IMPRINT

NIBMG in Bits and Bytes

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Scientist Talks

"There is a lot of inequity in the visualization of diversity"
-Prof. Partha Pratim Majumder

Publications

Recent Publications from NIBMG

Research Highlights

Researchers discuss the extent and scope of research at NIBMG

Creative Corner

Researchers at NIBMG explore their creative side

Cover Photo: Side view of the Institute.
Photo and Design By: Tuneer Ranjan Mallick

Contents

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Director's note

Prof. Arindam Maitra
Officiating Director

A systematic and clear understanding of geographical and ethnic variation in causal factors of disease of high prevalence in India and an in-depth estimation of the interaction between genetics and environmental factors are of paramount importance. The research focus of NIBMG has been to mount efforts to understand and estimate these parameters of major relevance to public health, to provide an in-depth understanding of genetics and epidemiology of common diseases-common not only in India but also in many other global regions. We are presently conducting many exciting studies on genomics of Cancer and Chronic diseases, Infectious diseases and in Statistical and Computation genomics, with the overarching goal of improving knowledge as well as patient care. In particular, our findings on gingivobuccal oral cancer and our recent involvement in the genomics surveillance of SARS-CoV-2, have made major contributions towards this direction. The Research Newsletter is being initiated to provide periodic information and updates on our research and to bring to light, interactions with the tall and the young personalities of NIBMG. My kudos to the Newsletter Team for taking this initiative and I wish the Newsletter a grand success.

From The Research Office

-Dr. Alpana Dave

Quoting Matt Ridley "The genome is a book that wrote itself, continually adding, deleting and amending over four billion years." We at NIBMG are continually working towards unravelling the contents of this book.

With the start of a new financial year, we have received five new extramural grants. Prof. Arindam Maitra, in collaboration with PGIMER, has received a grant to validate circulating tumor cell-based diagnosis and treatment prediction in Oral Squamous Cell Carcinoma. In another new project Dr. Nidhan K. Biswas will use existing cancer genomics data to develop state-of-the-art machine learning tool for identification of cancer driver mutations and develop a web-framework to enable usage of the tool by scientific community across the world. Extracellular vesicles (EVs) are small particles of nanometers scale which carry DNA/RNA and proteins released from various organs including tumors. In a recently funded study, Prof. Kartiki V. Desai will examine protein markers specific to tumor EVs and their potential use in breast cancer diagnosis and treatment response. To further her research on understanding the mechanism of breast cancer progression, in another project, Prof. Desai will investigate the interaction between JMJD-6, known to be associated with breast cancer, with YBX-1 and their role in regulating the cell cycle. In addition to this, Prof. Anupam Basu has recently been funded to investigate the role of methylation in E β-thalassemia and to identify novel drug targets. We are also pleased to share that we have signed an MoU with AIIMS Kalyani which will facilitate academic and research collaborations between the two Institutes. IMPRINT, NIBMG's Research Newsletter, is a new initiative that we have undertaken to bring to you a glimpse of our ongoing research and achievements.

The first issue of IMPRINT features the Interview of our Founder & Distinguished Professor and National Science Chair, Govt of India, Prof. Partha Pratim Majumder where he reflects on his professional journey and his personal favorites. We also showcase the recently published research work in the segment 'In Public Eye'. Another section of this Newsletter, 'Research Spotlight', highlights the ongoing PhD research projects. The newsletter also covers the 'Events & Awards' section, which as the name suggests, highlights the recent seminars and events at NIBMG along with the awards received by our Faculty, staff and students. Finally, you can envisage the artistic streak of our Staff and Students in the 'Creative Corner' segment. We hope you enjoy reading it.

SCIENTIST TALKS

Promenade with PPM

Arunima Acharya | Manisha Rout | Pratyusha Chikkala

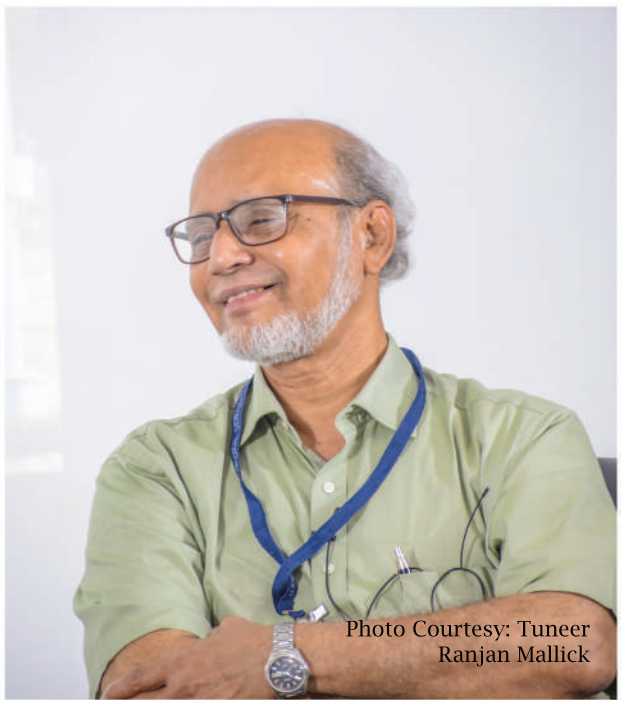


Photo Courtesy: Tuneer Ranjan Mallick

1. What does a typical day look like for Professor Majumder?

I normally wake up between 5:30 am and 5:45 am. After the usual chores, the first thing I do in the morning is to feed my cats. Then I usually work for an hour and complete any academic work I might have pended and after that get ready to come to the Institute. After coming to the Institute, you all know what I do. The usual things – teaching, research, some gossip. That is how the day ends. And then I go back home and am back with my laptop; have dinner around 9:30 pm, watch a bit of television and go to bed around 12:00-12:30 am.

2. How do you organize, plan, and prioritize your work?

I effectively manage work by planning meticulously, recognizing the necessity of adhering to deadlines.

