



16S Amplicon Metagenomics - A Fast and Reliable Service

Providing the Fastest Service on the Market

Microsynth offers the fastest 16S/ITS amplicon metagenomics service on the market. Our general turnaround time is just 3 - 4 weeks including bioinformatics.

Cost-effective Fixed Rates

We now also offer cost-effective fixed rates starting from just one sample.

Convenient and User-Friendly

All you need to do is provide us with the isolated DNA or alternatively provide it with your sample. Meaningful bioinformatics reporting offering a straightforward overview will then be delivered as the final output.

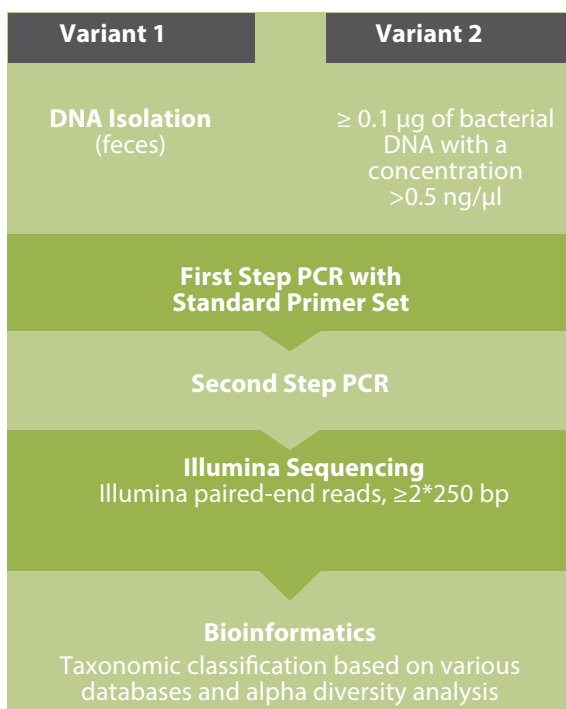
Introduction

Microbial communities exist in almost every environment. They are important drivers of biogeochemical processes, they have a major impact on human health, and they hold enormous potential for biotechnological applications. An important goal in analyzing a microbial community is identifying its taxonomic composition and diversity.

Sequencing of the ribosomal RNA (rRNA) gene and its internal spacer regions has become the gold standard for identifying microorganisms such as bacteria, archaea, and fungi. Its presence in all living organisms, the combination of conserved and hyper-variable genetic regions, and the availability of curated reference databases

make the rRNA gene an ideal phylogenetic marker. The combination of next generation sequencing (NGS) of subregions of the rRNA gene in combination with appropriate bioinformatics analysis is a powerful tool for exploring microbial community composition.

Workflow and Service Description



DNA Isolation: you can either perform the DNA isolation yourself or outsource this step to Microsynth. We have a standard pricing structure in place for feces samples but a range of other sample matrices are also possible upon request.

PCR Amplification: this follows a two-step protocol. In the first step, the locus-specific sequence is amplified. Meanwhile, in the second step, the Illumina sequencing adaptors and indices are added.

Bioinformatics: 16S/ITS analysis includes extensive quality filtering, denoising of operational taxonomic units (OTU), and taxonomic classification based on various databases and alpha diversity analysis (i.e. OTU diversity within a given sample).

Complementary options are available at a surcharge: For projects featuring very low amounts of starting material, we recommend our three-step PCR protocol. This includes two subsequent locus-specific PCRs to increase the yield of sequenceable amplicons.

The comparative statistics module includes beta diversity analysis (i.e. OTU diversity across samples) and the determination of differentially abundant OTUs including appropriate statistical measures. The functional profiling of the 16S amplicons module allows for the inference and prediction of functional profiles for 16S sequencing data.

Products

- Amplicon metagenomics by NGS¹
- Amplicon metagenomics by NGS including DNA isolation^{1,2}

¹ Fixed price per sample, which utilizes Microsynth's standard primer sets, including bioinformatics. Delivery of data within ≤4 weeks.

² Fixed add-on price per sample for DNA isolation is only valid for fecal samples. For other samples (e.g. bacteria cultures, soil, etc.) customized prices are provided on request.

Related Services:

- Bacterial de novo sequencing
- MLST Analysis
- Genomic epidemiology
- Shotgun Metagenomics
- Bacterial Resequencing