Linking changes in microbial communities to trophic variations in a tropical mangrove

Agnès Bouchez[1], Noémie Pascault[1], Cécile Chardon[1], Marc Bouvy[2], Philippe Cecchi[3], Mélanie Herteman[4], Luc Lambs[4], Christophe Leboulanger[2]

1 INRA UMR CARRTEL, Laboratoire RITOXE, BP 511, 74203 Thonon Cedex, France
2 IRD UMR 5119, Ecologie des systèmes marins côtiers, UM2, CNRS-IRD-Ifremer- UM1, 34095 Montpellier Cedex 5, France
3 IRD UMR G-eau, 361 rue Jean François Breton, BP 5095, 34196 Montpellier Cedex 5, France
4 CNRS UMR 5245, ECOLAB, 29 rue Jeanne Marvig, 31055 Toulouse, France

INTRODUCTION

Many coastal lagoons support mangrove ecosystems in **intertidal zones** which tolerate highly variable physicochemical conditions of salinity, flooding, light, temperature which give rise to the **biocomplexity** that distinguishes mangrove ecosystems.

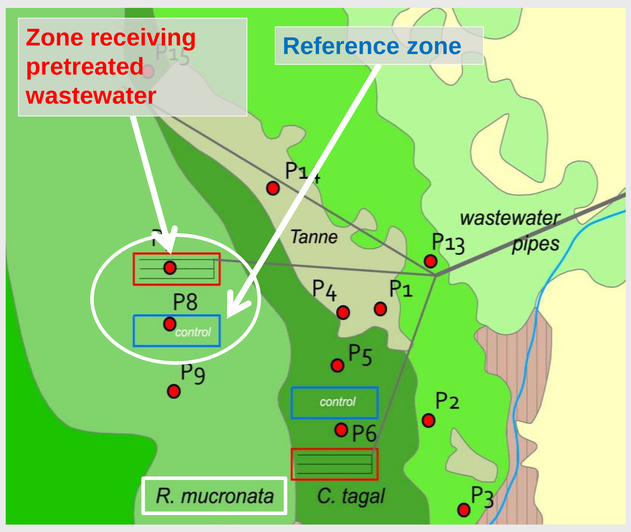
Microorganisms (heterotrophic bacteria and autotrophic eukaryotes) are efficiently participating to the mangrove ecosystem processes. Organized in **microbial biofilms,** they are present in the sediment upper-layer and on tree roots, **ensuring a number of different functions** as nutrient transformation, sediment stabilization, plant-growth promoting and even acting as a protective refugia for pathogens entering marine systems

To this day, works dedicated to **the use of mangroves as filters for nutrients and organic matter removal** have focused on global nutrient balance or on plant and animal compartments but not on microbial communities, although they may be both impacted and playing an active role in such processes.

This exploratory study focus on biofilm microbial communities in a tropical mangrove under two different trophic patterns. **Microbial communities sampled in two plots, receiving or not effluents from a domestic wastewater pretreatment device, were compared for their structure, diversity and functioning.**

MATERIEL AND METHODS

2 sampling plots in the zone of the mangrove with *Rhizophora mucronata.*
Effluent plot : receiving pretreated effluents
Reference plot : same zone, no effluents



Malamani mangrove,
Chirongui bay, southwest of Mayotte Island, Indian Ocean (12°55' S, 45°09' E)

Environmental sampling
3 substrata (roots, sediment, water)
2 plots * 2 dates (t0, t8)

Sampling of colonized biofilms
1 substrata (glass plates)
2 plots * 1 date (t8)

Mangrove zone with *Rhizophora mucronata* (Malamani mangrove) at high tide (left) and at low tide (right)

Sampling device for biofilms on the mangrove site (down) and after colonization (up)

✓The experiment lasted **8 days** (t0 to t8)

✓Environmental parameters were measured at the 2 plots : temperature, pH, sediment structure, salinity, NO_3^-, NO_2^-, NH_4^+, PO_4^{2-}

Parameters on communities

Community structure:
- Biomass (Chla – PhytoPAM)
- Number of cells of bacteria, pico and nanoeukaryotes (flow cytometry)

Community functioning:
- Photosynthetic efficiency (PhytoPAM)

Community diversity:
- Eukaryotic molecular fingerprinting (DGGE on rRNA 18s)
- Prokaryotic molecular fingerprinting (DGGE on rRNA 16s)

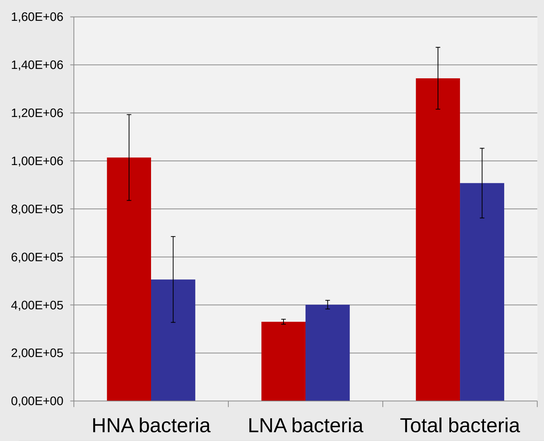
RESULTS AND DISCUSSION

✓ Sediment structure, pH, temperature, salinity : common characteristics in the 2 plots

