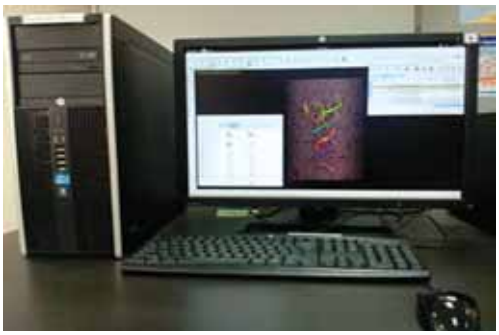
Hardware Infrastructure

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.

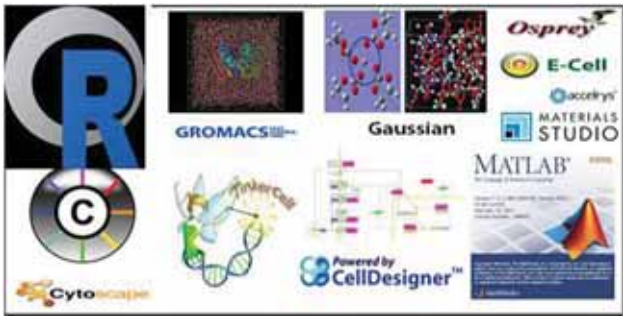
Network Modeling: CellDesigner

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



Visitors to the bioinformatics facility on the National Science day Open Day at NCCS

ab initio modeling: GAUSSIAN

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

Artificial Intelligence: SVMlight 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 / Training conducted at the Bioinformatics and High Performance Computing Facility:

In-house "Applications of Computational Biology" training to graduate students which helps them 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 helps them to develop inferences of the biological mechanism and hypothesis for further experimental testing.

Workshops are conducted regularly for students enrolled in the PhD coursework, from ARI, NIV, NCCS and Department of Biotechnology, Microbiology and IBB from SavitriBai Phule Pune University, (SPPU).

This includes -

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

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 363 volumes per year. The library holds approximately Fourteen thousand eight hundred thirteen bound journals, three thousand seven hundred fifty-four books, and three hundred and nine Ph.D. theses of students of NCCS. It subscribes to twenty scientific journals and twenty-four other periodicals in print form.

The staff and students are provided access to 734 online publications through DeLCON, the online journal consortium of DBT. This includes 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. 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, Ph.D. theses and other documents using the iThenticate anti-plagiarism software, prior to their submission to journals and the Savitribai Phule Pune University. The library has also made available the 'Grammarly' app for Windows desktops, to help with correcting and refining the language in documents like Ph.D. theses and manuscripts. An open access repository for the research publications of the NCCS scientists has been set up by the library, which is available on the following link - http://nccs.sciencecentral.in.

Computer Section

Dr. Sharmila Bapat

(Scientist In-charge)

The Computer Section provides various computing and network infrastructure services and training to NCCS Staff, personnel on extra-mural grants and students. Routine support includes setup and configuration of servers, desktops, laptops, printers, scanners, software and network services and management of their maintenance.

The section also is responsible for secured network services including the design of campus wide LAN/WAN solutions, intranet solutions besides making available basic computing infrastructure required for the implementation of ongoing R&D projects. Two Internet links are installed at NCCS viz. 100Mbps (NKN) and 30Mbps (Tata Communications Ltd.). Internet facilities are extended to all institute users, visitors to Guest house and student's hostel. The present Network security system has been upgraded with 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.
- Setting up temporary wifi network for Conferences, seminars and meetings.
- Providing Internet Connectivity to all Scientists, Staff and Students through NKN and Tata Links.
- Computer hardware Infrastructure Procurement, Installation, configuration and Maintenance
- Web Services include design and maintenance of NCCS and Website and its management.
- Providing User Support Services including new Desktop specifications, Software and Hardware installations, printers, scanners and other computer related devices.
- Providing E-mail Service to regular and project staff members including Scientists, Technical and Administrative Staff and Research scholars.
- Providing Technical support in Video Conferencing / SKYPE / DROPBOX / VPN access.

The Team

Mr. Rajesh Solanki *(Technical Officer)*
Mr. Shivaji Jadhav *(Technical Officer)*
Mrs. Rajashri Patwardhan *(Technical Officer)*
Mrs. Kirti Jadhav *(Technical Officer)*

- Management of Virtualised High-performance Servers for hosting services like WWW, DNS, E-mail, DHCP and Proxy.
- Network Management and maintenance of high-speed Routers, Switches and WL Access points.

New Initiatives:

1. Proposal for up gradation of exisiting Network

The present network was established in 2007-2008. We propose to install a new fiber optic backbone based high speed low latency network that will be a combination of Star and Ring topology for maximum uptime. This network will cover old building, new building, Animal House, Guest House, Hostels and all quarters in NCCS colony. It will provide cable and wifi network access to all users for online data analysis, high speed data transfer and skype/Video Conferencing. It will be managed and monitored by a network management software for network diagnosis, congestion / stress detection and troubleshooting. A survey was undertaken of all NCCS areas proposed to be covered by the network layout, and bill of material has been prepared considering additional requirements of LAN points of all sections and departments at NCCS.

2. Establishment of new Data Centre

The Computer section has been housed in the old stores area. A plan to install a new state of the art Data Centre (DC) for NCCS was developed. This proposed DC will provide centralized NCCS IT operations involving Computer servers and network infrastructure to store manage and disseminate data. The DC will house the network's most critical systems that are vital to the continuity of daily operations. As a beginning, the DC will house 6 racks collocating all servers and network devices. The DC will have centralised UPS, Precision Cooling, Secure biometric access, Smoke detector, Fire alarm and suppression, Water leak detection, Rodent repellent systems etc.

3. Secured SSL certificate for NCCS website

A new GeoTrust SSL certificate has been installed on NCCS website whereby, all website visitors will have secure protected access. This not only affirms NCCS identity but will also provide better search engine ranking.

4. Sun Server MANAV project

A separate SUN server X4450 has been setup and configured for MANAV project with UBUNTU 18.04 Operating System. This server has been configured to send confirmational e-mails to registered users through old e-mail system.

5. Migration to NIC E-mail service

As per the mandate of Government, we have smoothly migrated our e-mail services from NCCS to NIC email system. The necessary changes in the DNS server have been done to facilitate this transfer. All the NCCS user accounts have been created in NIC system.

6. New NCCS website and NCCS Logo

The RFP document for new NCCS website and NCCS logo was prepared after rigorous discussion and meetings, and the process of award of contract is in progress.

7. Bandwidth Upgradation of Tata Internet Connectivity

The 10 Mbps (1:1) Internet bandwidth from TATA Communications that is used for E-mail, DNS and browsing has been upgraded to 30 Mbps(1:1).

General Assistance

Regular maintenance and up-dating of the NCCS website, intranet website and uploading tenders / corrigendum's on CPP Portal is done by the Computer section. Several operating systems and common application software were installed / updated on user computers. These include MS Office 2010, Adobe Suite X, Sigma Plot Suite 12.0 and Reference Manager 12.0. Updation of Saral Paypack software that takes care of staff salary process which includes TDS, EPF and NPS deductions. Support is also provided in uploading notification material on the LED display screens placed across the campus.

Technical support provided

- FlowJO software workshop (29 Nov. 2019)
- NGS4ALL workshop (10 Dec. 2019)
- International Conference on Translational Research (ICTR-2019; 7 Nov.2019)
- LASA one day Conference (23 Nov. 2019)
- NCCS Open Day organised as a prelude to the India International Science Festival (IISF-2019; 23 Oct. 2019)
- National Science Day (28 Feb. 2020)
- Scientific Conference in Hindi- 'विकसित भारत में विज्ञान और प्रौद्योगिकी का योगदान' (04 March, 2020)
- A Ubuntu18.04 linux server was configured for Dr. Sahu to host web application named CoReDo, A tool to predict Complement Regulatory Domains.

Bio-Imaging Facility

The Team

- Dr. Arunkarthick S. - *Scientist C & Facility In-Charge*
- Dr. Ashwini N. Atre - *Technical Officer A*
- Mrs. Trupti P. Kulkarni - *Technician B*
- Mrs. Ketakee Pawar - *Laboratory Manager - Pune Bio-Cluster Project*
- Ms. Leena Thomas - *Laboratory Associate - Pune Bio-Cluster Project*
- Mr. Sourav Chowdhury - *Technical Assistant (Operator for HCA System provided by Thermo fisher Scientific and posted in NCCS)*

At the Bio-Imaging Facility, graduate and postdoctoral students are trained in microscope research techniques including advanced light microscopy, confocal microscopy, digital image processing of microscope images, and related laboratory techniques. Computer image processing and analysis is taught individually. In addition, the facility offers microscopy-related workshops, and training programs designed to train the student in modern and classical methods for preparing microscope slides. There are full time staff members who, among other things, demonstrate the correct use of the instruments, train students in the microscopic techniques required for successful cell biological research, and help with all aspects of light microscopy and computer image processing and analysis.

Microscopes Available at NCCS Bio-Imaging Facility:

i) Leica SP5 II
ii) Olympus FLUOVIEW FV10i
iii) Olympus FLUOVIEW FV3000
iv) Thermo Cellinsight CX7 LZR High Content System
v) Zeiss LSM510 META (Under repair)
vi) Zeiss LSM880 Airy Scan and ELYRA P.1

All the above confocal microscope systems are inverted microscopes and have a wide range of lasers. They are used by in-house users as well as by users from neighbouring organizations. 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. The softwares for confocal imaging, 3D imaging and

reconstruction, time lapse, colocalization, FRET (SE & AB), and FRAP are also available.

Usage of Microscopes during 2019-20:

The numbers of samples imaged during this year were approximately 5509 in-house, plus 64 samples received from various other nearby institutes.

Activities of Confocal Microscopy Facility:

1. Workshops / Training Programs Organized:

The Facility In-Charge, along with the NCCS Bio-Imaging facility staff, conducted the following training programs for the NCCS staff and students:

The Facility In-Charge coordinated with different companies and organized the following training programs / workshops for the NCCS staff and students:

1) "LSM 880 confocal microscope with AiryScan and Elyra P1 system" by Zeiss India on 05/08/2019 to 07/08/201.
2) IMARIS-The Ideal Solution to Interactively Analyze Microscopy Images - an one day training on Image analysis software by Bitplane & Nikon India on 10/08/2019.
3) Cilika digital microscope training by MedPrime Technologies, Mumbai held on 03/10/2019.
4) Nikon N-SIM super resolution microscope training by Nikon India & Tawa Optics during 24/10/2019 to 27/10/2019.
5) Training on Olympus FV3000 Confocal Microscope with OSR super resolution Capabilities by Olympus India during 06/01/2020 to 08/01/2020.
6) Training of Leica Thunder Imager by Leica Microsystems India during 16/01/2020 to 17/01/2020.
7) "Explore the Universe of the Cell: Cell imaging and Analysis Technologies". Training on GE OMX-SR: SIM based super resolution microscope by GE Healthcare Life Sciences during 20/01/2020 to 24/01/2020.

2. Technical Seminars Organized:

The Bio-Imaging Facility organized several technical seminars during the s

Sr. No.	Date	Microscope Lectures/ Technical Talks details
1	05-08-2019	LSM 880 with Airyscan: System overview and its applications
2	06-08-2019	IMARIS- Ideal Solution to Interactively Analyze Microscopy Images
3	26-09-2019	GE Life Sciences Delta Vision OMX Flex SIM microscope
4	01-10-2019	Introduction to Andor Dragonfly High-Speed Confocal Platform
5	24-10-2019	Presentation on Nikon N-SIM microscope
6	06-01-2020	Presentation on Olympus FV3000 Confocal Microscope Capabilities
7	20-01-2020	Explore the Universe of the Cell: Cell imaging and Analysis Technologies from GE Healthcare Life Sciences.
8	15-10-2019	Introduction to Andor Dragonfly High-Speed Confocal Platform

S. No.	Training Details	Date(s) of Training	No. of Participants
1	Hands-on Training on Olympus FV10i - Confocal Microscope (conducted in 6 batches)	15 April 2019 to 16 April 2019	49 students from NCCS
2	Hands-on Training Workshop on Leica SP5 II Confocal Microscope (conducted in 4 batches)	12 June 2019 to 01 July 2019	16 students from NCCS
3	Training on CX7 LZR - High Content Analysis system	11 September 2019 to 13 September 2019	5 students from NCCS
4	Hands-on Training Workshop on Leica SP5 II Confocal Microscope from NCCS	14 October 2019 to 13 November 2019	16 students
5	Three days Hands-on Training Workshop on Zeiss LSM 880 Confocal Microscope from NCCS	31 October 2019 to 1 November 2019	12 students
6	Training on CX7 LZR - High Content Analysis system	20-22nd November 2019	7 students from NCCS
7	Image Analysis using Fiji/ImageJ - a Basic course workshop (conducted in 3 batches)	07-11th October 2019	45 students from NCCS

3. Demonstration of Microscopes:

The facility organized a demonstration of three different microscopes at NCCS during the said year, as listed below.

Sr. No.	Microscope Demonstration Details	Date
1	Leica Thunder Imager by Leica Microsystems India during 16/01/2020 to 17/01/2020.	16/01/2020 to 0/01/2020
2	GE OMX-SR: SIM based super resolution microscope by GE Healthcare Life Sciences.	20/01/2020 to 24/02/2020
3	Nikon N-SIM super resolution microscope demo by Nikon India & Tawa Optics.	24/10/2019 to 17/02/2019.

4. Science Day: On the occasion of the National Science Day on 28th February 2020, the facility arranged a demonstration of microscopes available at the facility for all the visitors. Interesting cell images and videos acquired with our microscopes were shown to the participants, and the features of the microscopes were explained to them. Representatives for companies were also invited to display their instruments in NCCS reception area.

5. Purchase of new Microscopes & Consumables: The facility was involved in purchasing new microscopes with NCCS core funds and also from the Pune Bio-Cluster project. The Olympus FLUOVIEW FV3000 confocal microscope, Thermo Cellinsight CX7 LZR High Content System and Zeiss LSM880 confocal with Airy Scan and ELYRA P.1 microscopes were purchased and installed in the new Bio-Imaging facility during the said year. Consumables and spare parts for various instruments in the facility were also purchased.

6. Image analysis trainings: We provided training and assistance to individual students for post- acquisition analysis of images and data using the ImageJ, IgorPro and Matlab softwares.

7. Inauguration of New Bio-Imaging Facility: We were involved in planning of the new microscopy facility in the new building. Renovation work, ordering of furniture and necessary items were done. Centralized gas pipeline connections were done for the facility, for CO2, Zero Air and Nitrogen connections. The inauguration of the new Bio-Imaging facility was done by the Honorable Secretary of the Department of Biotechnology (DBT), Dr. Renu Swarup, on 23rd August 2019.

The Hon'ble Secretary of DBT, Dr. Renu Swarup, inaugurated the new Bio-Imaging facility at NCCS.

FACS Facility

The Team

Dr. Arunkarthick S. - *Scientist-C & Facility In-Charge*

Mr. Amit Salunkhe - *Technician C*

Ms. Ashwini Kore - *Technician B*

Mr. Dnyaneshwar Waghmare - *Technician B*

Mr. Atul Khirwale - *Flow Cytometry Operator (Operator provided by BD and posted in NCCS under BD-NCCS STEM CELL CoE)*

Flow cytometry is a powerful tool for the multi-parameter analysis of cells of all types. The Flow Cytometry Research Core facility provides a centralized resource for technical expertise and major equipment. The facility supports and enhances experimental design and execution of basic and applied researches that require flow cytometric cell analysis or cell sorting.

To achieve these objectives, the facility offers the following services:

- Expert consultation is provided through the Facility In-Charge & technical specialists
- FACS instruments are selected for complementary functions.
- Equipment use is accessible through dedicated technicians.
- Assistance with data analysis can be customized to the needs of individual investigators and research projects.

INSTRUMENTS AVAILABLE AT NCCS - FACS CORE FACILITY:

The NCCS FACS Core Facility has a total of six Flow Cytometer instruments, of which three are analyzers and other three are sorters. All six flow cytometer machines were purchased from Becton Dickinson (BD).

Benchtop Analyzers:

1) FACS Calibur: 2 Lasers, 4Colours. 2b-2r (Blue 488 nm, Red 633 nm)

2) FACS Canto II (Old): 3 Lasers, 8 Colours. 4b-2r-2v (Blue 488 nm, Red 633 nm, Violet 405 nm)

3) FACS Canto II (New): 3 Lasers, 8 Colours. 4b-2r-2v (Blue 488 nm, Red 633 nm, Violet 405 nm)

Cell Sorters:

1) ARIA II SORP: 4 Lasers, 11 Colours. 5b-2r-2v-2uv. (Blue 488 nm, Red 640 nm, Violet 405 nm, UV 355 nm)

2) ARIA III SORP: 5 Lasers, 16 Colours. 3b-2r-4v-3uv-4yg (Blue 488 nm, Red 640 nm, Violet 405 nm, UV 355 nm, Yellow Green 561 nm)

3) ARIA III STD: 5 Lasers, 11 Colours. 3b-2r-4yg-2 violet/yg.(Blue 488 nm, Red 633 nm, Violet 405 nm / UV 375 nm, Yellow Green 561 nm)

BD™ Cytometer Setup and Tracking (CS&T) beads, Rainbow QC and BD FACS Accudrop beads are used for quality control check.

Usage of Flow Cytometers during 2019-20:

The usage of the six instruments by NCCS users for 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	963	1917	–	–	1288	4168
FACS Canto II (Old)	7002	102	–	88	7257	14449
FACS Canto II (New)	3425	39	–	220	–	3684

STERILE SORTING:

EQUIPMENT	SORTING	ACQUISITION **
FACS Aria II SORP	116	340
FACS Aria III SORP	270	966
FACS Aria III Standard	255	796

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

Samples analyzed for external users:

Since the workload of external samples increased, NCCS made a policy in June 2012 to charge users from outside NCCS. The charges are less for academic and research institutes, and for private companies the charges are higher. Institutes /companies like Rasayani Biologies Pvt. Ltd., ARI, IISER-Pune & IRSHA have utilized our facility over April 2019 - March 2020. We had acquired around 910 samples for Surface / Intracellular staining and DNA cell cycle analysis.

Other Central Facility Instruments available at FACS Core Facility:

1) Bio-Plex 200 System from Bio-Rad

The Bio-Plex® 200 system is a suspension array system which offers protein and nucleic acid researchers a reliable multiplex assay solution that permits analysis of up to 100 biomolecules in a single sample.

2) Droplet Digital PCR Systems from Bio-Rad

Digital PCR is a breakthrough technology that provides ultrasensitive and absolute nucleic acid quantification. It is particularly useful for low-abundance targets, targets in complex backgrounds, allelic variants (SNPs), and for monitoring subtle changes in target levels that cannot be detected with real-time PCR.

ACTIVITIES OF FACS CORE FACILITY:

1. FACS facility trainings: We have organized the following training in batches on Analyzers (Canto-II and Calibur), Sorters and Biacore T200 instruments during the said year.

Training Details	Date(s) of Training	No. of Participants
One day Hands-on Training on Calibur flow cytometer	30th April 2019	11 Students from NCCS
One day Hands-on Training on Calibur cytometer flow	07th May 2019	14 Students from NCCS
One day Hands-on Training on Calibur flow cytometer	28th May 2019	15 Students from NCCS
One day Hands-on Training on Canto II flow cytometer	15th July 2019	07 Students from NCCS
Hands-on Training on Canto II flow cytometer	23rd September 2019	06Students from NCCS
Hands-on Training on Canto II flow cytometer	24th September 2019	06 Students from NCCS
Hands-on Training on Canto II flow cytometer	26th September 2019	03 Students from NCCS & 03 from outside institutes.
Hands-on Training on Canto II flow cytometer	27th September 2019	06 Students from NCCS
Three days Flow Cytometry Sorting Workshop.	20-22nd August 2019	03 Students from NCCS & 03 from outside institutes.

Training on BD FACS Calibur instrument at NCCS FACS Facility.

2. Workshop organized:

   1) Training on Flow cytometer: Cytoflex LX by Beckman Coulter India during 13 - 16th June 2019.
   2) FlowJo Analysis workshop Training by BD Life sciences on 28 - 29th November 2019.
   3) FCS EXPRESS 7 Software Training during 13th February 2020.

3. Demonstration of Instruments:

   Demonstrations of the Flow cytometer: Cytoflex LX by Beckman Coulter India were organized during 13 - 21st June 2019.

4. Science Day:

   On the occasion of the National Science Day Open Day on 28th February 2020, we presented a poster entitled "NCCS Flow Cytometry Core Facility". A demonstration of FACS machines available at the facility was also arranged for visitors to NCCS on this day. Videos about flow cytometers and its applications in various fields were also shown to the visitors.

5. Purchase of consumables & spare parts: Spare parts like Lasers for the instruments were purchased for the FACS facility. Purchase of consumables was also planned and implemented on time for the FACS machines, to ensure smooth functioning of the facility.

Other Facilities

1) 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 at NCCS 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. Several users from both academic as well as industrial organizations have been frequently using the facility.

2) DNA sequencing facility

The Team

Dr. Yogesh Shouche (Scientist and Facility In-charge)

Dr. Kamlesh Jangid *(Scientist In-Charge, NCMR)*

Dr. Abhay Bajaj *(Scientist)*

Dr. Sarang Satoor *(Technical Officer)*

Mr. Mandar Rasane *(Technician)*

Mr. Vikas Patil *(Technician)*

Mr. Sunil Dhar *(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 all sequence and data analysis software. The facility offers services related to sequencing of plasmids, PCR products and cloned inserts; primer walking; and genotyping and fragment analysis, to researchers from NCCS and other organizations. This facility caters to the needs of research institutions and industrial clients across the country, for the identification of bacterial and fungal isolates. In addition, the facility serves as the back-bone of culture authentication and identification for NCMR's preservation activities.

Over the year 2019-20, nearly 23541 sequencing reactions were run on the machine. The facility provided support to the internal institutional research

activity by delivering 23123 sequencing reactions. 418 services against payment were provided to 127 different academic and research institutions from 23 states across the country. Bacterial identification using 16S rRNA gene sequencing and fungal identification using the ITS region sequence were mainly performed. For the identification of bioprospection cultures stored in the biobank at NCMR, 653 cultures were processed. Also, 871 cultures 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 run on the machine during the aid period (490 96-well plates) : 23123.
c) No. of in-house users: 24
d) No. of extramural users benefited: 127 different institutions /universities from 23 states (Andhra Pradesh, Assam, Bihar, Chhattisgarh, Delhi, Himachal, Goa, Gujrat, Rajasthan, Jammu, Jharkhand, Karnataka, Kerala, Odisha, Punjab, Maharashtra, M.P., Tamilnadu, Telangana, Tripura, U.P., Uttarakhand and West Bengal).

3) Surface Plasmon Resonance Facility (SPR) Facility

The Team

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

Mrs. Mary Beulaa Jayapragasam *(Operator provided by Cytiva and posted at NCCS from June 2019)*

Name of the Instrument: Biacore T200 (Installed on 04 June, 2019)

A versatile system for high quality characterization of molecular interactions ranging from ions to viruses in real time using label free detection based on the phenomenon of surface plasmon resonance (SPR).

The usage of the equipment for the period under consideration is summarized below:

Lab	No Of Samples	Chips Used	Total Number Of Hours Used
Dr.Arvind Sahu	7	SA-3 & CM5-1	131h 29min
Dr.Janesh Kumar	2	L1 -1	25h 55min
Dr.Jomon Joseph	17	CAP-1	126h 36min
Dr.Shekhar Mande	6	NTA-1	92h 38min
Dr.Debashish Mitra	6	NTA-1	146h 59min
Dr.Vasudevan Seshadri	4	NTA-1& CAP-1	15h 15min
Total	42		539h 12min

Samples received from external users*:

Lab	No Of Sam -ples	Chips Used	Total Number Of Hours Used	Fund Generated (Rupees)
Dr. Virendra kumar-NIV, Pune	4	NTA-1 & L1-1	159h 5min	1,61,514
Zenia/Dr. Kiran Kulkarni-NCL, Pune	8	NTA-1	53h 18min	1,10,004
Total	12	-	212h 23min	2,71,518

* External users have to pay user charges, which are less for academic and research institutes, and higher for private companies.

ACTIVITIES:

1. SPR trainings and examination:

Two 3-days' training programs were conduceted during the period under report, as listed below.

Dates	Chips used	Total no of hours used for demo	No of students who attended and took the examination
23rd to 25th July 2019	CM5-FC 1,2	3h 49min	15
25th to 27th February 2020	CM5-FC 3,4	5h 31min	9

2. Science Day:

On the NCCS Open Day organized on the occasion of the National Science Day, facility operator, Beulaa presented a poster entitled "Surface Plasmon Resonance Facility", and explained the principles of the instrument and it's applications to the visitors.

Biacore T200 at the SPR Facility

Visitors on the Science Day Open Day learn about SPR

4) IVIS Imaging System

The Team

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

Dr. Mahadeo Gorain, *Technician*

The *In Vivo* Imaging System (IVIS) facility is one of the high-end central facility of the NCCS. This instrument can perform the Bioluminescent and Fluorescent Imaging of cells as well as whole small animal under in-vitro and in-vivo conditions. Since its installation at NCCS, the IVIS has been used by many researchers at NCCS and collaborators in different research institutes within country. They are using bioluminescence as well as fluorescence imaging in different strains of mice as well as for in-vitro studies. The instrument has been used for bioluminescence imaging of various tumors at primary sites as well as to determine the metastatic potential. The IVIS is also used to examine the tumor localization and bio-distribution of nanomaterials in conjugation or encapsulation of drugs by *in vivo* and *ex vivo* imaging.

The IVIS can perform bioluminescence and fluorescence imaging in living animals via novel in-vivo biophotonic imaging for real-time display 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 consist of a custom lens with 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. It has an integrated fluorescence system and 24-position emission filter wheel that enables easy switching between fluorescent and bioluminescent spectral imaging. Further, 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. Moreover, this camera system can quantitate the 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. A customized Living Image 3.0 software allows efficient image capturing and multi-optional image analysis such as signal quantification and spectral mapping etc as per the requirement.

Standard filter sets for IVIS Imaging System

Fluorescence Filters

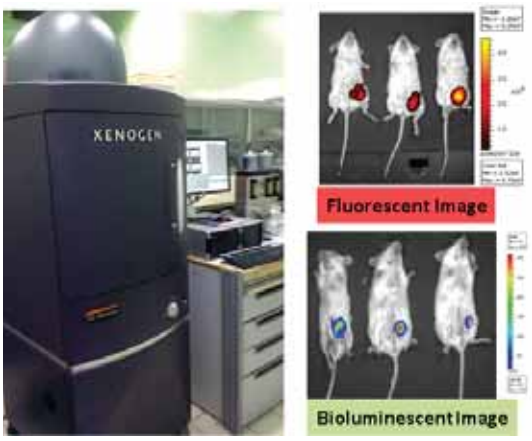
Set	Name	Excitation (nm)	Emission (nm)
1	GFP	445-490	515-575
2	DsRed	500-555	575-650
3	Cy5.5	615-665	695-770
4	ICG	710-760	810-875

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 *in vivo* imaging system

5) Central Sterilization Facility

The Team

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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 Resources (NCMR)

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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 Microorganisms 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 ofour 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

NCMR has made huge strides in the identification and value addition of its existing collection of isolates from the microbial bioprospecting project. The collection represents ~250 microbial taxa harboring an array of activities of human, industrial, environmental and ecological importance. Of these, *Acinetobacter, Aeromonas, Arthrobacter, Bacillus, Burkholderia, Enterobacter, Klebsiella, Ochrobactrum, Pseudomonas and Stenotrophomonas* represent the

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10 most abundant taxa with numerous applications known so far (Fig. 1). Additionally, through in-house screening for various bioactive compounds and enzymes, more than 1000 fungal cultures have been screened for production enzymes, such as laccase, cellulase, amylase and pectinase. Of these, 380 isolates have been found positive for these enzymes (laccase= 200; cellulose= 40; amylase= 90; pectinase= 50).

Over the last year, NCMR has enriched its collection by over 6000 microbial cultures. These include ~3000 cultures received as general deposits, 2747 isolates from marine environment, over 150 cultures from Wildlife Sanctuaries, 67 isolates from the Lonar crater lake, 15 isolates from industrial leachates, 14 *Clostridium spp.* from food waste, 24 anoxygenic phototrophic bacteria and another 14 anaerobic bacteria from the human gut. Further, NCMR has added another.

