Dissecting RNA world using NGS technology

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Sequencing the genome of an organism, or transcriptome of a cell line, or a tissue to know its composition, is the key to understand complex biological processes. The first-generation dideoxy Sanger DNA sequencing method has been used to sequence several genomes including viruses, bacteria, fungi, animals (including human), and plants. With the help of the whole genome information, scientists have identified many novel genes, genetic variations, functional elements, and expression pattern of genes in various tissues/cell types. However, this paradigm-changing technology until recently was confined to large-genome centers and was associated with high cost and labor. A relatively recent technological breakthrough, Next-Generation Sequencing (NGS) allows whole genomes to be sequenced at a much lower cost and in a short period allowing this technology to be within the reach of individual researchers/laboratory. The $1000 genome program (http://www.genome.gov/12513162) has transformed genomics by introducing several second-generation NGS technology platforms such as 454's pyrosequencing, Illumina's sequencing by synthesis, and Torrent *sequencing. More recently,* third-generation sequencers have emerged into the NGS market such as Pacific Biosciences and Oxford Nanopore.

The high-throughput parallel DNA sequencing has reduced the cost (from $100 million to $1000), time (months to hours), and manpower (thousands to an individual or automated) for human genome sequencing. The DNA sequencing throughput has increased to 10 fold per year, which compete with computing speed of "Moore's Law" (doubling every 24 months). Sequencing single genome is not enough, and hence thousands of population genome projects emerged to sequence 100,000 genomes (https://www.genomicsengland.co.uk); http://arthropodgenomes.org/wiki/i5K); https://b10k.genomics.cn; https://db.cngb.org/10kp, etc). All these developments will transform our understanding of life on earth and its evolutionary relationship at the deeper level.

However, DNA sequencing is one layer of complexity in the cell. Recently epigenetics and gene regulation are playing a very important role in the cell. Dr. Malali Gowda was one of the few scientists in the world, early access to NGS technology for deeper understanding of transcriptome or hidden RNA world. He has developed several high-throughput transcriptome profiling technologies such as Robust-Long Serial Analysis of Gene Expression (RL-SAGE) (Plant Physiology 2004; 134:890-897) and Robust Analysis of 5′-Transcript Ends (5′-RATE) (Nature Protocols 2008, 3:1018-1025, 34: e126), Massively Parallel Signature Sequencing (MPSS) and Microarray technology for genome-wide gene expression studies in plants and fungi (BMC Genomics 2006, 7:310). Recently his group established RNA sequencing methods to dissect transcriptome using NGS technology (Mahesh et al. Plant Physiology 2018; Shirke et al. PlosONE 2016; Mahesh et al. BMC Genomics 2016; Kuravedi et at.PeerJ 2015).

Dr. Malali Gowda is pioneer in genomics and bioinformatics where established the state-of-the-art cutting-edge technology; "**Next-Generation Genomic Facility**" at C-CAMP (Centre for Cellular and Molecular Platforms, NCBS-GKVK Campus, Bangalore. With in 3 years, over 1000 genomes (plants, animals, insects, microbes and environmental genomes) that are important to India have been sequenced including Tulsi, Neem, Rice, Sandalwood, etc. Recently he established the state-of-the- art "**Centre for Functional Genomics and Bioinformatics"**at TransDisciplinary University. The C-BFG, is carrying out large-scale sequencing, big data analysis and functional annotation of genomic elements (RNA, protein and molecules) and also train scientists and students on NGS, Bioinformatics and big data analysis and interpretation.