



Conference Abstract

Microbial Diversity, Biomass, and Community Structure Differences among Restored and Natural Saltwater Marshes, Louisiana

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Abstract

Tidally influenced, saltwater marsh construction projects are being completed in Louisiana to combat coastal erosion and land loss, as well as to restore critical fisheries and counteract ecosystem injuries caused by oil spills and other anthropogenic activities. Historically, metrics of success for restored marshes have been based on the amount of aboveground biomass, survival of planted vegetation, and recruitment of local endemic versus invasive species. The microbial communities responsible for cycling nutrients within restored soils are not typically evaluated. Therefore, we investigated microbial community structure, biomass, and diversity in marsh soils that had been created from nearby dredge material over the past 10 years in the Lake Hermitage, West Point a La Hache area, and compared the results to those from natural marsh soils from Bay Batiste, as determined using phospholipid fatty acid (PLFA) and gas chromatography/mass spectrometry (GC/MS) techniques and from 16S rRNA gene profiles. Soils were collected from two depths (0-2 cm and 8-10 cm) from four sampling locations along a 100-m transect that extended inland from the coastline. Soil organic carbon content and soil pH were consistently lower at restored sites compared to natural marshes. Natural marsh soil microbial diversity strongly correlated with the biomass of typical marsh plants (e.g., *Spartina alterniflora*, *Juncus roemerianus*), whereas restored soil diversity correlated to higher *Paspalum* spp. (crowgrass) and *Schoenoplectus pungens* (common bulrush) biomass. Created soils had

higher overall microbial diversity, but natural marsh soils had at least twice as much PLFA biomass than the created marshes at the shallow depth and 10X more biomass at the deeper depth. Biomass estimates ranged from below detectable levels to 6×10^4 pmol PLFA gdw^{-1} , with shallower soils from all sites exhibiting higher biomass (average 10^4 pmol PLFA gdw^{-1}) compared to deeper soils (average 10^3 pmol PLFA gdw^{-1}). Diverse PLFA profiles were observed. Shallow soils were dominated by terminally-branched and midchain-branched saturates that are indicative of Gram-positive microorganisms and actinomycetes. The shallow soils contained polyunsaturates indicative of phototrophs. Deeper soil profiles were dominated by monounsaturates associated with Gram-negative bacteria and sulfate- and metal-reducing bacteria. These monounsaturates contained on average 7% of the total PLFA profile as cyclopropyl fatty acids, which likely indicated anaerobic processes and the presence of nutritional stress. The shallow natural marsh soils exhibited more mid-branched saturates, branched monounsaturates, and polyunsaturates, whereas the shallow created marsh soils had more terminally-branched saturates. In the deeper soils, the natural marshes exhibited more terminally-branched saturates and monounsaturates, but the created marshes contained more saturates. GC/MS analyses of dimethyl disulfide derivatizations revealed shifts in microorganisms, as indicated by the types and bonding positions of monounsaturates, and the changes in the presence/absence of methanotrophic populations within the soils, which was also reflected in the 16S rRNA gene profiles. From these results, the microbial communities from the created marsh soils were different than the natural soil communities, and may reflect not being the best desired outcome for marsh restoration. With time, the expectation would be that created marsh above and belowground microbial diversity and biomass would begin to mimic natural marshes, but continued monitoring through time will be necessary to understand how these linkages develop and affect basic soil processes, nutrient cycling, and recruitment and sustenance of higher organisms like fish or crustaceans.

Keywords

community structure, phospholipid fatty acids, created marsh, natural marsh

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Conflicts of interest

The authors have declared that no competing interests exist.