NCMR was accorded the responsibility to function as "Bio-repository for resistant microbes/infective agents (Bacteria and Fungi)" and to carry out collection, storage, maintenance, preservation and characterization of these microbes across the country. NCMR has established a central AMR Repository and has signed MOU's under the KARSNET (Kerala AMR Surveillance Network) and MAHASAR (Maharashtra State Antimicrobial Resistance). NCMR has so far received 75 isolates as Deposits and two AMR/MDR isolates for Genome sequencing and has generated 400 AMR isolates under various surveillance projects at NCMR-NCCS.

NCMR has established two new facilities, genome sequencing and SEM facility. Whole-genome sequencing of two of the first phytoplasma genomes from India have already been completed. The new SEM facility has processed 39 bacterial and fungal samples so far.

In terms of human resource, NCMR organized IAM-2019, an International Conference of the Indian Association of Mycoplasmatologists, which was attended by 86 participants, including 6 international speakers, 18 national speakers and 8 resource persons. The conference was sandwiched between two hands-on workshops on the cultivation of mycoplasma (attended by 32 participants) and phytoplasma detection and taxonomy (attended by 24 participants).

Over the last year, 44 peer-reviewed publications have been published by NCMR. Of these, seven were novel taxa descriptions. While two novel bacteria were named after Dr. Tapan Chakrabarti as *Nitrincola tapanii* MCC 2863^T and *Chakrabartia godavariana* MCC 3406^T honouring his contributions to microbial taxonomy research in India, four novel fungi were named as *Naganishia indica* RNF072^T, *Leucosporidium himalayensis* MCC 1733^T (Fig. 2), Coniochaeta dendrobiicola MCC 1811^T and *Aureobasidium tremulum* MCC 1683^T.

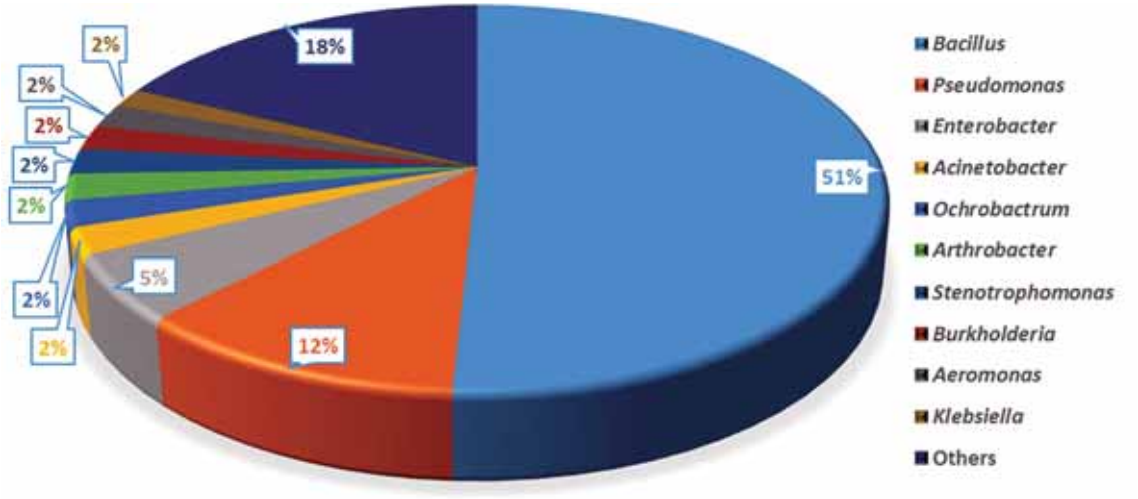


Fig. 1: Ten most abundant microbial taxa preserved and available at NCMR for further exploitation. The Others pie (18%) comprises of ~240 taxa in NCMR's collection, each with <1.5% relative abundance. Percentage abundance for each of the pies are round off to the nearest integer.

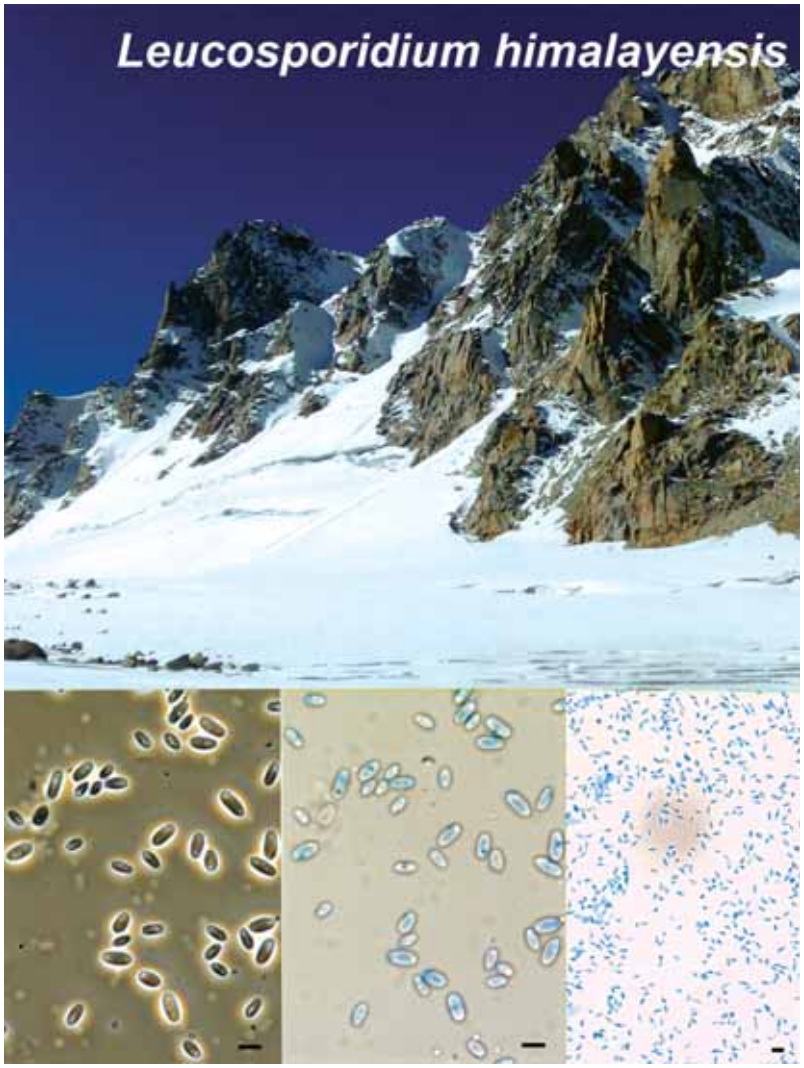
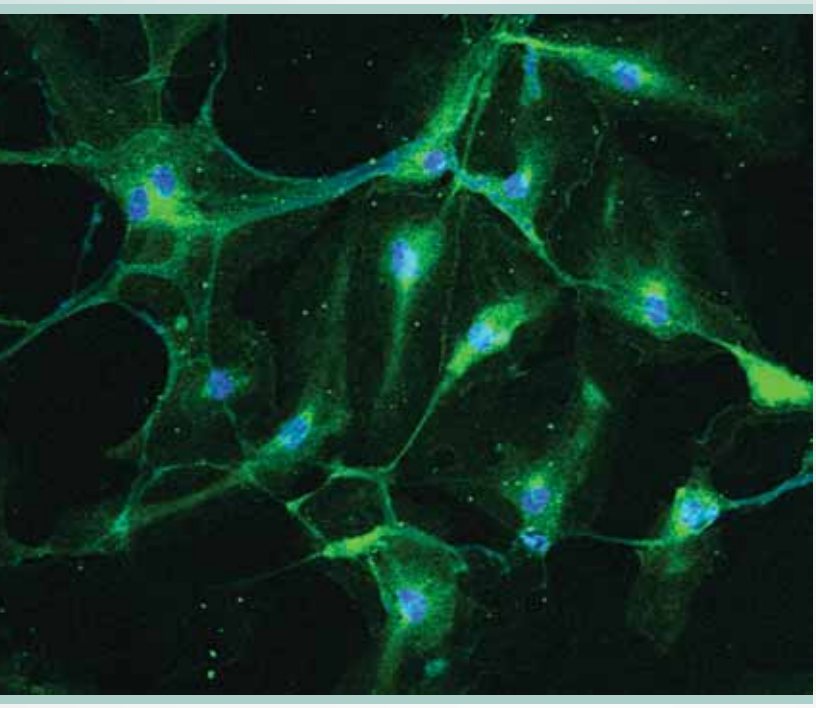


Fig. 2: Cells of *Leucosporidium himalayensis* at 100× under phase contrast and light (CMA after 10 d); yeast cells at 40× (SDA after 15 d). Scale bars = 5μm.



Other Information

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Review Articles

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6. Puri D, Subramanyam D. Stress - (self) eating: Epigenetic regulation of autophagy in response to psychological stress. FEBS Journal 2019; 286. 2447-2460. Review.
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Risk, Progression, Treatment, and Mortality. Cancers, 19 September 2019, 11(9), 1402. Review

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11. Varankar SS, Bapat SA. Uncoupling Traditional Functionalities of Metastasis: The Parting of Ways with Real-Time Assays. Journal of Clinical Medicine 2019 Jun 28;8(7). pii:E941. Review.
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Books / Book Chapters / Editorials

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2. Ingale P, Kabra R, Singh S. Structural sequence evolution and computationalmodeling approaches of the complement system in leishmaniasis (Chapter 10). Advances in Protein Chemistry and Structural Biology. Springer vol. 120: pg. 409-424. 2020.
3. Kalra RS, Bapat SA. Proteomics to Predict Loss of RXR-? During Progression of Epithelial Ovarian Cancer. Retinoid and Rexinoid Signaling Methods in Molecular Biology book series (MIMB, volume 2019) Springer pp 1-14. 30 July 2019.
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5. Ramteke P., Athavale D., Bhat M.K. (2019) Chapter 10-Dysregulated Signaling Pathways in Cancer: Approaches and Applications. In: Bose K., Chaudhari P. (eds) Unravelling Cancer Signaling Pathways: A Multidisciplinary Approach. Springer-Nature, Singapore. 2019 255-269.
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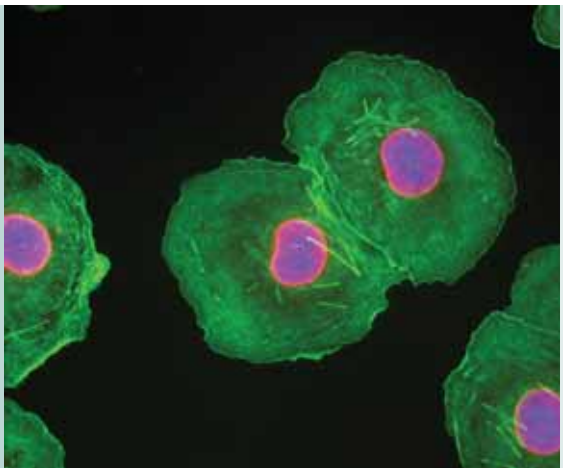
12. Pawar H, Sathe G, Patole MS. Genome-Wide Proteomics and Phosphoproteomics Analysis of *Leishmania* spp. During Differentiation. Trypanosomatids pp 161-176. Methods in Molecular Biology book series (MIMB, volume 2116). Protocol First Online: 28 March 2020
13. Prakash, O., Mahabare, K., Yadav, K.K., Sharma R. Fungi from Extreme Environments: A Potential Source of Laccases Group of Extremozymes In Fungi in Extreme Environments: Ecological Role and Biotechnological Significance, July 2019, pp 441-462. Springer.
14. Rahi P, Vaishampayan P. MALDI-TOF MS Application in Microbial Ecology Studies. Frontier Microbiology: System Microbiology 2020 Jan 10;10:2954. Editorial.
15. Thombre R, Jangid K, Shukla R, Dutta NK. Alternative Therapeutics Against Antimicrobial-Resistant Pathogens. Frontiers in Microbiology. 2019 Sep; 19;10:2173. Editorial

Patent Applications Filed / Granted

Sr.No.	Title	Inventors	Applicant	PCT/ Country	Patent No. (Filed)	Date of Filing / Grant
1	DAF-MCP chimeric protein, process to manufacture the same and use of the chimeric protein for treating pathological conditions involving the complement system	Sahu Arvind; Ojha Hina; Ghosh Payel; Barage Sagar H; Panwar Hemendra Singh	NCCS	India	201921014960	13.04.2019 (Filed)
2	A novel anti-cancer combination	Athavale Dipti Anil; Bhat Manoj Kumar	NCCS	India	201821039548	18.04.2019 (Filed)
3	A novel method for detection of cancer	Kundu Gopal C; Weber Georg F	NCCS	India	201821040459	26.04.2019 (Filed)
4	A nanohybrid, its method of preparation and use	Kundu; Sumit Das; GC. Amit Yadav; Mahadeo Gorain; Rohit Srivastava; Rajendra Prasad; Janahvi Devrukhar; Barkha Singh; Deepak Singh Chauhan	NCCS & IIT (Bombay)	India	201921020693	24.05.2019 (Filed)
5	Novel Peptides, Combination for Its Use in Leishmaniasis	Dr. Shailza Singh	NCCS	India	201921043619	26.10.2019 (Filed)
6	Novel Quinolizin based Leishmanial Compounds	Dr. Shailza Singh; Nutan Chauhan	NCCS	India	201921054193	27.12.2019 (Filed)
7	A tumor deconstruction platform for the analysis of intra -tumor heterogeneity	Bapat, Sharmila. A; Naik, Rutika. R	NCCS	United States of America	10429393	01.10.2019 (Granted)



Awards / Honours

Awards / Honours - NCCS Faculty

Sharmila Bapat

- Short Term ICMR-DHR International Fellowship for Senior Indian Biomedical Scientists 2019-20, availed from 2nd December, 2019 - 14th February, 2020 at the Institute for Systems Genetics, NYU School of Medicine, New York, USA.

Manoj Kumar Bhat

- Fellowship Scrutiny Committee, NASI, Allahabad (2019 onwards).
- Member, Animal Sciences & Biotechnology RC, CSIR, New Delhi (2019 onwards).

Radha Chauhan

- A research article published by Dr. Radha Chauhan and her team in Protein Science (Chopra et al, 2018) was among the top 10% of the most downloaded papers. In recognition of the immediate impact generated by this research, each author of the paper was awarded with a certificate of achievement by the journal publishers.

Jomon Joseph

- Elected as a 'Member of Guha Research Conference' in 2019.
- Selected member, Molecular Immunology Forum

Janesh Kumar

- Dr. Janesh Kumar was selected to be on the Editorial Boards of the following journals:
  - Communications Biology (Nature) - Editorial Board
  - Plos One- Editorial Board
  - Scientific reports -Editorial Board
  - FEBS OpenBio- Advisory Editorial Board

Gopal C. Kundu

- On the Editorial Board of -

- Molecular Cancer (Associate Editor) (IF 15.3)
- Journal of Cancer Metastasis & Treatment (Associate Editor)
- American Journal of Cancer Research (Senior Editor)
- Current Molecular Medicine (Editorial Board Member)
- Molecular Medicine Reports (Editorial Board Member)
- Current Chemical Biology (Editorial Board Member)
- World Academy of Sciences Journal (Editorial Board Member)
- International Journal of Oncology (Editorial Academy Member)

Girdhari Lal

- SwarnaJayanti Fellowship, from Department of Science and Technology, Ministry of Science and Technology, Government of India.
- 17th International Congress of Immunology (IUIS 2019) travel grant by American Association of Immunologists (AAI), USA.

Nibedita Lenka

- Chairperson, Institutional Ethical Committee and Member, IC-SCR, OCT Therapies & Research Pvt. Ltd. Mumbai.
- Keynote Speaker and Session Chair, International Conference on Recent Advances in Biotechnology and Biochemistry (ICRABB), NIT, Raipur, Jan. 8-9, 2020.

Srikanth Rapole

- Awarded the 'Eminent Mass Spectrometrist Award' by the Indian Society for Mass Spectrometry. 29 November, 2019

- General Secretary, Proteomics society of India (PSI)
- Member, Human proteome organization (HUPO)
- Editorial board member, Journal of Proteins and Proteomics

Mohan Wani

- Elected as Fellow of the Indian National Science Academy (INSA), 2020.
- Advisor, National Academy of Sciences (NASI), Pune Chapter, 2019-2021.

Awards / Honours - Postdoctoral and other Scientists, Students & Technical Staff

- Manoj K. Bhat's group
  - **Shyamananda Singh Mayengbam:** Received the following awards for presenting a poster at NCRI Cancer Conference, 03-05 November, 2019, Glasgow, UK -
  - National Cancer Research Institute (NCRI) Future of Research Bursaries Award
  - Centre for Co-operation in Science and Technology among Developing Societies (CCSTDS)" travel fellowship.
  - CSIR Foreign Travel Grant 2019
  - **Bhavana Deshmukh:** Best poster presenter award; Mumbai Healthcare Summit, 20-21 November, 2019, Mumbai, India.
- Samit Chattopadhyay's group
  - **Arpankumar Choksi:** 1st Prize in Poster presentation in 5th International Conference on Translational Research: Recent Trends in Pre-translational to Translational Research, 07-09 November 2019, Pune, India.
- Radha Chauhan's group
  - **Bhawna Burdak:** 3rd poster award; 5th International Conference on Translational Research: Recent trends in pre-transational research, 07-09 November 2019, Pune, India.
- Gaurav Das's group
  - **Madhav Sridharan:** Won a 'best poster' prize at the Asia Pacific Drosophila Research Conference (APDRC5), 06-10 January, 2020, Pune, India.
  - **Rusha Chakraborty:** Won a best poster prize at the "Signals from the Gut" mini symposium, 05, 06 January, 2020; NCCS, Pune, India.
- Jomon Joseph's group
  - **Poulomi Banerjee:** Travel grant from DBT to attend the ASCB:EMBO meeting, 7-11 Dec, 2019, Washington DC, USA.
  - **Indrasen Magre:** First author of the paper published in the Journal of Cell Science (17 June 2019) and recent

NCCS alumnus, was interviewed by JCS for their 'First Person' series. An image from this paper was also selected for the cover page of this issue of the journal.

- M. V. Krishnasastry's group
  - Ambati Raju: CSIR international travel grant to participate in the Keystone Symposium, Tuberculosis: Immunity and Immune Evasions, 16 - 20 January 2020, Santa Fe, New Mexico, USA.
- Janesh Kumar's group
  - **Rajesh Vinnakota:** The European Molecular Biology Organization (EMBO) short-term fellowship for working in The Netherlands for 3 months (July-September 2019).
  - **Ananth P. Burada:** The IFSM Students / Young Researchers Contest (IFSM-YRC) award at the 12th Asia Pacific Microscopy Conference, 3 - 7 Feb, 2020, Hyderabad, India.
- Srikanth Rapole's group
  - **Bhargab Kalita:** Won the travel award to pesented a poster at the 11th Annual Meeting of Proteomics Society, India (PSI) & International Conference on "Proteomics for System Integrated Bio-Omics, One Health and Food Safety" organised by NDRI, December 2-4, 2019 at Karnal.
- Manas Kumar Santra's group
  - **Tanisha Sharma:** First Prize for Poster Presentation, 'International Conference on Disease Biology: Diagnostics and Therapeutics', 4-6 March, 2020, S. P. Pune University, Pune, India.
  - **Tanisha Sharma:** Prize for best poster at the "7th international conference on molecular signalling, 23-25 January 2019, S. P. Pune University, Pune, India.
- Vasudevan Seshadri's group
  - **Shehnaz Bano:** Travel fellowship from the DBT to attend the Keystone Symposium on 'Diabetes: Glucose Control & Beyond', 27 - 31 January, 2020, Santa Fe, USA.
  - **Pranita Borkar:** Travel fellowship from the DBT to attend the EMBO Workshop: Protein Synthesis and Translational Control, Sep 2019, EMBL Heidlberg, Germany.
- Yogesh Shouche's group
  - **Rahul Bodkhe:** Young Investigator Award (1st runner up), 10th India Probiotic Symposium, 29 Feb - 01 Mar, 2020, New Delhi, India.
  - **Abhijit Kulkarni:** EMBO Travel Grant for attending the India-EMBO Symposium on Human Microbiome at the National Institute of Biomedical Genomics (NIBMG), Kalyani, India.

- **Om Prakash (Project Scientist at the NCCS CoE:** NCMR): Elected Chair of Subcommittee of Methanogenic Archaea of the International Committee on Systematics of Prokaryotes (ICSP).
- **Dr. Avinash Sharma:** Was selected for and participated as a member of the 38th Indian Scientific Expedition to Antarctica, to carry out studies to 'Understand novel anti-freezing proteins and lipid synthesis mechanisms of previously unknown, psychrophilic prokaryotes from extreme environment'.

Dr. Sharma collecting samples from Antarctica

- Shailza Singh's group
  - **Ritika Kabra:** Second Prize for Oral Paper Presentation at the 'International Conference on Disease Biology: Diagnostics and Therapeutics'; 4-6 March, 2020, Dept. of Biotechnology, S.P. Pune University, Pune, India.
  - **Prajakta Nimsarkar:** Third Prize for Poster Presentation at the 'International Conference on Disease Biology: Diagnostics and Therapeutics'; 4-6 March, 2020, Dept. of Biotechnology, S.P. Pune University, Pune, India.

- Sandhya Sitaswad's group
  - Rohini Dhat: Prof. C.C. Kartha Award for oral presentation, the International Conference on Cardiovascular Sciences, 21-23 Feb, 2020, New Delhi, India.

  - Megharani Mahajan: Best Poster Award at the International Conference on 'Role and Management of Oxidative Stress in Human Disease', 12-15 Feb, 2020, Mumbai, India.
- Deepa Subramanyam's group
  - Deepika Puri (DST Inspire Fellow): CSIR travel award received to attend EMBL Course: Chromatin Signatures During Differentiation: Integrated Omics. 02-06 September, 2019, held at EMBL, Heidelberg, Germany.
- Vidisha Tripathi's group
  - **Sonali Jathar:** DBT Indo-US GETin Fellowship (20 March - 10 Sept 2019), to work at the Medical University of South Carolina, USA.

- Alumni

  - **Rohan Kulkarni (NCCS alumnus from Dr. Vaijayanti Kale's group):** The 2019 STEM CELLS Young Investigator Award (YIA), for the groundbreaking work published in the March 2018 issue of Stem Cells. This work was led by Dr. Kale, and Dr. Rohan carried out this work under her guidance at NCCS.

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 Extension 14.03.2020	26.02.2020	Nil	DST	India
2	Dr. Sharmila A. Bapat	Development of a predictive algorithm for precision medicine in ovarian Cancer.	07.07.2017	06.07.2020	Nil	DBT	India
3	Dr. Bhaskar Saha	INLEISH: Immunometabolic Networks in the Regulation of Visceral Leishmaniasis.	26.05.2017	25.05.2020 Extension 25.11.2020	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
4	Dr. Bhaskar Saha	JC BOSE Fellowship	06.08.2018	05.08.2023	Nil	DST	India
5	Bhaskar Saha	Mode of CD40 clustering dictates its functional duality.	23.06.2017	22.06.2020 Extension 23.12.2020	Dr. Christoph G. Baumann, Dept. of Biology, University of York, UK	DST INT/UK	India
6	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
7	Dr. Gaurav Das	Neurobiology of food choice driven by nutrient specific memories and diet.	13.02.2018	12.02.2023	Nil	DST	India
8	Dr. Lalita Limaye	Identification of aging-induced epigenetic changes causing hematopoietic stem cell dysfunction: Rescue using in vitro niche (IVN) - technology.	09.02.2017	08.02.2020 Extension 08.05.2020	Nil	DBT	India
9	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 Bioinformatics, Bangalore; Dr. Partha P. Majumdar, National Inst. of Biomedical Genomics, WB; Dr. Shona Nag, Jehangir Clinical Development Centre, Pune	DBT	India
10	Dr. Girdhari Lal	Understanding the anti-tumor activity of natural killer (NK) & improving its adoptive cellular therapy potential to control tumor growth.	25.06.2018	24.06.2021	Nil	DST	India

11	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
12.	Dr. Girdhari Lal	Role of Gamma-delta Tcells in the generation and maintenance of transplantation tolerance	19.12.2016	18.12.2019	Nil	DBT	India
13	Dr. Lalita Limaye	Molecular analyses of extra-cellular vesicles isolated from bone marrow-derived mesenchymal stromal cells treated 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
14	Dr. Shekhar Mande	Centre of Excellence 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
15	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
16	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
17	Dr. Debashis Mitra	Centre of Excellence in Biomolecular Structure and Function on Host-Pathogens Interactions (Cellular Stress Proteins in HIV Infection: Biochemical and Functional Characterization).	28.12.2016	27.12.2021	Nil	DBT	India
18	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 Extension 31.03.2020	Dr. Supriya Sarkar, Head, Environmental Research, Tata Steel Limited	Tata Steel Limited	India
19	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
20	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

21	Dr. Sandhya Sitaswad	Therapeutic implication in ratio resistance mechanism of breast cancer stem cells (BCSC).	05.07.2018	4.7.2019 Extension 31.04.20200	Nil	DAE	India
22	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 Extension 26.06.2020	Nil	DST	India
23	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 Bioenginee-ring & Technology, Gauhati University.	DBT	India
24	Dr. Shailza Singh	Understanding the mechanism of ABC-type metal sequestering proteins: structure-based novel drug development against human pathogens.	20.01.2017	19.01.2020 Extension 19.07.2020	Dr. Shankar Prasad Kanaujia & Dr. Vikash Dubey, Dept. of Biosciences & Bioengineering, IIT, Guwahati, Assam	DBT (Twinning programme for the NE)	India
25	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
26	Dr. Anjali Shiras	Developing bank of human induced pluripotent stem cell for drug screening. Disease modelling and understanding disease biology.	26.05.2017	25.05.2020 Extension 25.11.2020	Nil	DST	India
27	Dr. Anjali Shiras	Altered microRNA and its targets in Giloblastoma cell lines	01.01.2016	31.12.2018 Extension 30.6.2019	Dr. Ravi Sirdeshmukh, Institute of Bioinformatics, Bengaluru	DBT	India
28	Dr. Anjali Shiras	Developing bank of human induced pluripotent stem cell for drug screening. Disease modelling and understanding disease biology.	26.05.2017	25.05.2020		DBT	India
29	Dr. Anjali Shiras	Derivation of functional hepatocytes from human induced pluripotent stem cells.	01.03.2017	28.02.2020	Nil	ICMR	India

30	Dr. Anjali Shiras	Investigating the role of RNA binding proteins in pluripotency & differentiation of induced pluripotent stem cell.	21.06.2017	20.05.2020	Nil	DBT	India
31	Dr. Yogesh Shouche	To set up Maharashtra Gene Bank in Maharashtra State.	02.01.2014	01.01.2020 Extension	Dr. Milind Watve, IISER, Pune	RGSTC	India
32	Dr. Yogesh Shouche	Establishment of Center of Excellence for "National Center for Microbial Resource (NCMR)".	30.03.2017	29.03.2020 Extension 30.9.2020	Nil	DBT	India
33	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
34	Dr. Srikant 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, University of Rostock, Germany; Dr Jose Sousa Camara, Chemistry Dept. University of Madeira; Dr.H.A. Nagarajaram CDFD, Hyderabad	DST	India
35	Dr. Vidisha Tripathi	Investing the role of long noncoding RNAs in mammalian gene expression regulation.	01.04.2015	31.03.2020	Nil	DBT	India
36	Dr. Vidisha Tripathi	Understanding the role of mammalian long noncoding RNAs [lnc RNAs] in regulating cellular quiescence''.	08.08.2016	08.08.2019	Nil	DST	India
37	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
38	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
39	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
40	Dr. Yogesh Shouche	Development of efficient and low cost biotechnology for colour removal of biomethanated spentwash from distillery.	22.06.2017	21.06.2020	Nil	DBT	India
41	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

