ITS Barcoding Metagenomics

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Small things that matter.

Taxonomic profile and diversity analysis service for **fungi** in all sample types.

The **Internal Transcribed Spacer (ITS)** is a non-coding fragment of DNA located between the genes of the ribosomal subunits of most species. Eukaryotes have two sequences: ITS1 and ITS2. Both are used for fungal taxonomic studies because of their properties: (1) they are highly abundant in fungal genomes, (2) they exhibit a high degree of nucleotide variation between species, due to their low evolutionary pressure, and (3) the flanking sequences of the genome are highly conserved. Selective sequencing of these hypervariable regions of DNA extracted from the sample allows analysis of the diversity and taxonomy present in the sample. Fungal identification is performed by comparing the sequences obtained with reference databases.

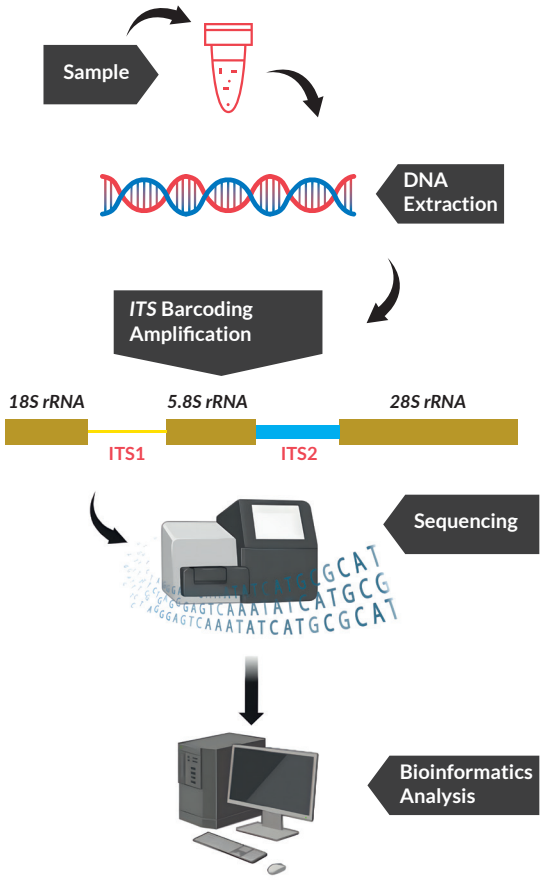
Molecular Biology Laboratory

Personalized scientific-technical consulting by our metagenomics experts for:

- Experimental Desing
- Sampling
- Project Tracking
- Results Delivery Meeting
- Drafting or Reviewing Publications

Molecular Biology Laboratory

A highly qualified team with extensive experience in metagenomics will carry out:



Sample quality control

Sample reception

- Biological sample reception 250 µl / 500 g*
  *According to the microbial load of the sample
- ADN up to 800 ng
  - Minimal volume = 40 µl
  - Minimal concentration = 20 ng/µl
  - Purity: OD260/280 = 1.8–2.0
    OD260/230 = 2.0

Certified Cleanroom

DNA extraction

- In anti-contamination **certified cleanroom**
- Experience with >50 different matrices
- Specific purification protocol

Amplification

- ITS1 o ITS2*
  *ITS2 is applied by default
- Possibility to customize primers
- **Use of positive and negative controls to monitor contamination**

