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SYMP 13-2: Microbial responses to changes in land use

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Background/Question/Methods

Land use change is one of the greatest threats to biodiversity worldwide. This is especially true for land use change that results in the destruction of intact forest, or "deforestation". Deforestation is causing a loss of biological diversity on an unprecedented scale, especially in the Tropics. It is unclear how the majority of the biodiversity on Earth – microbial biodiversity – is responding to these extraordinary rates of deforestation. I will provide an overview of our current understanding of microbial responses to deforestation. I will focus, as an example, on our current research regarding the effects of deforestation on the diversity of arbuscular mycorrhizal fungi (AMF), bacteria and archaea within Amazon Rainforest soils. This study takes advantage of an established chronosequence of primary rainforest, pastures of various ages, and secondary rainforest to determine the effect of deforestation on the taxonomic, phylogenetic and functional diversity of soil microorganisms, assayed using culture-independent methods.

Results/Conclusions

There is increasing evidence that deforestation significantly affects microbial diversity, and that "recovery" of microbial diversity in secondary forest soils is incomplete. For example, rarefaction curves suggest that the accumulation of AMF taxa is higher for Amazon primary forest soil relative to secondary forest soil. In addition, the community composition varies with land use; three AMF taxa were shared between primary and secondary forests, seven were found only in primary forest, and three were found exclusively in secondary forest soil. We also observed that the phylogenetic diversity of AMF is more reduced in secondary forest soils than expected given the regional pool of AMF taxa.