

Integrated Microbiome Analysis - Fungal & Bacterial

TC-S-MG-INT-MB

Applications

Method utilizes integrated amplicon sequencing of bacterial and fungal marker genes to comprehensively profile mixed microbial communities within a single study. Bacterial communities are characterized using 16S rRNA gene sequencing, while fungal communities are profiled using ITS (ITS1/ITS2) or 18S rRNA regions. This integrated approach enables simultaneous assessment of bacterial-fungal composition, diversity, and co-occurrence patterns across biological or environmental conditions. The use of long amplicons provides the ability to type microbial as well as fungal/plant samples present in a microbiome. These investigations are well suited to profile species richness, diversity, and abundances in microbiomes to infer changes in time-course or treatment-dependent studies. Inference of alterations in microbial abundances provides clues to shifts in microbial pathways.

These methods are suitable when host DNA is high, sample DNA is limiting, or as a pre-pilot for whole-genome, metagenome, or metatranscriptome investigations.

Pros

- Simultaneous profiling of bacterial and fungal communities
- Enables cross-kingdom interaction analysis
- Improved ecological and functional interpretation
- Suitable for complex microbiome studies

Notes

- Based on targeted marker gene sequencing
- Functional insights are predictive
- Taxonomic resolution depends on reference databases
- Sensitive to sample quality and inhibitors

Input



Microbial / Environmental DNA
≥ 10 ng recommended



DNA Qubit > 10ng

Sample Types



Soil



Extreme
environment
samples



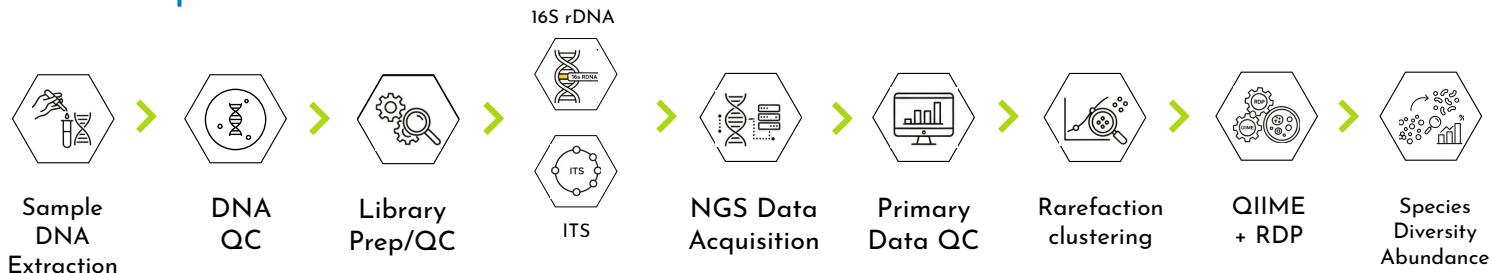
Biofilms and
sludge



Water

Platform ONT Long-read sequencing | 200K-250K reads 16s | 50K reads ITS

Process Map



Standard Deliverables

[Download Sample Report](#)

- Sample QC, Library QC, Summary of methods
- Data QC / Sequence data preprocessing summary
- 16S species match for typing and abundances
- ITS match for fungal and abundances
- Rarefaction Plots
- Species/Genus Identification with Shannon & Simpson Indices
- When multiple samples in time covers / treatment are provided in Beta diversity, differential heatmaps and PCA plots provided

References

- Estaki M et al. Curr Protoc Bioinformatics. 2020; PMID:32343490.
- Licata AG et al. Microbiol Spectr. 2025; doi:10.1128/spectrum.01673-25.