Bacterial taxonomy

Srujana Neelavar

Bacterial taxonomy is the method of naming and classifying organisms based on their characteristics. In bacteria, the species level classification is considered to be the most important as this helps in distinguishing one organism from another. Within one species, strains and subgroups might differ depending upon some characteristics, diseases they produce and their habitat. To distinguish bacteria at the species level, the current system of classification of bacterial species relies on a combination of phenotypic, genotypic and phylogenetic properties. To analyse those properties, many identification methods exist, such as fatty acid analysis, GC ratios, DNA profiling, DNA-DNA hybridisation, 16S-based phylogeny, etc. DNA-DNA hybridisation was extensively used in taxonomy and phylogeny before for species delineation where a known DNA is mixed with an unknown DNA and incubated to obtain single strands; and based on the level of hybridisation with each other, the species are demarcated. But this method is time-consuming and is difficult to perform in routine laboratories. Hence, 16S rRNA got widely accepted for species delineation. 16S rRNA is a part of the 30S subunit of the prokaryotic ribosome and is the most conserved region in most bacteria. Genome analysis of the species is performed by obtaining the 16S rRNA sequences of the two species from databases, e.g. EZBiocloud Server. If the 16S rRNA sequence similarity is less than 98.7%, it is termed as a new species; else, the overall genome relatedness index (OGRI) is calculated using an algorithm called average nucleotide identity (ANI). If the ANI value is greater than 95-96%, it is identified as a known species, hence enabling taxonomists to reclassify different bacterial species.