

Description for the general public

Bacteria from *Streptococcus* and *Enterococcus* genus are clinically significant opportunistic pathogens. Normally they are a part of normal human and animal microflora, but in special conditions, they can cause infections like bacteremia, endocarditis, abscesses, dental caries as well as urinary tract infections.

Streptococci and enterococci are groups of microorganisms which consist of many species. In routine diagnostics, their identification at the species level is based on phenotypic methods, which often cannot differentiate particular species. Nowadays, there are a few genetic techniques for streptococci and enterococci identification, but none of them can be used as a single method, because the results are not reliable. Therefore, there is a need to develop a diagnostic method with high discriminatory power. The method based on next generation sequencing of *16S-23S rRNA* region, which is present in all bacteria, comes across these needs. This method allows to obtain reliable results of identification at the species level within 24 hours and even culture-independent, directly from patients specimen. However, in widely used databases, there is a lack of reference sequences of *16S-23S rRNA* region, which will allow to compare the results obtained in diagnostic laboratories. The aim of this project is to develop reference sequences of *16S-23S rRNA* region for most *Streptococcus* and *Enterococcus* species.