extremely constructive. There were discussions on how to get the most out of scientific papers in a short time, ethics in research and writing and Matlab boot camping. There were paper discussions and abstract writing exercises, which kept the students in the exciting loop of scientific activity.

In summary, neuroscience is one of the most enthralling domains of science at present, which is interdisciplinary. Developing countries like India need to invest in this field and spread awareness, which would not only help ongoing research towards curing neurological disorders, but would create avenues for engineers, doctors, scientists, technicians, businessmen and others for pursuing studies in such interdisciplinary areas, thereby augmenting India's contribution to the world's cutting-edge research in neuroscience.

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MEETING REPORT

Non-coding genomics*

One of the major goals of the Human Genome Project was to identify all the protein-coding genes. With the advent of high-throughput sequencing technologies, we now know that 97% of the human genome is transcribed and the tissue-specific nature and conservation of the transcripts across species suggest that they are mostly involved in gene regulation.

Large-scale annotation of the human genome by the ENCODE project identified the non-coding RNAs which comprise non-coding parts of a protein-coding gene, non-coding genes (small RNAs, lncRNAs, tRNAs, rRNAs, spliced leader RNAs, spliceosomal RNAs, etc.), intergenic stretches, repeats and other low complexity regions. The discovery and functional characterization of these diverse non-coding RNA types is critical in advancing our understanding of disease biology, plant evolution and biological complexity. A symposium on non-coding genomics organized recently provided a forum for Indian researchers in this emerging area of genomics.

The symposium began with a plenary lecture by S. C. Lakhotia (Banaras Hindu University, Varanasi) chaired by Vidyanand Nanjundiah (IISc, Bangalore). Lakhotia introduced *hsrω*, the first non-coding gene discovered by his team in 1982 in *Drosophila melanogaster*, long before non-coding RNA was recognized as a regulatory molecule. Lakhotia's research has shown that multiple non-coding RNAs are transcribed by this locus during normal development as well as under stress. And most of the stress-related lncRNAs, which target multiple proteins, act by regulating their activity or by sequestering them away from the activity site. Lakhotia also noted that suppression of a few of these lncRNAs, which integrate multiple regulatory pathways, affects cellular homeostasis within the host.

In the second session, Rakesh Mishra (CCMB, Hyderabad) and M. V. Rajam (University of Delhi) presented an interesting aspect of secondary structures in non-coding DNA and their implications in molecular biology. Mishra explained how simple repeats are transcribed and assume secondary structures, and suggested that the non-random selection and distribution of some of these simple repeats has a higher-order role in gene regulation during development and in genome packaging. Rajam exemplified how yield of crop plants could be improved by employing RNA interference (RNAi) technology in his research with fungal resistant cotton and tomato that produce double-stranded RNA (dsRNA) with hairpin loop structures and target genes like ornithine decarboxylase and acetylcholinesterase essential for the growth and development of the pathogenic fungi.

The third session chaired by Usha VijayRaghavan (IISc) started with talks by two speakers from USA, Rakesh Nagarajan (Washington University, Saint Louis) and Ravi Sachidanandam (Mount Sanai University, New York).

Nagarajan discussed how prediction of miRNA and transcription factor (TF) binding sites can be integrated to build sophisticated networks. Using Schwann cell as a model system, he demonstrated that miRNAs can act both as repressors and activators and help in remyelination after nerve injury. Sachidanandam elaborated on the geometrical beauty of non-coding RNAs by bringing in the concept of circular RNA and providing evidence for its existence, and the mechanism which leads to its formation and function.

The fourth session was chaired by H. G. Sharat Chandra (Centre for Human Genetics, Bengaluru) in which the emphasis shifted from cells to chromosomes with presentations by Shrish Tiwari (CCMB), Priyanka Pandey (NIBMG, Kalyani) and S. V. Ramesh (Directorate of Soyabean Research, Indore).

Tiwari revealed that the heterochromatin region of Y-chromosome not only undergoes transcription but functions in conjunction with genes from autosomes. He presented evidence for two novel non-coding RNAs which were present in multiple copies on Yq12 and showed testis-specific expression while lacking active X-homologs. He pointed out that one of those non-coding RNAs trans-splices with CDC2L2 mRNA from chromosome 1p36.3 locus to generate a testis-specific chimeric beta sv13 isoform. According to Tiwari, this is the first reported evidence of trans-splicing between a Y-chromosomal and an autosomal transcript.

Pandey was the first to link non-coding RNAs to disease in this meeting. She employed metagenomics and

*A report on the symposium 'Advances in non-coding genomics' organized by the Institute of Bioinformatics and Applied Biotechnology, Bengaluru during 12–13 September 2013.

transcriptome sequencing to show that two loss-of-function genes – *PKD1* and *PKD2* – are regulated by miRNA both transcriptionally and at post-transcriptional level during polycystic kidney disease. Ramesh talked about conserved miRNAs that provide anti-viral resistance to plants during biotic and abiotic stress, thus emphasizing the importance of ncRNA not only in gene regulation and disease progression, but also in providing defence against pathogenic DNA.

