

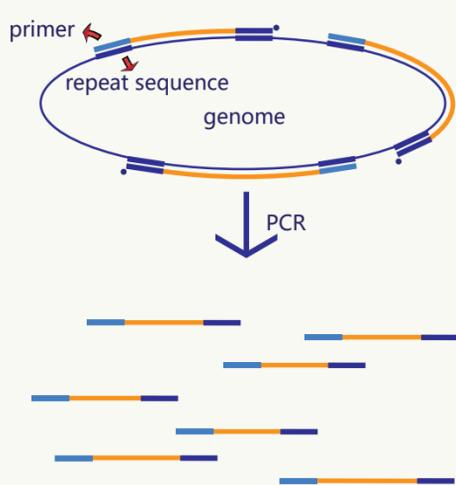
# How to Identify Microorganisms Quickly and Accurately?

Traditional culture-dependent microorganism identification methods lean heavily on morphology, physiology, pathology, and biochemical testing, which are time-consuming and labor-intensive. The advances of genetic technologies in recent decades have shined a light on microbial identification and promoted the soaring of microbiota research and the progress of medical science.

## Technologies for Microbial Identification

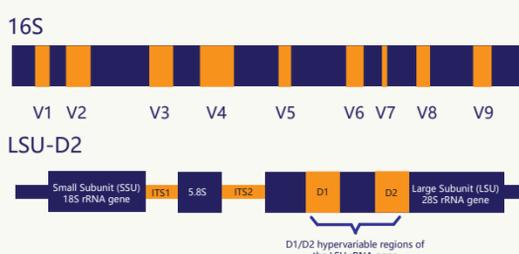
### Rep-PCR Profiling

REP (repetitive extragenic palindromic) sequences are highly conserved inverted repeats with strain-specific patterns, which can be scrutinized for bacterial fingerprinting by examining strain-specific patterns obtained from PCR amplification.



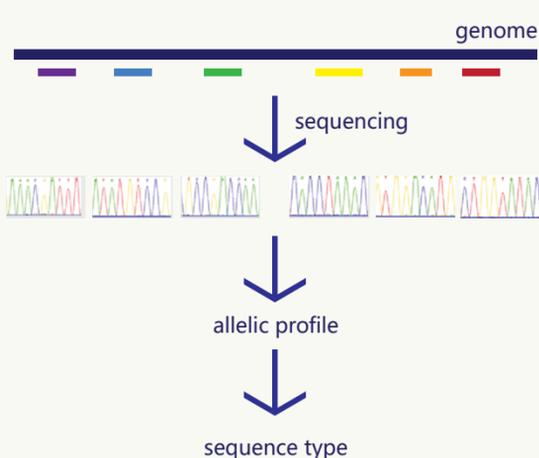
### MicroSEQ® Platform

MicroSEQ® platform (Applied Biosystems) provides rapid and accurate microbial identification based on PCR and Sanger sequencing of the 16S rRNA region (for bacteria) or LSU-D2 region (for fungi), providing much faster and more reliable identification approach than phenotypic methods.



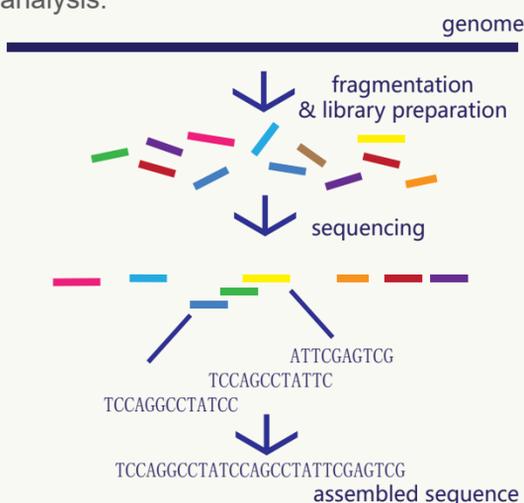
### Multi-Locus Sequence Typing

Multiple loci (internal fragments of 6-8 housekeeping genes) based multi-locus sequence typing (MLST) fulfills the identification and classification of microorganisms, allowing for the characterization of microbial species/strains with acceptable discriminatory power.



