Bacterial Community Structure in Sediment and Water Samples from Freshwater Marsh, Mangrove and Seagrass, in the Florida Everglades

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Abstract

Aquatic bacterial communities are important ecosystem engineers as they are known to play a significant role in nutrient cycling and organic matter processing. The main environmental factors which determine their numbers and composition, as well as ecosystem function, are a continuing line of research. The goal of this work was to assess the compositional structure of the both sediment and water column bacterial communities within different plant communities of the Florida Coastal Everglades (freshwater marsh, mangrove and seagrass) across seasons (dry and wet). Microbial diversity was assessed by molecular techniques based on LH-PCR profiles of 16S rRNA genes. The primary factor driving bacterial communities was matrix type (sediment vs water). Sediments had higher species number and Shannon diversity index. In both water and sediments, salinity was the next important driver; freshwater marsh samples always clustered separately from the more saline sites (mangrove and seagrass). Finally, some communities clustered according to a seasonal pattern (wet vs dry), especially the water samples from mangrove sites, but seasonal differences in the Shannon diversity index were not observed. Although community differences were profound, we still need to know more about functional aspects of the communities and how this affects ecosystem processes.

Objective

The main purpose of this experiment was to assess bacterial community structures and compare them according to:

i) type of samples: water and sediment

ii) plant communities: freshwater marsh (SRS 1,2,3 & TS 1,2,3), mangrove (SRS 4,5,6 & TS 6,7), seagrass communities (FB9,13,14,16,21,27)

iii)seasons: wet and dry

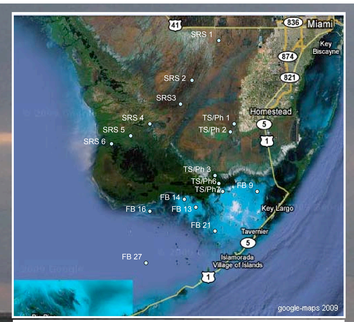

Fig. 1 Map of LTER sampling sites.

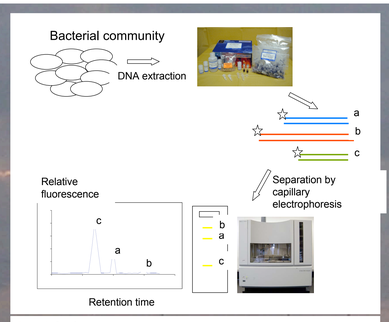

Fig. 2 Explanation LH-PCR process.

Materials and Methods

The samples were obtained from three different plant communities: freshwater marsh (SRS 1, 2, 3 and TS/Ph 1, 2, 3), mangrove (SRS 4, 5, 6 and TS/Ph 6, 7) and seagrass (FB 9, 13, 14, 16, 21, 27) in Florida Bay and Southern Biscayne Bay during the wet (September) and the dry (May) seasons. Fifty milliliter water samples were collected on a 0.22 _m (pore size) filter. Top surface sediment samples were taken at the same sites using a core. Only 500 milligrams of sediment were weighted for DNA extraction. For both water and sediment samples, DNA was extracted using a physical extraction method with glass beads. Amplification of the 16S rRNA gene was performed with primers universal for the domain Bacteria: 27f-6FAM and 355r by LH-PCR technique and the length of the fragments were resolved by capillary electrophoresis. Cluster analyses were done using the percentage of fluorescent of each fragment as an indicator of the proportional "abundance" of a particular Operational Taxonomic Unit (OTU), in a given sample. The similarity matrix was calculated with Morisita's index and a dendrogram was constructed using UPGMA algorithm. The Shannon index was calculated according to the formula *H'=-_pi ln pi* and the evenness index (J) by *J=H/Hmax* where *pi* is the proportion (relative abundance) of each fragment in the community. To assess differences between samples a one-way ANOVA test was used.

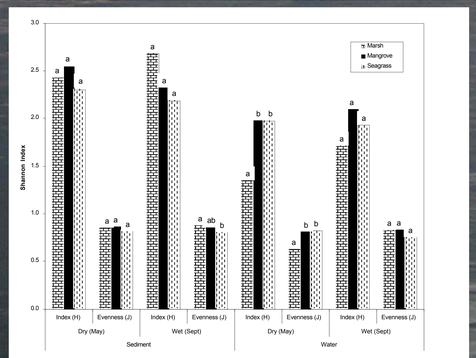

Fig. 4 Shannon and Evenness Indices assessed from LH-PCR profiles of bacterial communities from two types of samples and three plant cover types in two seasons. Bars with the same letter are not significantly different according to one-way ANOVA followed by Tukey's test ($p < 0.05$).