3. We know that over the years you have been quite successful in developing and maintaining effective working relations with other scientists, research groups, funding agencies and the public. What is your secret behind this?

I am not very sure that I am actually successful in all of these. Anyways, I do have a very cordial relationship with my colleagues, my PhD students and the students who are taking my courses. However, there is no secret to all of this. You just have to respect others irrespective of whether they are juniors or seniors and be mindful that they have their own aptitudes. One can achieve such relations by being respectful and mindful to others.

4. Why did you choose the academic institutions you went to? How much of it was planned? Have you ever allowed yourself to 'go with the flow'?

No, I do not go with the flow at all. I have a vision; I foresee what is coming and that is what drives my academic life. As you all know, I have grown up with statistics and slowly over a period, moved over to human genetics. And the reason I did that was, human genetics is the most quantitative aspect of biology. And even though I was good at mathematics and statistics, my heart was with biology. So, over a period of time, I drifted to that area of biology where there is a lot of quantification and use of statistical methods.

"No, I do not go with the flow at all. I have a vision; I foresee what is coming and that is what drives my academic life."

Indian Statistical Institute (ISI) is my alma mater where I have done my Bachelor's, my Master's, and my PhD. With the support of some of my colleagues at ISI, I formed the first Human Genetics department there. In around 2000, we got in touch with Dr. Purnendu Chatterjee, an investor from Kolkata now based in New York, and initiated the Centre for Population Genomics. We were able to obtain a several million dollar grant, the largest single grant from the National Institute of Health, US that ever came to India.

So, when the government decided that they would make some focused Institutes, I got a call from the secretary one morning asking me to formulate some ideas; by the end of the day, I wrote to him a paragraph on it. From that paragraph, we ended up making a 210 paged document which has now found its place in the Director's office.

After several scientific, administrative and financial discussions for about 6 months, the idea that a center or an institution of biomedical genomics should be formed was approved. And in 2009, the Parliament approved the formation of this Institute. I had to go to the Finance Ministry to defend that this Institute be formed. This was followed by a press release from Parliament. I along with working at the ISI, started coming to Kalyani to look for a plot of land and simultaneously for a building where we could set up for the initial days.

We got an entire floor in a hospital building where we started operations in 2010. The campus was then built on this 30-acre plot. Students were the first ones to move onto the campus, even before the faculty members moved in. We are all grateful to the students, your predecessors in fact, for getting the ball rolling and getting this campus started.

So that is the history of this Institute.

5. What is your take on how the academic field has evolved over the years?

General science covers a broad range of domains that flourished over different periods in time. From mid-1990s it started with major advances in conceptualization and development of technology. This period marked a breakthrough in genome science with the Human Genome Project, HapMap Project and many other genomics-based projects. Our Institute was involved in the study of cancer genomics.

"The strength is that they are much more informed and their breath of knowledge and information is far superior... The weakness is that in many of them the depth of knowledge is missing..."

We were successful in identifying the nature and extent of variation across individuals of various countries, establishing the characteristics of the genomes, cataloging them, and identifying the function of those variants that cause cancer. The whole field of artificial intelligence and machine learning, which was nascent when we were students, now has become a complete field by itself. They invade biological sciences and have been instrumental for meaningful inferences from data but there also exists the wrong sense of its usage. Simultaneously, we had other domains like physical sciences (atom smasher's accelerator), chemical and mathematical science and computer sciences flourish as well.

Overall, from the mid 1990s till today the impact of these advancements has been continuing and will continue.

6. What are the strengths and weaknesses of young researchers? What is the most challenging part of supervising them?

The strength is that they are much more informed and their breath of knowledge and information is far superior to what I was at their age for sure.

The weakness is that in many of them the depth of knowledge is missing and this might be due to not reading textbooks and only getting information from various data

sources. I wish this generation develops certain kinds of focused interests and go in to depths; that will be really helpful.

Coming to the challenging part, I have not had many students here because of the kind of work I had to do. I was doing brick and mortar as opposed to test tubes and petri dishes when I joined this Institute and started making it. But my relations with all my students have been fantastic and I have learnt a lot from them. Some students, of course, for a period of time would fall in love with someone and not come to the Institute; but such things were sporadic and transient. So honestly, I haven't faced any big challenges. I just wish some of my students had been more quantitative in their thinking and had quantitative arsenal to analyze their own data but that has been a part of my own learning of how to teach people who are not empowered with certain kinds of abilities.

misgivings. Given this, I do not know how our own work has panned out but I only hope that this is a passing phase and it is not going to stay for long.

8. If you could change any aspect of your life, what would it be?

I do not have an answer to this question. I have led a very happy and productive life. I really do not have any regrets.

9. If you had to switch professions with someone, who would it be and why?

I would probably switch to a medical profession, the reason being that it is very useful to help other people. Many doctors are very passionate and careful about their patients, and I really find that to be extremely heartening. I wish that I could also serve humanity in that way at least for a period of time.

11. If you had to pick any character in a book, movie, or TV show who is most similar to you, who would you choose and why?

My all-time favorite is Dennis the menace. I like his temperament, the way he deals with his people and his neighbors, but whether I would like to be Dennis the menace I am not sure.

12. What do you envision for NIBMG in the future?

I envision that all of you will get jobs in the Institute and steer the Institute forward and that our Institute will become one of the big names in India and probably in the world. That is what will make me really happy. We should excel both in research and in making an impact on society because after all Biomedical

"It is very depressing that even scientists are now thinking about racial purity. And that seems like a failure on our part."

Photo Courtesy: Tuneer Ranjan Mallick

"I enjoy Science primarily because every day is a new challenge, and you are meeting new kinds of problems trying to think of how to solve them..."

7. A large part of your research focuses on the evolution and diversity of the human race. In a country like India, with such diverse ethnicities and religious backgrounds, have you observed any change in the public reception of your research?