42	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 Program-me)	India
43	Dr. Manas Santra	Development of Novel Inhibitors of AKT: An Unorthodox approach Targeting the pleckstrin homology Domain.	12.01.2017	11.01.2020	Dr. Debasis Manna, Department of Chemistry, IIT, Guwahati	DBT	India
44	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 Extension 08.05.2020	Nil	DBT	India
45	Dr. Manoj K. Bhat	Scaling up of proprietary lab scale Fenugreek seed extract production for management of obesity.	22.03.2019	21.09.2020	Dr. Ankur Kumar, Basic Ayurveda Ltd.	BIRAC	India
46	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
47	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
48	Dr. Yogesh Shouche	Understanding the transmission of antibiotic resistance between hospitals and environment.	25.01.2019	24.07.2020	Nil	BIRAC	India
49	Dr. Jomon Joseph	Characterization of acute necrotizing encephalopathy 1(AEN-1) - associated mutations in Nup358.	07.03.2019	06.03.2022	Nil	DBT	India
50	Dr. Arvind Sahu	Role of anaphlyotoxins C3a, C4a and C5a generated intracellularly in the infection locale in providing protection against viral infection.	12.03.2019	11.03.2022	Nil	DBT	India
51	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
52	Dr. Girdhari Lal	To Evaluate the effect of Yakult on the immune system of late middle-aged Indian adults	27.04.2019	26.06.2020	Dr. Ashish Bavdekar, Department of Pediatrics, KEM Hospital, Pune; Dr. Anand Kawade,	NCCS	India

					Pediatric Research, KEMHRC-VADU; Dr. Sanjay Juvekar, Officer Incharge VADU-KEMHRC		
53	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
54	Dr. Deepa Subramanyam	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
55	Dr. Gopal C. Kundu	Chitosan nanoparticle mediated Andrographolide and / or Raloxifene delivery in Breast Cancer and its Implications in Multi-targeted Therapy	14.01.2016	13.01.2019	Nil	DBT	India
56	Dr. Gopal C. Kundu	Translational Development of Protein nanomedicine and multifunctional hydroxyapatite nano-contrast agent	18.03.2016	17.03.2019 Extension 18.09.2020	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
57	Dr. Shailza Singh	Molecular Motors as Nano circuits in Leishmaniasis: System cues guiding Synthetic Biology Device Construction.	18.05.2016	17.05.2019	Nil	DBT	India
58	Dr. Jomon Joseph	Role of Nup358 in the regulation of cytoplasmic mRNP granules.	12.01.2016	11.01.2019	Nil	DST	India
59	Dr. Deepa Subramanyam	The role of endocytosis 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
60	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
61	Dr. Samit Chattopadhyay	Metabolic stress induced epigenetic changes in the transcriptional regulator gene SMAR1	2017	31.12.2020	Nil	DBT	India
62	Dr. J. Singh	Understanding the role of RNAi - mediated antiviral host defense against DNA Viruses.	01.01.2018	31.12.2023	Nil	Wellcome Trust/ DBT	India

63	Dr. S.C. Mande	Structural perspective of molecular interactions in pathogenicity: Role of regulatory proteins of HIV-1 and heat shock proteins of M. Tuberculosis	28.12.2016	27.12.2020	Dr. Sharmishta Banerjee, Dept. Of Biochemistry, University of Hyderabad, Hyderabad.	DBT	India
64	Dr. Z. Kamal	Decoding organism related evolution of surviving, a hub protein.	01.07.2015	30.06.2020 Extension 30.06.2021		Wellcome Trust/DBT	India
65	Dr. Punam Nagvenkar	Establishment of GMP-compliant national repository for banking, safe deposit and supply of characterized mammalian cells for us in biopharma.	01.10.2019	30.09.2023	Nil	BIRAC	India
66	Dr. Yogesh Shouche	Study on distribution, function and genomic reconstruction of deep-subsurface abundant & rare microbial communities in different depth of the rock (Basalt-granite zone) at koyan-Waran region	05.02.2020	04.02.2022	Nil	Min. of Earth Sciences	India
67	Dr. Manoj Kumar Bhat, Dr.Yogesh Shouche	Human Microbiome Initiative of Select Endogamous Populations of India.	09.03.2020	08.03.2022	Dr. Girish Shreekrishna Tillu, AYUSH-COE SPPU, Pune. Prof. Shaunk Kulkarni, Dept. Of Anthropology, SPPU, Pune. Prof. Balakrihsnan S Ramakrishna, SRM Institutes for Medical Science, Chennai Dr. Sarangthem Indira Devi, Institute of Bioresources And Sustainable Development, Imphal, Manipur. Dr. Subrahmanya Kumar Institute of Trans Disciplinary Health Sciences and Technology, Bangalore. Dr. Sanjay Kamlakar Juvekar KEM Hospital and Research Centre, Pune. Prof. Govind K Makharia AIIMS, New Delhi, Prof. Vineet Ahuja, AIIMS, New Delhi. Dr. Anand Krishnan AIIMS, New Delhi. Dr. Amit Kumar Rai, Institute of Bioresources and sustainable	DBT	India

					development (IBSD) Regional Centre for IBSD (RCIBSD), Gangtok, Sikkim Mr. Shantanu Ozarkar, Dept.of Anthropology, SPPU, Pune. Mr. John Mechenro, SRM Intitututes for Medical Science, Chennai.		
68	Dr. Vidisha Tripathi	Deciphering the role of long noncoding RNAs (lncRNAs) in mediating replication stress response during cell division.	21.02.2020	20.02.2023	Nil	SERB	India
69	Dr. Arvind Sahu	Generation of neutralising human monoclonal antibodies against the SARS-CoV2 virus as a therapeutic strategy to contain the COVID -19 pandemic	29.05.2020	28.05.2021	Dr. D.N. Nayak, IIT, Indore Dr. Krishna Ella, Bharat Biotech International Ltd. Hyderabad, Dr. Kanury V S Rao, PredOmix Technologies Pvt. Ltd., Gurugram, Hariyana	CSIR	India
70	Dr. Sharmila Bapat	Proteogenomics based identification and characterization of a novel ITGB8 isoform in ovarian cancer and elucidation of its functional relevance	27.03.2020	27.03.2023	Nil	SERB	India
71	Dr. Akanksha Chaturvedi	Elucidating the role for toll-like preceptor 9 mediated extra cellular vesicle release from B cells.	26.03.2020	25.03.2023	Nil	SERB	India
72	Dr. Gaurav Das	The neurophysiological pathways of emesis in drosophila melanogaster.	09.06.2020	08.06.2023	Nil	SERB	India

Major Projects

Manav - Human Atlas Initiative:

This 3-year project encompasses to develop a software of portal of a comprehensive human map Atlas that can provide subcellular to organism level analysis and visualization based on available biological knowledge. A community of users and contributors would be developed for this initiative. The students contributing to this initiative will get exposure to diverse research articles and various cutting-edge technologies such as big data, analytics and machine learning. This will also provide an opportunity for students to understand various research methodologies, techniques and validation processes. This would help them to upskills and offer a better trained manpower to the nation.

Indian Human Microbiome Initiative:

Considering the fact that India has diverse biogeography and diet, it is expected that different populations in the country will have a different gut microbiome. Understanding this variation is important for the success of future microbiome-based therapies. The proposed project anticipates the assessment of microbial communities of the people of India and its association with ethnic, socio-economic and dietary habits of Indians. It will be using pan-India interdisciplinary approach to characterize gut microbiota of Indian population. We have selected 17 endogamous/tribal communities encompassing west, south, east, north and north east regions and who have maintained their traditional dietary patterns. The stool, urine and oral samples will be collected from the subjects. Communities will. This sampling scheme will provide us with an excellent opportunity to conduct several smaller analyses to explain microbiome patterning and to device future translational strategies based on microbiome therapy. The project has a duration of 2 years.

Establishment of GMP-compliant National Repository for banking, safe deposit and supply of characterized mammalian cells for use in biopharma

The ease of access to well-characterized, high quality and validated cell lines is one of the requirements for development of robust biopharma industry. The need for a National repository providing services similar to those offered by leading international repositories using global benchmarks in GMP is a need always articulated by the biopharma industry in the country. Further, the industry has a strong need for having a 'safe deposit' service for safe storage for their production and other proprietary cell lines under GMP conditions which they currently keep at international repositories paying exorbitant fees. In line with the demand, in this project, we intend to set up a GMP compliant wing in NCCS repository which would be best in class in world with respect to acquisition, characterisation, maintenance and supply of cell cultures through robust systems and processes audited and certified by international agencies. Moreover, the GMP-compliant cell bank would also provide the service of safe storage of cell lines under GMP conditions to Indian firms.

Research Fellows awarded with Ph. D. Degrees

(01.04.2019 – 31.03.2020)

No.	Research Scholar	Title of the Thesis	Date of award of Ph.D.	Research Guide
1	Ms. Prajakta Shinde	In depth studies on dendritic cells derived from haematopoietic stem cells	18.04.2019	Dr. L. S. Limaye
2	Ms. Sophia Fernandes	Studies on generation of induced pluripotent stem cells from umbilical cord tissue derived adult stem cell.	18.04.2019	Dr. L. S. Limaye
3	Ms. Parul Dutta	Elucidating the molecular mechanism of regulation of cell cycle regulators by FBXO31	14.05.2019	Dr. M. K. Santra
4	Ms. Shilpi	Role of gamma-delta T cells in the generation and maintenance of transplantation tolerance	07.06.2019	Dr. G. Lal
5	Mr. Sagar Varankar	Transciptional mechanisms governing epithelial and mesenchymal properties in ovarian cancer	14.06.2019	Dr. S. A. Bapat
6	Mr. Hemendra Panwar	Development and Characterization of C3-convertase inhibitors	17.06.2019	Dr. A. Sahu
7	Mr. Yadavalli Narayana	Understanding the Role of endocytosis in the regulation of embryonic stem cell pluripotency	19.06.2019	Dr. D. Subramanyam
8	Mr. Pravin Dewangan	Structural and Functional Studies on Nup62 Sub-complex of Nuclear Pore Complex	28.06.2019	Dr. R. Chauhan
9	Ms. Neha Gupta	Understanding the Regulation of APC/C complex	17.07.2019	Dr. M. K. Santra
10	Ms. Dipti Athavale	Hepatocellular carcinoma and hypercholesterolemia: molecular link and relevance in anticancer drug response	26.07.2019	Dr. M. K. Bhat
11	Ms. Rucha Sarwade	Delineating the role of PABP and PDI in translational regulation of insulin and insulin like UTR containing mRNA	31.07.2019	Dr. V. Seshadri
12	Mr. Anil Kumar	Studies on regulation of interleukin-3 receptor expression in T helper cells	02.08.2019	Dr. M. R. Wani
13	Mr. Suhas Mhaske	Studies on the molecular mechanisms involved in regulation of bone remodeling by interleukin-3	22.08.2019	Dr. M. R. Wani
14	Mr. Yousuf Ansari	Structural and Functional Characterization of Mycobacterial GroELs	11.09.2019	Dr. S. C. Mande
15	Mr. Jay Trivedi	Studies on Identification and Characterization of Novel Bioactive Molecules Inhibiting HV-1 Repication By Targeting Cellular Factors	16.09.2019	Dr. D. Mitra
16	Mr. Amit Yadav	Studies on the effect of Cyclic RGD-Peptide-Nanoparticle Conjugated Drug(s) on Tumor Growth and Angiogenesis in Breast Cancer	03.10.2019	Dr. G. C. Kundu
17	Ms. Hina Ojha	In silico annotation of complement regulatory RCA proteins and their experimental validation	19.11.2019	Dr. A. Sahu

No.	Research Scholar	Title of the Thesis	Date of award of Ph.D.	Research Guide
18	Ms. Meenakshi Setia	Studies on a pair of long non-coding RNAs Ginir and Giniras in cellular growth and development	16.12.2019	Dr. A. S. Shiras
19	Ms. Jyoti Kumari	Structural and functional characterization of Neuropilin and taloid like (Neto) Proteins	18.12.2019	Dr. J. Kumar
20	Mr. Ashwani Kumar	Structural and functional characterization of redox sensing proteins in *Mycobacterium tuberculosis*.	18.12.2019	Dr. S. C. Mande
21	Mr. Sachin Meshram	Genome-wide SCF Ubiqutin Ligase Screen to Identify F-box Proteins in NF-κB Activation	26.02.2020	Dr. M. K. Santra
22	Ms. Kriti Chopra	In - silico prediction and validation of evolved residues of interacting necleoporins	06.03.2020	Dr. R. Chauhan

Teaching, Training and Outreach

Talks / lectures delivered & hands-on activities / training conducted by NCCS faculty

Scientist	Topic / Symposium	Class / Department	Institution	Date
Janesh Kumar	Careers in Science	Standards VIII to XII (200 students)	Vilkhe Patil Memorial School, Pune	
Gopal C Kundu	INSPIRE Talk	Standard XI	Trident Academy, Bhubaneswar	07 January, 2020
Girdhari Lal	Phenotypic and functional plasticity of Th17 and T regs in inflammation and autoimmunity	Post-Graduate students	Post-Graduate Institute of Medical Education and Research (PGIMR), Chandigarh	09 December, 2019
Nibedita Lenka	Recent Advances in Stem Cell Delivery for Therapeutics. Dr. Lenka was a Mentor at the ICAR sponsored Winter School on "Clinical Applications of Stem Cells in Animals"	Veterinary Faculty and M.V.Sc. Students	ICAR-IVRI, Izatnagar, Bareilly	04 & 05 November, 2019
	Recent Advances in Stem Cell Delivery for Therapeutics.	M.Sc. and Ph.D. (Biotech)	Utkal University, Bhubaneswar	30 December, 2019
	To be or not to be, the Deubiquitinase and Cell fate modulation.	B.Tech, M.Tech. and Ph.D. students	National Institure for Science Education and Research (NISER), Bhubaneswar	01 January, 2020
Amitabha Majumdar	A role of cellular translation regulation associated with toxic Huntingtin protein	Masters students	National Brain research center, Manesar	25 February, 2020
	A role of cellular translation regulation associated with toxic Huntingtin protein. (Workshop on Molecular Neurobiology: From Genes, Neurons to behavior in health and disease)	Masters students	RCB, Faridabad	26 February, 2020
	A role of cellular translation regulation associated with toxic Huntingtin protein (A Day of Life' annual research Meet)	Masters students	IISER Tirupati	07 March, 2020
Debashis Mitra	Genomics in Health and Disease	Undergraduate and postgraduate students from different colleges of Kolkata. (more than 100)	Maulana Azad College, Kolkata	13 February, 2020
	Genomics in Health and Disease	Undergraduate and postgraduate students (more than 50)	Vivekananda College, Kolkata	14 February, 2020
Ajay Pillai	Grants Writing, The Know How	Post graduate and PhD Students in Pharmaceutical Sciences	R.C Patel Institute of Pharmaceutical Education and Research, Dhule, Maharashtra	08 June 2019
	Art and Science of Grants writing	Post graduate and PhD Students in Pharmaceutical Sciences	Dayananda Sagar University, Bangalore	21 November 2019
	Strategies for Successful Academic Collaborations towards Drug Discovery	Faculty, PhD and Post graduates in Pharmaceutical Sciences	Ramaiah University of Applied Sciences, Bangalore	20-22 November, 2019
Kamlesh Jangid (Project scientist, NCCS CoE: NCMR)	The Fantastic World of Microbiology	Std. V to X	Sadhana English Medium School, Pune	13 August, 2019
	The Diversity and Benefits of Microorganisms YOU around	Std. V to X	Shardabai Pawar VidyaNiketan, Baramati	25 July, 2019

Scientist	Topic / Symposium	Class / Department	Institution	Date
Kamlesh Jangid	Advances in microbial cultivation Mahavidyalay, Baramati	MSc Microbiology 2020	Shardabai Pawar	15 February,
	The Role and Importance of Culture Collection Centres.	MSc Biotechnology	Symbiosis International University, Pune	15 October, 2019
	The Bergey's Manual: Introduction, History and Use.	MSc Microbiology	Modern College - Shivajinagar, Pune	27 August, 2019
	Responsible Science Communication.	MSc Microbiology	Fergusson College, Pune	31 July, 2019
	Soil microbial communities at the Lonar Crater, a Martian analog for astrobiology research.	MSc Microbiology	Shardabai Pawar Mahavidyalay, Baramati	25 July, 2019

Classes taught by NCCS scientists for the Ph.D. course work (2019)

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

Scientist	Topic / Module
Dr. Arunkarthick S.	Quantitative methods; Cell biology - Bioimaging
Dr. Bapat Sharmila	Principles of metastases; Cancer stem cells and cellular plasticity. Co-ordinated the coursework for the elective - Advances in Cancer Biology along with Dr. Anjali Shiras.
Dr. Bhat Manoj K.	Cancer Therapy
Dr. Chauhan Radha	Structural Biology (Course coordinator); Quantative methods (Instructor)
Dr. Das Gaurav	Science Communication
Dr. Joseph Jomon	Advanced cell biology; Molecular biology techniques; Scientific communication
Dr. Krishnasastry M.V.	History of science; Protein chemistry (practicals)
Dr. Janesh Kumar	Quantitiative Methods; Structural Biology; Membrane Proteins
Dr. Lal Girdhari	Transplantation immunology; Tumor immunology
Dr. Lenka Nibedita	Ethics in Research (Mammalian Cloning: Pros - Cons and Ethics)
Dr. Rapole Srikant	Proteomics basics and applications; Mass spectrometry instrumentation; Quantitative proteomics
Dr. Santra Manas Kumar	Molecular Biology; Cancer Biology
Dr. Seshadri Vasudevan	Molecular Biology; Translation and control; Quantitative PCR; Science Communication
Dr. Shiras Anjali	Co-ordinated the coursework for the elective - Advances in Cancer Biology along with Dr. Sharmila Bapat.
Dr. Singh Shailza	Applications of Computational Biology (theory & practicals)
Dr. Singhal Nishant	Pluripotency / Reprogramming
Dr. Subramanyam Deepa	Stem cell biology; Molecular biology; History of science; Science communication
Dr. Tripathi Vidisha	Noncoding RNAs - Introduction; In development and disease; In cancer

Other Talks delivered by NCCS Faculty

Sharmila Bapat

- Invited talk titled "Read through Chimeric Transcripts in Ovarian Cancer" in the one-day Symposium on Molecular Genetics and Cancer at the Department of MRDG, IISc, Bangalore on 19 July 2019.
- Invited talk titled "CSCs and phenotypic plasticity in metastasis" in the 2nd MVR CANCON 2019 at Kozhikode, Kerala, on 30th Aug - 1st September, 2019.
- Invited talk titled "A decade of association with TCGA ovarian cancer datasets" in the 1st TCGA India 2019 conference at IISER, Pune on 21-22 September, 2019.
- Invited talk titled "Modeling human high-grade serous ovarian cancer in immune compromised mouse models" in the 9th International conference of LASA India at IISER, Pune on 21-23 November, 2019.
- Invited talk titled "Chimeric transcripts and peptides - mediating complexity through diversity" in the 15th Indo-Australian Biotechnology Conference on Contemporary strategies for the prevention and management of disease in the 2020s at The University of Adelaide Medical School, Adelaide Health and Medical Sciences, Adelaide, South Australia, November 16 -18, 2019.
- Invited talk titled "Chimeric transcripts and peptides - mediating complexity through diversity" at the Institute for Systems Genetics, NYU School of Medicine, New York, USA on 10th February, 2020.

- Invited talk titled "Chimeric transcripts and peptides - mediating complexity through diversity" at the Institute of Bioinformatics and Biotechnology, SPPU, Pune on 7th March, 2020.
- Invited talk titled "The different shades of cancer metastases" at the National Chemical Laboratory, Pune on 9th March 2020.

Radha Chauhan

- Molecular organization of central transport channel Nup93 sub-complex of mammalian nuclear pore complex. Invited talk, Cold Spring Harbor Asia meeting titled Cross Scale Biological Structure: From Macromolecular Complexes and Organelles to Cells and Tissues; 2-6 September, 2019, Suzhou, China.
- 'Protein chemistry and Ramachandran plot', Invited talk, Department of Biotechnology, SP Pune University, Pune India; 14 September, 2019.

Gaurav Das

- "Of Flies and Food" Nutrition specific memories and diet mediated brain plasticity in Drosophila; Invited talk at the "Workshop on Molecular Neurobiology: From Genes, Neurons to behavior in health and disease", 24.02.2020; Faridabad, NCR , India.
- "The Food Fly" Nutrition specific memories and diet mediated brain plasticity in Drosophila; Invited talk for the "Neuro-interest" group, 11.03.2020; IISER Pune, Pune, India.

Jomon Joseph

- Invited Speaker: '10th RNA GROUP MEET, RGCB, Uday Samudra, Kovalam, Trivandrum, India, May 2-4, 2019.
- Invited Speaker: 'Annual retreat of Department of Biological Sciences, TIFR, Mumbai, 21-23 August, 2019.
- Invited speaker, Guha Research Conference (GRC), Fort Rajwada, Jaisalmer, Rajasthan, 6-10 December, 2019.

M. V. Krishnasastry

- Conducted six lectures on software development for project staff of the "Manav: Human Atlas Initiative"; 01 February - 05 March, 2020.

Janesh Kumar

- Talks delivered at the 7th International Conference on Molecular Signaling ICMS-2019 held between 23-25 Jan, 2019 and Organized by Dept. of Zoology, Savitribai Phule Pune University, Pune, National Centre for Cell Science, Pune & The Society for Molecular Signaling

Gopal C. Kundu

- Invited Talk, National Institute of Biomedical Genomics (NIBMG), Kalyani, 5-6th July, 2019
- Invited Talk, Hannover Medical Center, Hannover, Germany, 6th September, 2019
- Invited Talk, Indian Institute of Technology (IIT), Guwahati, 24th September, 2019
- Invited Talk, Carcinogenesis Conference, Ahmedabad, 27th September, 2019
- Invited Talk, National Conference on Nanomaterials in Biology, University of Rajasthan, 10-11th October, 2019
- Talk, Inno Indigo Meeting, Janakpuri Super Speciality Hospital, New Delhi, 25th October, 2019
- Inaugural Talk, 5th International Conference on Translational Research (ICTR), NCCS, Pune, 7-9th November, 2019
- Invited Talk, Cancer Conference, Institute of Life Science (ILS), Bhubaneswar, 30th November, 2019
- Invited Talk, Department of Biotechnology, Goa University, Goa, 10th February, 2020
- Talk as Guest of Honour, National Conference, Rama Devi University, Bhubaneswar, 27th February, 2020.
- Invited Talk at the National Conference, University of Kalyani, 7th March, 2020.

Girdhari Lal

- Discipline, education, and territorial restriction of immune cells in the tissues for a healthy body and function. International symposium on basic and advanced translational immunology (BATI-2020) at Central University of Kerala, Tejaswini Hills, Periya, Kasaragod. On 5-7th March, 2020.
- Intrinsic signalling of CCR6 and T cell receptor alters the gene expression and cellular metabolism of Th17 cells during gut inflammation (Meitei HT, Shirolkar A, Rapole S and Lal G). Mini-symposium titled 'Signals from the Gut' at National Centre for Cell Science, Pune on 5-6th January (Invited talk).

- Importance of gamma-delta T cells in transplantation tolerance. Indian Immunology Society conference 2019 (Immunocon2019) to be held on 14-16th November, 2019, at Mumbai. (Invited talk).
- Effect of peripheral inflammation on blood-brain barrier structure and function in neuronal autoimmunity. International Brain Research Organization-Asia Pacific Regional Committee (IBRO-APRC) school on theme "Blood-brain Barrier: from basic physiology to Neurological Disorders" organized by Panjab University, Chandigarh from 4-9th November, 2019. (Invited Talk).
- CAR-T cell therapy- Opportunities and Challenges. 3rd Annual Conference of Cochin Cancer Research Centre (Canquer 2019) held at 8-9th November 2019, at KINFRA Biotechnology Park, Kalamassery, Kochi. (Invited Keynote Talk).
- Plasticity of CD4 T cell subsets in inflammation and autoimmunity. Society of Inflammation Research conference 2019 (SIRCON 2019) held on 13th October, 2019 at Chennai. (Invited talk).
- Neuro-immune communication during inflammation and autoimmunity. National Symposium on Basic and Translational Research in Cancer Biology held on 11-12th September, 2019, at Institute of Advance Research, Koba Institutional Area, Gandhinagar, Gujarat. (Invited Talk).
- Basic Research Questions in Inflammatory Bowel Diseases. In National Alliance for Translational Research In Autoimmune Diseases' (NATRAD) held at IICB, Kolkata on 20-21st June 2019 (Invited talk).
- Cells, cytokines, autoantibodies in Autoimmunity: Evidence and how to utilize the current information in model building. Autoimmunity: In Silico modeling consortium. Organized by ChanRe Hospital and Research Centre, Bangalore on 27th April 2019 (Invited talk).
- Activation of natural killer T (NKT) cells alter the tumor microenvironment and reduces the growth of solid tumor. Carcinogenesis 2019 conference, 'Emerging Horizons in Oncology: Molecules to Therapeutics Global Perspectives and Challenges held on 27-29th September 2019 at Gujarat University, Ahmedabad (Invited Talk).

Nibedita Lenka

- Recent Advances in Stem Cell Delivery for Therapeutics. ICAR sponsored Winter School (Nov.1-21, 2020) on Clinical Application of Stem Cells in Animals, Indian Veteriray Research Institute (IVRI), Izatnagar, Bareilly, Nov. 4-5, 2019 (Invited Speaker).
- The Biology and Promising Potentials of Enigmatic Stem Cells: from Bench to Bedside. International Conference on Recent Advances in Biotechnology and Biochemistry (ICRABB), NIT, Raipur, Jan. 8-9, 2020 (Keynote Speaker; Session Chair).

Debashis Mitra

- Cellular stress proteins as potential targets and repurposing of drugs in the fight against HIV/AIDS, Invited talk, 107th Indian Science Congress, University of Agricultural Sciences, GKVK, Bangalore, India, 3-7th January, 2020.
- Heat Shock proteins in HIV infection and their potential use as targets in the fight against HIV/AIDS, Invited talk, International Conference on "Emerging Areas in Biosciences and Biomedical Technologies-2, Indian Institute of Technology, Indore, India, 7-9th February, 2020.

Punam Nagvenkar

- Invited Talk: National Cell Repository - An Overview, 5th International Conference on Translational Research: Recent Trends in Pre-translational to Translational Research, National Centre for Cell Science, Pune, India; 7-9 November, 2019.

Ajay Pillai

- Managing Research Projects & Human Resource for the betterment of Science "Excellence on Leadership" - talk delivered for CSIR Directors at the CSIR-HRDC, Ghaziabad, 30-31 August 2019.

Srikanth Rapole

- 'Metabolomic profiling to investigate metabolic alterations in invasive ductal carcinoma of the breast', Invited talk at Symposium on Advances in Biomedical Mass Spectrometry organized by Saha Institute of Nuclear Physics, November 13-14, 2019 at Kolkata.
- 'Proteomics and functional study reveal MZB1 and XPO1 as potential targets for Multiple myeloma', Invited talk at 11th Annual Meeting of Proteomics Society, India (PSI) & International Conference on "Proteomics for System Integrated Bio-Omics, One Health and Food Safety" organised by NDRI, December 2-4, 2019 at Karnal.
- 'Mass Spectrometry based Quantitative Proteomics and Its Applications', Plenary talk at Skill development program on Mass Spectrometry based Proteomics organized by National Chemical Laboratory, December 9-20, 2019 at Pune.
- 'Mass Spectrometry for the Clinical Applications', Invited talk at Big Data & Precision Medicine organized by IIT-Bombay, March 3-7, Mumbai.

Arvind Sahu

- Invited talk: 'Self-nonself discrimination by the complement system - mechanistic insights' Centre for DNA Fingerprinting and Diagnostics (CDFD), Hyderabad, May 16, 2019.
- Invited talk: 'Molecular engineering of an efficient four domain DAF-MCP chimera reveals the presence of functional modularity in RCA proteins' 5th International Conference on Translational Research: Recent Trends in Pre-translational to Translational, National Centre for Cell Science, Pune, Nov 7, 2019.
- Plenary Lecture: 'Complement regulation: lessons from viruses' IMMUNOCON 2019, 46th Annual Conference of Indian Immunology Society, Anushakti Nagar, Mumbai, Nov 15, 2019.

