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Taxonomical and functional microbial responses to agriculture management of Amazon forest soils

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Land-use change is one of the greatest threats to biodiversity worldwide, and one of the most devastating changes in the use of land, especially in the tropics, is the conversion of forest to crop lands. Southeast Amazon region is considered the largest agricultural frontier in the world, where native forests are converted into soybean crop fields, a fact that highlights the social and economic importance of this system to Brazil. This study firstly, focused on the impact of land-use changes and agriculture management of Amazon forest soils on the size and composition of the acidobacterial community. Taxon-specific quantitative real-time PCR (qPCR) and pyrosequencing of 16S rRNA gene were applied to study the acidobacterial community in bulk soil samples from croplands, adjacent native forests and rhizosphere of soybean. Based on qPCR measurements, Acidobacteria accounted for 23%, 18% and 14% of the total bacterial signal in forest soils, cropland soils and soybean rhizosphere samples, respectively. From the sequences of Bacteria domain, the phylum Acidobacteria represented 28%, 16% and 17% of the sequences from forest soils, cropland soils and soybean rhizosphere samples, respectively. Acidobacteria subgroups 2-8, 10, 11, 13, 17, 18, 22 and 25 were detected with subgroup 1 as dominant among them. Subgroups 4, 6 and 7 were significantly higher in cropland soils than in forest soils, which subgroups respond to decrease of soil Aluminium. Subgroups 6 and 7 respond to high content of soil Ca, Mg, Zn, P, Fe, Mn and B. The results showed differential response of the Acidobacteria subgroups to abiotic soil factors, and indicated acidobacterial subgroups as potential early-warning bio-indicators of agricultural soil management effects in the Amazon area. Secondly, using 454 pyrosequencing, we investigated the metabolic diversity of microbial communities colonizing the rhizosphere and the bulk soil associated to soybean. The rhizosphere presented an overrepresentation of functional cores related to metabolism of nitrogen, iron, phosphorus and potassium, with bacterial groups linked to these cores found only in rhizosphere samples. Still, the network involving bacterial groups and metabolisms was less complex in rhizosphere, suggesting the specialization of some specific metabolic pathways. Taken together, these results indicate a rhizosphere effect over the soil functional community with a selection of some metabolic pathways, which could be related to plant benefits as nutrition and development. A better understanding of the functional role of the rhizosphere microbial communities is important to the development of a sustainable agriculture.