

# THE 2020 MILLENNIUM TECHNOLOGY PRIZE GOES TO...

Relevant for: Developmental Issues | Topic: Health & Sanitation and related issues

Perfect blend: The work of Shankar Balasubramanian (right) and David Klenerman brings together science and innovation. | Photo Credit: [Millennium Technology Prize](#)

The 2020 Millennium Technology Prize, announced in May, has been awarded to Shankar Balasubramanian and David Klenerman, “for their development of revolutionary DNA sequencing techniques.” Their work is a perfect blend of science and innovation, and very apt as we have all heard a great deal about genome sequencing in the context of the ongoing pandemic.

Awarded by the Republic of Finland, along with top Finnish academic institutions and industries, The Millennium Prize has a 21st century outlook, with a strong emphasis on innovation. Past winners include Tim Berners-Lee (for implementing the world-wide web) and Frances Arnold (for her work on directed evolution in a laboratory setting). Three of the eleven awardees so far have subsequently won Nobel prizes. We wait, with bated breath, for Balasubramanian and Klenerman!

Shankar Balasubramanian was born in Chennai, and has lived in England for most of his life. After his PhD, he joined the Chemistry Department, Cambridge University. He teamed up with David Klenerman, recruited by the Department around the same time. The initial aim was to build a microscope that could follow single molecules. Of special interest to him was the molecular machinery that DNA uses to make copies of itself. Somewhere in their discussions arose the germ of the idea for a new way to read the alphabet that make up DNA, and to thereby access the information stored in them.

DNA (or RNA, in some viruses), the genetic material of life forms, is made of four bases (A, T, G and C; with U replacing T in the case of RNA). A chromosome is the duplex of a long linear chain of these – and in the DNA sequence is information – the blueprint of life. Life famously can replicate, and DNA replicates when an enzyme, DNA polymerase, synthesises a complementary strand using an existing DNA strand as the template.

The breakthrough idea of Balasubramanian and Klenerman was to sequence DNA (or RNA) using this process of strand synthesis. They cleverly modified their ATGC bases so that each shone with a different colour. When copied, the “coloured” copy of DNA could be deciphered from the colours alone, using miniature optical and electronic devices.

A very significant advance in their “Next Generation Sequencing” (NGS) method lies in the size of DNA that could be sequenced at one go – more than a million base pairs can be sequenced, which translates to hundreds of genes or even the whole genome of an organism. This is made possible by simultaneously sequencing hundreds of pieces of DNA at the same time. Many copies of this long DNA “sentence” are randomly broken up into small pieces, each no more than a few hundred bases long, which are all sequenced together. The “reads” are then fitted together, in the manner of a puzzle, to give the final sequence.

This technology was spun off as a commercial entity, Solexa, with the initiative of Balasubramanian and Klenerman. This phenomenally successful startup was later acquired by the biotech company Illumina.

What about the cost of all this sequencing? When the Human Genome Project delivered the first, near-complete sequence of our genome, the cost was estimated to have been 3 billion dollars. As all our chromosomes together have 3 billion base pairs, it becomes an easy calculation – One dollar per sequenced base. By the year 2020, Next Generation Sequencing technologies had pushed the price for sequencing your genome down to a thousand dollars – when this technology becomes prevalent in India, this sum should become a few thousands of rupees!

To think that a coronavirus genome has not 3 billion but 30,000 RNA bases – not surprisingly, this has resulted in an explosion of data on the genomes of the novel coronavirus and its variants. Health authorities in the United Kingdom have sequenced the viral genome of one out of sixteen people who have tested Covid-positive. The popular genomic data sharing site GSAID has over two million submissions of Cov-2 genomic sequences, from 172 countries. NGS has been at the heart of monitoring the spread of viral variants across the globe, and tracing the source of outbreaks.

Shankar Balasubramanian continues to run a fine laboratory, focused on the design of therapeutic molecules that would tune down the uncontrolled expression of certain genes, and so control the damage they cause in conditions such as cancer.

*(This article has been written by D. Balasubramanian in collaboration with Sushil Chandani who is a professional computational biologist, sushilchandani@gmail.com )*

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This study was completed before the emergence of the Delta variant of SARS-CoV-2 now dominating in the U.K.

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