Manas Kumar Santra

- Delivered talk on August 29, 2019 in 5th ICTR at National Centre for Cell Science, NCCS complex, SP Pune University, Pune. Title: A novel small molecule AKT inhibitor suppresses tumorigenesis by directing FBXO31-mediated degradation of AKT.
- Delivered invited talk in National Symposium on Basic & Translational Research in cancer Biology Institute of Advanced Research, Gandhinagar, September 11, 2019. Title: Tumor suppressor FBXO31 functions as a dedicated gatekeeper to prevent oncogene-induced malignant progression.
- Delivered talk in Guha research conference at Fort Rajwada, Jaisalmer, Rajasthan on 7th December, 2019. Title: Understanding the importance of ubiquitination mediated protein degradation in maintaining the cellular homeostasis and cancer.
- Delivered invited talk in Phenotypic heterogeneity as a driver of cancer progression, IISc, Bangalore on January 6, 2020. Title: Ubiquitination determines on-off state of AKT signaling: Implication in cancer therapeutics.
- Delivered invited talk in International Symposia on Genome Instability: From Bench to Bedside, Manipal University on January 28, 2020. Title: F-box protein FBXO31: a novel gatekeeper to protect genome.
- Delivered invited talk in Role and Management of Oxidative Stress in Human Disease, 17th Annual Meeting, SFRR-INDIA-2020, BARC on February 12, 2020. Title: F-box only protein FBXO31: a dedicated genotoxic stress responder to maintain the genome stability.
- Delivered invited talk in 8th International Translational Cancer Research Conference Banaras Hindu University, Varanasi, India on February 14, 2020. Title: F-box protein FBXO31 abrogates proliferative signaling cascades to prevent breast cancer tumorigenesis.
- Delivered invited talk in Disease Biology: Diagnostics and Therapeutics, Department of Biotechnology, S. P. Pune University, March 5, 2020. Title: F-box only protein FBXO31: an important tumor suppressor plays crucial role in maintaining genome stability and cellular signaling.

Anjali Shiras

- Invited talk: Transformation of Neural Stem Cells to Tumor Stem Cells; the ways to assay them; 11th Annual Conference of Indian Society of Neuro-Oncology (ISNOCON Workshop) from 4th to 7th April, 2019 at BMRC (Bhopal Medical Research Centre), Bhopal.
- Invited talk: Attenuation of Tumor Suppressive function of microRNAs that contribute to Glioma Pathogenesis; International Conference on Cancer Biology; Basic Science to Translational Research (CBTR 2020) - Department of Stem Cell and Regenerative Medicine; DY Patil Medical College; 17th-18th January, 2020; Kolhapur.
- Invited talk: Tumor suppressive miRNA in GBM; their role in glioma progression; 5th International Conference on Translational Research (ICTR); Recent Trends in Pre-translational to Translational Research; 7th to 9th November at NCCS, Pune.

Yogesh Shouche

- Invited talk delivered at the University of Salford, Manchester, United Kingdom; 09 July, 2019.
- Invited talk delivered at Philips India, Pune, India; 09 September, 2019.
- Invited talk delivered at CGCM Shillim, Lonavala, India; 29 September, 2019.
- Invited talk delivered at the EMBO Symposium, NIBMG, Kalyani, India; 11 November, 2019.
- Invited talk delivered at the Bengaluru Tech Summit, Bangalore, India; 19 November, 2019.
- Invited talk delivered at the International Conformance on Human, Animal & Plant Mycroplasmas, Pune, India; 03 December, 2019.
- Invited talk delivered at the University of Delhi, New Delhi, India; 16 December, 2019.
- Invited talk delivered at the New Arts, Commerce & Science college, Ahmednagar, India; 13 January, 2020.

- Invited talk delivered at the 19th National Level Microbiolympiad, Auragabad, India; 15 February, 2020.
- Other invited talks were delivered at various organizations in Pune, India: .
  Smt. Kashibai Navale Medical College & Hospital, Narhe (09 April, 2019); Muktangan, (20 May, 2019); Garware College 20 June, 2019); Symbiosis College (25 July, 2019); Symbiosis College (16 October, 2019); Bharatiya Vidya Bhavan School (14 December, 2019)

Shailza Singh

- Engineering Immune Cells for Immunomodulation in Infectious Diseases; Invited Talk; University of Cambridge, London, UK, 24-28th June, 2019.
- Leveraging AI for Biomedicine in Infectious Diseases; Cray Intel Innovation Workshop at IISER Pune; 5th July, 2019.
- Oxidative stress complexity and Iron homeostasis in infectious disease: Emerging role in drug discovery; Invited Lecture; BARC, Mumbai, India; 1-3rd November, 2019.
- Systems Metabolic Engineering of Methylglyoxaland lipid hyperoxidase as holistic targets of Leishmania parasites; Amity University, Gurugram, India; 12-13th December, 2019.

Nishant Singhal

- Neurological disorders: An iPSCs approach to elucidate mechanisms and develop treatments (Invited Talk); International Conference on Disease Biology: Diagnostics and Therapeutics (DDT-2020)

Sandhya Sitaswad

- 'Redox regulation in Diabetic Cardiomyopathy: A journey': Invited talk; International Conference on IACS-India section meeting at Delhi Pharmaceutical Science and Research University; 21 February, 2020; New Delhi, India.

Deepa Subramanyam

- 'Stem Cells - A double-edged sword'. Invited talk at the Science Day Symposium of the Sophias College, 28 February, 2020; Mumbai, India.
- 'Cell fate decisions in development and disease'; All India Cell Biology Conference, December 2019, Mohali, India.
- 'Vesicular trafficking in embryonic stem cells.' Invited talk at IISER Thiruvavanthapuram, Department of Biological Sciences Symposium, November 2019.

" 'Balancing pluripotency in mouse embryonic stem cells through the action of intracellular trafficking pathways'. Poster presentation at the International Society for Stem Cell Research, ISSCR, San Francisco, USA, June 2019.

Mohan Wani

- "Mesenchymal stem cell therapy in animal model of human rheumatoid arthritis" on World Immunology Day held at Dr. D. Y. Patil Biotechnology & Bioinformatics Institute, Pune, April 30, 2019.
- "Cytokines in inflammation and osteoarthritis" in 3rd Annual Conference of Society of Inflammation Research held at Sankara Netralaya, Chennai, October 12-13, 2019.
- "Differential regulation of two functional forms of RANKL in osteoblasts" in 5th International Conference on Translational Research held at National Centre for Cell Science, Pune, November 7-9, 2019.
- "Impact of large animal models in translational research" in 9th International Conference of LASA (India) on Laboratory Animals in Biomedical Research-The way forward held at IISER, Pune, November 22-23, 2019.

Other Talks Delivered by Project Scientists of the NCCS CoE, NCMR

Amit Yadav:

- Genome Assisted Diagnosis of Phytoplasmas; Invited talk; Workshop; New Delhi, India; September 2019.

Kamlesh Jangid

- Enabling the cultivation of novel microbial taxa through in silico analysis; Invited talk; Workshop; Kolkata, February 2020.
- Emerging trends in microbial taxonomy; Invited talk; National Seminar; Pune, February 2020.
- Traditional and modern techniques of microbial diversity assessment; Invited talk; Faculty Development Porgram; Pune, February 2020.

- Diversity of microbes and associated statistics for its measurement; Invited talk; Faculty Development Porgram; Pune, February 2020.
- Microbial Succession during Ecosystem Development: from Metagenomics to Target State; Invited talk; National Seminar; Chandigarh, April 2019.

Om Prakash

- Landfill: A dumpyard or a graveyard (INSCAR-Meeting); Invited talk; Workshop; Rohtak, India, December 2019.
- Newer Technologies for Quicker Diagnosis/Identification of Bacteria; Invited talk; Workshop; Ahmednagar, India.
- Landfill: A dumpyard or a graveyard; Invited talk; Workshop; Allahabad, India, November 2019.
- OMICS as a Tool for Microbial Biodiversity Study; Invited talk; AMI-2019; Jant, Haryana, India, November 2019.

Rohit Sharma

- Present species concept in fungal taxonomy; Invited talk; Conference; Varansi, India; February 2020.
- Role of fungi in environmental biotechnology: Prospects and Challenges; Invited talk; Conference; Pune, India; February 2020.
- Role of fungi in waste treatment, other environmental problems and sustainability; Invited talk; Seminar; Pune, India; February 2020.
- Potential applications of fungi in industry; Invited talk; Panel Discussion; Pune, India; January 2020.
- Role of Fungi in Waste Treatment; Invited talk; Workshop; Pune, India; November 2019.

Other Outreach

National Science Day at NCCS — 28 February, 2020

Open days - *Displays and visits to the laboratories and central facilities*









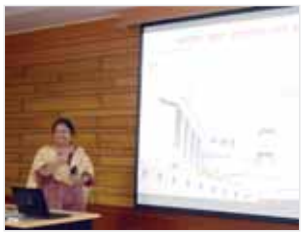
Two Open Days were organized to celebrate the National Science Day:

- 24th February - A visit to the NCCS CoE, NCMR campus was organized for 120 students from the 7th and 8th grade, from four different schools (DSK, VIBGYOR, Vidya Valley, and Ryan International School Pune).
- 28th February, 2020 - The NCCS campus was opened for the general public including students and anyone interested in visiting NCCS.

IISF-2019 Outreach Event: Open Day at NCCS 23 October 2019

An open day was organized at NCCS to create awareness among the general public about the activities of NCCS and about IISF-2019.

(a) 'Information session on IISF'
(b) A public talk in Marathi on cancer, 'कर्करोग जेव्हा आपल्याच पेशी बनतात आपल्या शत्रू!' (Cancer- When friends turn foes) was delivered by Dr. Anjali Shiras.
(c) Visits to the facilities and displays.




India International Science Festival (IISF 2019), Kolkata 5 - 8 November 2019

NCCS exhibited displays at the 5th India International Science Festival (IISF) organized by the Ministry of Science & Technology and the Ministry of Earth Sciences, Government of India, in association with Vijnana Bharati (VIBHA).




"Kutuhal" Science Exhibition 7 - 10 February, 2020

Extramural Outreach: NCCS displayed exhibits at the "Kutuhal" Science Exhibition organized by Vigyan Bharati, Pune, which attracted hundreds of people of various age groups from diverse backgrounds.





Workshop on 'Communicating Research out of the Lab' 18 October, 2019

(co-organized with EURAXESS & TIFR, Mumbai)



Foldscope Workshops

Workshop with Dr Jim Cybulski,
organized at the NCCS CoE, NCMR

Workshop on "Microbial World" at a
High School in Lauki, Shirpur
(17 September, 2019)

Workshop on "Microbial World and
foldscope" at a High School in Pawala,
Nandurbar (16 September, 2019)

'Foldscope: a wonder tool that triggers scientific temper' 18 November, 2019
A popular science talk organized for students of Magadh University,
Body Gaya, Bihar. 300 students of the 9th and 10th standards, and 100 students of the XI and XII satndards participated.

Workshop on foldscope assembly and preparation 28 April, 2019
Free workshop for students of class 5 and above conducted by
Dr. Praveen Rahi, Project scientist at the NCCS CoE-NCMR, at the Launcpad forum in Pune.

Other Public Talks

Public talks to commemorate the 150th Birth Anniversary of 'Ba and Bapu' 12 April, 2019
(organized by the National Academy of Sciences, India-Pune Chapter, in association with NCCS)

Climate Smart Agriculture in the Era of Plant Genomics'

- Prof. Paramjeet Khurana
Head, Department of Plant Molecular Biology, University of Delhi South Campus, New Delhi

'Lok Biradari Prakalp: A project for the health and development of tribal people in the dense forest of Gadchiroli district'

- Dr. Prakash Amte
Social Worker and Ramon Magasaysay Awardee, Hemalkasa, District: Gadchiroli, Maharashtra

Prof. B.K. Bachhawat Memorial Award Lecture 20 September, 2019
'Science, Technology, Innovation and Society' - delivered by Dr. Shekhar C. Mande
Director General, CSIR and Secretary, DSIR, New Delhi
(organized by the National Academy of Sciences, India Pune Chapter, in association with NCCS)

Prof. N. R. Dhar, Memorial Award Lecture 03 December, 2019
'Crystal Engineering: Present and Future'
delivered by Prof. Ashwini K. Nangia, Director, CSIR-NCL, Pune
(organized by the National Academy of Sciences, India, Pune Chapter, in association with NCCS)

Research training provided to extramural students and faculty
(in addition to the IAS Summer Training Fellows, 6 moths' / 1-year Project Trainees, students of the Ph.D. course work and cell repository workshop participants)

- Identification and prioritization of Actinobacteria for the metabolites against *Acinetobacter baumannii.*
  The NCCS CoE, NCMR provided training to 2 M.Sc. students from the Rajiv Gandhi Institute of IT and Biotechnology, BharatiVidyapeeth, Pune (September 2019 to March 2020).

- Prioritization of gut bacterial isolates for antagonistic potential against selected pathogens.
  (December 2019 to March 2020)
  The NCCS CoE, NCMR provided training to 1 M. Tech student from the Department of Technology, S.P. Pune University, Pune.

- Training on Fungal isolation, preservation and identification
  The NCCS CoE, NCMR provided training to 3 participants (1 faculty member, 1 PhD scholar & 1 MSc student) from Nar Bahadur Bhandari Degree College, Tadong, Sikkim (2019-20).

Other Popular Science and Public Talks

- 'Cancer-Conquering the enemy within'
  Talk delivered in Marathi by Dr. Anjali Shiras, at the Vasant Leela Auditorium, Mumbai on 5th March, 2020

- 'Animal Tissue Culture Workshop: Cancer Stem Cells - Facts and Fallacies'
  Talk delivered by Dr. Anjali Shiras at the Sir Parashurambhau College (SP College), Pune; 13 December, 2019.

- 'Stem Cells and Gene Editing -No God playing business'
  Public talk delivered by Dr. Deepa Subramanyam at the Pune 'Science on Tap" series. (attended by about a hundred members of the general public); September 28 2019.

- बायोप्रोस्पेक्टिंग द्वारा एनसीसीएस-एनसीएमआर के कवक संवर्धन (फंगल कल्चर) का मूल्य वर्धन
  Organized by the NCCS CoE-NCMR. 50 Students, Technicians, Scientists from National Insititutes of DST, DBT and CSIR attended. 02 March, 2020.

- 'Genomics in Health and Disease'
  Talk delivered by NCCS faculty, Dr. Debashis Mitra, at the Maulana Azad College, Kolkata (for more than 100 undergraduate and postgraduate students from different colleges of Kolkata), 13th February, 2020.

- 'Genomics in Health and Disease'
  Talk delivered by NCCS faculty, Dr. Debashis Mitra, at the Vivekananda College, Kolkata for more than 50 undergraduate and postgraduate students from the college; 14 February, 2020.

- 'Systems research-driven global innovation economy for human resilience'
  Talk delivered at NCCS by Prof. Kalidas Shetty, North Dakota State University, USA
  (organized jointly by the NCCS CoE-NCMR and the AMI Pune Unit)
  25 July, 2019

- 'Astrobiology: The hunt for alien life'
  Talk delivered by Prof. Lewis Dartnell, Professor in Science Communication, University of Westminster, UK
  (organized by the British Council, Pune, in association with the NCCS CoE-NCMR and the AMI-Pune Unit)
  01 August, 2019

Study visits by students to NCCS

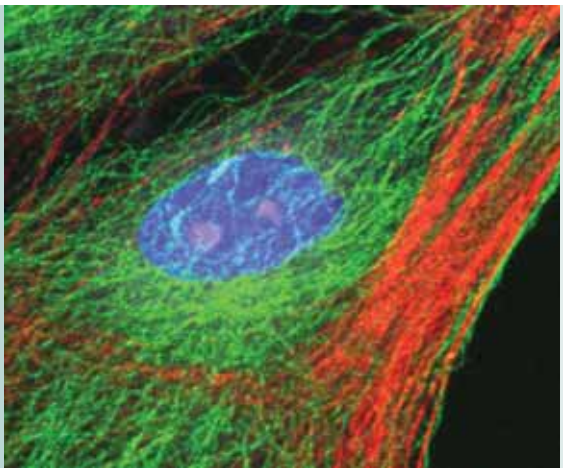
More than seven hundred students and faculty members from various schools, colleges and universities across India visited the campuses NCCS and the NCCS CoE, NCMR, during the period under report. The students were familiarized with the high-end techniques and equipment used in research in biology, as well as with the activities, facilities and services of NCCS.

Podcast

'Decoding Scientific Research and Stem Cell Behaviour'
Podcast by Dr. Deepa Subramanyam on Voice of Achievers; 01 February, 2020

Articles in Magazines / Newspapers

- 'Landfills: Dump-yards or Graveyards'
  Feature Article in Science Reporter, January 2020, co-authored by Dr. Om Prakash Sharma of the NCCS CoE, NCMR.
- 'मानव विष्ठा के सौदागर'
  Article in Hindi in Vigyan Pragti, April 2020, co-authored by Dr. Om Prakash Sharma of the NCCS CoE, NCMR.



Conferences / Workshops / Other Events

Participation by the NCCS Faculty

Manoj Kumar Bhat

- Global Bio-India 2019, 21-23 November 2019, Aerocity, New Delhi.
- IISF 2019, 5-8 November, 2019, Science City, Kolkata

Jomon Joseph

- Attended the 'Guha Research Conference 2019' at Jaisalmar 05-11 December, 2019.

Janesh Kumar

- 7th International Conference on Molecular Signaling ICMS-2019 held between 23-25 Jan, 2019 and Organized by Dept. of Zoology, Savitribai Phule Pune University, Pune, National Centre for Cell Science, Pune & The Society for Molecular Signaling

Nibedita Lenka

- Session Chair, 5th International Conference on Translational Research: Recent Trends in Pre-translational to Translational Research organized by Indian Society of Translational Research (ISTR), New Delhi and National Centre for Cell Science (NCCS), Pune, India, Nov. 7-9, 2019.

Amitabha Majumdar

- EMBO work shop on Protein quality control: From mechanisms to disease 28 April-3 May 2019, Costa de la Calma (Mallorca), Spain.
- APDRC meeting organized by IISER Pune, 06-10 January, Pune, India.
- Visiting scientist in the lab of Dr. Fatima Gebauer, CRG Barcelona, Spain, 25 April 2019- 20th August 2019.

Punam Nagvenkar

- Invited Talk: 'National Cell Repository - An Overview', 5th International Conference on Translational Research: Recent Trends in Pre-translational to Translational Research, National Centre for Cell Science, Pune, India; 7-9 November, 2019.

Arvind Sahu

- Attended the 'Guha Research Conference 2019' at Jaisalmar 05-11 December, 2019.

Manas Kumar Santra

- Attended the 'Guha Research Conference 2019' at Jaisalmar 05-11 December, 2019.

Mohan Wani

- Attended the 'Guha Research Conference (GRC) 2019' at Jaisalmar, Rajasthan, 06-10 December, 2019.

Participation by Other Scientists, Students and Staff of NCCS

Manoj K. Bhat's group

- **Shyamananda Singh Mayengbam:** 'Role of cholesterol in colon cancer and its impact on AOM/ DSS induced mouse intestinal tumourigenesis' (Mayengbam SS, Bhat MK). 2019 NCRI Cancer Conference, 3rd to 5th November 2019, Scottish Event Campus, Glasgow, UK.
- **Bhavana Deshmukh:** 'Serum associated factors alter DNA damage response and induce proliferation' (Deshmukh B, Bhat MK). 3rd World Cancer Congress 20-21November 2019, Mumbai, India.
- **Bhavana Deshmukh:** 'Stabilization of pH2AX level in colon cancer cells is dependent on inhibition of

dephosphorylation' (Deshmukh B, Bhat MK). World Congress on Cancer 3-5 February 2020, Mahatma Gandhi Medical College and Hospital Jaipur, India.

- **Abhijeet Singh:** 'Phenotypic alteration in immune cells and its association with enhanced tumor progression in obesity' (Singh A, Rani L, Wani MR, Mishra GC and Bhat MK). World Congress on Cancer 3-5 February 2020, Mahatma Gandhi Medical College and Hospital Jaipur, India.
- **Ankita Deb:** 'Molecular insights of resistin associated proliferation by inducing hypercholesterolemia in breast cancer' (Ankita Deb, Bhat MK). American Association of Cancer Research Annual meeting, 2020. 22nd and 24th June, 2020, e-conference, San Diego, US.

Samit Chattopadhyay's group

- **Arpankumar Choksi:** 'SMAR1 regulates PKM alternative splicing via HDAC6 mediated deacetylation of PTBP1' (Arpankumar Choksi and Samit Chattopadhyay). 5th International Conference on Translational Research: Recent Trends in Pre-translational to Translational Research (ICTR 2019), 07th -09th November 2019, Pune, INDIA.
- **Priyanka:** 'TLR4 mediated activation of SMAR1 renders an antitumor response in CRC (Priyanka, Vibhuti Kumar Shah and Samit Chattopadhyay). IMMUNOCON 2019, 46th Annual Conference of Indian Immunology Society: Advances in Immunology Research- Impact on Healthcare, 14th -16th November 2019, Mumbai, INDIA.
- **Vibhuti Kumar Shah:** 'Role of Chromatin remodeling protein SMAR1 in CD4+ Memory T cell differentiation' (Vibhuti Kumar Shah, Priyanka and Samit Chattopadhyay), IMMUNOCON 2019, 46th Annual Conference of Indian Immunology Society: Advances in Immunology Research- Impact on Healthcare, 14th -16th November 2019, Mumbai, INDIA.

Radha Chauhan's group

- **Sangeeta Niranjan:** Poster presentation: The dynamics of central channel nucleoporin complexes and architectural conservation across Species 45th Lorne International conference on protein Structure and function, 9-13 February, 2020; Lorne, Victoria, Australia.
- **Pankaj Kumar Madheshiya:** Oral presentation: Structural studies on the central transport channel-Nup93 complex (CTC-Nup93 complex) of mammalian nuclear pore complex. 12th Asia Pacific Microscopy conference & XL (40th) AGM meeting of EMSI, 03-07 Feb, 2020; Hyderabad, India.
- **Shrankhla Bawaria:** Poster/Oral presentation: Structural analysis of central transport channel (Nup54.Nup58.Nup62 complex) with Nup93 of mammalian Nuclear Pore Complex. CEM3DIP 2020: Single particle cryoEM of macromolecular-assemblies and cellular tomography. 19-30 January 2020, Kolkata, India.
- **Bhawna Budrak:** Poster/Oral presentation: Interactome analysis of Nup93 - Nup188/Nup205 complex in Nuclear Pore complex assembly. 5th International Conference on Translational Research: Recent trends in Pre-translational to translational research; 7 - 9 November, 2019; NCCS, Pune, India.

Gaurav Das's group

- **Mohandasan Radhika (JRF):** Poster titled "Introducing Y-maze as a simple method to assay olfaction associated learning in Drosophila", 5th Asia Pacific Drosophila Research Conference (APDRC5), 6th-10th January, 2020. Pune, India.
- **Manikrao Thakare (JRF):** Poster titled "A simple feeding protocol to simultaneously measure food consumption with gene expression, physiological or behavioural changes in Drosophila", APDRC5, 6th-10th January, 2020. Pune, India.
- **Rusha Chakraborty (Project Assistant):** Poster titled "A comparative study of stimulus responsive mesoporous silica nanoparticle in Drosophila", APDRC5, 6th-10th January, 2020. Pune, India.
- **Rusha Chakraborty (Project Assistant):** Poster titled "A comparative study of stimulus responsive mesoporous silica nanoparticle in Drosophila", Signals from the Gut, a mini symposium, 5th-6th January, 2020. NCCS, Pune, India.
- **Madhav Sridharan (Project Assistant):** Poster titled "Studying the neural basis of state dependent appetitive learning in Drosophila", APDRC5, 6th-10th January, 2020. Pune, India.
- **Fathima Iqbal (Project Assistant):** Poster titled "Probing exclusively post-ingestive mechanisms of nutrient perception using microencapsulated nutrients in Drosophila", APDRC5, 6th-10th January, 2020. Pune, India.

Jomon Joseph's group

- **Poulomi Banerjee:** Presented a poster at the ASCB: EMBO meeting, 7-11 Dec, 2019, Washington DC, USA.

M. V. Krishnasastry's group

- **Mahendra Kumar:** Esph noise: its significance in mycobacterial survival and virulence, Embo India symposium, Mycobacterial heterogeneity and host tissue

tropism, 11-02-2020 - 15-02-2020, February, 2020, New Delhi, India.

- **Raju Ambati:** Antibiotic-selected mycobacterial population show altered growth kinetics and reduced virulence, Keystone Symposium, Tuberculosis: Immunity and Immune Evasions, 16 January 2020 - 20 January 2020, January, 2020, Santa Fe, New Mexico, USA.

Janesh Kumar's group

- **Ananth P Burada:** 12th Asia Pacific Microscopy Conference - Structural Insights into Orphan Ionotropic Glutamate Receptors, 27-29 June 2018, NIMHANS, Bangalore, India.
- **Rajesh Vinnakota:** 12th International Symposium on Cell Surface Macromolecules (ISCSM 2020) held from 17th-21st February 2020, at IISER and NCL Pune.
- **Surbhi Dhingra:** 12th International Symposium on Cell Surface Macromolecules (ISCSM 2020) held from 17th-21st February 2020, at IISER and NCL Pune.
- **Prachi M. Boraste:** 12th International Symposium on Cell Surface Macromolecules (ISCSM 2020) held from 17th-21st February 2020, at IISER and NCL Pune.
- **Anshul Assaiya:** 12th International Symposium on Cell Surface Macromolecules (ISCSM 2020) held from 17th-21st February 2020, at IISER and NCL Pune.

Gopal C. Kundu's group

- **Deepti Tomar:** National Workshop on Microscopy Image Analysis, 6th-8th March 2019, Pune India.

Girdhari Lal's group

- **Chhatar S:** Effect of adrenergic receptor signalling in CD4 T cells during gut inflammation and autoimmunity (Chhatar S and Lal G). Mini-symposium titled 'Signals from the Gut' at National Centre for Cell Science, Pune on 5-6th January, 2020. (Poster Presentation.)
- **Padghan P:** CCR6 signaling modulates class-switch recombination in B cells during gut inflammation (Padghan P and Lal G). Mini-symposium titled 'Signals from the Gut' at National Centre for Cell Science, Pune on 5-6th January, 2020. (Poster Presentation.)
- **Meitei HT:** Chemokine receptor CCR6 signaling interacts with T cell receptor signaling and modulate the inflammatory function of Th17 cells (Meitei HT, Shirolkar A, Rapole S, Lal G). Indian Immunology Society conference 2019 (Immunocon2019) held on 14-16th November, 2019, at Mumbai. (Oral Presentation).
- **Karmakar S:** Role of serotonin receptors in anti-tumor immunity (Karmakar S and Lal G). 5th International conference on Translational Research: Recent Trends in Pre-translational to translational Research held at National Centre for Cell Science, Pune on 7-9th November, 2019. (Poster Presentation).
- **Mishra A:** Role of neurokinin 1 receptor on gut inflammation and autoimmunity (Mishra A and Lal G). Indian Immunology Society conference 2019 (Immunocon2019) held on 14-16th November, 2019, at Mumbai. (Oral Presentation)
- **Haldar N:** Acetylcholine receptors control the CD4+ T cell response during gut inflammation and autoimmunity (Haldar N, Kumar D and Lal G). Indian Immunology Society conference 2019 (Immunocon2019) held on 14-16th November, 2019, at Mumbai. (Oral Presentation)
- **Chhatar S:** Effect of adrenergic receptor signalling in CD4 T cells during gut inflammation and autoimmunity (Chhatar S and Lal G). Indian Immunology Society conference 2019 (Immunocon2019) held on 14-16th November, 2019, at Mumbai. (Poster Presentation)
- **Sonar SA:** IL-23 produced by Th17 cells in the central nervous system drives the apoptosis of neurons during experimental autoimmune encephalomyelitis (Sonar SA, Meitei HT, Lenka, and Lal G). In 17th International congress of Immunology to held between 18-23rd October 2019 at Beijing, China.

Nibedita Lenka's group

- **M. Bahir:** Synthetic porous 3D graft for bone tissue engineering (M. Bahir, N. Lenka.). International Indo-US Conference on Bio-engineering and Regenerative Medicine (ICBR), BHU, Varanasi, Feb. 27-29, 2020 (Oral Presentation).
- **M. Bahir:** Fabrication and Characterization of Synthetic Porous 3D scaffolds for Bone tissue Engineering (M. Bahir, N. Lenka). International conference on Disease Biology: Diagnostics and Therapeutics (DBDT), Savitribai Phule Pune University, Pune, Mar. 4-6, 2020 (Poster Presentation).