Plant community type			Type of sample Sediment/water		Season Dry/Wet
Freshwater marsh	Dry	F=16.7; P=0.003 (***)	Sediment	F=1.5; P=0.24 (n.s.)	
	Wet	F=79.3; P<0.001 (***)	Water	F=3.5; P=0.096 (n.s.)	
Mangrove	Dry	F=20.2; P=0.002 (***)	Sediment	F=0.5; P=0.491 (n.s.)	
	Wet	F=0.4; P=0.540 (n.s.)	Water	F=0.4; P=0.544 (n.s.)	
Seagrass	Dry	F=4.0; P=0.073 (n.s.)	Sediment	F=0.4; P=0.544 (n.s.)	
	Wet	F=1.8; P=0.215 (n.s.)	Water	F=0.07; P=0.792 (n.s.)	

Table 1 One-way ANOVA results comparing the bacterial diversity (Shannon index) between two types of samples (sediment and water) and two seasons (dry and wet).

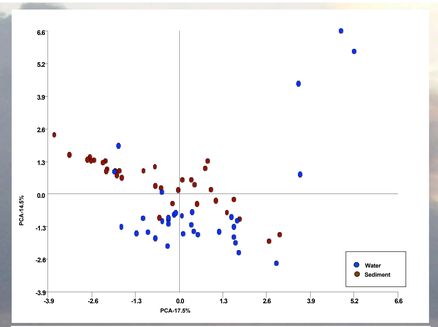

Fig. 3 Principal Component Analysis showing the degrees of similarity in the bacterial communities of water and sediment samples.

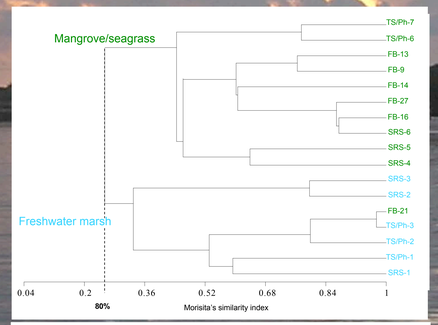

Fig. 5 UPGMA cluster analysis showing the relationship between sediment bacterial communities from different plant cover in dry season.

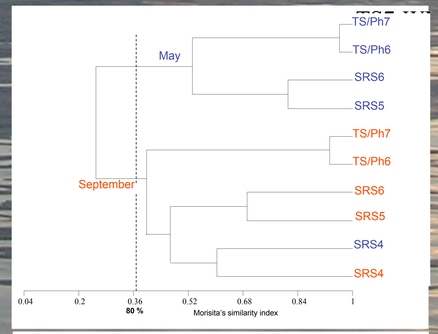

Fig. 6 UPGMA cluster analysis showing the relationship between bacterial communities in water samples from mangrove sites in two seasons.

Results and Discussion

The bacterial community structure differed between water and sediment samples throughout all types of plant communities and the two sampling seasons (Fig. 3). Furthermore, according to Shannon index, the bacterial diversity was higher in sediment than water samples during wet and dry seasons in the freshwater marsh and during the dry season in the mangrove communities (Fig. 4 and Table 1).

Groupings of samples showed differences across plant communities. Mangrove and seagrass samples always differed from freshwater marsh samples in both types of samples (water and sediment) and in wet and dry seasons (Fig. 5). These results suggest that the bacterial communities were strongly influenced by salinity.

Nevertheless, minor differences were observed in bacterial diversity where only the water samples of freshwater marsh were significantly different from mangrove and seagrass samples in the dry season (Fig. 4).

In general, the structure of bacterial communities was affected by season. Thus differences between freshwater marsh and mangrove samples were shown in wet and dry seasons. It was observed in water as well as in sediment samples. The most prominent example is shown in figure 6 where May samples differed from September samples in mangrove sites. On the contrary, seagrass samples were not clustered according to season. This result seems to indicate that the bacterial communities are more stable in seagrass ecosystems where the changes on abiotic factors are less pronounced. However, seasonal differences in the Shannon diversity index were not observed (Table 1).

Conclusions

1. Sediment bacterial communities had a higher diversity than those from water and were clustered in different groups. Therefore, sediment bacterial community does not have large influence on water column community structure.
2. Freshwater marsh samples always clustered separately from the more saline sites (mangrove and seagrass).
3. Some seasonal changes were observed, mainly in freshwater and mangrove, but the samples were not significantly different in bacterial diversity.

Acknowledgements

We wish to thank Jeff Absten and the Microbial Ecology field crew. This research was supported by the National Science Foundation through the FCE LTER program.