Metagenomics as a tool to uncover ecological diversity in Mangrove

Amélie LAPORTE
Olivier GROS
Silvina GONZALEZ-RIZZO
1. Introduction

$10^{11}$ stars in the galaxy. $10^{13}$ microbial cells in 1kg of soil.

Microbial communities are underestimated.
1. Introduction

Most microbes do not grow in lab culture. Most bacteria do not have a cultivated representative.

- Difficult nutritional requirements.
- Symbiotic system.
2. Problematic

Poor understanding of microbial community.

What can we do?

Find new techniques that do not rely on cultivation and isolation of microorganisms.
3. Metagenomics

Environment (eDNA) -> Lab -> High throughput sequencing technologies -> Bioinformatics

What is there? What is their function?
3. Metagenomics

Functional analysis

Shotgun

Amplicon-based

Taxonomic analysis
3. Metagenomics

Shotgun

Functional analysis

Amplicon-based

Taxonomic analysis
4. Applications in microbial ecology

Microbial community:
- Maintains biogeochemical cycles.
- Involved in all levels of ecosystems and trophic-chains.

Metagenomics is a basis for more in depth research in ecology.
5. Project: Marine mangrove sediments

Mangrove ecosystem is a sulfide environment and:

- a hotspot of microbial diversity.
- a shelter for the fauna.
- a protection for our coasts.

Marine mangrove sediment is composed of an:
- Aerobic top layer.
- Anaerobic bottom layer: CO$_2$ production by sulfate reducing bacteria (SRB).
5. Project: Marine mangrove sediments

Objectives of the project:

- Insight of the microbial community within marine mangrove sediments.

- Searching for putative pathogens as expected by the MALIN consortium.
5. Project: Data

We sampled 5 different types of sediments in Manche à Eau, Guadeloupe.

Anaerobic phase.

Dry and wet seasons

Amplicon-based metagenomics: targeting a region of the 16S rRNA gene -> Bacterial analysis.
6. Results

1. Statistical diversity analysis.

2. Taxonomic analysis.
6.2 Statistical analysis

Bioinformatics

Total: 127,052 sequences

→ 2000 - 4000 OTUs (Operational Taxonomic Units): Group of similar sequences that are considered as one specie.
6.2 Statistical analysis

Bioinformatics

Total: 127,052 sequences

→ 2000 - 4000 OTUs (Operational Taxonomic Units): Group of similar sequences that are considered as one specie.

Statistical analysis

α diversity: Diversity inside one sample.
β diversity: Diversity between different samples.

β diversity → Principal Coordinate Analysis (PCoA)
6.1 Statistical diversity analysis

PCoA: Principal Coordinates Analysis
6.1 Statistical diversity analysis

PCoA : Principal Coordinates Analysis
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PCoA : Principal Coordinates Analysis
6.2 Taxonomic analysis

Bioinformatics

Total: 127,052 sequences

→ 2000 - 4000 OTUs (Operational Taxonomic Units): Group of similar sequences that are considered as one specie.

Taxonomic analysis

Taxonomic classification of the OTUs in 69 phyla. Abundance calculation of each phylum.

Most abundant bacterial group: Proteobacteria.
### Proteobacteria

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7. Discussion

The database are not precise enough for the study at specie level for this type of environment.

We found bacteria involved in sulfur and iron cycles. We did not find abundant pathogens.

Each sampling possess a specific bacterial composition.

Further research needs to be conducted in order to understand the functional activity of the bacterial community.
8. Conclusion

- Metagenomic is a powerful tool.

- Allows a new multidimensional understanding of an ecosystem.

- Is important for ecological, biodiversity and conservation researches.
Before heading to the questions I would like to express my appreciation to:

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Université des Antilles
And the laboratory of Mangrove biology
Université de Bordeaux
Thanks!

Any questions?

You can contact me at amelie.lpe@sfr.fr