

Functional diversity and dynamics of microbial communities in soil profiles along a 2000-year paddy soil chronosequence

Qingfang Bi (1,2,3), Andreas Richter (1), Xianyong Lin (2), and Yong-Guan Zhu (3)

(1) Terrestrial Ecosystem Research, Department of Microbiology and Ecosystem Science, University of Vienna, Vienna, Austria (qfbi@zju.edu.cn), (2) MOE Key Laboratory of Environment Remediation and Ecological Health, College of Environmental and Resource Sciences, Zhejiang University, Hangzhou, People's Republic of China, (3) Key Lab of Urban Environment and Health, Institute of Urban Environment, Chinese Academy of Sciences, Xiamen, People's Republic of China

Long-term intensive cultivation in paddy soils strongly impacts soil pedogenesis and leads to accumulation of organic matter and the stratification of nutrients and oxygen in the soil profile. However, knowledge about the dynamics of soil microbial communities during continuous rice cultivation at long time scales including progressive and retrogressive stages is limited. In particular, the driving forces of community assembly also still remain poorly resolved. Therefore, we characterised the temporal and spatial changes in soil bacterial, fungal communities and functions using high-throughput sequencing and quantitative-PCR-based chip (targeting 64 microbial functional genes for C, N, P, S and methane metabolism) along a 2000-year chronosequence of soils under paddy and adjacent non-paddy management in the Yangtze delta of China, a coastal region where paddy soils originated. Soil depth profiles were sampled from the paddy fields (6, 50, 100, 300, 700, 1000, and 2000 years of paddy use), the adjacent arable chronosequence (50, 100, 300 and 700 years of dryland use) and a tidal wetland (estuarine sediment, representing the parent material for paddy and arable soil reclamation). Results showed that across multiple time-scales ranging from decades to millennia, significant shifts in soil bacterial and fungal communities with soil depths occur, indicating paddy soil development and a microbial succession since reclamation from tidal wetlands. The initial stages of paddy and dryland soil development exhibited a higher phylogenetic β -diversity than the soils at later successional states. Patterns of α -diversity for microbial groups differed along soil chronosequence and with depth. Microbial α -diversities in topsoil was greatest in soils of intermediate age, while the α -diversities in subsoil was greatest in 1000-year cultivation. Moreover, allogenic succession of microbial communities was mostly driven by shifts in the soil physicochemical properties, especially pH and nutrient availability including organic matter and phosphorus during paddy soil development. Further network analysis showed that soil microbial communities were more interconnected at late successional stages than at initial stages, coinciding with a higher dynamics in turnover and environmental variability. Our study implies that, long-term rice cultivation substantially alters topsoil and subsoil microbial functional structure, leading to functional homogenization. Additionally, soil functions related to the acceleration of nutrient cycling, necessary for high crop yields, are promoted by long-term rice cultivation.