✓ In the "effluent" plot NO_3^-, NO_2^-, NH_4^+ concentrations were higher in the interstitial water of the sediment surface layer than in the reference plot

✓ In the "effluent" plot PO_4^{2-} concentrations were higher in the interstitial water of the sediment deeper layer (100 cm) than in the reference plot

Community structure



number of cells of bacteria (flow cytometry) in the colonized biofilms (sampling device)
HNA (high nucleic acid content) LNA (low n.a. content)

✓ The number of cells of bacteria is significantly higher in the plot receiving pretreated effluents

✓ This is due to the active bacteria fraction with high nucleic acid content

✓ According to fluorescence ratios (phytoPAM, results not shown) green algae and diatoms contribution was higher in the "effluent" plot than in the reference one for colonized biofilms.

Community functioning

✓ No difference observed for photosynthetic efficiency of colonized biofilms

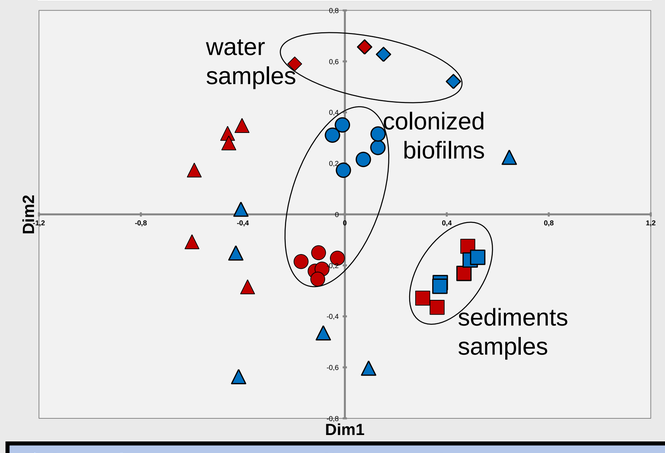
✓ But no measured parameters linked to bacteria activity

Community diversity

Sediment
Root biofilm
Colonized biofilm
Water

RED = effluent plot
BLUE = reference plot

Environmental & colonized samples
MDS on presence/absence results of DGGE on 16S rRNA

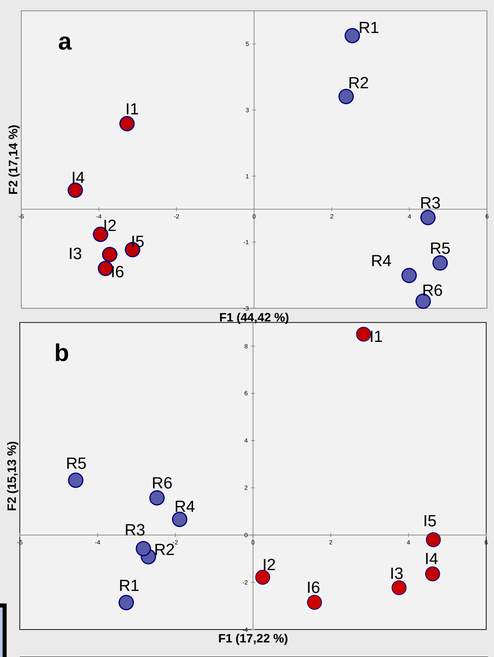


✓ Samples group according to substrata, except root biofilms which are more heterogeneous.

✓ Colonized biofilms samples are at the center they represent an average diversity of natural communities.

✓ With an average richness of 19, colonized biofilms are between root (13) and sediment (26) samples.

Zoom on colonized biofilms
PCA on relative band intensity of DGGE on (a) 16S rRNA and (b) 18S rRNA



✓ The first axis is related to the sample origin. Though prokaryotic and eukaryotic diversity appears to be different in the "effluent" plot and in the reference plot.

CONCLUSIONS AND PERSPECTIVE

✓ Biofilms colonized on glass plates in a sampling device seem to give a good image of the diversity of bacterial communities in the mangrove

✓ **Due to the deposed effluent, a trophic pattern was observed in the interstitial water of sediments, with more nutrients in the sediments upper layer (N forms) or lower layer (P)**

✓ **Together with this increase in nutrients, we observed an increase in active bacteria cells in the plot receiving effluents**

✓ **The trophic pattern highly influenced the diversity pattern of both eukaryotic and prokaryotic communities**

Perspectives: increasing knowledge on such ecosystems is still required. Data mining remains necessary as diversity; structure and functioning of microbial communities in mangroves are still sparsely studied. Insight in functional diversity of these communities is particularly required in order to better understand their ability to transform the effluents from the pre-treatment device, especially for communities acting in nitrogen cycling.

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