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The match between microbial community structure and soil properties is modulated by land use type and sample origin within an integrated agroecosystem

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Introduction It is of global concern to adopt measures to mitigate land degradation caused by agricultural production systems. One of the strategies proposed is to replace degraded pastures with agrosilvopastoral systems, which integrate three different land-use types: crop production, pasture and forestry plantation (denoted ICLF). However, little is known about the differences between ICLF and other land use types in terms of their impact on soil microbial community structure. In this study, we tested the hypothesis that introducing ICLF as replacements for degraded pastures leads to a change in the response of phenotypic composition of the soil microbial community to individual soil chemical variables.

Material and Methods The study was conducted in one of the ~203 technology reference units in ICFL (http://www.cnpgl.embrapa.br/nova/silpf) of the Brazilian Agricultural Research Corporation (Embrapa) on the Boa Vereda farm located within the municipal limits of Cachoeira Dourada, Goiás, Brazil (18°27'43.19"S, 49°35'58.53"W). Distance matrices based on individual soil chemical properties and individual soil microbial variables were correlated by Procrustes analysis and these relationships yielded vectors of residuals depicting these correlations (matches) (Lisboa et al., 2014a). These vectors were used as univariate response variables in an ANOVA framework in order to investigate how the match sizes (the strength of correlation/covariance) between individual soil chemical properties and individual soil microbial variables vary across land use types (levels: ICLF; degradated pasture; improved pasture; and a native cerrado fragment) and also across sample origin within ICLF (levels: soil samples under the influence of the exotic tree forest stand (canopy); soil samples under influence of the pasture; samples within the transition between the forest stand and the pasture). For more details please see Lisboa et al. 2014b).

Results and Conclusions While the strength of the correlation between soil microbial structure variables and phosphorus availability was typically land use type dependent, the response of the microbial structure to exchangeable base cations was mainly affected by the sample origin within ICLF. Finally we concluded that increases in the heterogeneity of vegetation within integrated crop, pasture and forestry systems are an important driver of microbial community response to environmental changes, and may be one means by which to increase the sustainability of tropical agroecosystems.

References cited Lisboa et al. (2014a) Plos One (doi:10.1371/journal.pone.0101238); Lisboa et al. (2014b) Soil Biol Biochem (doi:10.1016/j.soilbio.2014.07.017)