

**New Updates. New initiatives. New Breakthroughs. New Technologies.**  
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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

**Ms. Milina Bose**

Executive Director & V.P.

#### Business

**Mr. Bipul Banerjee**

General Manager - Sales

#### Technical

**Dr. Prashanth Bagali**

Associate Vice President  
Genomics Research and Diagnostics

**Dr. Srinivas Vudathala**

General Manager  
NGS Services

**Dr. Sanjay Singh**

Sr. Manager-Sequencing & R & D Services

**Chandan Badapanda**

Sr. Scientist, Bioinformatics

### Dr. Sanjay Singh:

Sr. Manager-Sequencing & R&D services

Dr. Sanjay Singh heads Sequencing and R&D services at Xcelris Labs. He has expertise in Sequencing services, MID, Oligo synthesis and has developed various protocols for nucleic acid isolation for NGS. He has more than 13 years of research and industry experience in Sanger sequencing, Nucleic acid purification portfolios, Gene expression, Molecular Virology, Bacterial genetics, Animal Cell culture and has been acknowledged across various platforms.

## Multi Locus Sequence Typing (MLST)

### "A new road map for microbial identification on ABI 3730xl"

**Multi-Locus Sequence Typing (MLST)**, a method based on partial Sanger sequencing is a powerful tool to unveil taxonomic relationships within bacterial populations up to species level.

This is an approach of molecular typing technique, whereby using the partial sequence analysis of chosen seven to ten housekeeping genes(loci), sequence homology and variation among the pathogens is studied. The combination of each identified allelic profile generates the uniqueness of pathogen being studied; determining strain discrimination among the close relatives. Hence, this method can be considered, as a prime typing tool for epidemiological investigations of microorganisms

Each sequence of a given locus is screened with much higher frequency of recombination. So, if a derived sequence varies, it is considered as a new haplotype. It offers a unique advantage in screening of distinct known sequences and allelic profiling for various pathogens. MLST is been used successfully to study population genetics within bacterias and reconstruct micro-evaluation of epidemic bacteria and other microorganisms.

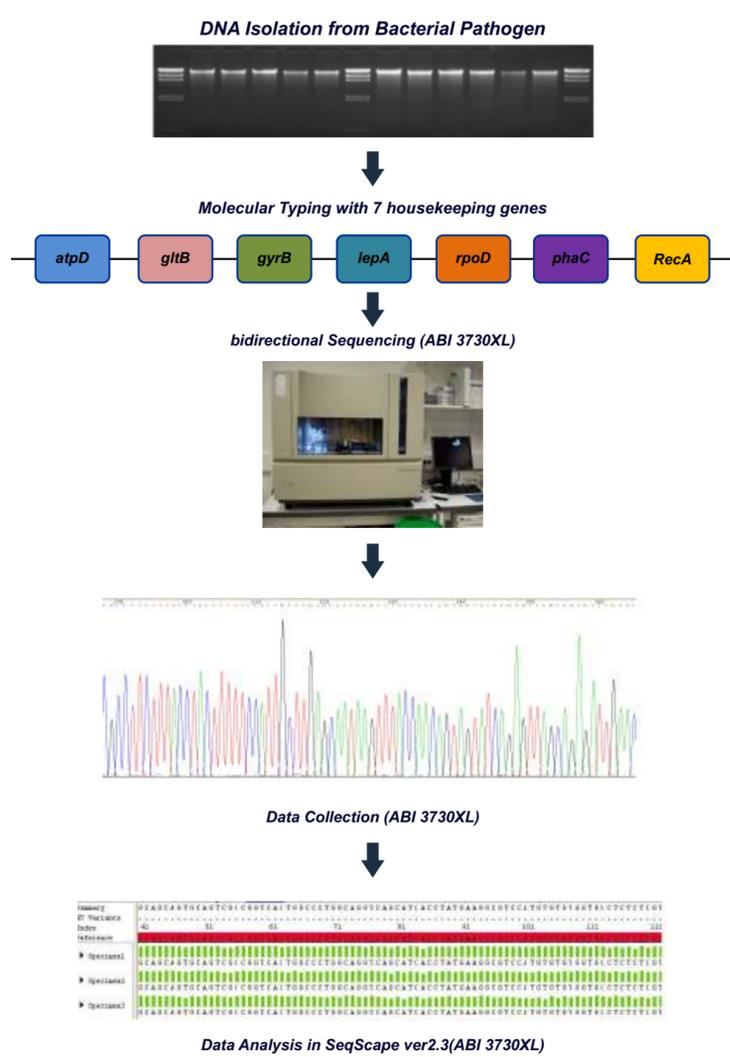
Molecular methods like 16S rDNA based molecular identification study of bacteria has been used for the last few decades and is a method of choice, if our goal is to have the overall diversity (Hung et al., 2005), but if our need is to find out the closest related pathogen, MLST will be one of the gold standard method (Gevers et al., 2005).

In recent past, few bacterial and fungal pathogens have been well studied and characterized using MLST approach like *E. coli*, *Salmonella enterica*, *Klebsiella pneumoniae*, *Campylobacter*, *Acinetobacter baumannii*, *Pseudomonas aeruginosa*, *Cryptococcus neoformans/Cryptococcus gattii species complex*, *Scedosporium aurantiacum*, *Scedosporium apiospermum*, *Pseudallescheria boydii* and *Pneumocystis jirovecii*.

At Xcelris, we have developed and standardized MLST protocol for nucleotide based approach (Sanger sequencing) typing of bacterial and fungal pathogens using ABI 3730xl platform. In recent past, more than 5 bacterial species on 50 different bacterial isolates have been successfully performed and identified. Approx 700 bp of selected loci are sequenced and well separated by capillary electrophoresis. The generated profiles are analyzed using SeqScape (ABI) software for base calling alignment, trimming and allelic library matching.

The application of MLST is huge, and in future it have immense potential as a resource for the scientific, public health, veterinary communities as well as the food industry.

### MLST workflow



## It's time to win goodies from "Xcelris NEWSBYTES"

Answer 2 simple questions within 2 days of receiving this mail.

**Q1: What type of coverage is performed in Sanger sequencing for MLST?**

(A) Partial (B) Complete

**Q2: Which is the method of choice to identify closest related pathogen?**

(A) Microbial Identification by 16S (B) Multi Locus Sequence Typing (MLST)

Hurry Up  
& Win  
goodies



(\*Winner will be announced after 6th issue.

\*Person with maximum right answers & on first come first serve basis will be announced as a winner.)

Reply us on: [bdgenomics.corp@xcelrislabs.com](mailto:bdgenomics.corp@xcelrislabs.com)



Next article

**Chandan Badapanda:**

"Metagenomics: Tools for Analyzing NGS data derived from Biodiversity studies"

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