WE MAKE DNA SPEAK

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NEWSBYTES

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About Xcelris

Xcelris Labs Limited is a life sciences based innovative research organization delivering solutions across domains such as Agriculture, Environmental Genetics, Animal science, Nutrition and Human health. We operate through two key divisions i.e Genomics and Medical Genetics. At Xcelris Genomics Division, we partner with more than 1000 research institutions across India and world to provide key services like Sanger Sequencing, Next Generation Sequencing, Molecular Biology kits and Oligo synthesis. In a span of 10 years, we have completed 15,000+ sequencing projects and 1000+ Next Generation Sequencing projects. Through our Xcelris Medical Genetics (XMDx) division we offer genetic testing service based on Sequencing for cancer diagnosis and therapy selection, infectious diseases and inherited genetic disorders in humans.

Key People

Management

Milina Bose
Executive Director & V.P.

Business

Bipul Banerjee
General Manager-Sales

Technical

Dr. Prashanth Bagali
Associate Vice President
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Dr. Srinivas Vudathala
General Manager
NGS Services

Dr. Sanjay Singh
Sr. Manager-Sequencing & R & D Services

Chandan Badapanda
Sr. Scientist, Bioinformatics

Xcelris Labs @ 19th ADNAT Convention, Bengaluru

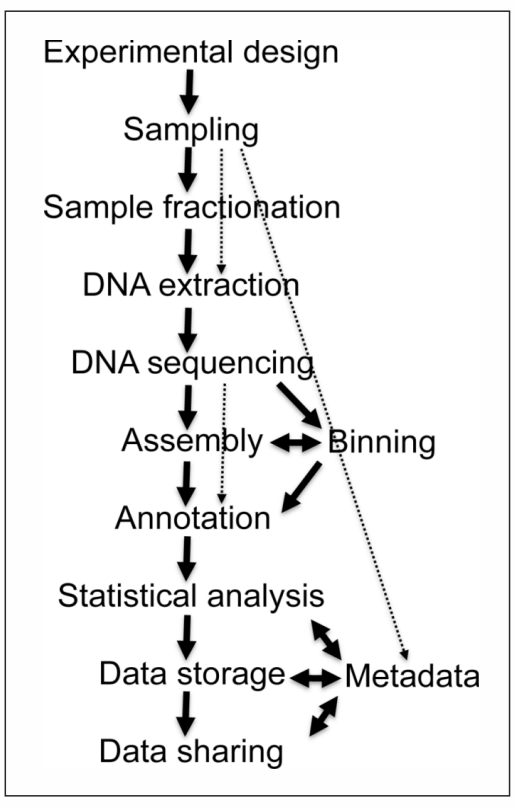
Dr. Srinivas Vudathala (General Manager - NGS Services) was invited as one of the keynote speakers at 19th ADNAT Convention, International Symposium on Microbiome in Health and Disease at NIANP, Bengaluru. His presentation on "Insights into the microbial worlds: Factors affecting metagenome mapping" explained in depth about the impact of several factors which affects metagenomics research.

This comprehensive presentation covered minutest factors right from sample collection, isolation techniques, choice of primers, sequencing platforms and finally the bioinformatics tools used for deducing the microbiomes. The novel ideas and the strategies shared by him were well received and applauded by the scientific community.

Insights into the microbial worlds: Factors affecting metagenome mapping

Dr. Srinivas Vudathala, General Manager – Sequencing Services

A wide range of environments-deep seas to upper stratosphere and other intermediary spheres of life in between them, are teeming with zillions of microbes. And every process in these environs is affected by the transformative powers of microbes. Metagenomics - a combination of Genomics, Bioinformatics and Systems Biology - has revolutionized the understanding of the enormity of the microbial world and its impact on every aspect of the world. This field of science has became a powerful norm in unravelling microbial communities in any environment. The onus squarely lies on the methodologies adopted at every stage of the study on the outcomes of the accurate analysis of the diversities in divergent microcosmos. An attempt is made to map all the factors involved in the study design, which includes sampling strategies, isolation methods, type of sequencing, the choice of primers, platforms, and finally, the bioinformatics tools used for deducing the microbiomes and understanding the true nature of abundances and community structures.