That is a very good question, a very thoughtful question. I think overall, there has been an appreciation of the diversity that is embodied in the human kind in India. I think that it has sunk in very well that there is a lot of diversity. The problem is with the interpretation of this diversity. There have been times when people have identified themselves well with this diversity and at times people have felt that this diversity has certain underpinnings which do not treat this entire gamut of diversity as equals. So, there is a lot of inequity in the visualization of diversity. But right now, we are passing through times where diversity is not being respected in an equitable manner. It is very depressing that even scientists are now thinking about racial purity. And that seems like a failure on our part. And many of us are

But sometimes you look at something from a distance and believe that that is what you should be doing but once you start doing that, you get bored. So honestly, I like that profession but I don't think I can endure it for long because it is a lot mechanical. I enjoy Science primarily because every day is a new challenge, and you are meeting new kinds of problems trying to think of how to solve them and that is very interesting.

10. How is your walk with God?

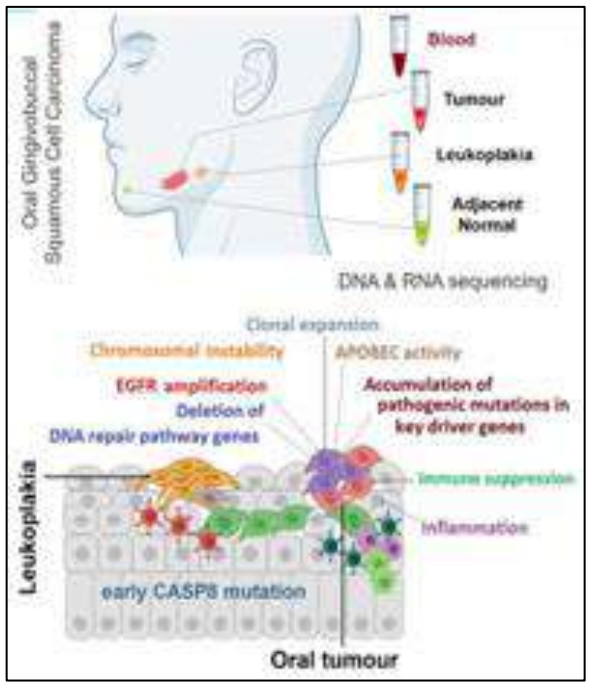
What is God? Can you define that for me? I would not say I am disrespectful, but I am kind of not interested. Even though I live in a neighborhood where they celebrate Durga Puja and I have been President of the Durga Puja Committee. But I do not believe in rituals. Durga Puja is wonderful because it brings people together, and we sit there for three or five days, chat and eat together. I like the social aspect of that, but I am not really a believer of rituals.

Genomics is something that needs to be translated to society and it is not theoretical physics that you are solving. So, as long as we are able to do research that brings some solace to humanity and people who are suffering, that would be absolutely fantastic and I would like to see the Institute prospering in that way and all of you are actively working in this field of Biomedical Genomics and contributing.

~

In Public Eye

Aditya Agarwal | Anjali Gupta | Bandana Mondal | Piyali Mondal | Sukanya Mitra



Multiomics analysis reveals signatures of tumor initiation and progression in gingivo-buccal oral cancer

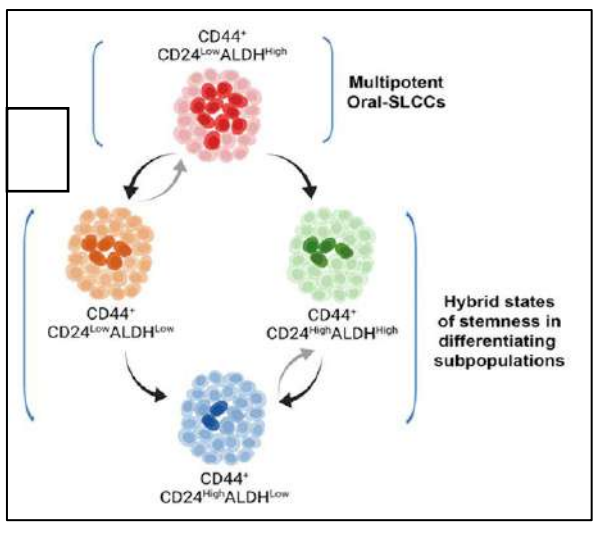
Leukoplakia is a condition in which thick, white patches are formed in the oral cavity because of injury or chronic irritation. In a fraction of the individuals (~9%), this develops into oral squamous cell carcinoma. The genomic sketch of how a benign lesion progresses towards a malignant tumor was described by Dr. Nidhan K. Biswas and his team. The collaborative study between NIBMG and Dr. R. Ahmed Dental College & Hospital revealed how molecular and immune deregulation transforms an oral tissue lesion into a malignant tumor. Multiomics analysis of patient samples showed mutational changes responsible for such a transformation. Mutations in the *CASP8* gene were found to be the key reason behind such malignant transformation. Additional associated mutations were seen in other genes such as *TP53*, *NOTCH1*, *HRAS*, DNA-repair genes, *NOTCH1*, etc. Such alterations were likely associated with immune suppression that promoted tumor initiation and progression. This study from Dr. Biswas's lab throws light on the mechanism behind the progression to malignancy, which was previously unknown. This study was featured on the cover page of Journal of Pathology, August 2022 issue.

