Microbial Ecology

Analysis of Bacterial Communities in Seagrass Bed Sediments by Double-Gradient Denaturing Gradient Gel Electrophoresis of PCR-Amplified 16S rRNA Genes

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Bacterial communities associated with seagrass bed sediments are not well studied. The work presented here investigated several factors and their impact on bacterial community diversity, including the presence or absence of vegetation, depth into and Double

seagrass decline and enhance efforts in seagrass restoration. It is therefore important to define the dynamics of bacterial communities associated with seagrasses.

Many strategies for examining microbial diversity entail analysis of ribosomal RNA (rRNA) sequences, including denaturing gradient gel electrophoresis (DGGE) [26, 29]. DGGE is a genetic fingerprinting technique that enables the separation of equally sized DNA fragments

Table 2. Assignment of banding patterns to month groups by jackknife analysis (Dice coefficient)

	Banding patterns (%) assigned to groups		
Month collected	Feb	Jun	Oct
Feb	81.4	4.7	14.0
June	24.4	57.8	17.8
Oct	21.2	6.1	72.7

ERCCs of patterns to host class are in boldface. The mean ERCC was 70.7%.

ison. Within Bionumerics, optimization refers an adjustment of bands beyond normalization and was necessary when imperfect normalization resulted in residual shifts. Likewise, tolerance refers to the total distance that bands in different lanes differed by before they were determined to be distinct. The default values were used for optimization and tolerance and were 0.17 and 3.5%, respectively. At these values, bands that differed by more than 3.5% of

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sediment. Although this study does not refute the fact that depth into sediment greatly influences the microbial community, it highlights the fact that such influences may not be consistent enough over the seasons or in the presence or absence of vegetation as to be elucidated using this community DNA fingerprinting technique. It is also possible that the DGGE method is insufficiently sensitive to detect differences with depth.

The ERCC for assignments based on month (as a proxy for season) was high, and a likely explanation is that the bacterial communities for a given month were likely responding to the seasonal status of the seagrasses. Microbial activities in seagrass bed sediments show strong seasonality and are highest when the plants are actively growing [10, 38].

The ERCC for assignments based on the presence of vegetation was also significantly higher than random. Seagrass bed sediments support higher numbers of bacteria and greater bacterial activities than nonvegetated sediments because of enrichment with organic carbon [10, 19, 20, 38]. Bacterial communities in unvegetated sediment do not experience these inputs and would be expected to differ at some level from the seagrass bed sediment communities. In contrast, Bagwell et al. [2] obtained one reproducible DGGE banding pattern for nifH sequences amplified from seagrass bed sediments in an oligotrophic environment and nearby nonvegetated sediments. Similarly, Smith et al. [38] concluded that the community composition of sulfate-reducing bacteria, based on comparisons of dissimilatory sulfite reductase genes, at the same site used in the present study did not vary substantially between vegetated and unvegetated sediments. Smith et al. [38] did find some small groups of sulfate-reducing bacteria unique to either the vegetated or nonvegetated sediment and suggested they could represent responses to available carbon sources, either root exudates or benthic algae, respectively. Similarities in microbial communities between vegetated and nonvegetated sediment are therefore to be pat.374 0 Td(10)TjEM-194.9 (could)]TJ0 -1.138 TDarbe.5 s]TJ/T1_2 1iTJc196.8 (se)(a

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