Srikanth Rapole's group

- **Sai Kiran Jajula:** Pesented a poster, "Investigation of bone marrow interstitial fluid proteome alterations in Acute Myeloid Leukemia" at 11th Annual Meeting of Proteomics Society, India (PSI) & International Conference on "Proteomics for System Integrated Bio-Omics, One Health and Food Safety" organised by NDRI, December 2-4, 2019 at Karnal.
- **Bhargab Kalita:** Pesented a poster, "Identification of FBXL16 interactome using immunoprecipitation mass spectrometry

analysis: insights into the role of FBXL16 in breast cancer" at 11th Annual Meeting of Proteomics Society, India (PSI) & International Conference on "Proteomics for System Integrated Bio-Omics, One Health and Food Safety" organised by NDRI, December 2-4, 2019 at Karnal. (Won the travel award).

- **Osheen Sahay:** Presented a poster, "From Foe to Friend quicker than ever: Dynamic Relationship of FBXO31 and γH2AX in DNA Damage Repair Pathway" at 5th International Conference on Translational Research: Recent Trends in Pre-translational to Translational Research organised by NCCS, November 7-9, 2019, Pune.

Arvind Sahu's group

- **Palak Agrawal:** Differential requirements of complement factor H domains for the regulations of cell surface and fluid phase alternative pathway activation (Palak Agrawal, Devraj Mogare and Dr. Arvind Sahu), International symposium on cell surface macromolecules (ISCSM2020), 17 - 21, February, 220, IISER, Pune, India.
- **Renuka Nawadkar:** Role of complement anaphylatoxins C3a, C4a and C5a generated in the infection locale in providing protection against viral infection (Renuka Nawadkar, Ashish Kamble, Pradipta Pal, Giridhari Lal, Jayati Mullick, Arvind Sahu), IMMUNOCON 2019; 46th Annual Meeting of Indian Immunology Society, 16 - 18, November, 2019, BARC, Mumbai, India.
- **Renuka Nawadkar:** Role of localy produced complement anaphylatoxins C3a and C5a in controlling vaccinia virus infection. (Renuka Nawadkar, Ashish Kamble, Pradipta Pal, Giridhari Lal, Jayati Mullick, Arvind Sahu), Diagnostics and Therapeutics (DBDT-2020), S. P. Pune University, 4 - 6, March, 2020, Pune, India.

Manas Kumar Santra's group

- **Yashika Agarwal:** Delivered talk at the 5th ICTR at National Centre for Cell Science, NCCS complex, SP Pune University, Pune, 29 August, 2019.
- **Ganesh Kumar Barik:** Presented poster in "Disease Biology: Diagnostics and Therapeutics international conference, Department of Biotechnology, S. P. Pune University, March 5, 2020.
- **Osheen:** Presented poster poster in "International Symposia on Genome Instability: From Bench to Bedside", Manipal University on January 28, 2020.
- **Tanisha Sharma:** Presented poster poster in "Disease Biology: Diagnostics and Therapeutics international conference, Department of Biotechnology, S. P. Pune University, March 5, 2020.
- **Osheen:** Presented poster in "Disease Biology: Diagnostics and Therapeutics international conference, Department of Biotechnology, S. P. Pune University, March 5, 2020.

Yogesh Shouche's group

- **Abhijit Kulkarni:** 'A comprehensive microbiome analysis of Rongmei tribal community from North-East India', 'India | EMBO Symposium on Human Microbiome' at National Institute of Biomedical Genomics (NIBMG), 9-12th Nov 2019, Kalyani, India.
- **Abhijit Kulkarni:** 'A comprehensive microbiome analysis of Rongmei tribal community from North-East India', 10th India Probiotic Symposium, 29th Feb-1st Mar 2020, New Delhi, India.
- **Akshay Gaike:** 10th India Probiotic Symposium, 29th Feb-1st Mar 2020, New Delhi, India.
- **Rahul Bodkhe:** 10th India Probiotic Symposium, 29th Feb-1st Mar 2020, New Delhi, India.

Shailza Singh's group

- **Ritika Kabra:** Oral Presentation entitled "Theoretical and Experimental Insight into the Allosteric Modulation of Transporter Proteins in Miltefosine resistant Leishmania major" (Ritika Kabra, Shailza Singh), International Conference on Disease Biology: Diagnostics and Therapeutics (DBDT-2020), 4 - 6th March, 2020, Pune, India.
- **Prajakta Nimsarkar:** Poster Presentation entitled "Systems studies unravels the role of miR-146a in regulating Host-Pathogen interaction in leishmaniasis" (Prajakta Nimsarkar, Shailza Singh), International Conference on Disease Biology: Diagnostics and Therapeutics (DBDT-2020), 4 - 6th March, 2020, Pune, India.
- **Nikhil Samarth:** CTCA-TCGA Conference, IISER - Pune, India; 21-22nd September, 2019.
- **Anurag Kumar:** Participated in Global Bio-India, 2019, New Delhi, India; 21st-23rd November, 2019.

Sandhya Sitaswad's group

- **Subhajit Das:** Attended "Second UK-India Cancer Bio-Informatics Workshop; 31 October-2nd November 2020; ACTREC, Navi Mumbai, India.
- **Megharani Mahajan:** Presented 'Role of redoximiRs in breast tumor angiogenesis and metastasis: Nrf2 as a target protein' (Ms. Megharani Mahajan and Dr. Sandhya Sitasawad); 17th Annual Meeting of SFRR-India (SFRR-INDIA-2020) & International Conference on "Role and

Management of Oxidative Stress in Human Disease"; 12 -15 Feburary 2020; BARC, Mumbai, India.

- **Deepali Bhadane:** Presdented 'Role of NOX4 in regulation of breast cancer cell migration and invasion' (Ms. Deepali Bhadane and Dr. Sandhya Sitasawad) 17th Annual Meeting of SFRR-India (SFRR-INDIA-2020) & International Conference on "Role and Management of Oxidative Stress in Human Disease"; 12 -15 Feburary 2020; BARC, Mumbai, India.
- **Rohini Dhat:** Presented 'Hyperglycemia induced DNA hypermethylation of antioxidant genes and its role in the pathogenesis of Diabetic cardiomyopathy' (Ms. Rohini Dhat and Dr. Sandhya Sitasawad), International conference of cardiovascular sciences at Delhi Pharmaceutical Science and Research University; 21-23 February 21-23, 2020; New Delhi, India.

Deepa Subramanyam's group

- **Deepika Puri (DST-Inspire Fellow):** Poster title: 'Epigenetic regulation of autophagy in development differentiation and disease'. EMBL Course: Chromatin Signatures During Differentiation: Integrated Omics. 02/09/2019- 06/09/2019 held in EMBL, Heidelberg , Germany.
- **Deepika Puri (DST-Inspire Fellow):** Poster title: 'Epigenetic regulation of autophagy in development differentiation and disease'. Signals from the Gut 05/01/20-06/01/20 Held in NCCS Pune, India.

Mohan Wani's group

- **Dr. Amruta Naik (DST Woman Scientist):** Attended the Summer Training Workshop by "MANAV-Human Atlas Initiative" Persistent Systems, Pune, May 21-31, 2019.
- **Dr. Amruta Naik (DST Woman Scientist):** Attended the 5th International Conference on Translational Research: Recent Trends in Pre-translational to Translational Research organized by National Centre for Cell Science, Pune, November 7-9, 2019.
- **Dr. Dr. Milanjeet Kour (Research Associate):** Attended the 5th International Conference on Translational Research: Recent Trends in Pre-translational to Translational Research organized by National Centre for Cell Science, Pune, November 7-9, 2019.
- **Shubhanath Behera :** Attended Global Bio India at Aerocity, New Delhi, November 21-23,2019.
- **Adrita Guha:** Attended the 9th International Conference of LASA (India), on Laboratory Animals in Biomedical Research-The way forward held at IISER, Pune, November 22-23, 2019.
- **Juilee Karhade:** Attended the 9th International Conference of LASA (India), on Laboratory Animals in Biomedical Research-The way forward held at IISER, Pune, November 22-23, 2019.

Tehnical Staff

- **Ashwini Atre, Technical Officer 'A' (Bio-imaging facility):** Attended the 8th training programme on Science and Technology for Rural Societies for Women Scientist &Technologist at New Delhi; 25- 29 November, 2019.
- **Bhimashankar Utage, Technician 'C':** Attended the 'International Conference on Disease Biology: Diagnostics and Therapeutics', organised by the S. P. Pune University (SPPU), 04-06 March, 2020.
- **Prachi Chopade, Technician 'B':** Attended the 'International Symposium on Cell Surface Macromoleculs (ISCSM2020)' held at the Institute of Science Education and Research (IISER), Pune between 17.02.2020 to 20.02.2020.

Project Staff on the NCCS Centre of Excellence, NCMR

- Kirdat K., Thorat V., Tiwarekar B., and Yadav A. Genome assisted taxonomy of phytoplasmas. SCGS phytoplasma, a case study. Oral Presentation at XIth National Symposium of Indian Association of Mycoplasmologists (IAM). December 2 to 5, 2019, Pune, India.
- Kirdat K., Thorat V., Tiwarekar B. and Yadav A. Enrichment of Phytoplasma Genomic DNA for Whole Genome Sequencing. Oral Presentation at XIth National Symposium of Indian Association of Mycoplasmologists (IAM). December 2 to 5, 2019, Pune, India.
- Tiwarekar B., Kirdat K., Thorat V., and Yadav A. Bioinformatics analysis pipeline for phytoplasma genome assembly. Poster Presentation at XIth National Symposium of Indian Association of Mycoplasmologists (IAM). December 2 to 5, 2019, Pune, India.
- Thorat V., Kirdat K., Tiwarekar B. and Yadav A. Improved phytoplasma 16s rRNA specific nested PCR primers. Poster Presentation at XIth National Symposium of Indian Association of Mycoplasmologists (IAM). December 2 to 5, 2019, Pune, India.
- Kirdat, K., Thorat, V. and Yadav A. (2019). A new elm yellows phytoplasma strain associated with leaf yellowing disease of Tamarindus indica in India. Poster Presentation at fourth International Phytoplasmologist Working Group (IPWG) meeting. September 8 to 12, 2019, Valencia, Spain.
- Kirdat, K., Sundararaj, R., Mondal, S., Reddy, M. K., Thorat, V. and Yadav, A (2019). Novel aster yellows phytoplasma subgroup associated with sandalwood spike disease in Kerala, India. Oral Presentation at fourth International Phytoplasmologist Working Group (IPWG) meeting. September 8 to 12, 2019, Valencia, Spain.

Global Bio-India 2019 (21-23 November, 2019)



NCCS participated in the Global Bio-India 2019 expo at New Delhi organized by the Department of Biotechnology.

Conferences / Workshops / Other Events Organized

NCCS Foundation Day

(26th August, 2019)

Foundation Day Oration:
'Ethics in biology research & education - A perspective'

by
by Prof. K. Muralidhar (University of Hyderabad)

Felicitation of members of the NCCS family who have completed 20 years of service at NCCS

5th International Conference on Translational Research: Recent Trends in Pre-translational to Translational Research — 7-9 November, 2019

9th International Conference of LASA India (LASACON 2019) on 'Laboratory Animals in Biomedical Research - The way forward' *(organized jointly with IISER-Pune)* — 21-23 November, 2019




International conference on 'Ayush for Future Health Challenges: Strengthening trans-disciplinary research' *(organized by S.P. Pune University is association with NCCS)* — 28 November - 01 December, 2019

International Conference on Human, Animal and Plant Mycoplasmas 03, 04 December, 2019

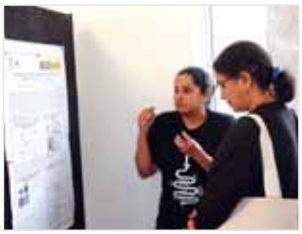
(organized by the NCCS CoE-NCMR)

This two-day international conference was attended by 82 participants, mostly from India and 26 speakers from India, China, Taiwan, Israel, Netherlands and France.

'SIGNALS from the GUT' 05, 06 January, 2020

An international satellite mini-symposium to the 5th Asia Pacific Drosophila Research Conference (APDRC5)



Science Conference in Hindi 04 March, 2020

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

Theme: 'विकसित भारत में विज्ञान और प्रौद्योगिकी का योगदान' (Contribution of Science and Technology to Developed India).






Other Workshops / Training Programmes / Demonstrations Conducted

Workshop on 'Microbial Identification by BIOLOG & VITEK' 23 April 2019

Organized by the NCCS CoE, NCMR.

20 participants from pan-India participated (1 lecturer, 5 Assistant professors and 14 Ph.D. students and postdoctoral researchers)

Workshop on 'MALDI-TOF MS based microbial identification' 24 April 2019

Organized by the NCCS CoE, NCMR.

33 participants from pan-India participated (22 faculty members and 11 Ph.D. students)

23 April, 2019

24 April, 2019

Workshop on 'Writing Grant Proposals' 11 June, 2019

Organized jointly with the DAAD Information Centre, Pune for Ph.D. students from research institutes in Pune. 9 students engaged in research in the biological sciences participated.

Workshop on 'Sample preparation and mass spec analysis of proteome' July & August, 2019

In-house training for Ph.D. students, imparted by the proteomics facility staff

'Nikon A1R HD 25 Confocal Laser Scanning Microscope' 03-11 September, 2019

Demonstration workshop & hands-on training

(organized under the aegis of the Pune Bio-Cluster by the Bio-Imaging Facility of NCCS)

Workshop on Molecular Detection and Cultivation of Mycoplasmas 02 December, 2019

Conducted by the NCCS CoE-NCMR, under the auspices of the XIth National Symposium of Indian Association of Mycoplasmologists

Workshop on Phytoplasma Detection & Taxonomy 05 December, 2019

Conducted by the NCCS CoE-NCMR, under the auspices of the XIth National Symposium of Indian Association of Mycoplasmologists (IAM)

The workshop was attended by 26 participants (including M. Sc and Ph. D students pan-India), and mentored by Dr Amit Yadav (Project Scientist, NCCS CoE-NCMR, Pune), Dr Manimekalai (SBI, Coimbatore), Dr Chih-Horng Kuo (Academia Sinica, Taiwan), Dr Kamlesh Jangid (Project Scientist, NCCS CoE-NCMR, Pune) and Dr Tushar Lodha (Project Scientist, NCCS CoE-NCMR, Pune).



Hands-on Workshop on Next-Generation Sequencing Data Analytics — 10 December, 2019

Organized for the NCCS students, postdoctoral researchers and scientists, by Bionivid Technology Pvt. Ltd.

Workshop on Statistical Methods in Microbiome Research — 16-20 December, 2019

Organized by the NCCS CoE-NCMR

Conducted by Prof. Dr. Susan Holmes (Dept. of Statistics, Stanford University, USA) & Dr. Leo Lahti (University of Turku, Finland). 30 researchers (PhD scholars, Postdoctoral Fellows and Early Career Researchers) from academia and industry across India participated.

** Additional workshops / training programmes / demonstrations conducted by the bio-imaging and FACS facilities are listed in the individual reports of these respective core facilities.

Workshops in Hindi

'प्रयोजनमूलक हिंदी एवं उसकी आवश्यकता' — 18 December, 2019

(Functional Hindi and its necessity)

Conducted by Mrs. Archana Nair (Senior Hindi Translator, AFMC, Pune)

'तिमाही हिंदी रिपोर्ट' (Quarterly Hindi Report) — 24 January, 2020

Information on how to fill in the quarterly report format)

Conducted by Mrs. Smita Khadkikar (Junior Hindi Translator, NCCS, Pune)

'हिंदी के प्रचार-प्रसार में मोबाईल एवं कंप्यूटर की भूमिका' — 04 February, 2020

(Role of mobile phones and computers in the promotion of Hindi)

Conducted by Shri. Rajendra Prasad Verma (Assistant Director, Hindi Teachning Scheme, Pune)




December 2019 January 2020 February 2020

Talks Delivered at NCCS by Invitees

- 'A conserved Cdk9-PP1 kinase-phosphatase switch regulates the elongation-termination transition of RNA polymerase II'
  Dr. Pabitra Parua
  (Department of Oncological Sciences, Icahn School of Medicine at Mount Sinai, USA); 11 Apr, 2019.

- 'An intricate pathway that protects epithelia against mechanical rupture'
  Dr. Bipul Acharya
  (Centre for Stem Cells & Regenerative Medicine, King's College London, UK); 02 May, 2019.

- '38th Indian Scientific Expedition to Antarctica: A Tale of Uncertainty, Patience and Endurance'
  Dr. Avinash Sharma
  (Wellcome Trust-DBT, India Alliance Fellow; Scientist, NCCS CoE-NCMR); 21 May, 2019.

- 'Early cell lineage commitment in mammals: a molecular perspective'
  Dr. Pratik Home
  (Institute for Reproduction and Perinatal Research, Univ. of Kansas Medical Center, USA); 28 May, 2019.

- 'Indo-German Funding Opportunities & Grant Proposal Writing Workshop'
  Information Session
  Representatives from the DAAD Information Centre, Pune; 11 June, 2019.

- Information Session: 'A Primer to The Cancer Genome Atlas (TCGA)' -
  Dr. Anamika Krishanpal (Persistent Systems, Pune),
  Dr. Madhura Kulkarni & Dr. Santosh Dixit (Centre for Translational Cancer Research); 30 July, 2019.

- 'Social regulation of insulin signalling and the evolution of eusociality in ants'
  Vikram Chandra,
  (The Rockefeller University, New York, USA); 23 August, 2019.

- The Web of Science database
  Information & demonstration session; 03 Sep, 2019.

- Effect of co-solutes on the emergence of molecules of an RNA world'
  Dr. Sudha Rajamani
  (IISER Pune); 27 Sep, 2019.

- Rhes engineers cell-to-cell membranous tunnels and transports Huntington disease protein'
  Dr. Srini Subramaniam
  (Dept. of Neuroscience, The Scripps Research Institute, USA); 03 Oct, 2019.

- 'Stem Cell Research to Therapy: Lessons from Ophthalmology'
  Prof. Geeta K Vemuganti
  MD, DNB, FAMS, FICP, FARVO (School of Medical Sciences, University of Hyderabad, Hyderabad); 22 Oct, 2019.

- 'A spatio-temporal kinase gradient ensures sequential events of cell division'
  Dr. Saravanan Palani
  Centre for Mechanochemical Cell Biology, University of Warwick, UK; 11 Nov, 2019.

- 'HIF-1 is the central regulator of nucleus pulposus cell metabolism'
  Prof. Makarand Risbud
  Director, Division of Orthopaedic Research,
  Sidney Kimmel Medical College, & Professor, Thomas Jefferson University, Philadelphia, USA; 14 Nov, 2019.

- 'Molecular interactions of hepatitis E virus with the host cell signaling machinery'
  Dr. Kavita Lole
  National Institute of Virology, Pune; 15 Nov, 2019.

- 'Innate immune surveillance by surfactant protein D against allergy and cancer'
  Dr. Uday Kishore
  Brunel University, London, UK; 18 Nov, 2019.

- 'T cell costimulation and anti-tumor responses: A personal perspective'
  Prof. Dipankar Nandi
  Dept. of Biochemistry, IISc, Bengaluru; 19 Nov, 2019.

- Tumor Progression and Metastasis: Hijacking the Host'
  Prof. Rakesh Kumar Singh
  (University of Nebraska Medical Center and Eppley Institute for Cancer Research, USA); 02 Dec, 2019.

- 'Exploiting genomics to elucidate virus-host-microbiome interactions'
  Dr. Suman Das
  (Division of Infectious Diseases, Vanderbilt University Medical Center, USA); 12 Dec, 2019.

- Infection and Immunity in the old age - what goes wrong and what can be fixed?'
  Prof. Janko Nikolich-Zugich
  (Bowman Professor and Head, Department of Immunobiology; Co-Director, Arizona Center on Aging, University of Arizona College of Medicine, USA); 17 Dec, 2019.

- 'Genetic interaction between BRCA1 and FANCM in stalled replication fork repair'
  Dr. Arvind Panday
  (Beth Israel Deaconess Medical Center, Harvard Medical School, Boston, USA); 19 Dec, 2019.

- 'Our attempts at understanding enzyme specificity with a focus on vitamin biosynthesis'
  Dr. Amrita Hazra
  (IISER, Pune); 20 Dec, 2019.

- 'Development of an immunology-based therapy for human papilloma virus-induced pre-cancers and cancers'
  Dr. Prakash Bhuyan
  MD PhD (Vice President, Clinical Development of Inovio Pharmaceuticals, & Adjunct Assistant Professor, University of Pennsylvania, USA); 24 Dec, 2019.

- 'The ups and downs of oncogenic Wnt signaling: signals to MYC and MAPK'
  Dr. Babita Madan
  (Duke-NUS, Singapore); 07 Jan, 2020.

- 'The Enigma of Gravitation: Newton to Einstein and Beyond'
  Dr. Sanjeev Dhurandhar
  (Professor Emeritus, IUCAA); 10 Jan, 2020.

- 'Role of protein translation in neurodegenerative diseases' & 'Arc, an master regulator of synaptic plasticity'
  Dr. Sudarshan Patil
  (Institute of Biomedicine, University of Bergen, Norway); 14 Jan, 2020.

- 'Cell Cycle and Biomaterial Engineering for Injured Brain Regeneration'
  Dr. Itsuki Ajioka
  (Tokyo Medical and Dental University, Japan); 29 Jan, 2020.

- 'Sex specific adipose tissue imprinting of T reg cells'
  Dr. Ajithkumar Vasanthkumar
  (University of Melbourne, Australia); 27 Jan, 2020.

- 'Reward Circuits in the brain are modulated by CART neuropeptide'
  Dr. Nishikant Subhedar
  (Visiting Faculty, IISER Pune). 21 Feb, 2020.

- 'From ubiquitin-dependent degradation to ubiquitin degradation - An emergency role of proteasomes under human pathology'
  Dr. Indrajit Sahu
  (EC Senior Researcher, Technion - Israel Institute of Technology). 27 Feb, 2020.

- 'Introduction to Prime PCR solutions for advanced qPCR applications & CFX Maestro, all in one analysis software'
  Technical Seminar by Dr. Yann Jouvenot
  (Bio-Rad Laboratories, Inc. USA); 07 August, 2019.

** Additional technical seminars organized by the bio-imaging and FACS facilities are listed in the individual reports of these respective core facilities.

Other Happenings

Launch of the 'Manav: Human Atlas Initiative' 10 May, 2019
at the Department of Biotechnology, New Delhi

'Manav' is a collaborative project between NCCS,
IISER-Pune and Persistent Systems Limited (PSL), co-funded by the DBT and PSL.

Inauguration of the Pune Biotech Cluster by Dr. Renu Swarup 23 August, 2019



International Day of Yoga 21st June, 2019



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

Rashtriya Ekta Diwas (National Unity Day) 31 October, 2019

The staff and students of NCCS participated in a 'run for unity' within the campus of the S. P. Pune University, and took a pledge to preserve and strengthen the unity, integrity and security of our nation.




Activities under Swachh Bharat Initiative

Appropriate handling, segregation and disposal of laboratory and other waste is carried out at NCCS. The housekeeping staff is given training for this purpose.



NCCS commemorated the "Constitution Day & Dr. Ambedkar Jayanti" with the following activities:

a) Two books in Hindi and one book in English related to the Constitution of India were purchased, as listed below, which will be available to the staff and students of NCCS from the NCCS library:

i) भारत का संविधान - विष्णु खरे

ii) भारत का संविधान - एक परिचय - दुर्गा दास बसु

iii) The constitution of India - Durga Das Basu

b) An e-book in Hindi (PDF book) on The Constitution of India (published by the Govt. of India, Ministry of Law and Justice, Legislative Dept.) was shared with the NCCS staff via email.

c) A talk on, "The Constitution of India & International Security" was organized on 22nd January 2020. This talk was delivered by Prof. (Dr.) Vijay Khare, who is the Head, Department of Dr. Ambedkar Studies; Professor & Head, Department of Defence & Strategic Studies; Director, Yashwantrao Chavan National Center of International Security and Defence Analysis (YC-NISDA); and Director, International Centre, at the Savitribai Phule Pune University, Pune.

d) Short video films: "The Preamble" and "Our Constitution" (made by the Films Division-Mumbai, Ministry of Information and Broadcasting, Govt of India), were displayed on all TV monitors located across the campus of NCCS.




