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Extracellular enzyme activities in a tropical mountain rainforest region of southern Ecuador affected by low soil P status and land-use change

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Little is known about the enzymatic response of microorganisms in soils having a low P status and being subjected to global change phenomena, such as forest disturbance and land-use change. Along a land-use sequence (natural forest - young pasture - old pasture - abandoned pasture - shrubland) in the Andes of southern Ecuador mineral topsoils of Cambisols / Umbrisols were investigated. We tested whether the activities of the six hydrolytic enzymes (cellobiohydrolase, β-glucosidase, N-acetylglucosaminidase, α-glucosidase, xylanase, acid phosphomonoesterase) were affected by nutrient status and land-use induced alterations in soil pH (pHH_2O from 3.7 to 5.2), resource quantity and quality (e.g. a SOC:N:P ratio from 182:13:1 to 1050:38:1) and microbial community structure (as monitored by phospholipid fatty acids). Microbial production of acid phosphatase responded to the low P status of the sites by a higher investment in the acquisition of P compared to C. We determined three major drivers of enzyme activities: 1.) Microbial demand for P regulated the production of acid phosphatase, provided that N and C were available. At the natural forest site the two-fold higher specific activity of acid phosphatase pointed to a high microbial P-demand, whereas the production of acid phosphatase was constrained by the availability of N and DOC after pasture abandonment. 2.) Microbial biomass that was controlled by pH and resource availability (total soil N (organic and inorganic N), organic P (Bray-fraction)) was the main driver for cellobiohydrolase, β-glucosidase and N-acetylglucosaminidase activities. 3.) Substrate induction due to increased litter inputs of herbaceous plant species seemed to regulate α-glucosidase and xylanase activities during secondary succession. In contrast, alterations in the abundance of microbial groups affected the variation in extracellular enzyme activities only marginally. At the level of broadly defined microbial groups (PLFA), our results point to functional similarity in the decomposition of simple organic material.