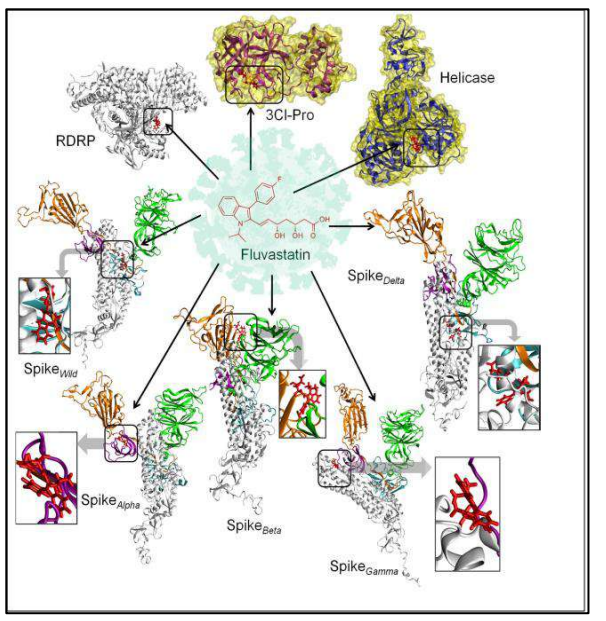
Ghosh et al.; doi: 10.1002/path.5900

Non- genetic intratumoral heterogeneity in oral cancer

Taking one step further towards precision medicine, work published from Dr. Sandeep Singh's lab sheds light on non-genetic intra-tumoral heterogeneity, responsible for the emergence of the hybrid state of cancer stem cells (CSC). Four heterogeneous, interconvertible CSC populations were characterized based on phenotypic markers like CD44, CD24 and ALDH in oral tumors. Phenotype specific-RNA sequencing-based gene expression profiles were used to understand the maintenance of hybrid states of CSCs and correlated with poor prognosis of the oral cancer patients.

Vipparthi et al.; doi:10.1016/j.isci.2022.104317





Fluvastatin: a member of statin group of drugs against SARS- CoV-2

In a collaborative effort coordinated by Dr. Amlan Das, a team of researchers from NIBMG attempted to decipher the molecular mechanism of statin group of drugs against SARS-CoV-2 pathogenesis using computational predictions. Using blind docking of SARS-CoV-2 functional proteins with statin group of drugs, Fluvastatin was found to bind to multiple target proteins of SARS-CoV-2 including the spike-mutant proteins.

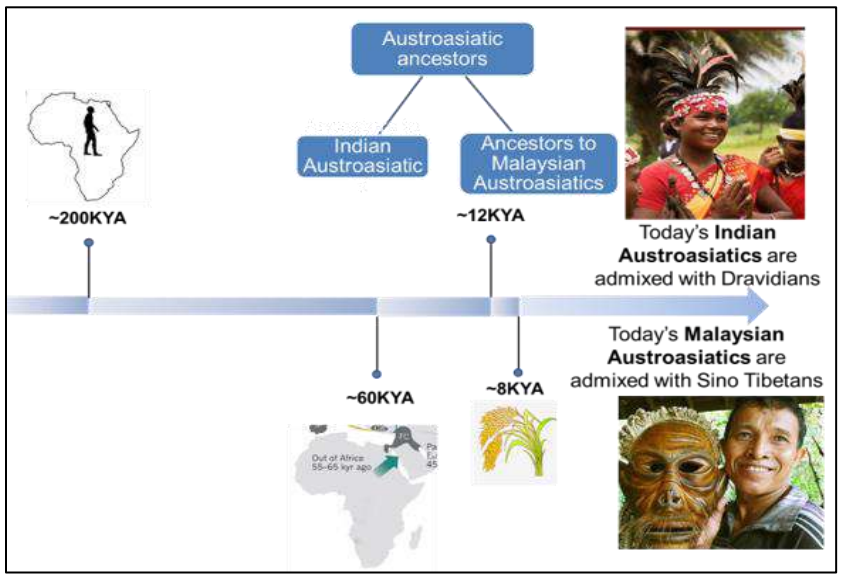
Ghosh et al.; doi:10.1038/s41598-022-09845-y

Collaborative studies

We have also contributed to a collaborative study with Indian Statistical Institute to examine the mutation background of patients with Birt-Hogg-Dubé syndrome (BHDS), a rare monogenic disorder. In another collaborative study with National Institute of Mental Health And Neurosciences, novel variations in sarcoglycan genes were identified in a large cohort of genetically confirmed patients with sarcoglycanopathy and disease progression was reported.

Ray et al.; doi: 10.1186/s13023-022-02326-5, **Bardhan et al.;** doi: 10.1007/s10048-022-00690-9

Research spotlight



Tracing the past from genomes

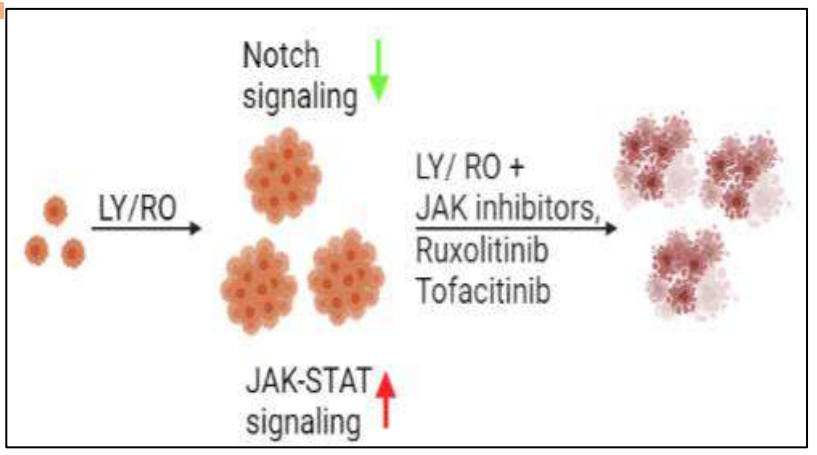
Debashree Tagore, SRF
(PI: Dr. Analabha Basu)

Once upon a time, around 200 thousand years ago (200KYA), the earth saw the appearance of a new species that changed the world: our species, the homo sapiens (modern humans) came into existence in Africa. After spending over half of its existence in Africa, a group of modern humans left Africa around 60KYA and eventually occupied every corner (almost!) of the earth. This journey of modern human ancestors of ours wasn't easy: they faced climate change, geographical barriers, various evolutionary forces and met other human-like species. Such encounters over a prolonged period of time shaped their genetic material and ultimately led to the genetic differences between populations as we see today.