### NGS Identification

NGS (next-generation sequencing) is a culture-independent and high-throughput sequencing technology with the ability to sequence billions of DNA molecules simultaneously and independently. **16S/18S/ITS amplicon sequencing** and **shotgun metagenomic sequencing** can both be prepared for reliable identification and metagenetic studies, and allow for the taxonomic assignment of microbial species in complex microbial communities, evolutionary studies, network analysis, and correlation analysis.



## Technology Comparison

	Rep-PCR Profiling	MicroSEQ® Microbial Identification	Multi-Locus Sequence Typing	NGS-Based Microbial Identification
<b>Target(s)</b>	Repetitive extragenic palindromic sequences	16S rRNA region (for bacteria) LSU-D2 region (for fungi)	Internal fragments of 6-8 housekeeping genes	16S/18S/ITS amplicon Whole genome
<b>Bacteria/ Fungi</b>	Bacteria Fungi	Bacteria Fungi	Bacteria Fungi	Bacteria Fungi
<b>Bacteria/ Fungi Coverage</b>	High	High	Limited	High (16S/18S/ITS amplicon sequencing) Limited (shotgun sequencing)
<b>Application</b>	<ul style="list-style-type: none"> <li>Study the clonality of strains</li> <li>DNA fingerprinting for strain discriminations</li> <li>classification of strains and genetic relationship analysis.</li> </ul>	<ul style="list-style-type: none"> <li>Identify and classify unidentified bacterial or fungal sequences</li> <li>Perform a wide range of reliable microbial identification tasks and routine QC microbiology tests for pharmaceutical, medical, clinical, public health laboratories, etc.</li> </ul>	<ul style="list-style-type: none"> <li>Provide resources for the scientific, public health, and veterinary communities as well as the food industry</li> </ul>	<ul style="list-style-type: none"> <li>Allow for the taxonomic assignment of microbial species in complex microbial communities, evolutionary studies, network analysis, and correlation analysis.</li> </ul>
<b>Turnaround Time</b>	1 -2 days	1 day	2 days	10 days
<b>Accuracy</b>	99%	Highly accurate (above 99%)	Highly accurate (above 99%)	99%
<b>Throughput</b>	Low	Medium	Medium	Very High
<b>Advantages</b>	<ul style="list-style-type: none"> <li>Rapid and cost-effective</li> <li>Adequate discrimination power (better than the restriction analysis of the 16S/18S rRNA gene or the 16S-23S spacer region) of the DNA fingerprint analysis for related bacteria strains</li> <li>Reproducible results</li> <li>Generate results in real time</li> </ul>	<ul style="list-style-type: none"> <li>Optimized design and user-validated custom libraries, integrated workflow, and superior accuracy</li> <li>Working gold standard for the identification of most bacteria</li> </ul>	<ul style="list-style-type: none"> <li>Highly unambiguous and portable</li> <li>Reproducible, automated, and scalable</li> <li>Can be used to investigate evolutionary relationships among bacteria</li> <li>Provide good discriminatory power to differentiate isolates</li> </ul>	<ul style="list-style-type: none"> <li>High sequencing depth</li> <li>High sensitivity and discovery power</li> <li>High throughput</li> <li>Ability to sequence hundreds to thousands of genes simultaneously</li> <li>WGS (whole-genome sequencing) can detect gene information across the entire genome</li> <li>Cost-efficient and fast-turnaround for large sample volumes</li> </ul>
<b>Limitations</b>	<ul style="list-style-type: none"> <li>Less discriminatory compared to PFGE, making it suitable for initial screening of bacteria species</li> </ul>	<ul style="list-style-type: none"> <li>Rare instances in which MicroSeq® does not correctly identify a strain</li> </ul>	<ul style="list-style-type: none"> <li>Sometimes lacks the discriminatory power to differentiate bacterial strains, which limits its use in epidemiological investigations</li> <li>Sequencing 6-8 loci separately, gain less information than NGS</li> <li>Databases are limited</li> </ul>	<ul style="list-style-type: none"> <li>Less cost-effective and time-consuming for sequencing low numbers of targets</li> </ul>

CD Genomics provides comprehensive microbial identification based on the state-of-the-art platforms and proceeds versatile downstream analyses to meet your specific needs. Our excellent microbial identification platforms include Rep-PCR, MicroSEQ®, NGS-based microbial identification, multi-locus sequence typing, and mycoplasma detection, aiming to identify microorganisms efficiently and economically in a high-throughput, and simple manner.