Identification of Bacteria by 16S rRNA Gene Sequencing

Sequencing of the 16S rRNA gene is commonly used for identification of bacteria as it is a highly conserved component of the translational machinery of all bacteria and is highly suited as a target gene for universal identification.

MultiLocus Sequence Typing (MLST)

MLST is a procedure for unambiguous sub-species discrimination of bacterial isolates of a variety of common species using the sequences of internal fragments of several house-keeping genes.

Whole Genome Sequencing

Whole genome sequencing provides the ultimate characterisation of any organism. We can generate a draft de novo assembly of the genome or raw data mapped to any reference bacterial genome provided by the customer. Further analysis is also available.

Microbial Community Profiling

This service provides data to determine the relative abundance of all bacterial taxa found in complex samples including faeces, soil or clinical specimens.

Beyond traditional culture, our scientists have expertise in a wide range of technologies eg. MALDI-ToF, BIOLOG, and access to extensive bacterial isolate libraries and data sources. They also have in depth knowledge of animal and zoonotic diseases, wide experience of food safety, environmental and public health issues and a commitment to high quality standards including ISO9001 and ISO17025.

Many of the techniques are based on DNA sequencing and we are well equipped with a wide range of capillary and next generation DNA sequencing instruments.

APHA Scientific also offers other services including bacterial identification by traditional culture, MALDI-TOF and phenotypic characterisation using BIOLOG techniques. Please contact us to discuss any other requirements you may have for analysis based on DNA sequencing or data analysis using bioinformatics.