Exploring these differences provides clues to the genetic relationship between different populations, helps in tracing their genetic history and identifying past evolutionary events. And this is what I do. I have studied the DNA of populations of East, South and Southeast Asia with particular interest on the Austroasiatic tribes residing both in India and Malaysia. They have existed for over 40,000 years, speak languages that can till today be classified to a single language family (Austroasiatic) and have mostly remained foragers and hunter gatherers. Interestingly, these Indian and Malaysian Austroasiatics aren't genetically closest. Instead, the Indian Austroasiatics are genetically similar to the Dravidians (from Southern India) while the Malaysian Austroasiatics to the Tibeto Burman (a language group belonging to Sino-Tibetan language family). Their ancestors had however separated nearly 12KYA who likely spoke some proto-Austroasiatic language that has led to today's linguistic commonality. This phenomenon of DNA segment exchange as a result of mating between individuals of distinct populations is called admixture. The Indian Austroasiatic admixed with the Dravidians making them genetically close. The genetic similarity between Malaysian Austroasiatics and the Tibeto-Burmans was because both had admixed with Sino-Tibetan language speaking neighbours of East Asia. This was further substantiated from my Ancient DNA analysis from Southeast Asia. These are DNA extracted and sequenced from bones of individuals who died at least 100 years ago. I found that after the advent of agriculture in East Asia around 8000 years ago, East Asian farmers had started migrating toward southwards admixing with the ancestors of Tibeto Burmans and Malaysian Austroasiatics on their way. Thus, my work has shed light on genetic history but also provided new insights to the linguistic history of India and Southeast Asia.

Synthetic lethality against stemness in Oral Cancer cells

Subhashish Ghosh, SRF
(PI: Dr. Sandeep Singh)



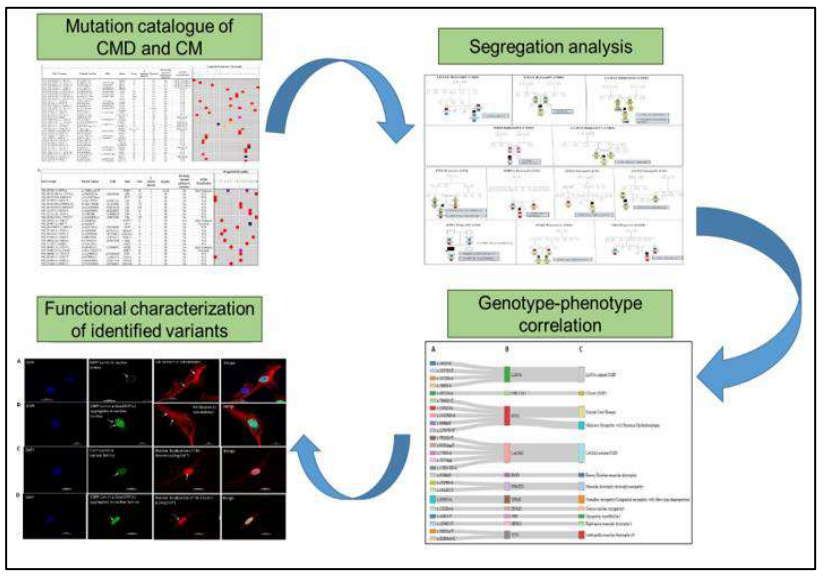
Oral Cancer poses is a huge public health burden as it is the most common cancer type in Indian males. Notch is a cell surface receptor which plays an important role in signalling pathways implicated in development and malignant transformation. Genes involved in Notch-signaling are frequently altered in Oral Cancer. Inactivating mutation in Notch1-receptor is reported as a drive tumor evolution or progression in Oral Cancer. Concurrently, several reports have suggested activation of Notch-signaling in subsets of Oral tumor. Therefore, a bimodal role of Notch has been suggested in Oral Cancer. Stem-like cancer cells (SLCCs) are a subset of tumor cells which are capable of initiating tumors and this property is called Stemness.

My work aims to understand the role of these two opposite alteration statuses of Notch-pathway in maintaining stem-like cancer cell states in oral squamous cell carcinoma (OSCC). Oral-tumor derived cancer cell lines were used for this study and cancer stem cells (CSC) were enriched in 3D-spheroids culture. These 3D-spheroids retain the complexity of a tumor. Notch-active and inactive conditions were artificially maintained by genetic and pharmacological tools. Gene expression studies clearly suggested the maintenance of states of stemness in 3D-spheroids generated from both Notch-active and inactive conditions. RNA-sequencing study revealed more proliferative state of stemness in Notch-inactivated state. Further, these cells showed activation of Janus Kinase-Signal Transducer and Activator of Transcription (JAK-STAT) signaling. This pathway is crucial in several cellular processes including development of the immune system and haematopoiesis. Perturbation of JAK-STAT signaling components in Notch-inactivated state of Oral cancer stem cells resulted in significant reduction in stemness under both *in vitro* and *in vivo* condition. Since SLCCs are associated with aggressive cancer behaviour; our findings suggest a novel therapeutic option of inactivation of Notch signaling with JAK-STAT perturbation in OSCC in a synthetic lethal manner.

