



Soil and Water Science

Research Brief

University of Florida

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Characterization of Cellulolytic and Fermentative Processes in Wetland Soils, with Emphasis on *Clostridium* Species

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Nutrient runoff from nearby agricultural areas has resulted in a variety of ecological changes in the northern Florida Everglades, including changes in the amount and types of plants that provide valuable nutrients, such as carbon, to the rest of the ecosystem. Increases in nutrients also resulted in increases in the numbers and types of the bacteria that control the biogeochemical cycles that form the basis for ecosystem functioning. Oligotrophic (low nutrient) and eutrophic (high nutrient) regions are dominated by sawgrass and cattail, respectively, as the primary source of carbon. Differences in plant material may affect the rate and pathways through which carbon is mineralized in the different areas. Cellulolytic and fermentative species are responsible for decomposing dead plant material and converting it into simple molecules which serve as sources of carbon for other groups in the Everglades microbial food web. Changes in environment or substrate quality will likely affect fermentative bacteria and, hence, affect the entire microbial food web and the biogeochemical cycles they control. The overall goal of this research was to gain a more complete picture of nutrient impacts on carbon cycling, including establishing linkages between carbon input and microbial community structure and function. The study was conducted with soil and benthic periphyton (algal mats growing on top of soil) collected from four sites in the Everglades Water Conservation Area 2A (WCA-2A), including samples collected from sites with different levels of

eutrophication (oligotrophic, transition, and eutrophic), and from a slough in the oligotrophic region. Historic flow patterns of water through the Everglades created a series of ridges and sloughs in WCA-2A. The vegetation in sloughs differs from that in the ridges, and it may be that the dominant bacteria that decompose carbon in the ridges differ from those in the sloughs (Fig. 1).

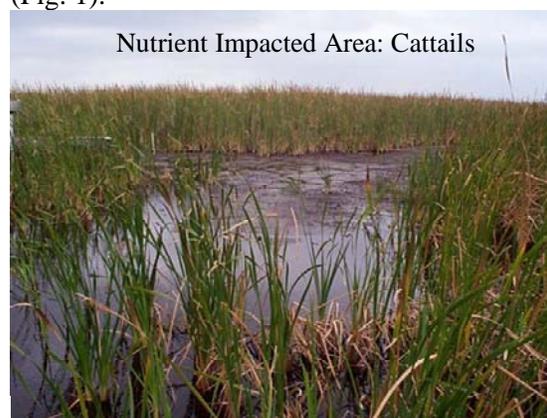


Figure 1. Ridges in eutrophic (nutrient-impacted) region dominated by emergent cattail; sloughs are dominated by submerged vegetation.

Cellulolytic bacterial numbers in eutrophic, transition and oligotrophic ridge soils were approximately 10 fold greater than in oligotrophic slough area soils, and numbers of fermentative bacteria were similar in samples taken from the three ridges. Microcosm experiments indicated that carbon cycling (cellulose conversion to methane) was more active in eutrophic soils than in oligotrophic soils, and that eutrophic and transition soils harbor microbial communities that are poised to eliminate excess fatty acids or other by-products more efficiently than are oligotrophic soils.

Differences in the dominant plant species (cattail in eutrophic areas, sawgrass in oligotrophic areas) may be responsible for

differences in fermentation products. In order to investigate this possibility, microcosms were constructed with soils from the oligotrophic and eutrophic regions and incubated with dried cattail or sawgrass tissue. The type of plant material as carbon and nutrient source appeared to be significant with respect to methanogenesis only in eutrophic soils; cattail slightly inhibited methanogenesis in eutrophic microcosms, possibly due to its higher phenolic content. However, cattail supported greater numbers of fermentative bacteria, possibly because of more readily available carbon, such as sugar, pectin, and proteins.

Decomposition of plant material is not the only source of carbon utilized by the microbial food web in these soils. Benthic algal mats and root exudates likely provide a significant portion of carbon needed for microbial communities in oligotrophic soils. Benthic algal samples harbored 100 times more fermentative bacterial than did the underlying soils, strongly suggesting that anaerobic decomposition is very active in this component of the ecosystem. Members of the microbial food web that are dependent on fermentation products were also shown to be more active in periphyton mats than in underlying soils.

Both environment and species of bacteria determine the types of substrates produced by fermentative bacteria. We applied DNA-based techniques to characterize the dominant fermentative bacteria in the oligotrophic and eutrophic ridge soils to identify possible differences between the dominant bacteria in the two regions. *Clostridium* is the dominant fermentative bacterial group present in Everglades soils and includes bacterial species involved in cellulose degradation and fermentation. DNA-based techniques targeting genes characteristic of *Clostridium* revealed that differences in the types of *Clostridium* were based on soil sample origin. This may affect the production of specific fermentation products and affect bacteria composition and activities in the food web. Other studies have revealed differences in the composition of the food

web, which may be attributable to differences in *Clostridium* species found in the different areas of WCA-2A (Fig 2).



Figure 2. Consortium of bacteria from eutrophic region dependent on fermentation products.

Our studies elucidate differences between eutrophic and oligotrophic soils of WCA-2A in the microbial communities that control carbon decomposition and mineralization. Differences observed in the structure of the microbial food web in nutrient-impacted regions of the Everglades may be affected by differences in numbers, activities and species of *Clostridium*, the primary cellulolytic and fermentative bacterial group in these soils. A detailed understanding of the microbial ecology of the Everglades will provide a greater understanding of the mechanisms by which eutrophication affects ecosystem functioning, including biogeochemical cycling, and may provide sensitive indicators of nutrient status and progress toward restoration of these marshes.

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