

Editor's Message

Environmental sustainability is the ability to maintain an ecological balance in our planet's natural environment and conserve natural resources to support the wellbeing of current and future generations. The United Nations aptly defines sustainable development as "meeting the needs of the present without compromising the ability of future generations to meet their own needs." However there are key pain-points of the journey of sustainable development that are required to address urgently. Those include – biodiversity loss, water scarcity, climate change, carbon offsetting, social and economic disparity, emerging diseases, food scarcity. It requires a holistic approach to address them effectively.

United nations has clearly identified the strategy and have developed sustainable development goals. The Sustainable Development Goals (SDGs), also known as the Global Goals, were adopted by the United Nations in 2015 as a universal call to action to protect the planet from marching at the tipping point of destruction. For achieving SDGs it demands a coordinated effort by natural and social scientists, engineers, technologists as well as the lawmakers and diplomats.

Total seventeen integrated SDGs are defined and through these it is ensured that development must balance social, economic and environmental sustainability. The creativity, knowhow, technology from all of society is necessary to achieve the SDGs in every context. Ultimately what is most required is 'Embracing sustainability as opportunity!'

The intelligent multilevel and multidirectional use of science can help us achieve the SDGs. Today's science is going to pave way for tomorrow's technology! The scientific data help us realize the burden individual living being has on nature and suggests measures to reduce the same. It would help us manage the existing resources wisely and create alternate energy sources. Development of new plant breeds, environmental friendly fertilizers and pesticides, zero budget farming techniques can help the farmers to have hopeful and peaceful life by serving community with healthier livestock. The development of technologies can help us meet the growing demand for a better quality of life and achieve a new direction.

The ever-dynamic field of science and technology will be redundant if it does not reach the common people. That will be only possible with right communication. Nothing in science has any value to society if it is not communicated. This particular issue of the multidisciplinary scientific journal of the college -JBNB, is a step forward to convey new ideas, technologies through research papers, review articles, short communications, reveals the theme that are directly or indirectly contributing to 'sustainable tomorrow'!

Dr. Kalpita Mulye

Dr Jayashree Pawar

THE GENOMEINDIA PROJECT: AMBITIOUS LEAP IN BIOLOGY!

Jayashree Pawar & Kalpita Mulye

Department of Biotechnology and Microbiology, VPM's B. N. Bhandodkar College of Science, Thane, India

Every human being is made up of cells containing genome, the complete set of all genetic material within an organism, essentially encompassing all the DNA sequence present in a cell. This genome sequence, is one of the most important structures that defines the 'identity' of an individual. Various platforms available today, from Sanger's sequencing, to Next-generation sequencing (NGS), combined with bioinformatics tools, can determine the entire genome sequence of the organism, identifying the order of the bases A, C, G, and T, in DNA, thus defining the individual at 'molecular level'! Two individuals, though would have genomes 99% similar, would still have millions of variations in their genomes. About 1 in every 1000 positions in the DNA differ between any two individuals on average, resulting in diverse genetic outcomes.

Human genome sequencing can detect these variations in the genomes, including polymorphisms and chromosomal rearrangements, that are responsible for various traits like disease predispositions, including rare inherited disorders. They could determine our predispositions to certain diseases as well as response to drugs. They would also help us track migration and evolutionary patterns of population groups.

The Human Genome Project began in 1990 by an international team of scientists under the guidance of Prof. James Watson. Both strategies, 'shotgun sequencing' and 'whole genome sequencing' were used for this purpose. The project was completed in 2003, quite ahead of schedule (13 years), with cost of roughly one billion USD. The project gave valuable insights into genomes of western populations. It produced a high-quality human genome sequence, that accounted for only 92% of the human genome. Remaining 8% couldn't be 'read' using methods available at that time.

Several new methods for DNA sequencing have since been established along with better bioinformatics tools, during the last twenty years, to make it a faster process, one genome sequenced in five days! The cost of genome sequencing also has decreased, so much so, that a genome can be sequenced at around 1,20,000 INR today! A 'truly complete' ('telomere-to-telomere') human genome sequence has been generated in 2022 using the advanced tools.

The 'GenomeIndia Project' launched on 3rd January 2020, is an enterprise by the Government of India, funded through the Department of Biotechnology, Ministry of Science and Technology, with a modest budget of Rs 238 crore. It is Led by the Centre for Brain Research at the Indian Institute of Science, Bengaluru, in collaboration with twenty more research institutions in India.

The 1.43 billion Indian population is one of the oldest populations in the world. It is made of more than 4600 population groups, and several ethnicities, many of which are endogamous. This leads to highly diverse genomes in Indian population, quite distinct from genomes of western populations sequenced earlier. The GenomeIndia project aims at creating a reference genome for Indian population. Whole Genome Sequencing and data analysis of 10,074 individuals, from 99 communities was successfully completed on 5th January 2025. Huge dataset of 8 petabytes would be stored at the Indian Biological Data Centre (IBDC), India's first national repository for life science data, in Faridabad.

