

Bacterial Identification Database

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The scientific approach to bacterial identification testing is to compare characteristics of an unknown organism to a collection of known bacteria, the most homologous known bacteria being assumed to be the putative matching identification. The bacterial species is the ultimate group (taxon) encompassing individuals with defined common traits. Hence, very early, microbiologists, set up databases of known bacteria's traits. The challenge lies in the countless number of bacteria, the number of traits, the representativity of included species and the comprehensiveness of the database in order to generate the most accurate identification.

Over 10,000 species of bacteria have been described and accepted as valid to this taxonomic rank through publication in peer reviewed journals, to date. Moreover, from 700 to 900 new species are published each year (two per day) and validated through inclusion in the "Approved list of bacterial names" (International Journal of Systematic and Environmental Microbiology [IJSEM]). This constitutes a form of official registration/indexing of that name through a centralized system. The corresponding "Type strain," the most representative strain of the species of each new species, is deposited in two international collections of microorganisms (e.g. IP, ATCC, DSMZ, NCTC, etc.) in

two countries. As well, the nearly full-gene sequence of the 16S rRNA gene (small ribosomal sub-unit RNA encoding gene : roughly 1,500 base pairs) of this type strain, which was used to perform taxonomic studies as part of the polyphasic description, is deposited in an international public database (e.g. NCBI).

DNA sequence-based analyses have been established as the preferred methods (genotypic) to characterize bacteria because they are highly reliable, quick, and constitute the scientific reference in taxonomy. In particular, the comparative sequencing method consists in targeted sequence amplification of one gene (Unilocus) or multiple genes (Multilocus) by PCR (Polymerase Chain Reaction), then sequencing of both strands of the amplified DNA (e.g. Sanger's method), followed by comparison of the generated sequence to reference sequences contained in a database of reference sequences. The goal is to determine the most related reference sequence in order to identify the unknown at the appropriate taxonomic rank, ultimately at the species level.

For 16S rRNA gene Comparative Sequencing, Eurofins IDmyk has developed and validated, the most comprehensive commercial sequence-database made up of valid species type strain sequences.

This database, called Eurofins Microbial Sequencing Index (EMSI), contains over 9,000 full-gene sequences of type strains (9,000 entries in the index, which is highly representative of the whole known bacterial world). Eurofins BioPharma Product Testing has harmonized the analytical process of identification by Comparative Sequencing, hence, any unknown isolate received for identification by Comparative Sequencing in the EBPT labs is analyzed through a harmonized analytical process : 16S rRNA near full-gene sequencing, both strands of the DNA, and comparison to EMSI in order to determine the taxonomic rank of identification (order, genus, and ultimately species level).

This approach using Eurofins EMSI allows us to generate highly reliable results, improve the resolution of the method, and take into account most of the potential species that we may encounter in the Bio/Pharma industries. This is a real breakthrough in comparative sequencing identification of bacteria, since taxonomic quality identification is made available to our customers with the most comprehensive and representative database.

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