Research spotlight

Investigation of genomic signatures in rare muscle disorder patients from India

Shamita Sanga, SRF
(PI: Dr. Moulinath Acharya)

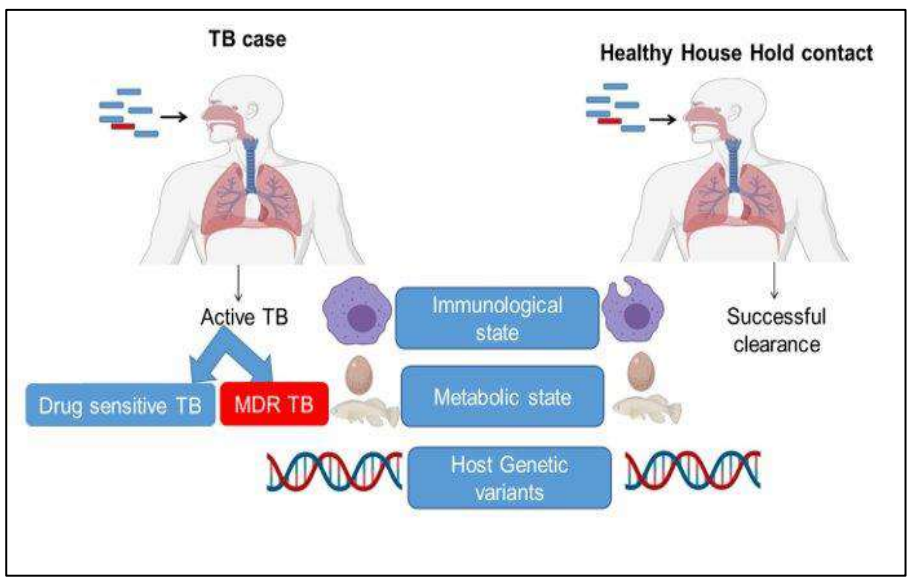


Congenital muscular dystrophies (CMDs) and congenital myopathies (CMs) are a group of genetically and clinically heterogeneous degenerative primary muscle disorders with onset at birth or during infancy. It is characterized by progressive muscle weakness and degeneration, diminished muscle tone, contractures, spinal rigidity and delays in reaching motor milestones. Due to vast heterogeneity, clinical examination and protein-based analyses often fail to identify the genetic causes of these diseases. Fortunately, with the advances in genomic technologies in the past few years, addressing the complexity of the genotype-phenotype relationship has become possible. The aim of my study is to identify the spectrum of causal variants in a cohort of 36 difficult-to-diagnose CMD and CM cases of Indian origin using whole exome sequencing (WES) methods to understand the genotype-phenotype correlation and achieve a genetic diagnosis.

We identified two novel pathogenic mutation c.448C>T; p.(Arg150*) in the *Desmin* (*DES)* gene and c.590T>C;p.(Leu197Pro) in the *Lamin* (*LMNA)* gene. *DES* encodes for the Desmin protein which is a muscle specific member of the intermediate filament family. while *LMNA* encodes Lamins which are structural protein components of nuclear lamina and constitute a class of intermediate filaments. Functional characterization of these mutations was performed in primary human skeletal muscle cells to understand their pathological role in disease phenotypes. Based on family pedigrees and WES, a total of 33 and 21 rare and deleterious mutations were identified in 28 genes previously reported in CMD and CM based on OMIM, ClinVar and Orphanet, respectively. Taking into consideration ancillary investigations such as muscle biopsy, magnetic resonance imaging (MRI), immunohistochemistry (IHC) and clinical examinations, we could accurately diagnose 60% patients (n = 14/23) in the CMD group and 46% patients (n = 6/13) in the CM group. Furthermore, analysis of the confocal micrographs of cells with p.(Arg150*) *DES* construct elucidated the formation of aggregates and migration of truncated desmin proteins into the nucleus of the cells. On the other hand, cells transfected with p.(Leu197Pro) *LMNA* construct showed formation of aggregates and disappearance of laminar rims in the nuclei of the muscle cells. This provides insights to the pathogenicity of the two mutations identified in our cohort. The aggregates might disturb the cellular homeostasis and organelle positioning thereby impacting the mechano-transduction signalling.

Tuberculosis: A host of answers

Anuradha Gautam, SRF
(PI: Dr. Bhaswati Pandit)



Infectious diseases represent an interaction between two genomes: a host and a pathogen genome. Apart from a substantial exposure to the pathogen, both host and pathogen genetic factors must interact to determine if an exposure to a pathogen may lead to a successful infection and to determine the outcome of this infection. Tuberculosis (TB) is one such infection of the lungs caused by the *Mycobacterium tuberculosis* complex (MTBC). Although, one third of the world population is expected to be latently infected by *M.tb*, only 5%-10% individuals manifest active tuberculosis. TB is a substantial public health crisis for India with the country accounting for 27% of the world TB cases.

Its management is further complicated by the emergence of multi-drug resistant (MDR)-TB: resistance against at least two first line drugs Isonazid (INH) and Rifampicin (RIF). Determinants for developing drug resistant TB include non-adherence to therapy, inadequate drug regimens, drug metabolism and immunological state of the host. Resistance to standard antibiotic therapy allows for the drug-resistant *M.tb* to linger longer in the host and induce immuno-pathological changes different from that caused by their drug-susceptible counterparts. Therefore, to appreciate the impact of host genetic factors in susceptibility to drug sensitive and MDR-TB, we analyzed the DNA and plasma samples from individuals infected with drug sensitive TB, MDR TB and their uninfected household contacts. Despite the same exposure these three groups had widely different outcomes which were guided by their immunological state, metabolic state and genetic variants. The immunological and metabolic states of the hosts are intricately modulated by the various genetic factors of the host. To link these physiological changes with the host genetic factors, entire genomes of the study participants have been probed by genome wide genotyping assay. This is a powerful approach that will help detect rare genetic variants by capitalizing on the vast knowledge of human genetic variants produced by seminal projects such as the Human Genome Project, Hap-Map project and 1000 Genomes Project.

