

Ecology of
Soil Microorganisms

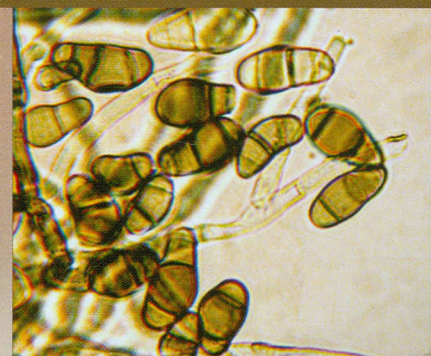
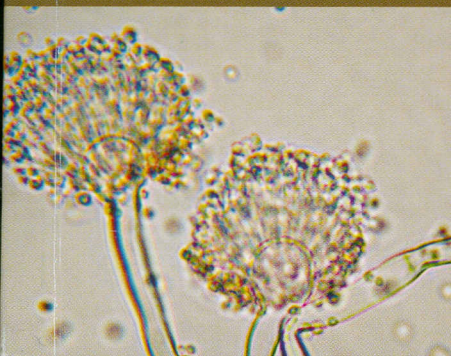
2011

Abstract Book

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Microbes as Important Drivers of Soil Processes

27.4. - 1.5. 2011, Prague, Czech Republic

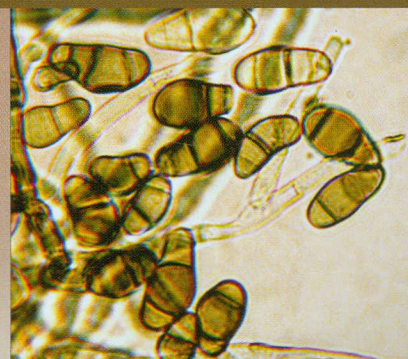


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THURSDAY, 28 April 2011

Influence of land use change on denitrifier community composition in Terra Preta de Índio (Amazonian Dark Earth) soils of Central Amazonia

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Land use change represents one of the major impacts on terrestrial ecosystems, drastically influencing plant communities and decreasing biological diversity. These effects are particularly important in humid tropical soils because of its natural acidity and low fertility. In the Amazon, soil fertility is the limiting factor for the development of sustainable agriculture. However, the existence of small patches of Terra Preta de Índio-TPI (Amazonian Dark Earth) soils are gaining considerable attention because these soils are highly fertile and do not rapidly degrade even in tropical conditions or under agricultural use. An important process which influences soil and water fertility and atmosphere chemistry is denitrification, the sequential reduction of nitrate and nitrite to dinitrogen via the intermediates nitric oxide and nitrous oxide. This microbiological process which is central to nitrogen cycling on earth removes nitrogen from soils and constitutes a major source of N₂O emissions in agricultural soils. In this context, the main aim of this research was to investigate the effect of vegetation cover on the structure and density of denitrifier communities in TPI and adjacent (ADJ) soils from the Amazonas region, Brazil. Structure and density of denitrifier communities is believed to at least in part determine ecosystem functioning. For assessing denitrifier communities across a conversion in land use, two sites in secondary forest (SF) and two sites under manioc plantation (MP) were selected. The structure and density of denitrifier communities was assessed by the fingerprinting technique Terminal Restriction Fragment Length Polymorphism (T-RFLP) and quantitative PCR, respectively, based on nosZ genes encoding nitrous oxide reductase as a functional marker gene for denitrification. Multivariate analyses of T-RFLP patterns showed that denitrifier communities differed between the soil types TPI and ADJ, but significant differences were also observed with land use at SF and MP. Moreover, denitrifier community composition from TPI soils was associated with high levels of pH, Ca²⁺ and microbial biomass nitrogen while that from ADJ soils was associated with higher levels of Al³⁺. Denitrifier abundance was significantly higher only in TPI-SF soil than in any other soil during rainy season. These results suggest that denitrifier community may regulate an important function in TPI soils and that vegetation cover influences the structure of these communities.

FRIDAY, 29 April 2011

Microbial community structure in the Amazonian Dark Earth soils by pyrosequencing analyses: the role of biochar in the N-cycling and sustainability of tropical soils

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We report a ribosomal tag pyrosequencing study of the phylogenetic diversity of Bacteria in soils from the Brazilian Amazon Dark Earth with two contrasting histories; anthrosols and their adjacent non-anthrosol soils with the same mineralogy. The anthrosols, also known as the Amazonian Dark Earths (ADE) or "Terra Preta de Índio", exhibit approximately three times more organic matter, nitrogen and phosphorus and 70 times more Biochar (BC) content when compared to their adjacent infertile soils (ADJ), without a past history of anthropogenic activities by the Amazonian pre-Colombian native. We sampled paired anthrosol and unmodified soils from two locations (Hatahara [HAT] and Balbina [BAL]) in Manaus, Amazonas-Brazil, which differed in their current land use and soil type. Fragments of biochar found in ADE were separated directly from soil using a tweezer and storage at 4 C. The V4 region of the SSU rRNA gene was amplified from samples representing the ADE, ADJ soil and BC. The total number of bacterial sequences presents in the samples studied was 16,875 and this number was dependent on the type of soil sample under different vegetation covers. The 16,875 sequence tags analyzed represented 4,752 unique sequences. The highest species diversity was observed in ADE soils. Comparisons of unique sequences revealed a low degree of overlap between communities at each sample. Values of richness estimations indicated higher operational taxonomic units (OTUs) richness in ADE libraries (1927.4 HAT; 1654.7 BAL), followed by lower OTUs richness and diversity in ADJ (703.6 HAT; 1317.2 BAL). Data libraries (1605.7 HAT; 1589.5 BAL) indicated higher bacterial diversity in BC than in ADJ soils. Bacterial diversity was higher in ADE than ADJ at both locations. Differences were noted in the total bacterial community composition in ADE, ADJ soil and BC and a higher bacterial diversity present in anthrosols revealed by pyrosequencing. The most abundant bacterial phyla in samples studied were Proteobacteria, Acidobacteria, Actinobacteria and Firmicutes. The phylum Nitrospira that is a key part of global nitrogen cycling was only found in BC library (46 OTUs). Our data suggest that soil microbial community structures may be strongly influenced by the historical soil management, anthropogenic origins, with the support of the biochar, which may sustain a particular and unique habitat for the microbes [FAPESP and CNPq-Brazil, NSF-USA].