

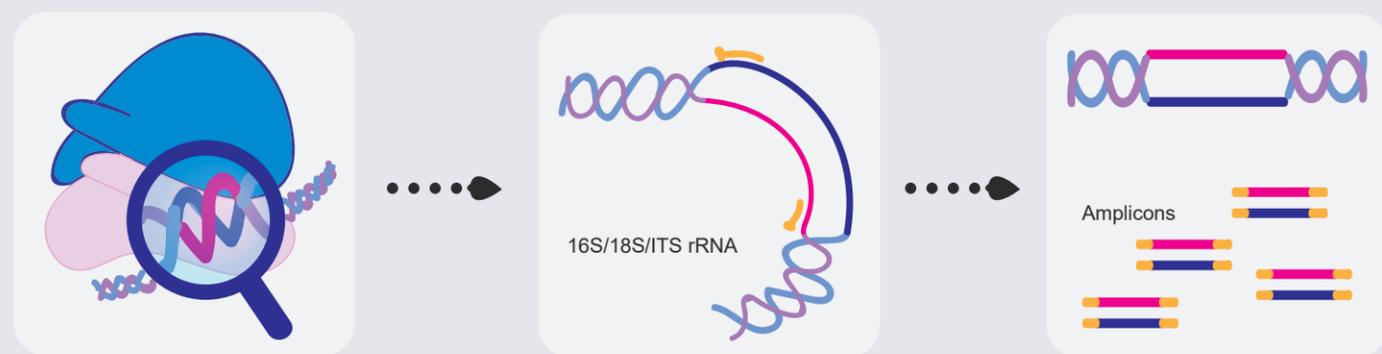
# MICROBIOME STUDIES: 16S/18S/ITS Amplicon Sequencing or Metagenomics?

Microorganisms are ubiquitous in all kinds of environments – they live in soil, water, inside or on the surface of animals and plants, and even survive in extreme conditions. Due to the various interactions between microorganisms and the environments, the studies of microbiome can provide us with a broader perspective to explain the law in nature that may help us make the most of microbial resources as well as turn the tide against microbial dysbiosis.

Microbiome profiling can illuminate the structures and functions of specific microbial communities. With the advancement of the next-generation sequencing (NGS) technologies, researchers can interpret comprehensive genetic information of all kinds of microorganisms including bacteria, archaea, fungi, and viruses, of which the majority are unculturable and have not been thoroughly studied. NGS technologies can offer distinct strategies for high-throughput sequencing of the microbiome, among which 16S/18S/ITS amplicon sequencing and metagenomics are two of the most widely used and the most representative technical approaches.