NCCS featured in the media


NCCS studies decode 2 key brain receptors

hindustantimes

Pune research group gives new hope for targeted therapy to ovarian cancer patients

CITIES

Ministry of Science & Technology

Posted On: 24 JUN 2020 12:58PM by PIB Delhi

New biomolecules to fight drug resistance in Kala- azar

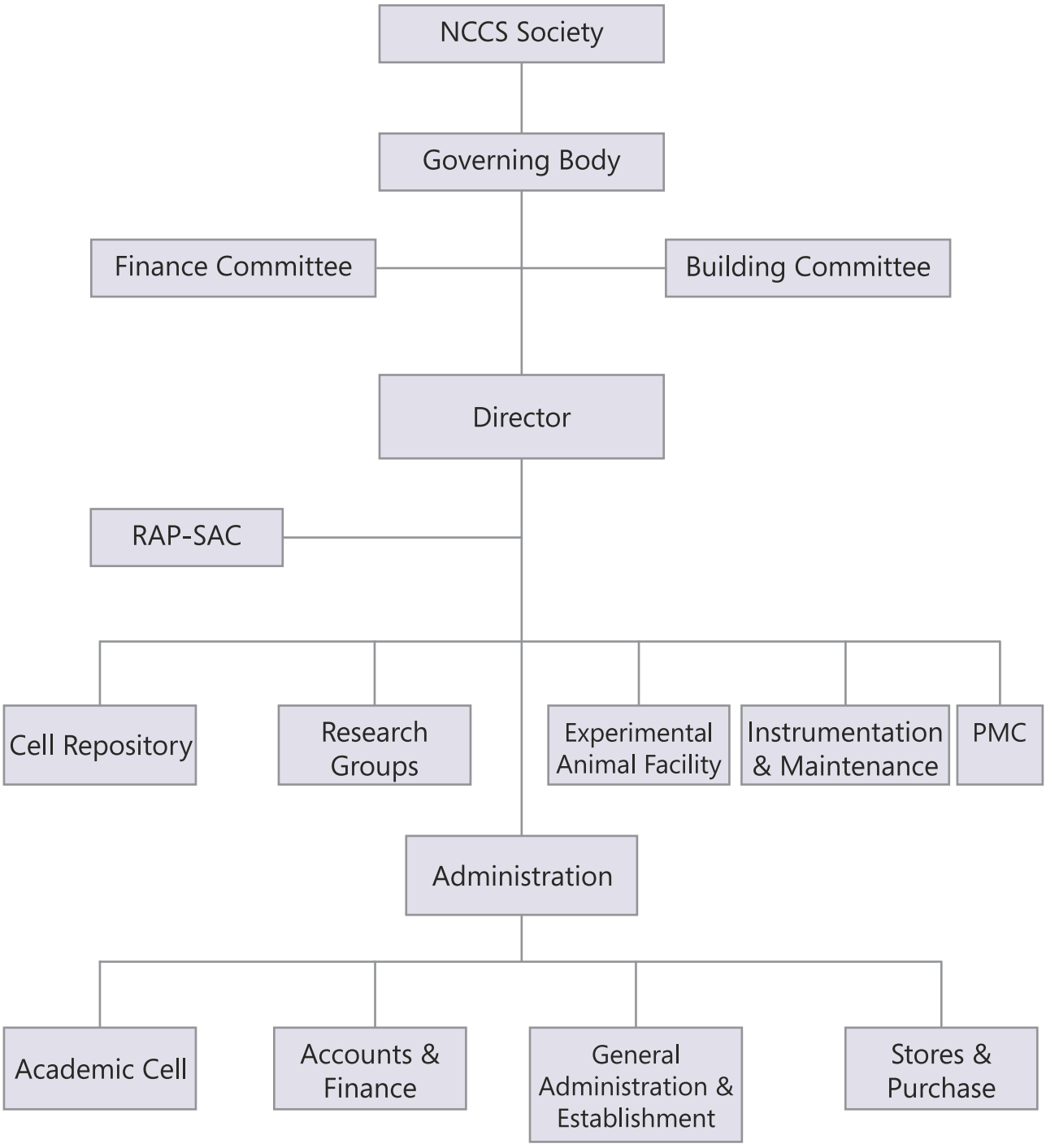

शरीरातील मायक्रोबायोममध्ये वाढत्या वयानुसार बदल

राष्ट्रीय पेशीविज्ञान संस्थेचे संशोधन


As prelude, NCCS to hold open day today


Big research institutes expect max footfall on Science Day this Friday

NCCS Organization



NCCS Committees

NCCS Society Members

1 **Dr. Harsh Vardhan** — President
Honorable Minister of Science &
Technology & Earth Sciences,
Anusandhan Bhawan,
2, Rafi Ahmed Kidwai Marg, New Delhi - 110 001
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2 **Dr. Renu Swarup** — Ex-Officio Member
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Department of Biotechnology,
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CGO Complex, Lodhi Road,
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3 **Prof. (Dr.) Nitin R. Karmalkar** — Ex-Officio Member
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8 **Dr. T. Mohapatra** — Ex-Officio Member
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Indian Council of Agricultural Research
And Secretary, Dept. of Agricultural Research
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9 **Prof. Kalpana Pai** — Non-Ex-Officio Member (nominated by Vice Chancellor SPPU)
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NCCS Society Members

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11 **Prof. Vineeta Bal** — Non-Ex-Officio Member (Nominated by Secretary DBT)
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13 **Dr. Manoj Kumar Bhat** — Ex-Officio Member Secretary
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NCCS Governing Body Members

1 **Dr. Renu Swarup** — Ex-Officio Chairperson
Secretary
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2 **Prof. (Dr.) Nitin R. Karmalkar** — Ex-Officio Member
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3 **Dr. Suchita Ninawe** — Ex-Officio Member
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6 **Dr. Balram Bhargava** — Ex-Officio Member
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	Director General, Indian Council of Medical Research meetings) (ICMR), Ansari Nagar, Post Box 4911 New Delhi - 110029 Phone- 011-26588204 Email -secy-dg@icmr.gov.in	
7	**Dr. T. Mohapatra** Director General Indian Council of Agricultural Research And Secretary, Dept. of Agricultural Research & Education, Krishi Bhavan New Delhi - 110 114 Phone: -011-23382629, 23386711 E-mail: dg.icar@nic.in	Ex-Officio Member
8	**Prof. Kalpana Pai** Head of Department of Zoology Savitribai Phule Pune University Ganeshkhind Pune 411007 Ph. - 020-25601436 Email: kalpanapai@unipune.ac.in	Non-Ex Officio Member (nominated by Vice Chancellor, SPPU)
9	**Prof. N. K. Ganguly** Former DG-ICMR Global Health Strategies 18/1, IInd floor, Shaheed Bhawan Aruna Asaf Ali Marg New Delhi - 110067 Cell - 09811504314 Email - ganguly1nk@gmail.com	Non-Ex-Officio Member (Nominated by Secretary DBT)
10	**Prof. Vineeta Bal** Visiting Professor Indian Institute of Science, Education and Research (IISER), Pune, Dr. Homi Bhabha Road, Pune - 411 008 Phone - 020- 25908129 Email - vineeta@iiserpune.ac.in	Non-Ex-Officio Member (Nominated by Secretary DBT)
11	**Dr. Yogesh Shouche** Scientist 'G' NCCS, Pune - 411 007 Phone - 020 25329026 Email - yogesh@nccs.res.in	Non-Ex-Officio Member (Nominated by Secretary DBT)
12	**Dr. Manoj Kumar Bhat** Director, NCCS Pune - 411 007 Phone - 020-25708121 Email - director@nccs.res.in	Ex-Officio Member Secretary

NCCS Finance Committee Members

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1. **Dr. Dinakar Salunke** — Chairman
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2. **Dr. Debashis Mitra** — Member
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3. **Shri. Pushkar M. Kanwinde** — Member
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4. **Dr. Sukhanand Sopan Bhosale** — Member
   Prof. & Head Department of
   Civil Engineering, College
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5. **Dr. Agarwal Anil** — Member
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6. **Shri. Nitin D. Ohol** — Member
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7. **Executive Engineer,** — Member
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8. **Director,** — Member
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9. **In-Charge Maintenance** — Convener
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10 **Dr. Y. S. Shouche** — Special Invitee
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11 **In-Charge Administration** — Special Invitee
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12 **In-Charge Accounts** — Special Invitee
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NCCS Research Area Panels - Scientific Advisory Committee (RAP-SAC) Members

1. **Prof. N. K. Ganguly** — Chairman
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2. **Dr. Rajan Sankaranarayan** — Member
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   Structural Biology Laboratory,
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3. **Prof. Tapas Kundu** — Member
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   Member

6. **Prof. Udaykumar Ranga** — Member
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7. **Prof. Kumarvel Somasundaram** — Member
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13. **Prof. Roop Malik** Member
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14. **Dr. Suchita Ninawe** Member
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Senior Scientific Advisor
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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	:	32
Administrative Staff	:	40
Technical Staff	:	73

Total	:	145

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, quarterly and yearly reports of all the vigilance-related matters including probity report, information about foreign tours of the staff and 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. The 2019 Vigilance Awareness Week was being observed from 8 October to 2 November, 2019 with the theme "Integrity- A way of life".

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 the Official Language Implementation Committee to implement the orders of the Government of India to use the Official Language in day-to-day official work.

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' 'Translation" and 'Hindi elocution'. hese competitions were judged by external & internal examiners to ensure unbiased assessment. Dr. Swati Chaddha-Hindi Officer, CSIR-NCL, Pune, Dr. Rekha Singh, Hindi Officer- R&D(E), Dighi, Shri. M. K. Mishra, Hindi Officer, VAMNICOM, Pune and Mrs. Archana Nair-Senior Hindi Translator, AFMC, Pune, were invited as external examiners/ judges for these competitions. Dr. Girdhari Lal, Mrs. Sushama Namjoshi, Mrs. Nalini Chavan, Mrs. Prachi Dani and Mr. Rameshwar Nema were deputed as internal examiners-cum-supervisors for these competitions. To

encourage students and staff with diverse linguistic abilities to participate in these competitions, the tradition of giving separate prizes to "Hindi Bhashi" & "A-Hindi Bhashi" particpants was followed this year as well, which consequently elicited an overwhelming response. Dr. Yamini Bhushan Tripathi, Professor- Department of Medicinal Chemistry & Dean- Faculty of Ayurveda, Banaras Hindu University, Varanasi, graced the Hindi Day function held on 16th September, 2019, as the Chief Guest. On this day, the seventh issue of the annual Hindi magazine, 'Meemansa' was released at the hands of Dr. Yamini Bhushan Tripathi, Dr. G. C. Mishra (former Director of NCCS), Dr. Manoj Kumar Bhat (Director, NCCS) and Dr. Gopal Kundu (Sr. Scientist & Dean-Academic Cell, NCCS). The chief guest expressed his views on the importance of using Hindi in official work. He also emphasized the importance of Hindi while communicating science to the general public, by conducting his scientific presentation in Hindi. Dr. M. K. Bhat gave an overview of the day-to-day activities conducted / organized in Hindi, at the Institute. Dr. G. C. Mishra, also shared his thoughts on the usage of the official language. The Hindi Day event was compered by Mrs. Prachi Dani, Technical Officer (Accounts), NCCS.




Quarterly workshops in Hindi conducted by external experts were organized regularly. To promote the use of the official language, and to provide a platform to the staff members to express their ideas in Hindi, workshops in Hindi conducted by the NCCS staff were also initiated.

A Scientific Conference entitled- 'विकसित भारत में विज्ञान और प्रौद्योगिकी का योगदान ' (the role of science and technology in was organised in Hindi on 4th March, 2020 at NCCS, Pune in association with CSIR-NCL and ARI, Pune, to promote the usa of the official language in the field of science. Research articles in Hindi were invited under these 8 subtopics- Health, Bio Energy & Water Conservation, Biotechnology, Biodiversity & Environment, Skill Develoment & Employment Generation, Digital India, Make in India, Industrial Research. This received an overwhelming response, with 42 abstracts being received. From among these, 20 were shortlisted for presentation at the conference. The conference was inaugurated by the Chief Guest, Prof. Girishwar Mishra, renowned educationist, psychologist, sociologist, writer & editor, & ex-VC of the Mahatma Gandhi International Hindi University at Wardha. Dr. G. C. Mishra, Former Director, NCCS and the Directors of the host Institutes viz Dr. Manoj Kumar Bhat (NCCS), Dr. Ashwani Kumar Nangia (CSIR-NCL) and Dr. Prashant Dhakephalkar (ARI) shared the dais with the chief guest for the inaugural ceremony. An abstract book was released at the hands of the dignitaries present on the dais during the inaugural session. In his inaugural address, the Chief Guest emphasized the need to embrace the concept of development continuously. He also stressed that the outcomes of scientific activities need to reach policy makers, in addition to the general public, which can be best achieved through the language of the people. In addition, he stated that it is important to recognize the value of traditional knowledge, and that it needs to be connected to modern science through research. 125 participants from different institutes across India participated in the conference. Presentations were conducted in three different sessions on the same day. Senior scientists from the host institutes chaired these sessions. Dr. G. C. Mishra, chaired the Valedictory Session. In the Valedictory speech Dr. G. C. Mishra expressed the need to increase the use of Hindi in the field of science, for which we need to change our tendency to give less importance to Hindi and regional languages, as compared to English. This conference provided participants at all levels, such as students, scientists, technical staff members and Hindi officers, with an opportunity to present their work and other scientific concepts in simple language through the medium of Hindi. The success of the conference in reaching a wider audience was evident from the fact that it was appreciated by people from different backgrounds, including administrative staff. The entire event was co-ordinated by Mrs. Smita Khadkikar, Jr. Hindi Translator, NCCS, Dr (Mrs). Swati Chaddha, Hindi Officer, CSIR-NCL & Mrs. Manjusha Tiwari, Admin Officer, ARI. We received immense co-operation and support by Dr. Girdhari Lal, Dr. Shailja Singh, Dr. Jyoti Rao, Shri. Rameshwar Nema, Shri. Vijay Jinralkar, Mrs. Kirti Bhosale of NCCS, Dr. Rajesh Gonnade of CSIR-NCL and Dr. Sanjay Singh, Dr. Gurudatta Wagh of ARI as members of the Organising Committee of the conference.

NATIONAL CENTRE FOR CELL SCIENCE

An Autonomous Institute of
Department of Biotechnology, Govt of India
NCCS Complex, Savitribai Phule Pune University Campus,
Ganeshkhind, Shivaji Nagar Pune 411044.

AUDITED STATEMENTS OF ACCOUNT

FOR

F.Y. 2019-2020

AUDITORS

ASHOK PATIL & ASSOCIATES,
CHARTERED ACCOUNTANTS,
Flat No.1, Ranjeet Apartment, Walvekar Nagar, Opp Big Bazar,
Pune, Satara Road, Pune-411009.
Tel : 020-24227938
admin.dept@apa.org.in

INDEPENDENT AUDITOR'S REPORT

TO
THE DIRECTOR
NCCS Complex, P.B. No.40,
Ganesh Khind P.O.,
Pune-411007

Opinion

We have audited the accompanying standalone financial statements of **National Centre for Cell Science, (hereinafter referred as "the Institute"),** Situated at NCCS Complex, Pune University Campus, Ganesh Khind Road, Pune-411007, which comprise the Balance Sheet as at 31st March, 2020, the Statement of Income and Expenditure Account, Receipt and Payment Statement for the year then ended, and a summary of the significant accounting policies and other explanatory information prepared as per common format of accounts for all autonomous institutes as per letter no. BT/MED/NCCS/ADMN/2002/ Dt. 10th June 2002 of department of biotechnology, New Delhi and Comptroller and Auditor General of India letter no. OA-VII (MISC/CORRES/2002-03-1165 Dt. 16th October 2002.

In our opinion, the accompanying financial statements of the Institute are prepared, in all material respects, in accordance with aformentioned format for all autonomous institutes.

Basis for Opinion

We conducted our audit in accordance with Standards on Auditing (SAs). Our responsibilities under those Standards are further described in the Auditor's Responsibilities for the Audit of the Financial Statements section of our report. We are independent of the institute in accordance with the ethical requirements that are relevant to our audit of the financial statements, and we have fulfilled our other responsibilities in accordance with these requirements. We believe that the audit evidence we have obtained is sufficient and appropriate to provide a basis for our opinion.

Responsibilities of Management and Those Charged with Governance for the Financial Statements

Management is responsible for the preparation of the financial statements in accordance common format for autonomus institutions and for such internal control as management determines is necessary to enable the preparation of financial statements that are free from material misstatement, whether due to fraud or error.

In preparing the financial statements, management is responsible for assessing the institute's ability to continue as a going concern, disclosing, as applicable, matters related to going concern and using the going concern basis of accounting unless management either intends to liquidate the institute or to cease operations, or has no realistic alternative but to do so.

Those charged with governance are responsible for overseeing the Institute's financial reporting process.

Auditor's Responsibility

Our objectives are to obtain reasonable assurance about whether the financial statements as a whole are free from material misstatement, whether due to fraud or error, and to issue an auditor's report that includes our opinion. Reasonable assurance is a high level of assurance, but is not a guarantee that an audit conducted in accordance with SAs will always detect a material misstatement when it exists. Misstatements can arise from fraud or error and are considered material if, individually or in the aggregate, they could reasonably be expected to influence the economic decisions of users taken on the basis of these financial statements.

FOR ASHOK PATIL & ASSOCIATES
CHARTERED ACCOUNTANTS
FIRM REG. NO. 122045W

(SAURABH P. AGRAWAL)
PARTNER
M.NO.131312
UDIN NO.: 20131312AAAAFB1728

Date: 16/09/2020
Place: Pune

NATIONAL CENTRE FOR CELL SCIENCE, PUNE - 411 007.

SCHEDULES FORMING PART OF BALANCE SHEET AS ON 31.03.2020

BALANCE SHEET AS AT 31.03.2020

Amount (Rs.)

CORPUS/CAPITAL FUND AND LIABILITIES	Schedule	2019-20	2018-19
CORPUS/CAPITAL FUND	1	1,027,246,633.41	960,566,184.13
GENERAL RESERVE	2	-	-
EARMARKED/ENDOWMENT FUNDS	3	317,194,600.77	135,264,440.81
CURRENT-LIABILITIES & PROVISIONS	4	133,522,723.78	90,929,698.00
Total		**1,477,963,957.96**	**1,186,760,322.94**
ASSETS			
FIXED ASSETS	5	846,966,868.56	808,729,552.98
INVESMENTS - OTHERS	6	-	1,000.00
CURRENT ASSETS, LOANS, ADVANCES	7	630,997,089.40	378,029,769.96
MISCELLANEOUS EXPENDITURES (to the extent not written off or adjusted)			
Total		**1,477,963,957.96**	**1,186,760,322.94**
SIGNIFICANT ACCOUNTING POLICIES	15		
CONTINGENT LIABILITIES AND NOTES ON ACCOUNTS	16		

The schedules referred to above form an integral part of the Balance Sheet.
This is the Balance Sheet referred to in our report of even date.

EXAMINED AND FOUND CORRECT AS PER BOOKS OF ACCOUNT PRODUCED AND INFORMATION GIVEN, SUBJECT TO OUR SEPARATE REPORT OF EVEN DATE

Date: 16/09/2020
Place: Pune

FOR ASHOK PATIL & ASSOCIATES
CHARTERED ACCOUNTANTS
FIRM REG.NO. 122045W

राष्ट्रीय कोशिका विज्ञान केंद्र पुना

Officer 'C' Accounts
NCCS

वैभव अ. अरगडे
Vaibhav A. Argade
अधिकारी 'ग'(लेखा)
Officer 'C' (Accounts)
रा.को.वि.के./NCCS Pune-411007

ASHOK PATIL ASSOCIATES AURANGABAD

Director
NCCS

18/09/2020

मनोज कुमार भट, पीएच डी
निदेशक, एनसीसीएस, पुणे
Manoj Kumar Bhat, PhD
Director, NCCS, Pune

(SAURABH P. AGRAWAL)
PARTNER
M.NO.131312

NATIONAL CENTRE FOR CELL SCIENCE, PUNE - 411 007.

SCHEDULES FORMING PART OF BALANCE SHEET AS ON 31.03.2020

INCOME AND EXPENDITURE ACCOUNTS FOR THE YEAR ENDED 31.03.2020

Amount (Rs.)

INCOME	Schedule	2019-20	2018-19
INCOME FROM SALES/SERVICE	8	8,870,161.00	7,418,818.68
GRANTS/SUBSIDIES	9	450,000,000.00	465,000,000.00
FEES/SUBSCRIPTIONS	10	18,220.00	50,004.00
INTEREST EARNED	11	233,353.00	8,850,499.00
OTHER INCOME	12	1,982,768.00	2,747,804.00
TOAL (A)		**461,104,502.00**	**484,067,125.68**
EXPENDITURE			
ESTABLISHMENT EXPENSES	13	236,665,698.00	223,554,023.87
OTHER ADMINISTRATIVE EXPENSES	14	219,765,803.71	221,198,242.56
DEPRECIATION	5	117,992,551.01	112,392,830.45
TOTAL (B)		**574,424,052.72**	**557,145,096.88**
BALANCE BEING SURPLUS/(DEFICIT) CARRIED TO			
CORPUS/CAPITAL FUND		**(113,319,550.72)**	**(73,077,971.20)**
SIGNIFICANT ACCOUNTING POLICIES	15		
CONTINGENT LIABILITIES AND NOTES ON ACCOUNTS	16		

The schedules referred to above form an integral part of the Income & Expenditure Account.
This is the Income & Expenditure Account referred to in our report of even date.

EXAMINED AND FOUND CORRECT AS PER BOOKS OF ACCOUNT PRODUCED AND INFORMATION GIVEN, SUBJECT TO OUR SEPARATE REPORT OF EVEN DATE

Date: 16/09/2020
Place: Pune

FOR ASHOK PATIL & ASSOCIATES
CHARTERED ACCOUNTANTS
FIRM REG.NO. 122045W

राष्ट्रीय कोशिका विज्ञान केंद्र पुना

Officer 'C' Accounts
NCCS

वैभव अ. अरगडे
Vaibhav A. Argade
अधिकारी 'ग'(लेखा)
Officer 'C' (Accounts)
रा.को.वि.के./NCCS Pune-411007

ASHOK PATIL ASSOCIATES CHARTERED ACCOUNTANTS AURANGABAD

Director
NCCS

18/09/2020
मनोज कुमार भट, पीएच डी
निदेशक, एनसीसीएस, पुणे
Manoj Kumar Bhat, PhD
Director, NCCS, Pune

(SAURABH P. AGRAWAL)
PARTNER
M.NO.131312

NATIONAL CENTRE FOR CELL SCIENCE, PUNE - 411 007.
RECEIPTS & PAYMENTS ACCOUNTS FOR THE YEARR ENDED 31ST MARCH 2020

Amount (Rs.)

Receipts	Amounts	Amounts	Payments	Amounts	Amounts
Opening Balance		354,844,271.36	**Current Liabilities**		504120361.09
Bank Accounts			Hostel Charges Recovery-Payable	145,510.00	
NCCS Bank Accounts			Medical Insurance -Payable	54,942.00	
Axis BANK	219,091.00		Dr Mitra - Pension Contribution Payable	475,785.00	
Bank of India - 4911	153,289,219.42		Duties & Taxes	43,724,438.00	
State Bank of India	29,326,137.79		Sundry Creditors	293,596,253.09	
Project Bank Account			Salary Payable	164,898,748.00	
Bank Of India 4912	171,959,823.15		Security Deposit	257,026.00	
Cash-in-hand	50,000.00		Earnest Money Deposit	327,050.00	
			payable	640,609.00	
Current Liabilities		1,379,758.00			
Conti-Welfare Fund	101,946.00		**Fixed Assets**		125,136,744.59
PBG	723,288.00		Library	2,261,620.94	
Student - Caution Money	554,524.00		Equipments	121,774,515.65	
			Advance-Central Public Works Department	1,099,108.00	
Current Assets		24,271,386.20	Furniture and fixture	1,500.00	
Sundry Debtors	21,946,286.20				
Receivable	2,325,100.00		**Current Assets**		2,876,480.00
Sales Accounts		943,680.00	Loans & Advances (Asset)	2,876,480.00	
Income From Salaes and Services	903,680.00				
NCMR Income From Sales & Services	40,000.00				
			Earmarked Fund		188,682,238.44
Indirect Incomes		6,958,246.38			
Interest Earned	6,498,989.38		**ESTABLISHMENT EXPENSES**		29,541,487.00
Audotorium charges	16,000.00		Admin Charges	484,887.00	
Cont-mis income	1,220.00		Salaries	29,056,600.00	
Guest house charges	332,961.00				
Interest on HBA	30,856.00		**OTHER ADMINISTRATIVE EXPENSES**		41,328,904.51
Tender Fees	18,220.00		Bank Charges	24,725.23	
Transit house charges	60,000.00		Eligibility Fees	7,600.00	
			Rent Rates and Taxes	22,026,386.00	
CORPUS/CAPITAL FUND		180,000,000.00	Consumables	9,678,293.68	
Corpus/Capital Fund	180,000,000.00		Contingencies	6,741,667.60	
			TA-DA	2,850,232.00	
Earmarked Fund		541473735.49			
			PROVISION		59,934,482.00
FEES/SUBSCRIPTIONS			Provision for works on contract	45,811,017.00	
Tender Fees			Provision for leave encashment and graduity	10,762,835.00	
			Provision for electricity and power	3,360,630.00	
GRANTS/SUBSIDIES		450,000,000.00			
Grant in Aid General	210,000,000.00		**Closing Balance**		
Grant in Aid Salary	240,000,000.00		Bank Accounts		609,751,758.80
			Axis BANK	226,883.00	
Other Income		1,501,379.00	Bank of India - 4911	241,028,375.26	
Application Fees	46,084.00		State Bank of India	9,756,702.73	
Hostel Room Charges	129,292.00		Bank Of India 4912	346,483,323.31	
Ph.D Fees	1,180,100.00		Cash-in-hand	128,742.00	
hostel charges recovery	145,903.00		Bank of India-SERB 8403	12,127,732.50	
Total		**1,561,372,456.43**	**Total**		**1,561,372,456.43**

SIGNIFICANT ACCOUNTING POLICIES **SCH "15"**
CONTINGENT LIABILITIES AND NOTES ON ACCOUNTS **SCH "16"**

The schedules referred to above form an integral part of the Receipts & Payments Account.
This is the Receipts & Payments Account referred to in our report of even date.

EXAMINED AND FOUND CORRECT AS PER BOOKS OF ACCOUNT PRODUCED AND INFORMATION GIVEN, SUBJECT TO OUR SEPARATE REPORT OF EVEN DATE

Date: 16/09/2020
Place: Pune

वैभव अ. अरगडे
Vaibhav A. Argade
Officer 'C' Accounts
NCCS
अधिकारी 'ग'(लेखा)
Officer 'C' (Accounts)
रा.को.वि.के./NCCS Pune-411007

18/09/2020
मनोज कुमार भट, पीएच डी
निदेशक, एनसीसीएस, पुणे
Director
NCCS
Manoj Kumar Bhat, PhD
Director, NCCS, Pune

ASHOK PATIL ASSOCIATES AURANGABAD CHARTERED ACCOUNTANTS

FOR ASHOK PATIL & ASSOCIATES
CHARTERED ACCOUNTANTS
FIRM REG.NO. 122045W

(SAURABH P. AGRAWAL)
PARTNER
M.NO.131312

NATIONAL CENTRE FOR CELL SCIENCE, PUNE - 411 007.

SCHEDULES FORMING PART OF BALANCE SHEET AS ON 31.03.2020

SCHEDULE 1 - CORPUS/CAPITAL FUND

(Amount-Rs.)

Particulars	2019-20	2018-19
SCHEDULE 1- CORPUS/CAPITAL FUND:		
Balance at the beginning of the year	960,566,184.13	883,644,155.33
Add /(Deduct) : Balance of net income /(expenditure)	-	-
Deduct : Capital grants written off	-	-
	960,566,184.13	883,644,155.33
Add : Contribution towards Capital Fund	180,000,000.00	150,000,000.00
Add : General Reserve		
	1,140,566,184.13	1,033,644,155.33
Add/(Deduct) : Bal. Of net income/(expenditure) transferred from the Income and Expenditure A/c.	(113,319,550.72)	(73,077,971.20)
BALANCE AS AT THE YEAR - END	**1,027,246,633.41**	**960,566,184.13**

NATIONAL CENTRE FOR CELL SCIENCE, PUNE - 411 007.

SCHEDULES FORMING PART OF BALANCE SHEET AS ON 31.03.2020

SCHEDULE 2 -GENERAL RESERVE

Amount (Rs.)

Particulars	2019-20	2018-19
General Reserve	-	-
Grand Total	-	-

NATIONAL CENTRE FOR CELL SCIENCE, PUNE - 411 007.

SCHEDULES FORMING PART OF BALANCE SHEET AS ON 31.03.2020

SCHEDULE-3 EARMARKED/ENDOWMENT FUND

(Amount-Rs.)

SR. No.	Name of the Project & P.I.	Opening Balance	Additions Grant. Recd.	Interest & Other Recd.	Total	Utilization/Expenditure			Closing Balance
						Capital	Revenue	Total	
1	AB/JK/DBT-RA-DR. AJINKYA BENDRE	574,520.00	201,780.00	8,005.00	784,305.00	-	745,211.00	745,211.00	39,094.00
2	AB/MW/BIOCARE/07/9813-AMRUTA BARHANPURKAR	(288,776.00)	-	-	(288,776.00)	-	-	-	(288,776.00)
3	AC/SERB/CRG/004981-DR. AKANKSHA CHATURVEDI	-	2,490,133.00	-	2,490,133.00	-	-	-	2,490,133.00
4	AM/BT/PR-25893-DR. MAJUMDAR	1,861,280.00	1,000,000.00	70,858.00	2,932,138.00	753,224.00	518,011.66	1,271,235.66	1,660,902.34
5	AM/DBT-WELLCOME-DR. MAJUMDAR	789,531.00	5,245,459.00	110,332.00	6,145,322.00	238,475.00	6,826,326.14	7,064,801.14	(919,479.14)
6	AM/ECR/SERB/000429-DR. MAJUMDAR	(95,038.00)	2,200,000.00	13,979.00	2,118,941.00	-	910,463.00	910,463.00	1,208,478.00
7	AN/MW/SR/WOS-A/LS-25-DR. AMRUTA NAIK	910,000.00	-	13,300.00	923,300.00	-	1,094,084.00	1,094,084.00	(170,784.00)
8	AS/BT/PR-10708-DR. SHIRAS	213,076.00	-	-	213,076.00	-	213,076.00	213,076.00	-
9	AS/BT/PR-10852-DR. SHIRAS	382,793.00	-	7,776.00	390,569.00	-	262,831.00	262,831.00	127,738.00
10	AS/BT/PR-15178-DR. SHIRAS	788,660.00	1,370,835.00	18,677.00	2,178,172.00	-	592,127.00	592,127.00	1,586,045.00
11	AS/BT/PR-28506-DR. A K SAHU	2,504,800.00	-	53,389.00	2,558,189.00	-	1,616,811.00	1,616,811.00	941,378.00
12	AS/BT/PR8739-DR. SHIRAS	389,191.00	-	3,480.00	392,671.00	-	332,097.00	332,097.00	60,574.00
13	AS/BT/PR-9725-DR. A K SAHU	(193,404.00)	-	-	(193,404.00)	-	-	-	(193,404.00)
14	AS/DST/IPSC (CORE)-DR. SHIRAS	-	3,000,000.00	22,420.00	3,022,420.00	-	-	-	3,022,420.00
15	AS/DST/VI-D&P/551-DR. SHIRAS	(642,872.00)	9,000,000.00	17,909.00	8,375,037.00	6,386,134.74	3,170,577.00	9,556,711.74	(1,181,674.74)
16	AS/ICMR/90-DR. SHIRAS	68,324.00	1,047,303.00	14,547.00	1,130,174.00	-	1,130,174.00	1,130,174.00	-
17	AS/PR-14258-DR. SHIRAS	(73,843.00)	-	-	(73,843.00)	-	-	-	(73,843.00)
18	AS/UNILEVER-DR. SHIRAS	926,992.00	-	-	926,992.00	-	255,078.00	255,078.00	671,914.00
19	AS/WELLCOME-DR. AVINASH SHARMA	-	1,829,446.00	16,863.00	1,846,309.00	297,318.00	793,436.00	1,090,754.00	755,555.00
20	ASHWINI DHAMANGE/GM/NASI/620/3	435,480.00	500,520.00	6,007.00	942,007.00	-	561,600.00	561,600.00	380,407.00
21	AY/YS/EEQ/2016/000752-DR. AMIT YADAV	40,466.00	700,000.00	9,419.00	749,885.00	-	590,687.00	590,687.00	159,198.00
22	AY/IPWG-SPAIN-DR. AMIT YADAV	-	122,534.00	-	122,534.00	-	122,534.00	122,534.00	-
23	AY/SEB/000889/CONFERENCE-DR. AMIT YADAV	-	150,000.00	-	150,000.00	-	145,243.00	145,243.00	4,757.00
24	BAHIR/WOS-LS-602-DR. BAHIR	(234,983.00)	1,100,000.00	-	865,017.00	-	781,048.00	781,048.00	83,969.00
25	BHATNAGAR AWARD-DR. KUNDU	-	75,000.00	-	75,000.00	-	30,000.00	30,000.00	45,000.00
26	BIVALKAR/WOS-A/LS/2016-DR. BIVALKAR	(49,772.00)	500,000.00	71.00	450,299.00	-	610,752.00	610,752.00	(160,453.00)
27	BK/SR/DBT-RA/DR. BHARGAB KALITA	-	562,020.00	1,275.00	563,295.00	-	561,938.00	561,938.00	1,357.00
28	BS/INFECT-ERA/33-DR. BHASKAR SAHA	1,509,185.00	-	19,855.00	1,529,040.00	-	1,607,081.00	1,607,081.00	(78,041.00)
29	BS/BT/PR10785 - DR. SAHA	(460,986.00)	-	-	(460,986.00)	-	-	-	(460,986.00)
30	BS/BT/PR-718-DR. SAHA-27.09.11TO26.09.16	(656,982.00)	-	-	(656,982.00)	-	-	-	(656,982.00)
31	BS/BT/PR-7505-DR. BHASKAR SAHA	(117,090.00)	-	-	(117,090.00)	-	-	-	(117,090.00)

(Amount-Rs.)

