

# Forest conversion changed the structure and functional process of tropical forest soil microbiome

G Lan<sup>1</sup>, Zhixiang Wu<sup>2</sup>, Chuan Yang<sup>3</sup>, Rui Sun<sup>3</sup>, and Bangqian Chen<sup>3</sup>

<sup>1</sup> Rubber Research Institute, Chinese Academy of Tropical Agricultural Sciences

<sup>2</sup>RRI,CATAS

<sup>3</sup>Rubber Research Institute, Chinese Academy of Tropical Agricultural Sciences

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## Abstract

The effects of forest conversion from natural forest to agricultural system on soil microbial composition still need further study. Especially, impact on soil function after forest conversion is not yet known. In this study, by using metagenomic sequencing as well as 16S and ITS sequencing technology, we evaluated the soil microbial composition, diversity and functions based on a large number of soil samples of tropical rainforest and rubber plantation across the whole island of Hainan, south China. The results showed that (1) forest conversion changed microbial composition from bacterial groups of Proteobacteria to Chloroflexi, and fungal groups from Basidiomycota to Ascomycota. (2) The bacterial alpha diversity, beta diversity as well as the total diversity did not decrease after forest conversion. However, beta diversity of fungal community reduced resulting a net loss of total OTU richness. (3) There was no difference in soil functional compositions and diversity between rubber plantations and rainforest, however, the relative gene abundance of most COG functions, KEGG functions, CAZy functions as well as Antibiotic gene were significantly different between rubber plantation and tropical rainforest. (4) Soil pH and environmental heterogeneity were the main driver for microbial taxonomic composition and gene functional composition. Land use did not result in changes of functional gene composition, but the relative abundance of functional gene. The changed relative abundance gene would alter the ecosystem processes. In conclusion, our results confirmed that land use changes alter the soil microbial community structure and can have profound effects on ecosystem functions and processes.

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