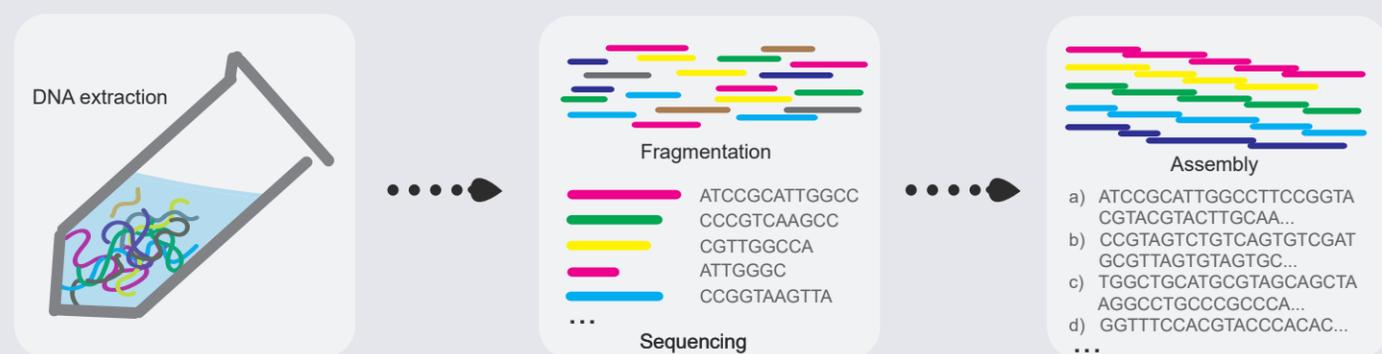
## 16S/18S/ITS amplicon sequencing

Amplicon-based NGS enables fast, accurate, and cost-effective microbial profiling by detecting genetic variation in specific genomic regions in a complex sample. Ribosomal RNA contains multiple conservative and variable regions distributed in 16S, 18S, and ITS. 16S sequencing is widely used for bacterial and archaeal phylogeny and taxonomy studies, particularly in diverse metagenomics samples. 18S rRNAs in eukaryote cells are the counterpart of 16S rRNAs in bacteria and archaea. Thus, 18S sequencing can be applied in microbiome profiling with regard to microbial eukaryotes such as fungi and protists. ITS sequencing is also a preferred approach in the ecological studies of fungi, which is typically useful for molecular systematics at the genus and even species level.



## Metagenomic sequencing

Metagenomic sequencing overcomes many limitations of amplicon sequencing and provides comprehensive information on the microbiomes, which is an unbiased sequencing technology that detects pre-fragmented billions of DNA base pairs in a single run. Instead of only concerning with the targeted regions as amplicon-based sequencing, metagenomic sequencing independently sequences all DNA fragments that are randomly sheared in analogy with the pattern of a 'shotgun'. Some of these reads will be generated from taxonomically informative regions such as 16S, 18S, and ITS1/2, while others will be generated from coding sequences to gain insight into the biological functions encoded in the genome, which simultaneously provides insight into biodiversity and function of a microbial community.



### A comparison of 16S/18S/ITS amplicon sequencing and metagenomic sequencing

	16S/18S/ITS amplicon sequencing	Metagenomic Sequencing
<b>Principle</b>	Use oligonucleotide probes designed to target and capture regions of interest, followed by next-generation sequencing to provide genetic information of the amplified sequences.	Randomly shear the DNA of the microbial genome into small fragments, followed by sequencing and splicing the fragmented sequences into a longer sequence through assembly.
<b>Research Objectives</b>	Phylogenetic relationship of species; species composition; biodiversity	Taxonomic analysis that amplicon sequencing can provide; in-depth research on genes and functions
<b>Taxonomic Resolution</b>	Microorganisms can be reliably identified at the genus levels, and some at species levels.	Microorganisms can be identified at the species levels and even provides discrimination power for subspecies and strains.
<b>Advantages</b>	Cost-efficient; Applicable to high host DNA contamination; Many well-developed tools available; Lower false positives risk.	Exact estimation of present and absent genes/functions; Novel gene detection; High variation of tools available; Detection of all genetic information of prokaryotes, eukaryotes, and even viruses; High resolution; Functional profiling available.
<b>Disadvantages</b>	Priori knowledge is required; Lower resolution; Functional profiling not available.	In a highly contaminated sample, other DNA should be removed to avoid unnecessary sequencing costs; High sequencing and bioinformatic analysis costs; Higher false positives risk.
<b>Recommended Applications</b>	Evaluating the differences in a large number of microbiota samples across different environments	Deeply investigating a smaller number of samples

The studies of the microbiome have provided valuable knowledge on various ecological systems and promoted the development of microbial resources. And most recently, a large amount of research are investigating all sorts of the microbiome that exist in the human body, such as oral microbiome, skin microbiome, and the gut microbiome. The correlation between microbiome and host/habitat is bilateral, which makes microbiome profiling and functional interpretation a complex and significant task.

CD Genomics is specialized in gene sequencing. Based on our state-of-the-art NGS platforms, we provide comprehensive microbiome profiling services with accuracy and supreme data quality. You can choose our amplicon-based NGS or metagenomic NGS for your specific microbiome research project. CD Genomics is dedicated to providing the most suitable solutions for your sequencing project and making sure your project runs smoothly in a cost-efficient manner.