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Soil Microbial Diversity as Controlled by Pedodiversity in New South Wales, Australia

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The potential link between soil biodiversity and pedodiversity have not been explored at global scales. Anthropogenic threats and decays on soil biodiversity and their impacts on soil functioning - as recently warned - might differ by soil habitats. A global assessment beforehand is needed on what to define actions and cautions concordant with the different soil natures around the world. Soil attributes (e.g. soil pH, soil C) has been primary drivers of soil microbial diversity in both biogeographic studies and in-depth surveys. However, by only knowing that key factors regulate the soil biota is not a comprehensive knowledge yet and, furthermore, there are every so often ambiguous results that a deeper analysis at a soil diversity level (e.g. by soil horizons, classes, types) is frequently suggested. As never before, this is possible thanks to the access into both soil microbial DNA data from NGS technology and a profound soil physicochemical characterisation by pedometrics approaches. On this basis, the hypothesis tested was that soil microbial diversity is controlled by pedodiversity (e.g. by soil type) and, therefore, a co-spatial correlation between them would be established across a region. Observed data from forty-nine sampling sites were taken following two orthogonal transects (~1000 km each) across New South Wales (Australia). Paired soils were sampled at both natural and disturbed ecosystems. Soil biodiversity was estimated from archaea, bacterias and fungi communities (16SrDNA and ITS genes). The cospatial relations between soil microbial diversity and soil properties were assessed by bootstrapped regression trees models whose output enabled predictions of soil microbial distribution at 1km across NSW. Diversity and dissimilarity of the soil microbes (α -diversity and β -diversity) were comparable to soil type's distribution (ASC system) even beyond other remarkable environmental factors (e.g. altitude). Indeed, there was an increase in microbial diversity towards western NSW,





Brazilian Soil Science Society



however, the diversity of *fungi* and *archaea* were significantly lower and higher in *Vertosols,* respectively. *Bacteria* showed also similarities with soil distribution but did not reveal a determined preference – e.g. soil preferences for different abundant *bacteria* groups would be obscuring a clear result. Then, a co-spatial exploration is suggested at a higher microbial taxonomic (e.g. family) and pedodiversity (e.g. soil spectra) levels.

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