Events & Outreach

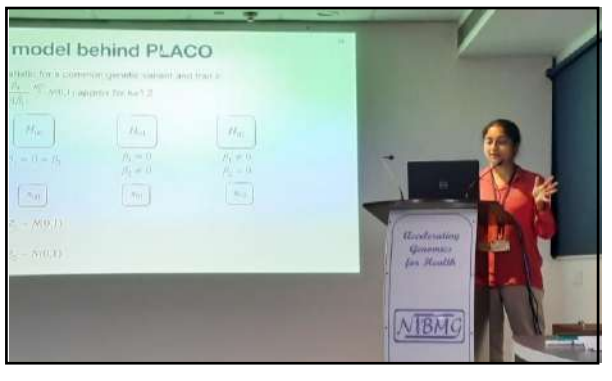
Jyotishman Sarma | Vinay More

A glimpse of dynamic activities at National Institute of Biomedical Genomics

NIBMG is committed to capacity building in the field of Biomedical Genomics. In the past months we re-opened our doors for students from Dinabandhu Andrews college (Microbiology Department) and Sister Nivedita University (Biotechnology), Banwarilal Bhalotia College, Asansol and the Department of Physiology from West Bengal State University. Our faculty members delivered lectures to provide them with an overview of the ongoing research. They were also given a tour of the institute, our research facilities and the Genome Hall.

To mark the discovery of DNA double helix and completion of the Human Genome Project, we celebrated DNA Day 2022 on 25th April. An Infographics contest, Extempore and Quiz competitions were organized. Enthusiastic participation from our students and staff made this program a grand success.

We also had the privilege of having Dr Debashree Ray, Assistant Professor, John Hopkins University, USA visit our Institute. She delivered a fascinating talk on "Identifying genetic overlap between diseases and prostate cancer, and rare birth defects". This was followed by an engaging discussion with our students and Faculty members.



As a part of the Scientific Advisory Committee (SAC) meeting, our students presented posters on their research work. The Members interacted with the students and gave them valuable suggestions

Following the NIBMG tradition, we commemorated Kabiguru Rabindranath Tagore's birth anniversary on 9th May with vibrant cultural programs comprising of songs, dances, recitations, and drama.

8th International Day of Yoga was celebrated on 21st June 2022. Ms Madhumita Singha Roy, an eminent Yoga therapist, demonstrated popular yoga therapies in this programme.

A tree -plantation drive was organized on campus on 27th June.

A Mini symposium was organized to celebrate World Microbiome Day. Our guest speaker was Dr. Sandip Paul, Associate Professor, JISIASR. This was followed by talks by Dr. Suman K. Paine and Ms. Mousumi Sarkar about ongoing microbiome research at NIBMG

Awards

Urvashi Yadav

Since the beginning of this year, our students have bagged several awards at National and International forums.

Mr. Sudipta Chakraborty

Mr. **Sudipta Chakraborty** (PI: Dr. Moulinath Acharya) received the ARVO India Chapter Affiliate Grant 2022 to attend the Virtual Association for Research in Vision and Ophthalmology (ARVO-2022) Annual Meeting. Earlier in the year, he had also received the SERB-DST, Govt. of India Travel Award to attend the Annual Clinical Genetics Meeting 2022 at the American College of Medical Genetics and Genomics (ACMG).

Ms. Debashree Tagore

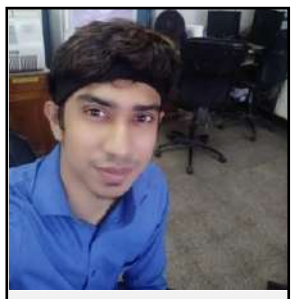
Awarded for her Science Communication skills, **Ms. Debashree Tagore's** (PI: Dr. Analabha Basu) write-up for her PhD work was selected among the Top 100 Popular Science Stories under the DST AWSAR program.

Ms. Mousumi Sarkar

Ms. Mousumi Sarkar (PI: Dr. Souvik Mukherjee) was awarded the 1st Prize in the Young Investigator Award category at the 12th India Probiotic Symposium.

Ms. Shamita Sanga

Ms. Shamita Sanga (PI: Dr. Moulinath Acharya) received the DBT Travel Grant to attend European Society of Human Genetics Conference (ESHG-2022), held in Austria Center Vienna.



