



Effects of anthropogenic degradation of an Andean temperate forest on the soil nutrients and on the diversity and function of the soil microbial community

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Soil microorganisms are an essential component of forest ecosystems being directly involved in the decomposition of organic matter and the mineralization of nutrients. Anthropogenic disturbances such as logging and livestock modify the structure and composition of forests and also the structure and diversity of soil microbial communities changing critical biogeochemical processes in the soil. In this research we evaluated the effect of anthropic disturbance on the soil in a degradation gradient of Andean temperate forest. This gradient comprises mature forest stands dominated by *Nothofagus dombeyii*, secondary forests dominated by *Nothofagus alpina* with medium degradation, a highly degraded forests dominated by *Nothofagus obliqua* and a highly degraded grassland. We evaluate the reservoir of the main soil nutrients (TC, TN, NO₃⁻, NH₄⁺) and the structure, diversity and functions of the soil microbial community (bacteria and fungi) via NGS-Illumina sequencing and metagenomic análisis with DADA2 pipeline in R-project. The results show a higher amount of TC, TN, NO₃⁻ and C:N ratio in the most degraded condition (degraded grassland). There are no significant differences in the amount of TC, TN and NH₄⁺ along the forest degradation gradient. This reflects a C:N:P stoichiometry that tends to decrease as forest degradation increases. The soil bacteria community was mainly dominated by Phyla *Proteobacteria* (45.35%), *Acidobacteria* (20.73%), *Actinobacteria* (12.59%) and *Bacteroidetes* (7.32%). At genus level there are significant differences, *Bradyrhizobium* has a higher relative abundance in the condition of mature forest which tends to decrease along the gradient of degradation forest. The soil fungi community was dominated by the Phyla *Ascomycota* (42.11%), *Mortierellomycota* (28.74%), *Basidiomycota* (24.61%) and *Mucoromycota* (2.06%). At genus level the condition of degraded grassland has significantly lower relative abundance of the genera *Mortierella* and *Cortinarius*. The degraded grassland soil microbial community is significantly less diverse in terms of bacteria ($D' = 0.47 \pm 0.04$) however it is significantly more diverse in terms of fungi ($H' = 5.11 \pm 0.33$).