Library Quality Control

Sequencing

- Illumina MiSeq 2x300 pb
- 60.000 guaranteed reads per analysis

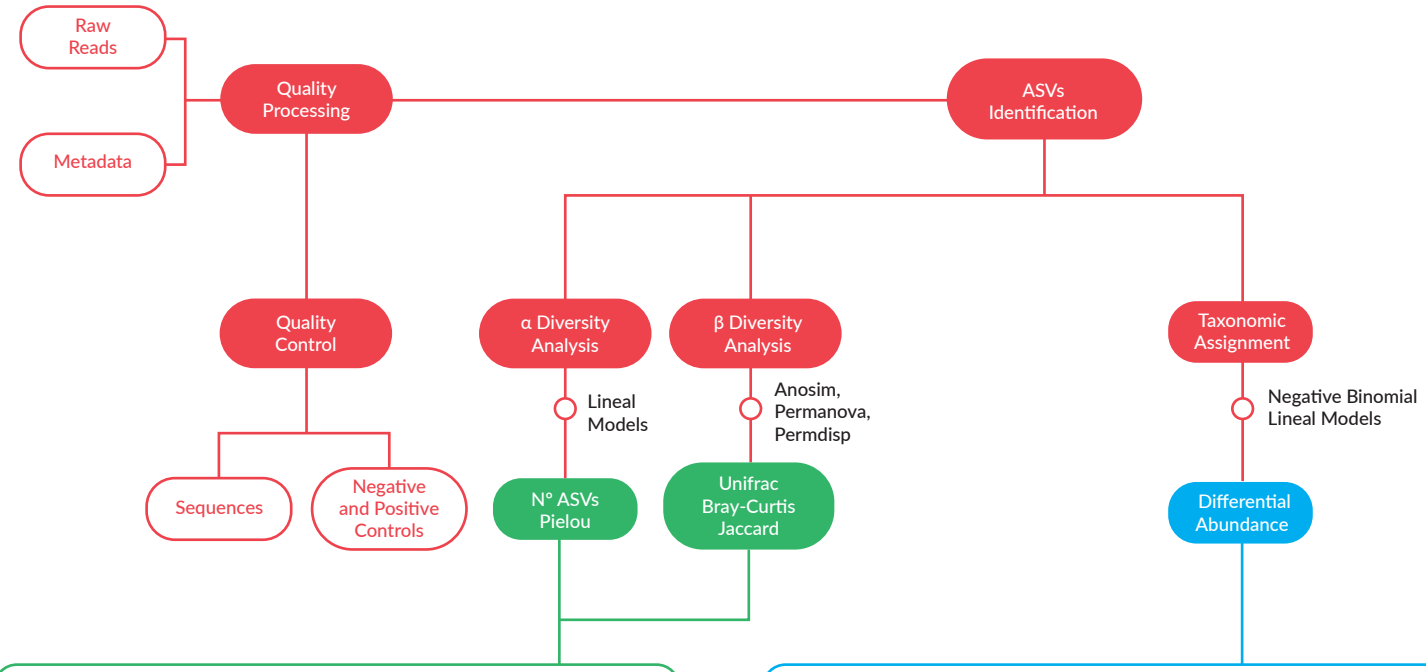
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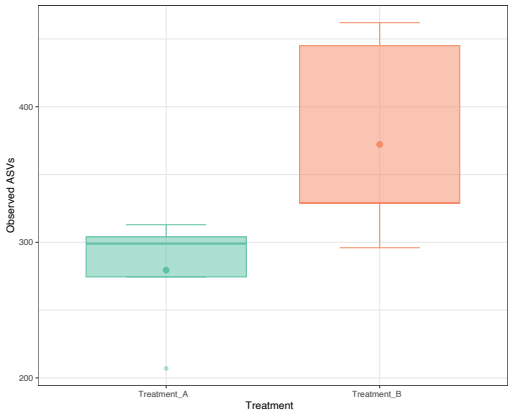
Bioinformatic and Statistical Analysis

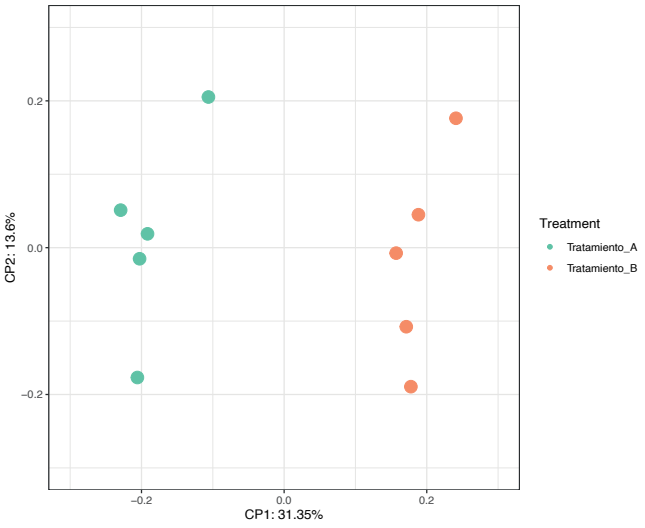
Our Bioinformatics Department has **pipelines designed to customize each analysis** according to the study's needs, addressing:



Diversity Analysis

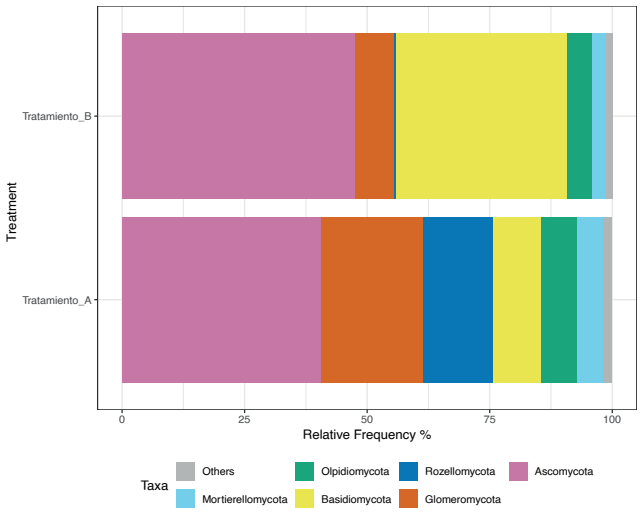
Study of the microbial ecological diversity present in each sample (**α**) and among samples (**β**).





Taxonomic Assignment

Identification of fungi present in the sample with **high taxonomic resolution** down to the **genus level**. Adapted approach for some species.



Association or correlation studies with qualitative or quantitative variables.

Complementary services

Customized bioinformatics analysis: bioinformatics analysis consulting service, **which includes 2 hours of post-delivery analysis in any complete study.**

Express service: possibility of reducing the turnaround time for the complete analysis.

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