Day 1 of the symposium also hosted nine poster presentations from various research institutions. The poster included research that was not covered in the earlier presentations, and ranged from interlinking disease diagnosis, ncRNA and RNAseq to the role of ncRNA in developing disease/stress-resistant plants. The various topics included: (i) the application of RNAseq from patient-derived cell lines in early diagnosis or prognosis of CNS disorders in humans by studying differential expression profiles of coding genes and lncRNAs; (ii) the role of miRNAs in regulating protein–protein interaction networks in cervical cancer; (iii) the role of ncRNA in X-chromosome inactivation for diagnosis of heterozygous X-linked gene that leads to recurrent spontaneous abortions; (iv) miRNA profiling in finger millet and the use of RNAi to develop disease-resistant varieties; (v) involvement of lncRNA (ginir and giniras) in cellular transformation; (vi) exploiting miRNAs for developing abiotic stress-tolerant plants; (vii) sequencing the promoter region of *PR-10a* gene in *Jatropha curcas* using the techniques of molecular biology; (viii) utilization of publicly available RNAseq data to discover and validate prostate cancer-specific lincRNAs, and (ix) the efforts to characterize repetitive elements in *Amaranthus hypochondriacus*, an edible plant species *de novo* sequenced in-house.

On the second day, the fifth session witnessed talks by Beena Pillai (IGIB, Delhi), Anjali Shiras (NCCS, Pune) and K. N. Balaji (IISc). Pillai provided a refreshing talk emphasizing the interplay between miRNA and transcription factors in neurogenesis and neurodegeneration. She raised the point that deregulation of certain miRNAs is associated with malfunctioning of parts of the brain.

Shiras introduced a fascinating pair of long non-coding RNAs called ginir and giniras that work antogonistically to each other. She showed that overexpression of one led to de-regulated cell-cycle progression, genomic instability and cellular transformation *in vitro* and tumourigenicity and high metastatic potential *in vivo*, and vice versa. Balaji discussed the role of miRNAs in regulating the battery of genes associated with divergent functions in M1/M2 macrophages following activation of sonic hedgehog signalling-based BCG-mediated down-regulation of TLR2. Their genome-wide studies pointed to SHH signalling responsive miR-31 and miR-150 targeting MyD88, which leads to the suppression of TLR2 responses.

In the sixth session, Malali Gowda (C-CAMP, Bangalore), C. V. S. Siva Prasad (IIIT, Allahabad) and J. Sridhar (Madurai Kamaraj University) talked about different applications of studying the non-coding genome. Gowda discussed interrogating host and pathogen transcriptomes using various methods. His work revealed that the transcriptomes of rice and *Magnaporthe oryzae* are highly dynamic and produce diverse RNA species, including antisense transcripts, siRNA, CPA-sRNA, miRNAs and tasiRNA. Siva Prasad emphasized the need for tools to predict miRNA. He talked about SVM-based models, and introduced tools such as RAmiRNA and UTRpred which work on sequence complementarity and thermodynamics principles. He also introduced a few validation methods such as Vienna RNAcofold and iFoldRNA. Sridhar introduced the world of non-coding RNAs in prokaryotes. Non-coding RNAs assume complex secondary structures in prokaryotes, and he mentioned about the ongoing work where the effects of structure-disrupting mutations in the genomes of pathogens are studied.

The seventh session was chaired by Nagasuma Chandra (IISc) and comprised lectures by Vinod Scaria (IGIB), P. V. Shivaprasad (IISc) and Subhashini Srinivasan (IBAB). Scaria reported that functional regions in long non-coding RNAs are conserved across species with distinct spatio-temporal expression patterns. He also described long and small non-coding RNA interactions. Using genome-wide assays for protein–RNA binding, RNA processing, and variation frequencies, he expects to define potential functional elements in lncRNAs. Shivaprasad presented his work on regulatory cascade in tomato triggered by small RNAs from an unusually diverse superfamily in which miR482 and miR2118 are prominent members. His team has confirmed that miR482 targets NBS-LRR disease resistance proteins that cause mRNA decay. This silencing cascade mediated by miR482 is suppressed in plants infected with viruses or bacteria. He also emphasized that the process allows pathogen-induced expression of NBS-LRR proteins and that it contributes to a novel layer of defence against pathogen attack. Srinivasan talked about the discovery and characterization of a lincRNA specific to prostate cancer using data from public repositories and showed evidence for potential coregulation of *QSOX1* gene, a known tumour-suppressor factor, near the same locus as the lincRNA.

No genomics meeting can be considered complete without a session on tools that help scientists interrogate large volumes of genomics data. Vamsi Veeramachaneni (Strand Life Sciences, Bangalore) talked about the challenges of developing tools that address all aspects of non-coding genomics.

Bibha Choudhary (IBAB) wrapped up the symposium by summarizing all the talks and giving due acknowledgements.

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