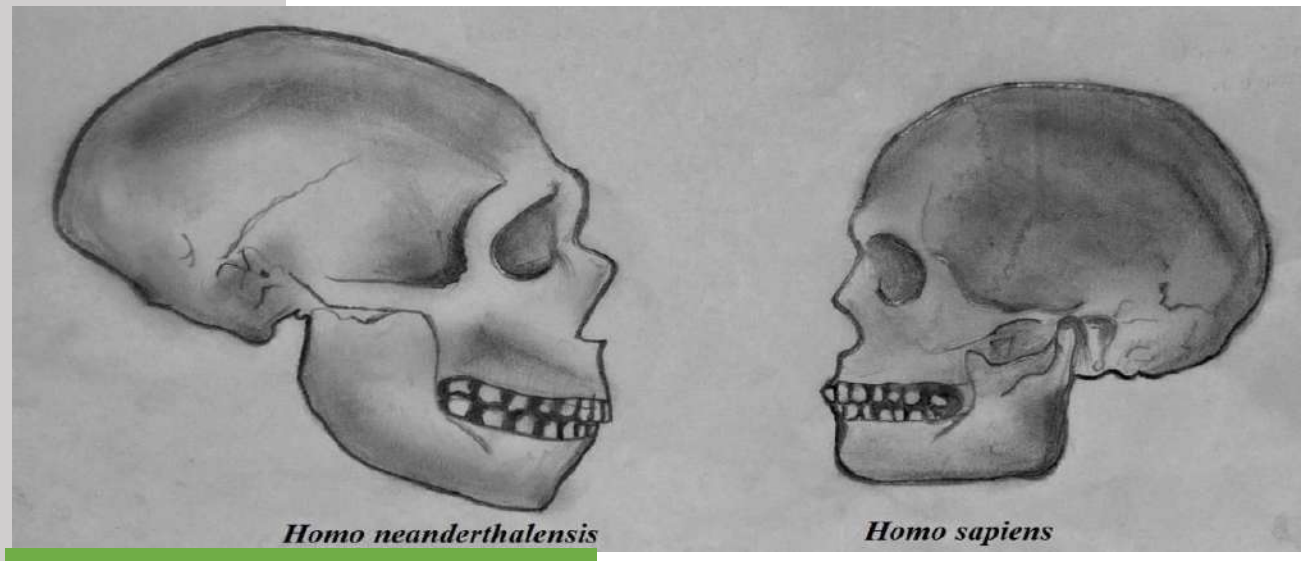
Mr. Aritra Gupta

Ms. Paromita Mitra

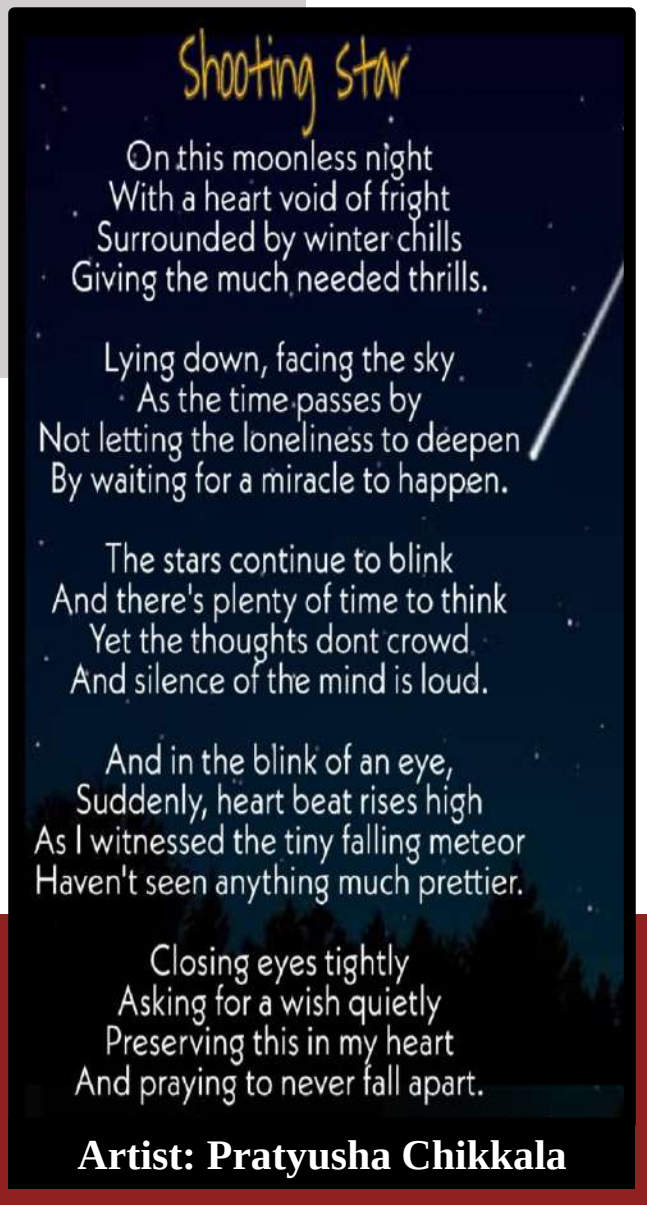
Mr. **Aritra Gupta** (PI: Prof. Kartiki V. Desai) and **Ms. Paromita Mitra** (PI: Dr. Sandeep Singh) received the Amity Best Poster Presentation Award at the 41st annual conference of Indian Association of Cancer Research – an International Symposium on: Cancer and Stem Cells.

CREATIVE corner

Artist: Sayan Ghorai



Artist: Vinay More

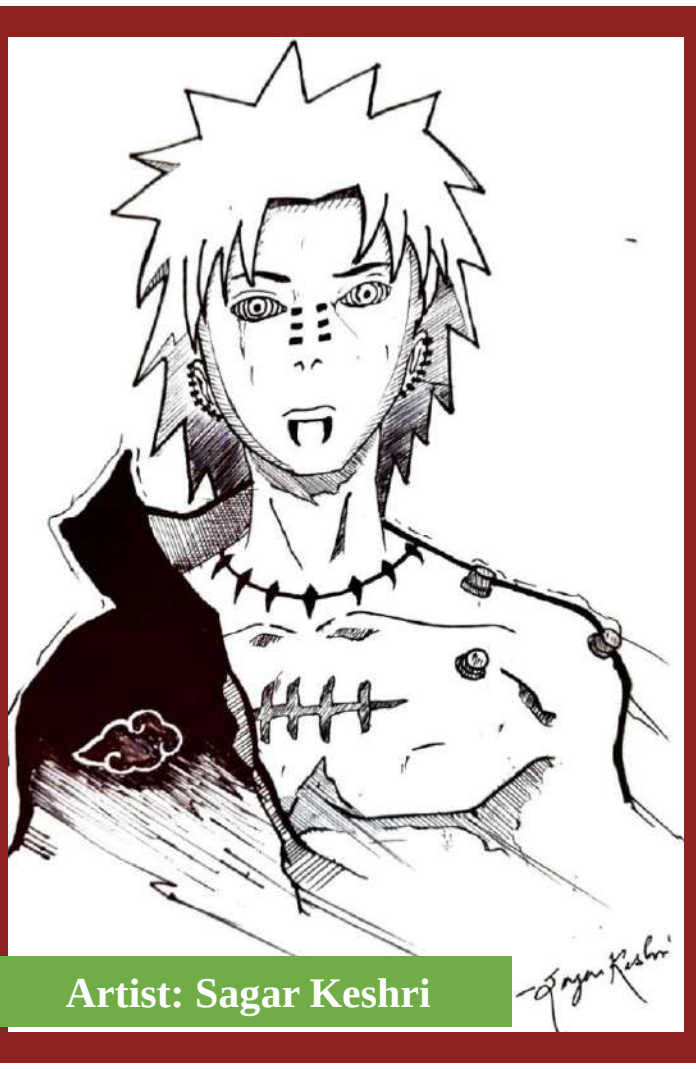


Artist: Pratyusha Chikkala

Artist: Urvashi Yadav

Artist: Ankita Maddheshiya

Artist: Debashree Tagore



Artist: Sagar Keshri