The fluctuations of the relative abundances of an organism in a community over time or among different instances of the community need to be understood and taken care for sampling. This of course, also includes seasonal, geographical and host variations.

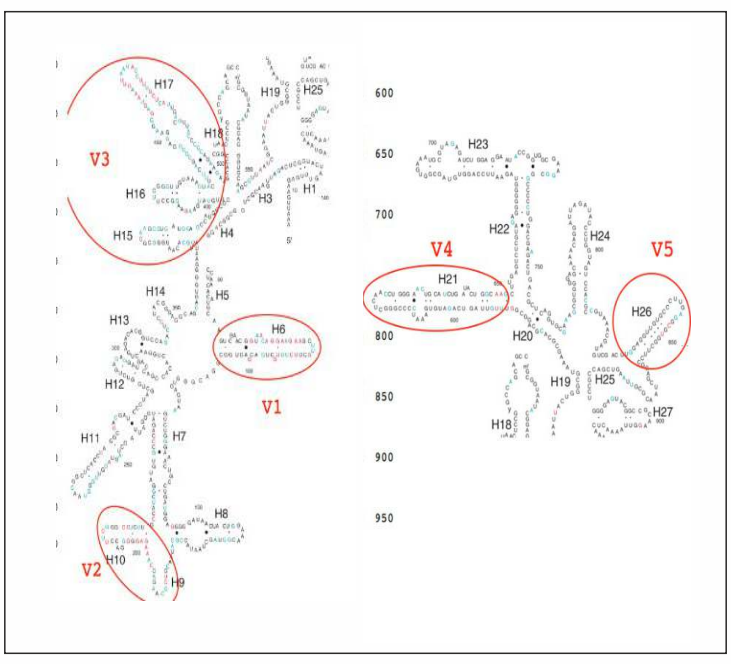
Biases are also introduced at other stages too. For a proper representation of all the members in the community, it is essential that the DNA from all members is extracted properly. Various DNA extraction techniques, and at times, in multiples, need to be introduced into a single study to allow access to different parts of the microbial diversity for achieving a proper representation. Another important variability is induced by the procedural contamination too.

Culturing and identifying the microbe is passé. 16S Metagenomics has transformed the first level of identification and does give a preliminary peek into the abundances. The choice of a single variable region to dual variable region to full length 16S sequencing and further down to whole Metagenomics, the methods have important bearing on the outcomes. Even for the 16S variable regions, there are no truly universal PCR primers, and reports stating that even the most comprehensive pair covers approximately 85% of the known taxa. This too, poses a challenge to an accurate identification. Factors like read lengths in various platforms, the quality of sequencing, the percentage of stitching are also important and worth being considered. The advent of the longer read capabilities now offers an opportunity for better diversity analysis than before.

Other interesting areas are the lateral gene transfers, phage-host interactions and metagenomic complementation that are now being better understood by deep Metagenomics rather than just with 16S gene sequencing.

The final factor is the Bioinformatics tools used for the analysis. The analyses depend on the availability of database, computational capabilities, the algorithms for assemblies, de-convolution and others. A wide range of variations in abundances has been reported in the analysis done using different tools using the same data set (MG-RAST, QIIME and many other tools).

The accurate mapping of the microbiomes by Metagenomics techniques is crucial as this field is gaining prominence in aiding various fields including Earth Sciences, Life Sciences, Environmental Remediation, Energy, Biotechnology, Agriculture, Biodefense and Microbial Forensics and all allied industries.



Key Notes: Scientists can obtain high quality of interpretable microbiome diversity analysis, if proper attention is paid on such small measures which will ultimately make a big difference in their research work. At Xcelris Labs, we have been instrumental in controlling the impact of such limiting factors, leading to successful completion of more than 1000+ Next Generation Sequencing Project.

Next article

Industry overview by Xcelris Team

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