SR. No.	Name of the Project & P.I.	Opening Balance	Additions Grant. Recd.	Interest & Other Recd.	Total	Utilization/Expenditure			Closing Balance
						Capital	Revenue	Total	
32	BS/DST/INDO-UK/P-123-DR. SAHA	1,129,852.00	-	14,243.00	1,144,095.00	-	1,176,065.00	1,176,065.00	(31,970.00)
33	BS/PR-14435-DR. SAHA	(421,933.00)	-	-	(421,933.00)	-	-	-	(421,933.00)
34	BS/SERB/JCB-DR. SAHA	1,719,840.00	1,100,000.00	36,832.00	2,856,672.00	-	1,900,000.00	1,900,000.00	956,672.00
35	CICS-ISRF FELLOWSHIP-MR. SUJIT SHAH	8,450.00	-	277.00	8,727.00	-	-	-	8,727.00
36	CSIR	(25,480,721.05)	6,157,680.00	-	(19,323,041.05)	-	561,872.00	561,872.00	(19,884,913.05)
37	CSIR-RA FELLOWSHIP	(1,325,946.00)	-	-	(1,325,946.00)	-	-	-	(1,325,946.00)
38	DBT-BINC FELLOWSHIP	146,760.00	378,210.00	1,417.00	526,387.00	-	263,950.00	263,950.00	262,437.00
39	DBT FELLOWSHIP	(3,518,375.00)	15,773,901.00	14,796.00	12,270,322.00	-	12,322,717.00	12,322,717.00	(52,395.00)
40	DBT-JRF PROGRAMME	369,213.00	-	8,410.00	377,623.00	-	-	-	377,623.00
41	DBT - PDF PROGRAMME	2,225,233.00	-	69,006.00	2,294,239.00	-	-	-	2,294,239.00
42	DBT RAMLINGASWAMY CONCLAVE CD318	(85,735.00)	85,735.00	-	-	-	-	-	-
43	DBT TWAS FELLOWSHIP	-	858,400.00	2,885.00	861,285.00		361,871.00	361,871.00	499,414.00
44	DM/BIRAC-DR. MITRA	245,479.00	-	2,699.00	248,178.00	-	470,807.00	470,807.00	(222,629.00)
45	DM/BT/HRD/35/01/03-DR.MITRA	(46,996.00)	-	-	(46,996.00)	-	-	-	(46,996.00)
46	DM/BT/PR-14226-DR. MITRA	(476,857.00)	-	-	(476,857.00)	-	-	-	(476,857.00)
47	DM/BT/PR-15450-DR. MITRA	(50,028.00)	1,547,067.00	13,715.00	1,510,754.00	-	1,716,447.00	1,716,447.00	(205,693.00)
48	DM/JCB/18-19-DR. MITRA	167,574.00	-	2,158.00	169,732.00	-	166,674.00	166,674.00	3,058.00
49	DM/SERB/003331-DR. MITRA	798,846.00	-	16,378.00	815,224.00	-	817,804.00	817,804.00	(2,580.00)
50	DM/THSTI-DR. MITRA	(18,445.00)	-	-	(18,445.00)	-	-	-	(18,445.00)
51	DP/PACER-POP/BS-01-DR. DHIRAJ PAUL	-	1,199,000.00	14,463.00	1,213,463.00		557,571.00	557,571.00	655,892.00
52	DP/YSS/SER8/2015/000513-DR. DHIRAJ PAUL	43,500.00	-	-	43,500.00	-	43,500.00	43,500.00	-
53	DS/BATTELE INDIA-DR. DEEPA	(22,472.00)	-	-	(22,472.00)	-	-	-	(22,472.00)
54	DS/BT/PR-25883 - DR. DEEPA	1,720,912.00	-	38,008.00	1,758,920.00	292,667.00	1,433,062.66	1,725,729.66	33,190.34
55	DS/BT/PR-30450-DR. DEEPA	-	1,761,280.00	27,237.00	1,788,517.00		1,255,967.78	1,255,967.78	532,549.22
56	DST INSPIRE FELLOWSHIP	(2,204,489.00)	2,305,606.00	859.00	101,976.00	-	1,552,054.00	1,552,054.00	(1,450,078.00)
57	DS/WELLCOMETRUST-DR. DEEPA	2,281,078.58	53,950.00	47,122.00	2,382,150.58	23,190.00	1,792,688.00	1,815,878.00	566,272.58
58	GD/SB/S2/RJN-048/2017-DR. GAURAV DAS	(58,070.00)	825,000.00	7,866.00	774,796.00	-	703,740.00	703,740.00	71,056.00
59	GK/5TH INTERNATIONAL CONF. TRANSLATION RES.-DR. KUNDU	-	741,463.44	-	743,963.44	-	460,430.00	460,430.00	283,533.44
60	GK/BT/MED/30/VNCI-Hr/BRCA-DR. KUNDU	1,078,190.00	-	24,445.00	1,102,635.00	-	1,366,617.00	1,366,617.00	(263,982.00)
61	GK/BT/PR-14430-DR. KUNDU	101,267.00	-	5,238.00	106,505.00	-	-	-	106,505.00
62	GK/BT/PR-2573-DR.KUNDU	(352,346.00)	-	-	(352,346.00)		-	-	(352,346.00)
63	GK/BT/PR-28794-DR. KUNDU	1,661,600.00	137,760.00	36,994.00	1,836,354.00	-	1,372,303.24	1,372,303.24	464,050.76
64	GK/BT/PR-3021-DR.KUNDU	(368,191.00)	-	-	(368,191.00)		-	-	(368,191.00)
65	GK/BT/PR-4569 - DR. KUNDU	(108,652.00)	-	-	(108,652.00)		-	-	(108,652.00)

(Amount-Rs.)

SR. No.	Name of the Project & P.I.	Opening Balance	Additions Grant. Recd.	Interest & Other Recd.	Total	Utilization/Expenditure			Closing Balance
						Capital	Revenue	Total	
66	GK/BT/PR-7665-DR. KUNDU	(483,620.00)	-	-	(483,620.00)	-	29,166.00	29,166.00	(512,786.00)
67	GK/CSIR-DR. KUNDU	(47,957.00)	-	-	(47,957.00)	-	-	-	(47,957.00)
68	GK/DST/IMRCD/INNO-INDIGO-DR. KUNDU	1,199,780.00	-	16,941.00	1,216,721.00	-	1,019,068.00	1,019,068.00	197,653.00
69	GK/MANAV/BT/PR-27731-DR. KUNDU	29,455,000.00	-	764,418.00	30,219,418.00	484,650.00	5,900,386.00	6,385,036.00	23,834,382.00
70	GK/PR-12730-DR. KUNDU	(534,424.00)	-	-	(534,424.00)	-	-	-	(534,424.00)
71	GK/BT/PR-17945	-	350,000.00	5,894.00	355,894.00	-	299,255.00	299,255.00	56,639.00
72	GK/SERB/002298-DR. KUNDU	-	1,728,000.00	15,860.00	1,743,860.00		356,438.00	356,438.00	1,387,422.00
73	GK/SR/SO/HS-70-DR. KUNDU	(332,350.00)	-	-	(332,350.00)	-	-	-	(332,350.00)
74	GL/BT/03/IYBA-DR. LAL	(562,237.00)	-	-	(562,237.00)	-	-	-	(562,237.00)
75	GL/BT/PR-14156-DR. LAL	440,608.00	1,631,395.00	22,695.00	2,094,698.00	-	1,064,584.00	1,064,584.00	1,030,114.00
76	GL/BT/PR-15533-DR. LAL	167,910.00	1,509,106.00	18,689.00	1,695,705.00	-	2,371,379.46	2,371,379.46	(675,674.46)
77	GL/DST/SJF/LSA-01-DR. LAL	-	4,921,280.00	87,274.00	5,008,554.00	-	1,384,994.14	1,384,994.14	3,623,559.86
78	GL/EMR/2016/007108-DR. LAL	738,338.00	868,000.00	9,062.00	1,615,400.00	464,779.00	315,994.00	780,773.00	834,627.00
79	GL/KEMHRC-DR. LAL	1,222,367.00	-	-	1,222,367.00	-	161,676.00	161,676.00	1,060,691.00
80	GL/KEMHRC-II-DR. LAL	-	13,011,950.00	-	13,011,950.00	80,171.00	6,860,048.00	6,940,219.00	6,071,731.00
81	GM/NASI PLATINUM JUBILEE CHAIR-DR. MISHRA	1,664,900.00	2,585,433.00	42,553.00	4,292,886.00	-	3,207,583.00	3,207,583.00	1,085,303.00
82	ICMR	(2,783,182.02)	2,755,216.00	-	(27,966.02)	-	2,757,988.00	2,757,988.00	(2,785,954.02)
83	INSPIRE FACULTY AWARD-DEEPIKA PURI	745,061.00	2,431,096.00	18,237.00	3,194,394.00	-	2,042,225.00	2,042,225.00	1,152,169.00
84	INSPIRE FACULTY AWARD-DR. DEBASRI MUKHARJEE	(42,253.00)	-	-	(42,253.00)	-	-	-	(42,253.00)
85	INSPIRE FACULTY AWARD-DR. JYOTI SINGH	-	-	-	-	-	3,497.00	3,497.00	(3,497.00)
86	INSPIRE FACULTY AWARD-PRIYANKA DUTTA	457,599.00	2,299,000.00	27,562.00	2,784,161.00	-	2,244,070.00	2,244,070.00	540,091.00
87	INTRAMURAL PROJECT-IM-001	2,009,309.00	2,500,000.00	43,572.00	4,552,881.00	-	5,252,705.74	5,252,705.74	(699,824.74)
88	INTRAMURAL PROJECT-IM-002	-	3,280,000.00	12,220.00	3,292,220.00		1,368,846.80	1,368,846.80	1,923,373.20
89	IUSSTF-SONALI JATHAR	-	-	-	-	-	-	-	-
90	IUSSTF FELLOWSHIP	12,500.00	-	285.00	12,785.00	-	-	-	12,785.00
91	JJ/BT/PR-14537-DR.JOSEPH	(488,490.00)	-	-	(488,490.00)	-	-	-	(488,490.00)
92	JJ/BT/PR-27451-DR. JOSEPH	2,743,129.00	-	45,444.00	2,788,573.00	445,353.00	1,994,070.00	2,439,423.00	349,150.00
93	JJ/PR-727-DR. JOSEPH	(259,430.00)	-	-	(259,430.00)	-	-	-	(259,430.00)
94	JJ/SERB/001092	(85,886.00)	-	-	(85,886.00)	-	-	-	(85,886.00)
95	JK/DBT/WELLCOME-DR.JANESHKUMAR	1,757,559.00	119,989.00	45,382.00	1,922,930.00	10,598.00	1,444,852.00	1,455,450.00	467,480.00
96	JS/WELLCOME - DR. JYOTI SINGH	36,219.00	4,578,061.00	79,433.00	4,693,713.00	168,399.00	2,143,434.00	2,311,833.00	2,381,880.00
97	LL/BT/PR-11928-DR. LIMAYE	195,574.00	1,402,863.00	12,544.00	1,610,981.00	-	1,061,503.00	1,061,503.00	549,478.00
98	LL/BT/PR-12696-DR. LIMAYE	346,542.50	1,484,239.00	15,854.00	1,846,635.50	-	1,803,738.40	1,803,738.40	42,897.10
99	LL/BT/PR-23620-DR. LIMAYE	12,865.00	342,406.00	5,225.00	360,496.00	-	149,768.00	149,768.00	210,728.00

ASHOK PATIL ASSOCIATES AURANGABAD CHARTERED ACCOUNTANTS

(Amount-Rs.)

SR. No.	Name of the Project & P.I.	Opening Balance	Additions Grant. Recd.	Interest & Other Recd.	Total	Utilization/Expenditure			Closing Balance
						Capital	Revenue	Total	
100	LL/DAE/37B/BRNS-DR. LIMAYE	(108,965.00)	-	-	(108,965.00)	-	-	-	(108,965.00)
101	LL/JAI RESEARCH FOUNDATION-DR. LIMAYE	(2,167,671.00)	1,819,952.00	-	(347,719.00)	-	2,199,087.00	2,199,087.00	(2,546,806.00)
102	MB/BIRAC/BT/CRS0400/PACE-DR. BHAT	555,000.00	370,000.00	11,161.00	936,161.00	-	720,074.00	720,074.00	216,087.00
103	MB/BT/PR-23968 - DR. BHAT	-	81,379,440.00	-	81,379,440.00	-	-	-	81,379,440.00
104	MB/ITC/CONSULTANCY - DR. BHAT	823,389.00	-	-	823,389.00	-	-	-	823,389.00
105	MS/BT/PR-15889-DR. SANTRA	145,779.00	-	2,726.00	148,505.00	-	309,154.00	309,154.00	(160,649.00)
106	MS/BT/PR-25181-DR. MANAS SANTRA	699,992.00	-	15,384.00	715,376.00	-	567,101.00	567,101.00	148,275.00
107	MS/CSIR/37/(1655)/15/EMR-II-DR. SANTRA	33,962.00	186,620.00	1,896.00	222,478.00	-	183,820.00	183,820.00	38,658.00
108	MS/EMR/002277-DR. SANTRA	(567,584.00)	1,500,000.00	-	932,416.00	(74,146.00)	486,788.00	412,642.00	519,774.00
109	MS/HRD/NBA/39-DR. MANAS SANTRA	500,000.00	-	7,668.00	507,668.00	-	479,799.00	479,799.00	27,869.00
110	MS/PR-152/TWINNING-DR. MANAS SANTRA	55.00	-	1.00	56.00	-	-	-	56.00
111	MS/UNILEVER-DR. SANTRA	2,000,399.50	-	-	2,000,399.50	-	-	-	2,000,399.50
112	MW/BHU-DR. WANI	285,529.00	-	3,884.00	289,413.00	-	269,086.00	269,086.00	20,327.00
113	MW/HRD/35/01/04/2018-DR. WANI	58,707.00	841,000.00	11,251.00	910,958.00	-	377,307.00	377,307.00	533,651.00
114	MW/SERB/004441-DR. WANI	1,316,667.00	-	27,503.00	1,344,170.00	-	1,262,184.00	1,262,184.00	81,986.00
115	MW/SPPU/AYUSH-DR. WANI	400,716.00	400,000.00	10,856.00	811,572.00	-	348,892.00	348,892.00	462,680.00
116	NAM S&T FELLOWSHIP	7,417.00	-	232.00	7,649.00	-	-	-	7,649.00
117	NAS/141/7/2014-15-DR. RANI LEKHA	(234,000.00)	-	-	(234,000.00)	-	-	-	(234,000.00)
118	NE/SB/FT/CS-067/2014-DR. N D ERANDE	(75,165.00)	-	-	(75,165.00)	-	-	-	(75,165.00)
119	NL/BT/MUTAGENESIS(INDO AUS) DR.LENKA	(187,406.00)	174,198.00	-	(13,208.00)	-	-	-	(13,208.00)
120	NL/BT/PR-16655-DR. LENKA	677,485.00	-	14,725.00	692,210.00	-	417,815.00	417,815.00	274,395.00
121	NL/BT/PR-8219/31.03.14-30.03.16-Dr. Lenka	(110,957.00)	-	-	(110,957.00)	-	-	-	(110,957.00)
122	NL/ICMR/47/80-DR. LENKA	182,660.00	-	5,664.00	188,324.00	-	-	-	188,324.00
123	OP/EMR/2016/006589-DR. OM PRAKASH	581,612.00	-	13,959.00	595,571.00	-	673,741.00	673,741.00	(78,170.00)
124	OP/YSS/BT/PR-13969-DR. OM PRAKASH	131,544.00	-	2,187.00	133,731.00	-	378,208.00	378,208.00	(244,477.00)
125	PD/SERB/CRG/001727-DR. PRIYANKA DUTTA	-	364,000.00	-	364,000.00	-	24,000.00	24,000.00	340,000.00
126	PN/BT/NBM0166/04/19/BIRAC-DR. NAGVENKAR	-	122,316,000.00	228,527.00	122,544,527.00	-	-	-	122,544,527.00
127	PR/BT/IN/INDO-US/FOLDSCOPE/39-DR. PRAVEEN RAHI	293,673.00	31,388.00	5,621.00	330,682.00	-	308,114.00	308,114.00	22,568.00
128	PR/NMHS-DR. PRAVEEN RAHI	-	1,277,000.00	23,679.00	1,300,679.00	-	497,126.00	497,126.00	803,553.00
129	Project Overheads	17,959,881.96	3,675,441.00	-	21,635,322.96	-	1,274,448.80	1,274,448.80	20,360,874.16
130	PR/YSS/SERB/2015/000149 - DR. PRAVEEN RAHI	138,977.00	-		138,977.00		138,977.00	138,977.00	-
131	PS/DBT RA-DR. PARSHURAM SONAWANE	-	183,580.00	-	183,580.00		58,280.00	58,280.00	125,300.00
132	PS/ICMR/53/6/BM-DR. PADMA SHASTRY	(660,992.00)	-	-	(660,992.00)	-	-	-	(660,992.00)
133	PUNE BIOCLUSTER-DR. SHEKHAR MANDE	91,387,966.00	-	2,426,220.00	93,814,186.00	30,180,305.22	7,388,224.00	37,568,529.22	56,245,656.78

ASHOK PATIL ASSOCIATES AURANGABAD CHARTERED ACCOUNTANTS

(Amount-Rs.)

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						Capital	Revenue	Total	
134	PV/JJ/DBT-RA-PALLAVI VARSHNEY	141,643.00	68,880.00	2,265.00	212,788.00	-	215,519.00	215,519.00	(2,731.00)
135	RC/BT/PR-15450-DR. RADHA CHAUHAN	(869,546.00)	1,505,831.00	1,697.00	637,982.00	-	917,935.00	917,935.00	(279,953.00)
136	RC/BT/PR-26398-DR. RADHA CHAUHAN	1,726,107.00	-	43,399.00	1,769,506.00	-	1,058,515.00	1,058,515.00	710,991.00
137	RC/BT/PR7118/15-18-DR. RADHA CHAUHAN	(96,573.00)	-	-	(96,573.00)	-	-	-	(96,573.00)
138	RC/SB/SO/BB-0030/13-16-DR.RADHA CHAUHAN	(246,623.00)	-	-	(246,623.00)	-	-	-	(246,623.00)
139	RC/SERB/000272-DR. RADHA CHAUHAN	153,778.00	857,000.00	3,226.00	1,014,004.00	-	221,979.00	221,979.00	792,025.00
140	RL/SR/WOS-A/LS-456-DR. RANI LEKHA	871,269.00	-	19,041.00	890,310.00	-	596,681.00	596,681.00	293,629.00
141	RS/BT/PR-25368-DR. ROHIT SHARMA	609,081.00	-	11,175.00	620,256.00	-	526,653.00	526,653.00	93,603.00
142	RS/BT/PR-25490-DR. ROHIT SHARMA	202,450.00	-	3,237.00	205,687.00	-	390,928.00	390,928.00	(185,241.00)
143	RS/BT/PR-29526-DR. ROHIT SHARMA	1,111,280.00	-	21,664.00	1,132,944.00	395,483.00	796,090.00	1,191,573.00	(58,629.00)
144	SANDHYA/DAE/35/14/31-BRNS-DR. SANDHYA	620,759.00	-	16,625.00	637,384.00	-	254,790.00	254,790.00	382,594.00
145	SANDHYA/SR/SO/BB-0119-DR.SANDHYA	(33,598.00)	-	-	(33,598.00)	-	-	-	(33,598.00)
146	SB/BT/11465-DR. BAPAT	(372,384.00)	-	-	(372,384.00)	-	-	-	(372,384.00)
147	SB/HRD-35/01/04-DR. BAPAT	(15,783.00)	890,000.00	9,920.00	884,137.00	-	805,457.00	805,457.00	78,680.00
148	SB/BT/INDO-FINNISH-DR. BAPAT	(174,378.00)	-	-	(174,378.00)	-	-	-	(174,378.00)
149	SB/CRG/2019/001157 - DR. BAPAT	-	2,262,120.00	-	2,262,120.00	-	146,000.00	146,000.00	2,116,120.00
150	SB/GODAVARI BIOREFINERIES-DR. BAPAT	18,600.00	-	-	18,600.00	-	-	-	18,600.00
151	SB/INDO AUSTRALIA SYMPOSIUM-DR. BAPAT	(16,664.00)	-	-	(16,664.00)	-	-	-	(16,664.00)
152	SC/AMRITA THERAPEUTICS-DR. SAMIT	(108,000.00)	-	-	(108,000.00)	-	-	-	(108,000.00)
153	SC/BT-11381-DR.SAMIT	(530,464.00)	-	-	(530,464.00)	-	-	-	(530,464.00)
154	SC/BT/8068-DR. SAMIT CHATTOPADHYAY	(152,055.00)	152,055.00	-	-	-	-	-	-
155	SC/CSIR/37(1572)-DR.SAMIT	(227,473.00)	-	-	(227,473.00)	-	-	-	(227,473.00)
156	SC/SB/S2/JCB-II/2013-18-DR.SAMIT	-	2,600,000.00	19,241.00	2,619,241.00		2,488,695.00	2,488,695.00	130,546.00
157	SC/SB/S2/JCB/2013-18-DR.SAMIT	(406,008.00)	-	-	(406,008.00)	-	(406,008.00)	(406,008.00)	-
158	SERB PDF	1,542,322.00	2,133,575.00	50,165.00	3,726,062.00	-	2,597,659.28	2,597,659.28	1,128,402.72
159	SK/YS/BT/PR-19641-DR. SNEHAL KULKARNI	273,805.00	1,441,147.00	7,161.00	1,722,113.00	-	985,117.00	985,117.00	736,996.00
160	SM/BT/47/TE/TBP-DR. MANDE	(90,175.00)	-	-	(90,175.00)	-	-	-	(90,175.00)
161	SM/BT/IN/NEW INDIGO/05/SB/TB-OMICS-DR.MANDE	(32,671.30)	-	-	(32,671.30)	-	-	-	(32,671.30)
162	SM/BT/NEW INDIGO/18-DR. MANDE	(659,959.00)	-	-	(659,959.00)	-	-	-	(659,959.00)
163	SM/BT/PR-15450 (CORE GRANT)-DR. MANDE	4,378,566.00	-	74,663.00	4,453,229.00	3,186,782.00	858,199.00	4,044,981.00	408,248.00
164	SM/BT/PR-15450 (PROJECT 1)-DR. MANDE	(160,235.00)	1,687,039.00	13,695.00	1,540,499.00		1,802,744.00	1,802,744.00	(262,245.00)
165	SM/BT/PR-25395-DR. MANDE	497,377.00	-	13,086.00	510,463.00		218,211.00	218,211.00	292,252.00
166	SM/BT/PR-3260/BRB/2012-17	170,086.00	-	5,252.00	175,338.00	-	-	-	175,338.00
167	SM/BT/PR-7265-DIRECTOR,NCCS	249,575.00	-	7,739.00	257,314.00	-	-	-	257,314.00

ASHOK PATIL ASSOCIATES AURANGABAD CHARTERED ACCOUNTANTS

(Amount-Rs.)

SR. No.	Name of the Project & P.I.	Opening Balance	Additions Grant. Recd.	Interest & Other Recd.	Total	Utilization/Expenditure			Closing Balance
						Capital	Revenue	Total	
168	SM/DST/INDO-RUSSIA/23.04.14-22.04.16-Dr. Mande	(107,683.00)	-	-	(107,683.00)	-	-	-	(107,683.00)
169	SM/DST/INT/RFBR/P-89-DR. MANDE	(238,142.00)	-	-	(238,142.00)	-	-	-	(238,142.00)
170	SM/DST/SPAIN/P-26/23.7.12-22.7.15-DR. MANDE	(430,348.00)	-	-	(430,348.00)	-	-	-	(430,348.00)
171	SR/BT/PR-10536-DR. SRIKANTH	(28,775.00)	-	-	(28,775.00)	-	-	-	(28,775.00)
172	SR/BT/PR-10855-DR. SRIKANTH	656,706.00	2,360,603.00	38,447.00	3,055,756.00	-	2,366,104.00	2,366,104.00	689,652.00
173	SR/BT/PR-4152/BRB/2013-DR.SRAPOLE	(44,269.00)	-	-	(44,269.00)	-	-	-	(44,269.00)
174	SR/DST/IMRCD/INNO-INDIGO-DR. SRIKANTH	585,495.00	-	5,635.00	591,130.00	-	816,866.00	816,866.00	(225,736.00)
175	SS/BT/PR-10286-DR. S SINGH	74,728.00	-	890.00	75,618.00	-	122,836.00	122,836.00	(47,218.00)
176	SS/BT/PR-16065-DR. S SINGH	(32,617.00)	-	-	(32,617.00)	-	298,330.00	298,330.00	(330,947.00)
177	SS/NATL. CONF. ON EMERGING TRENDS-REGN. FEES	240,446.00	-	-	240,446.00	-	113,243.00	113,243.00	127,203.00
178	SS/NATIONAL CONF. ON EMERGING TRENDS IN DMS-DBT	(150,025.00)	150,000.00	-	(25.00)	-	-	-	(25.00)
179	SS/NATIONAL CONF. ON EMERGING TRENDS IN D.M.S.-NASI	(180,694.00)	180,000.00	-	(694.00)	-	-	-	(694.00)
180	SS/BT/LS-400-DR. SINGH	(1,303.00)	-	-	(1,303.00)	-	-	-	(1,303.00)
181	STRUCTURAL BASED DRUG DESIGNING (SBDD)	(157,063.00)	-	-	(157,063.00)	-	-	-	(157,063.00)
182	SUSPENSE A/C	8,898,516.96	(6,813,887.45)	251,794.00	2,336,423.51	-	-	-	2,336,423.51
183	TL/SERB/SRG/2019/001818-DR. TUSHAR LODHA	-	635,500.00	3,562.00	639,062.00		166,357.00	166,357.00	472,705.00
184	TRAVEL GRANT - CD318	45,887.00	-	-	45,887.00	-	-	-	45,887.00
185	UGC	(9,436,254.00)	159,610.50	-	(9,276,643.50)	-	43,106.00	43,106.00	(9,319,749.50)
186	VK/BT/PR-14036-DR. KALE	(201,332.00)	-	-	(201,332.00)	-	-	-	(201,332.00)
187	VK/BT/PR-4227-DR.KALE	(37,115.00)	-	-	(37,115.00)	-	-	-	(37,115.00)
188	VK/DAE/PR-37B/BRNS-DR.KALE	(247,647.00)	-	-	(247,647.00)	-	-	-	(247,647.00)
189	VS/BT/PR-14109-DR.SESHADRI	(136,955.00)	-	-	(136,955.00)	-	-	-	(136,955.00)
190	VS/BT/PR-25858-DR. TRIPATHY	494,398.00	-	8,598.00	502,996.00	-	552,942.00	552,942.00	(49,946.00)
191	VS/SERB/2014/001093-DR. SESHADRI	18,458.00	-	1,467.00	19,925.00	-	-	-	19,925.00
192	VT/RLF-DR. VIDISHA TRIPATHI	132,575.00	-	3,675.00	136,250.00	-	195,793.00	195,793.00	(59,543.00)
193	VT/SERB/004159-DR. TRIPATHI	-	1,698,000.00	-	1,698,000.00		126,756.00	126,756.00	1,571,244.00
194	VT/SERB/000242-DR. TRIPATHI	(327,706.00)	-	-	(327,706.00)	-	(305,370.00)	(305,370.00)	(22,336.00)
195	YS/BHORUKA CHARITABLE TRUST-DR. SHOUCHE	92,142.00	-	-	92,142.00	-	40,523.00	40,523.00	51,619.00
196	YS/BIRAC-DR. SHOUCHE	1,740,000.00	1,160,000.00	18,534.00	2,918,534.00	507,949.00	1,853,555.00	2,361,504.00	557,030.00
197	YS/BT/PR-1489-DR. SHOUCHE	(398,473.00)	-	-	(398,473.00)	-	-	-	(398,473.00)
198	YS/BT/PR-14956-DR. SHOUCHE	(140,225.00)	-	-	(140,225.00)		-	-	(140,225.00)
199	YS/BT/PR-20390-DR. SHOUCHE	191,476.00	-	2,498.00	193,974.00		480,486.00	480,486.00	(286,512.00)
200	YS/BT/PR-31340-DR. SHOUCHE	-	2,214,000.00	24,308.00	2,238,308.00		152,696.00	152,696.00	2,085,612.00
201	YS/BT/PR-3461-DR.SHOUCHE	(168,241.00)	-	-	(168,241.00)		-	-	(168,241.00)

ASHOK PATIL ASSOCIATES AURANGABAD CHARTERED ACCOUNTANTS

(Amount-Rs.)

