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

Business

Ms. Milina Bose
Executive Director & V.P.

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General Manager - Sales

Technical

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Associate Vice President
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Sr. Manager-Sequencing & R & D Services

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Sr. Scientist, Bioinformatics

GBS: New Service Offered by Xcelris on NextSeq™500 Platform

Genotyping-by-Sequencing: Applications and Approaches

by Dr. Srinivas Vudathala

In the genomic data analysis domain, Genotyping-By-Sequencing (GBS) is fast gaining popularity in identifying confidence markers through NGS for any species in a much faster and lower data requirement regimen. GBS is now being widely used for population studies, germplasm characterization, breeding and trait mapping in diverse organisms by high-density SNP discovery and genotyping.

For any SNP discovery program, one would have used typically the GWAS on microarrays or a Whole Genome Sequencing (WGS) approaches.

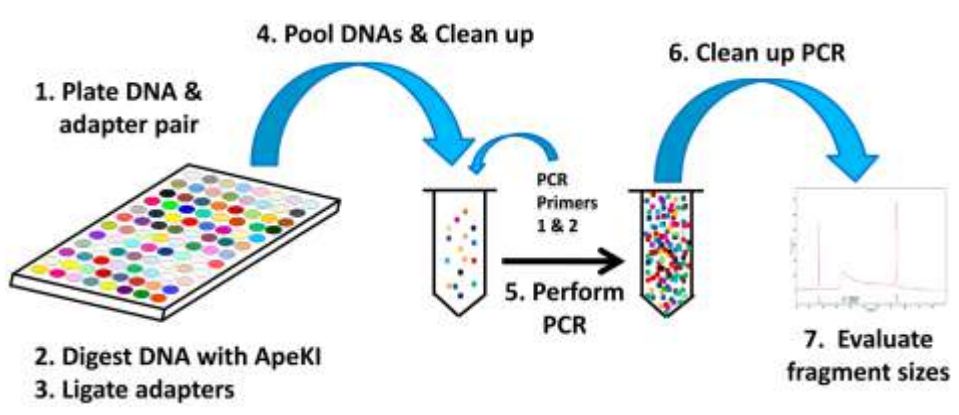
The microarray method has restricted use, as microarrays require invariant primer binding sites in order to obtain consistent results. It would also require designing and manufacturing arrays depending on the species being studied. This would become an expensive proposition.

In case of WGS approach, large amounts of data need to be generated. Also, the task becomes much more humongous if the reference sequence of that species is not available. This is another level of complexity and invariably is a very resource and finance-intensive approach.

That's where GBS comes handy. GBS uses a highly multiplexed, cost-effective approach that includes the use of restriction enzymes to reduce genome complexity and next generation sequencing technologies for SNP analysis.

What does reducing genome complexity mean? To put it in very simple terms, reducing the complexity means- instead of doing a complete genome sequencing to mine for the genome-wide SNPs, we use the restriction enzymes (RE) to digest the DNA and sequence only those regions around the cut sites. This reduces the need to generate large amounts of data. By choosing appropriate restriction enzyme (ApekI, EcoRI, PstI, MspI., to name a few), repetitive regions of genomes can be avoided and lower copy regions can be targeted with two to three fold higher efficiency.

The most important advantage is that the SNP analysis can also be done in non-model organisms using denovo approach. The parental lines or any one sequence from the population set can serve as the template for SNP discovery across the populations. This approach has been demonstrated to be robust across a range of species and capable of producing tens to hundreds of thousands of molecular markers (Elshire et al., 2011; Poland et al., 2012). Other key advantages of GBS methodology include reduced sample handling, fewer PCR and purification steps, no size fractionation, and inexpensive barcoding. The methodology is depicted below as described by Elshire et al., 2011:



GBS is making rapid strides in the arena of Cattle and Plant Genomics. One of the primary objectives of functional genomics in agricultural species is to connect phenotype to genotype and use this knowledge to make phenotypic predictions and select improved plant types. **The application of GBS to breeding, conservation and population surveys allow plant breeders to conduct genomic selection on a novel germplasm or species without first having to develop any prior molecular tools. For conservation biologists, it helps in determining population structure without prior knowledge of the genome or diversity in the species.**

Xcelris Labs Achievement

We have developed and standardized GBS pipelines for identifying high density genetic maps, population genomics and phylogeography. **For the first time in India, Jute GBS was performed successfully at Xcelris for building a high density genetic map of 503 RAD markers. This enabled us to develop a tool for marker assisted selection in Jute as published in the reputed peer reviewed international journal** (*reference available on request). **In GBS workflow, the most suitable RE is selected (based on cut-frequency across the genome, generation of 3-4 base sticky ends) and the primers are designed incorporating the complementary bases for the cut sites. The upper and lower strand primers are annealed to make the barcoded adaptors for ligation to the RE digested gDNA. The adaptor-ligated GBS libraries are then sequenced on NGS platforms. We are capable of handling large scale GBS projects and has successfully multiplexed 96 samples per GBS run on NextSeq™ 500.**

Dr. Srinivas Vudathala
General Manager, NGS Services , Xcelris Labs Ltd.

Dr. Srinivas Vudathala heads the Next-Gen Sequencing services at Xcelris Labs for the past few years. He is credited with successfully completing more than 150 runs on NGS platforms and upscale of 700 projects in various NGS domains. He has a strong cross-functional domain expertise of 20 years encompassing of Next Generation Sequencing, Microarrays, Bioinformatics (3D Protein Modelling/Drug Discovery), Proteomics, Automation and IT (SAP).

Next article

Dr. Prashanth Bagali : Impact of Whole-Exome Sequencing (WES) in healthcare.

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