INSTITUTIONS INVOLVED IN GENOMEINDIA PROJECT:

Sample Collection, Sequencing and Analysis Centres:

Centre for Brain Research (CBR), IISc Campus, Bengaluru

CSIR - Centre for Cellular and Molecular Biology (CSIR-CCMB), Hyderabad

CSIR - Institute of Genomics & Integrative Biology (CSIR-IGIB), New Delhi

iBRIC - National Institute of Biomedical Genomics (iBRIC-NIBMG), Kolkata

Sample Collection Centres

All India Institute of Medical Sciences (AIIMS), Jodhpur

Gujarat Biotechnology Research Centre (GBRC), Gandhinagar

iBRIC - Institute of Bioresources & Sustainable Development (iBRIC-IBSD), Imphal

Indian Institute of Science Education and Research (IISER), Pune

iBRIC - Institute of Life Sciences (iBRIC-ILS), Bhubaneswar

Mizoram University (MZU), Aizawl

National Institute of Mental Health & Neurosciences (NIMHANS), Bengaluru

iBRIC - Rajiv Gandhi Centre for Biotechnology (iBRIC-RGCB), Thiruvananthapuram

Sher-i-Kashmir Institute of Medical Sciences (SKIMS), Srinagar

Method Development Centres

iBRIC - Centre for DNA Fingerprinting and Diagnostics (iBRIC-CDFD), Hyderabad

Indian Institute of Information Technology (IIITA), Allahabad

Indian Institute of Science (IISc), Bengaluru

Indian Institute of Technology Delhi (IITD), New Delhi

Indian Institute of Technology Jodhpur (IITJ), Jodhpur

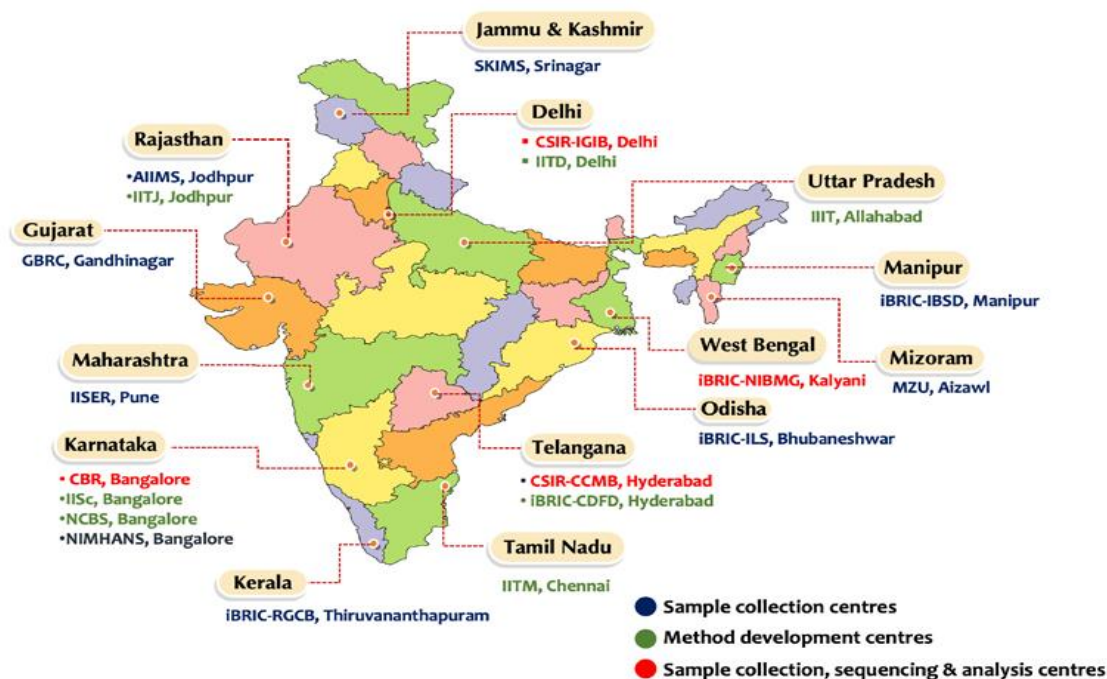
Indian Institute of Technology Madras (IITM), Chennai

National Centre for Biological Sciences (NCBS), Bengaluru

Biobanking and Data Archival Centres

Biobank at the Centre for Brain Research (CBR)

Data Archival at Indian Biological Data Centre (IBDC)



GenomeIndia collaborating institutions

RESULTS SO FAR....

The data of 5750 samples has been published so far, and more than 135 million genetic variations, have been identified. These mostly comprise of biallelic single nucleotide polymorphisms (SNVs), short insertions/ deletions (INDELs), and a small proportion of multi-allelic variants. Most SNVs and INDELs have been reported to be present within intergenic and intronic regions. Common, rare and ultra-rare variants have been identified in order to design studies for identifying genetic factors underlying common traits. Interestingly, many of the common variants are rare or non-existent in global variant databases, highlighting the uniqueness of Indian genomes. The data can also be used for designing gene-chips for diagnosing genetic disorders particularly for Indian populations.

Some medically significant findings have also been mentioned. For example, ten novel missense variants of the *LDLR* gene with role in familial hypercholesterolemia have been reported in Indian populations. In view of high prevalence of familial hypercholesterolemia in India, this is a highly significant finding.

Certain pathogenic sequence variants have been found to be less frequent in overall population, while prevalent in particular Indian populations. Another study has specified particular gene variants in certain population/s implicated in decreasing the efficiency and efficacy of anticoagulant, anti-retroviral, and anti-viral drugs. These findings are important for designing genomics based public health solutions and personalized health care in the post-genomics era.

Since the sampled populations represent the four major linguistic groups (Indo-European, Dravidian, Austro-Asiatic, and Tibeto-Burman) in India, the sequence data has also thrown light upon Indian population history.

CONCLUSION:

Indian genome sequencing would have invaluable applications in diagnostics and personalized medicine in near future. In today's era of genomics, getting a person's genome sequenced has become an achievable task. This however has multiple ethical and regulatory concerns that need to be thought about crucially.

REFERENCES:

<https://genomeindia.in/>

https://dbtindia.gov.in/sites/default/files/GenomeIndia-Digest-27-02-2024_1%20%281%29.pdf