SR. No.	Name of the Project & P.I.	Opening Balance	Additions Grant. Recd.	Interest & Other Recd.	Total	Utilization/Expenditure			Closing Balance
						Capital	Revenue	Total	
202	YS/DNB-DR. SHOUCHE	(127,174.00)	-	-	(127,174.00)	-	-	-	(127,174.00)
203	YS/ES/PO/SEISMO/1(361)/2019	-	1,621,280.00	-	1,621,280.00	-	50,000.00	50,000.00	1,571,280.00
204	YS/MCC-DR. SHOUCHE	(50,286,201.44)	-	-	(50,286,201.44)	-	-	-	(50,286,201.44)
205	YS/MS/RGSTC/FILE 2007-DR.SHOUCHE	1,355,191.00	-	22,714.00	1,377,905.00	-	1,608,040.00	1,608,040.00	(230,135.00)
206	YS/NCMR-DR. SHOUCHE	32,668,976.12	143,308,562.00	5,038,540.69	181,016,078.81	17,338,534.86	115,002,751.30	132,341,286.16	48,674,792.65
207	YS/SSY/2018/000789-DR SHOUCHE	-	250,000.00	-	250,000.00	-	250,000.00	250,000.00	-
208	YS/TATA STEEL/PHASE-I-DR. SHOUCHE	530,423.00	-	-	530,423.00	-	649,873.00	649,873.00	(119,450.00)
209	YS/TATA STEEL/PHASE-II-DR. SHOUCHE	814,864.00	1,259,128.00	-	2,073,992.00	-	919,288.00	919,288.00	1,154,704.00
210	YS/UNILEVER-DR. SHOUCHE	64,782.00	-	-	64,782.00	-	-	-	64,782.00
211	ZK/WELLCOME-DR. ZAHID KAMAL	2,090,097.00	2,959,401.00	64,304.00	5,113,802.00	-	1,971,381.00	1,971,381.00	3,142,421.00
212	CCSTDS/TRAVEL GRANT-SUNIL KUMAR	-	30,000.00	-	30,000.00	.	30,000.00	30,000.00	-
213	CCSTDS/TRAVEL GRANT-MR. MAYENGBAM S SINGH	-	30,000.00	-	30,000.00	.	30,000.00	30,000.00	-
214	DBT/CTEP/01/2014-15 WORKSHOP	168,591.00	-	-	168,591.00	-	-	-	168,591.00
215	DBT/CTEP/02-PRANITA BORKAR	-	100,679.00	-	100,679.00	-	100,679.00	100,679.00	-
216	ITS/2018/2706-DR. AVINASH SHARMA	-	183,624.00	-	183,624.00	-	-	-	183,624.00
217	ITS/2018/003276-DR. PRAVEEN RAHI	71,002.00	-	-	71,002.00	-	-	-	71,002.00
218	ITS/2019/002052-RUJUTA KUHIKAR	-	183,010.00	-	183,010.00	-	183,010.00	183,010.00	-
219	IUIS2019 TRAVEL GRANT-DR. LAL	-	125,188.00	-	125,188.00	-	125,188.00	125,188.00	-
220	MASSTRICH UNIV. PROJECT	(350,730.00)	-	-	(350,730.00)	-	-	-	(350,730.00)
221	Receivable	(276,756.00)	13,747.00	263,009.00	-	-	-	-	-
222	SHYAMANAND CSIR TA/DA	-	44,394.00	-	44,394.00	-	-	-	44,394.00
223	SPONSORSHIP FEE-SIGNALS FROM GUT SYMPOSIUM -ARUN K	-	140,000.00	-	140,000.00	-	-	-	140,000.00
224	SVETNER INNOVATIONS P LTD. - DR. SHOUCHE	23,600.00	-	-	23,600.00	-	-	-	23,600.00
225	TA/DA-CTEP CLAIM-MR. ROHAN KULKARNI,EX SRF. CSIR	(45,887.00)	-	-	(45,887.00)	-	-	-	(45,887.00)
226	TA/DA-DST/JANGID/SCOTLAND	90,400.00	-	-	90,400.00	-	-	-	90,400.00
227	TG/10763/18/HRD-TRAVEL GRANT-MR. SEHBANUL ISLAM	-	79,147.00	-	79,147.00	-	79,147.00	79,147.00	-
228	TRAVEL GRANT/CSIR-DEEPIKA PURI	-	62,925.00	-	62,925.00	-	62,925.00	62,925.00	-
229	TRAVEL TA/DA-ASHOK PATIDAR	-	91,748.00	-	91,748.00	-	91,748.00	91,748.00	-
	Grand Total	**135,264,440.81**	**492,161,041.49**	**10,966,724.69**	**638,394,706.99**	**61,179,866.82**	**260,020,239.40**	**321,200,106.22**	**317,194,600.77**

ASHOK PATIL ASSOCIATES ★ AURANGABAD ★ CHARTERED ACCOUNTANTS

NATIONAL CENTRE FOR CELL SCIENCE, PUNE - 411 007.

SCHEDULES FORMING PART OF BALANCE SHEET AS ON 31.03.2020

SCHEDULE 4 - CURRENT-LIABILITIES

Amount (Rs.)

Particulars	2019-20	2018-19
Canteen Deposit	10,000.00	10,000.00
Earnest Money Deposit	2,214,248.00	2,657,698.00
Gardening Contract Deposit	30,000.00	30,000.00
Laundry Deposit	500.00	500.00
Security Deposit	3,217,692.00	2,677,977.00
Security Deposit/ Caution Money	3,479,524.00	2,925,000.00
Tele. Deposit	3,164.00	3,164.00
* M/s Shalaka Infra-Tech(I) Pvt. Ltd.	1,555,516.00	1,555,516.00
For Leave Encashment & Gratuity	72,667,587.00	66,625,839.00
GST Payable	190,256.00	422,319.00
Tax Deducted at Source payable	566,407.00	2,137,894.00
Sundry Creditor	33,211,407.58	423,670.00
Advanc from Customers	2,082,053.20	-
EPF Payable	996,008.00	908,075.00
NPS Payable	437,490.00	389,747.00
NPS Payable-Mr. Mahadeo	12,000.00	12,000.00
Provision for Charity Commissioner	2,366,064.00	1,566,676.00
Provision for Electricity & Power	3,245,290.00	3,360,630.00
Provision for Works on Contract	3,839,187.00	2,761,940.00
Provision of Auditors Fee	33,630.00	33,630.00
Salary GSLI Payable (Mr. Mahadeo)	660.00	1,380.00
Salary P Tax Payable	52,000.00	54,575.00
Medical Insurance Payable	-	(38,028.00)
Performance Bank Gurantee	993,288.00	282,310.00
Payable from Extra Mural projects	1,135,228.00	640,609.00
Centre Reserve Funds	10,000.00	10,000.00
Conti.-Welfare Fund	795,575.00	682,302.00
Dr. Mitra-Leave Salary Payable	318,490.00	318,490.00
Dr. Mitra Pension Contri. Payable	-	475,785.00
salary payable	16,259.00	-
Salary welfare payable	43,200.00	-
Grand Total	**133,522,723.78**	**90,929,698.00**

*** Note**

Amount hold against M/s Shalaka Infra-Tech(I) Pvt. Ltd. due to non-completion of work within contract period.

NATIONAL CENTRE FOR CELL SCIENCE, PUNE - 411 007.

SCHEDULES FORMING PART OF BALANCE SHEET AS ON 31.03.2020

SCHEDULE 5 - FIXED ASSETS

(Amount-Rs.)

DESCRIPTION	Rate	GROSS BLOCK				DEPRECIATION / AMORTIZATION				NET BLOCK	
		As at beginn- ing of the year	Additions during the year	Deduction during the year	Cost valuation at the year-end	As at the beginning of the year	Additions during the year	Deduction during the year	Total up to the Year-end	As at the Current year-end	As at the Previous year-end
A. FIXED ASSETS:											
1. BUILDINGS:	**4.87%**										
a> Jopasana		6,026,554.30	-	-	6,026,554.30	3,512,991.93	122,410.49	-	3,635,402.42	2,391,151.88	2,513,562.37
b> Jidyasa		6,914,265.25	-	-	6,914,265.25	3,987,329.87	142,541.75	-	4,129,871.62	2,784,393.63	2,926,935.38
c> University Campus		486,326,956.46	8,226,812.00	-	494,553,768.46	144,377,620.48	16,946,865.14	-	161,324,485.62	333,229,282.84	341,949,335.98
2. Lease Hold Land Baner											
a> Lease Hold Land - Baner		15,441,563.00	-	-	15,441,563.00	1,029,437.54	514,718.77	-	1,544,156.31	13,897,406.69	14,412,125.46
b> Lease Hold Land - Baner - Construction			-		-	-	-	-	-	-	-
3.Furniture & Fixtures	**25.89%**	71,030,561.73	2,562,090.00	-	73,592,651.73	50,888,260.99	5,564,225.67	-	56,452,486.66	17,140,165.07	20,142,300.74
4.Library Books	**18.10%**	97,877,822.53	3,068,832.94	-	100,946,655.47	76,684,389.66	4,163,529.04	-	80,847,918.70	20,098,736.77	21,193,432.87
5.Equipment	**18.10%**										
a> Institute		1,443,985,422.00	141,273,023.65	-	1,585,258,445.65	1,040,161,187.76	90,533,431.08	-	1,130,694,618.84	454,563,826.81	403,824,234.24
b> Fetal Liver project		200,000.00	-		200,000.00	187,160.37	2,323.97	-	189,484.34	10,515.66	12,839.63
6.Vehicles	**39.30%**	1,311,895.00	-	-	1,311,895.00	1,305,520.69	2,505.10	-	1,308,025.79	3,869.21	6,374.31
Total A		**2,129,115,040.27**	**155,130,758.59**	**-**	**2,284,245,798.86**	**1,322,133,899.29**	**117,992,551.01**	**-**	**1,440,126,450.30**	**844,119,348.56**	**806,981,140.98**
Capital WIP											
A) Lease Hold Land-Baner-Construction		1,748,412.00	-	-	1,748,412.00	-	-	-	-	1,748,412.00	1,748,412.00
B) Advance CPWD		-	1,099,108.00	-	1,099,108.00	-	-	-	-	1,099,108.00	-
Total B		**1,748,412.00**	**1,099,108.00**	**-**	**2,847,520.00**	**-**	**-**	**-**	**-**	**2,847,520.00**	**1,748,412.00**
Total (A+B)		**2,130,863,452.27**	**156,229,866.59**	**-**	**2,287,093,318.86**	**1,322,133,899.29**	**117,992,551.01**		**1,440,126,450.30**	**846,966,868.56**	**808,729,552.98**

Note: The aforesaid expenditure is incurred out of Govt. Grants, disposal of which is subject to conditions attached to these Grants.

NATIONAL CENTRE FOR CELL SCIENCE, PUNE - 411 007.
SCHEDULES FORMING PART OF BALANCE SHEET AS ON 31.03.2020
SCHEDULE 6 - INVESMENTS - OTHERS

Amount (Rs.)

Particulars	2019-20	2018-19
Bank Fixed Deposit	-	1,000.00
Grand Total	**-**	**1,000.00**

NATIONAL CENTRE FOR CELL SCIENCE, PUNE - 411 007.

SCHEDULES FORMING PART OF BALANCE SHEET AS ON 31.03.2020

SCHEDULE 7 - CURRENT ASSIT LOAN AND ADVANCES

Amount (Rs.)

Particulars	2019-20	2018-19
CURRENT ASSET		
Cash-in-hand	128,742.00	50,000.00
SAVING ACCOUNTS		
Axis Bank	226,883.00	219,091.00
Bank of India - 4911	241,028,375.26	153,289,219.42
Bank of India - 4912	346,483,323.31	171,959,823.15
State Bank Of India	9,756,702.73	29,326,137.79
Bank of India-SERB 8403	12,127,732.50	-
TOTAL (A)	**609,751,758.80**	**354,844,271.36**
LOAN AND ADVANCES		
Advance-LTC	82,541.00	158,507.00
Advance - TA/DA	229,000.00	188,100.00
Advance - Contingency	91,200.00	164,460.00
Staff Computer Advance	15,565.00	50,756.00
Staff Vehicle Advance	2,973.00	9,321.00
Deposit for Compressor for AC Plant	3,829,000.00	3,829,000.00
Deposit to DAE-University Campus	5,977,000.00	5,977,000.00
Equipment-Security Deposit	38,663.60	38,663.60
Gas Deposit	49,650.00	49,650.00
MSED Deposit	7,312,600.00	7,312,600.00
MSED Deposit (Kothrud)	282,200.00	282,200.00
Telephone Deposit	121,701.00	121,701.00
Advance for International Conference on Microbiome Res.		750,000.00
Prepaid Expnditure Postage	3,835.00	3,737.00
TDS Receivable FY 2016-17	865,968.00	865,968.00
TDS Receivable FY 2017-18	620,934.00	620,934.00
TDS Receivable FY 2018-19	808,568.00	808,568.00
TDS Receivable FY 2019-20	533,212.00	
Advance to customers	-	964,533.00
Project Receivable	380,720.00	989,800.00
TOTAL (B)	**21,245,330.60**	**23,185,498.60**
Grand Total	**630,997,089.40**	**378,029,769.96**

NATIONAL CENTRE FOR CELL SCIENCE, PUNE - 411 007.

SCHEDULES FORMING PART OF BALANCE SHEET AS ON 31.03.2020

SCHEDULE 8 - INCOME FROM SALES/SERVICE

Amount (Rs.)

Particulars	2019-20	2018-19
Cell Culture Workshop	67,800.00	70,240.00
Cell Line Authentication	126,000.00	25,323.00
Cell Line Handling	7,394,580.00	6,905,368.68
FACS Analysis Charges	740,820.00	88,000.00
Fragment Analysis Charges	-	36,000.00
GC MS Analysis	162,000.00	-
Mycoplasma Testing Charges	-	21,600.00
Bio Imaging Facility	6,000.00	-
Proteomene Analysis of chronomus samples	40,000.00	-
Guest House\ Hostel Fees	332,961.00	272,287.00
Grand Total	**8,870,161.00**	**7,418,818.68**

NATIONAL CENTRE FOR CELL SCIENCE, PUNE - 411 007.

SCHEDULES FORMING PART OF BALANCE SHEET AS ON 31.03.2020

SCHEDULE 9 - GRANTS/SUBSIDIES

Amount (Rs.)

Particulars	2019-20	2018-19
GRANTS/SUBSIDIES	450,000,000.00	465,000,000.00
Grand Total	**450,000,000.00**	**465,000,000.00**

NATIONAL CENTRE FOR CELL SCIENCE, PUNE - 411 007.

SCHEDULES FORMING PART OF BALANCE SHEET AS ON 31.03.2020

SCHEDULE 10 - FEES/SUBSCRIPTIONS

Amount (Rs.)

Particulars	2019-20	2018-19
Tender Fees	18,220.00	50,004.00
Grand Total	**18,220.00**	**50,004.00**

NATIONAL CENTRE FOR CELL SCIENCE, PUNE - 411 007.

SCHEDULES FORMING PART OF BALANCE SHEET AS ON 31.03.2020

SCHEDULE 11 - INDIRECT INCOME

Amount (Rs.)

Particulars	2019-20	2018-19
Bank Interest Earned	-	8,569,246.00
Interest On Staff Computer Adv.	28,088.00	41,841.00
Interest On Staff HBA	201,123.00	192,744.00
Interest On Staff Vehicle	4,142.00	46,668.00
Grand Total	**233,353.00**	**8,850,499.00**

As per guidelines received from Department of Biotechnology the interest received from bank refunded to DBT vide DD.NO. as follows

D.D.No.	Date	Amount
058555	13.5.20	999,999.00
058556	13.5.20	999,999.00
058557	13.5.20	999,999.00
058558	13.5.20	999,999.00
058559	13.5.20	999,999.00
058560	13.5.20	999,999.00
058561	13.5.20	999,999.00
058562	13.5.20	160,080.88
	Total Rs.	**7,160,073.88**

NATIONAL CENTRE FOR CELL SCIENCE, PUNE - 411 007.

SCHEDULES FORMING PART OF BALANCE SHEET AS ON 31.03.2020

SCHEDULE 12 - OTHER INCOME

Amount (Rs.)

Particulars	2019-20	2018-19
Application Fee	46,084.00	53,200.00
Hostel Charges Recovery	156,613.00	331,432.00
Hostel Room Charges	129,292.00	-
Ph.D Fees	1,195,800.00	1,581,695.00
Registration Fees-Seminar	-	64,410.00
License Fee	211,400.00	221,063.00
Sale of Scrap	27,783.00	105,642.00
Auditorium Charges	16,000.00	76,000.00
Buy Back	-	32,100.00
Transit House Charges	60,000.00	76,633.00
Usage of Premises for ATM	14,386.00	2,177.00
Conti (Mis Income)	20,410.00	40.00
Income from Road Show	105,000.00	203,412.00
Grand Total	**1,982,768.00**	**2,747,804.00**

NATIONAL CENTRE FOR CELL SCIENCE, PUNE - 411 007.

SCHEDULES FORMING PART OF BALANCE SHEET AS ON 31.03.2020

SCHEDULE 13 - ESTABLISHMENT EXPENSES

Amount (Rs.)

Particulars	2019-20	2018-19
Salaries	218,399,539.00	207,192,783.87
Contribution to Provident Fund	11,393,886.00	11,439,867.00
Contribution to NPS	5,372,273.00	4,921,373.00
Grand Total	**236,665,698.00**	**223,554,023.87**

NATIONAL CENTRE FOR CELL SCIENCE, PUNE - 411 007.

SCHEDULES FORMING PART OF BALANCE SHEET AS ON 31.03.2020

SCHEDULE 14 - OTHER ADMINISTRATIVE EXPENSES

Amount (Rs.)

Particulars	2019-20	2018-19
Consumables	61,216,594.68	68,271,359.42
Contingencies (as per attached details)	29,392,203.60	31,603,665.94
TA-DA	4,869,867.00	6,148,581.08
Work On Contract	45,801,917.00	41,926,803.00
Bank Charges	24,725.23	15,923.12
Eligibility Fees	7,600.00	14,150.00
GST Fee	-	1,000.00
Rent Rates and Taxes	78,452,896.20	73,216,760.00
Grand Total	**219,765,803.71**	**221,198,242.56**

NATIONAL CENTRE FOR CELL SCIENCE, PUNE - 411 007.

SCHEDULES FORMING PART OF BALANCE SHEET AS ON 31.03.2020

CONTINGENCIES BIFURCATION

Amount (Rs.)

Particulars	**2019-20**
Conti-Local Conveyance	2,119,825.00
Conti-Advertisement and Publicity	1,174,487.00
Conti-Vehicle Petrol Exps	118,243.00
Conti-Auditors Remunerations	33,630.00
Conti-Fees Registration& Membershi Chg	291,187.18
Conti-Honorarium	782,167.00
Conti-Hospitality Expenses	1,273,113.00
Conti-Vehicle Insurance	26,825.00
Conti-Laundry Exps	146,940.00
Conti-Meeting Exp.	168,476.00
Conti-Misc. Purchase	2,898,068.00
Conti-MIS EXP	627,591.00
Conti-Postage and Telephone	3,698,658.00
Conti-Printing and Stationery	3,306,656.00
Conti-Professional & Legal Charges	1,764,403.42
Conti-Repairs and Maintenance	1,403,970.00
Conti-Repairs and Maintenance- Contract	7,154,375.00
Conti-Repairs and Maintenance - Vehicle	5,661.00
Conti-Seminar / Symposia	1,617,928.00
NCCS manpower	780,000.00
Grand Total	**29,392,203.60**

SCH. "15" : SIGNIFICANT ACCOUNTING POLICIES AND NOTES ON ACCOUNTS FOR THE YEAR 2019-2020

A. SIGNIFICANT ACCOUNTING POLICIES

1) ACCOUNTING CONVENTION :

The financial statements are prepared on the basis of historical cost convention, unless otherwise states and on the accrual method of accounting

2) INVENTORY VALUATION :

Inventory is valued at cost or realizable value whichever is less. At the year end value of inventary is NIL.

3) INVESTMENTS :

Investments classified as " long term investments" are carried at cost

4) REVENUE RECOGNITION

All Receipts are accounted for on accrual basis except Guest House/ Hostel fees & FDR interest.

5) FIXED ASSETS :

Fixed assets are stated at cost of acquisition inclusive of inward freight, duties and taxes and incidental and direct expenses related to acquisition.

6) DEPRECIATION /AMORTIZATION:

i) Depreciation is provided as per rates specified in the Companies Act 1956 at W.D.V. method except depreciation on cost adjustment arising on account of conversion of foreign currency liabilities for acquisition of fixed assets, which is amortized over the residual life of the respective assets. Depreciation is provided at half the rate for assets purchased after 30th september.

ii) Assets costing Rs. 5000/- or less each are fully provided.

iii) The annual amortization expense for a leasehold land is the cost of the leasehold land divided by the lease term, assuming straight-line amortization.

7) GOVERNMENT GRANTS/SUBSIDIES :

i) Where the Government Grants are in the nature of capital contribution, i.e., they are given with reference to the total or part investment or by way of contribution towards its total or part capital outlay, are recognized as "Contribution towards Capital Fund" under head "Corpus/Capital Fund" and if received as compensation for expenses or losses incurred or to be incurred in a previous accounting period are recognized as income under income & expenditure account. Grants received from Sponsoring agencies for specific Projects are recognized as " Earmarked Funds"

ii) Government grants/subsidy's are accounted on realization basis.

8) FOREIGN CURRENCY TRANSACTION:

Transactions denominated in foreign currency are accounted at the exchange rate prevailing at the date of the

9) RETIREMENT BENEFITS :

i) Liability towards gratuity payable on deth/retirement of employees is made on the basis of estimated liability to the extent of employees retiring in next five years.

ii) Provision for accumulated leave encashment benefit to the employees is accrued and computed on the assumption that employees are entitled to receive the benefit as at each year end.

10) CURRENT ASSETS, LOANS & ADVANCES.

It is explained to us that, the value of all current assets, advances and deposits, outstanding income and other realisable assets, if any, are not less than their realisable value in the ordinary course.

Date: 16/09/2020
Place: Pune

FOR ASHOK PATIL & ASSOCIATES,
CHARTERED ACCOUNTANTS,
FIRM REG.NO. 122045W

Officer 'C' Accounts
NCCS

Director
NCCS

मनोज कुमार भट, पीएच.डी.
निदेशक, एनसीसीएस, पुणे
Manoj Kumar Bhat, PhD
Director, NCCS, Pune

(SAURABH P. AGRAWAL)
PARTNER
M. NO. 131312

SCH. "16" : CONTINGENT LIABILITIES AND NOTES ON ACCOUNTS FOR THE YEAR 2019-2020

1) The Accounts are prepared as per the common format of accounts for all Autonomus Institute as per letter No. BT/MED/NCCS/ADMN/2002 dtd.June 10,2002 of Department of Biotechnology, New Delhi and comptolier & Auditor General of India letter No. OA-VII(MISC/CORRES/2002-03/1165)dtd.16 October 2002.

2) As per the standard accounting practices depreciation on Fixed Assets has been provided from 2002-2003 as per the rates specified in the Companies Act,1956

3) Taxation:- Inview of there being no taxable income under Income Tax Act 1961, No provision for Income Tax has been considered necessary.

4) It is explained by the management it has maintained fixed assets register and has also conducted physical verification of fixed assets during the financial year 2019-20. We verified the fixed assets register as well as fixed assets on random basis.

5) As informed to us, the land on which the NCCS complex is situated is owned by the State Government of Maharashtra. Agreement for the ground rent/ lease rent payable, if any, for the use of land is not entered into and no provision in respect of the same has been made.

6) As informed to us, the land situated at Baner, is owned by the Municipal Corporation of Pune. Agreement for the same has been executed by paying requisite stamp duty to the State Government of Maharashtra.

7) Interest earned on investment of capital grants has been credited to the Income & Expenditure Account and interest earned on Grants received towards Earmarked funds has also been credited to their respective project fund account.As per the instruction received from DBT New Delhi, Interest earned on core fund interest earned on MSED deposit is transferred to DBT New Delhi

8) Unspent/Overspent grants and receivables in respect to Projects are subject to confirmation from the granting authorities, reconciliation and consequential adjustments, if any.

9) Amount of GST credit, GST payable and GST TDS are subject to reconciliation.

10) **EARMARKED/ENDOWMENT FUND :**

i) As explained to us, Grants/Funds received from Sponsoring agencies for specific Projects are recognised as " Earmarked Funds". These Grants/Funds are credited to respective Project Funds as per the norms associated with these Projects. In some instances, the said funds received directly from these Sponsoring Agencies without any prior maping towards the projects. These unmaped funds are credited to "Suspense Account" till the maping done or any written communication received by/from these sponsoring agencies. The Suspence account having balance amount of Rs. 23,36,423.51/-/- is due to not able to map the grant received from sponsoring agency, the same will account for to the concern project after getting the payment advice from the sponsoring agency.

ii) Negative balances are due to fund are not received timly from Sponsoring agency.

Date: 16/09/2020
Place: Pune

FOR ASHOK PATIL & ASSOCIATES,
CHARTERED ACCOUNTANTS,
FIRM REG.NO. 122045W

वैभव अ. अरगडे
Officer 'C' (Accounts)
Officer 'C' Accounts
NCCS

Director
NCCS

मनोज कुमार भट, पीएच.डी
निदेशक, एनसीसीएस, पुणे
Manoj Kumar Bhat
Director, NCCS, Pune

(SAURABH P. AGRAWAL)
PARTNER
M. NO. 131312

National Centre for Cell Science
An autonomous institution aided by the Department of Biotechnology, Govt. of India

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