



## Soil bacterial community structure in Chinese wetlands

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### ABSTRACT

Soil microbial communities are crucial in maintaining the functions of wetland ecosystems. Understanding the microbial community structure and the key factors driving the assemblages of wetland soil microbiota are important to reveal the connections between microorganisms and functions of wetland ecosystems. In this study, soil bacterial community compositions and the factors shaping them were investigated in three groups of wetlands across China, including Tibet plateau wetlands (TW), inland wetlands (IW) and coastal wetlands (CW). Overall, Bacterial community structure and turnover showed distinct patterns in different groups. Bacterial phyla were mainly composed of *Proteobacteria* followed by *Chloroflexi*, *Acidobacteria*, *Actinobacteria* and *Bacteroidetes* in all groups of wetland samples. At genus level, random forest model showed that *Coprothermobacter* and *Acetobacter* were two most important genera explaining the differences among groups. The abundances of these genera were very low in IW relative to the other two groups. The alpha diversity of IW was significantly higher than those of TW and CW. The relative contribution of environmental factors was larger in the assemblages of bacterial communities in TW and CW than that in IW. The pH and conductivity were recognized as the most important measured environmental factors influencing bacterial community structure. Our results suggested that the bacterial communities of wetlands in different regions were shaped with different mechanisms. The communities in CW and TW regions owned lower alpha diversity and were more influenced by deterministic processes than those in IW. In conclusion, the spatial pattern of soil bacterial community assembly in Chinese wetland was scale-dependent.

### 1. Introduction

Wetlands are unique ecosystems frequently or continually inundated with water, including swamps, marshes, bogs and fens (Mitsch and Gosselink, 2000). Wetland soils constitute big reservoirs of terrestrial carbon including decayed herbaceous and woody organic matter (Gorham, 1991). Microorganisms play key roles in biogeochemical processes in the wetlands such as greenhouse gas emission and nutrient cycling. Therefore, the structure of microbial communities and their responses to environmental changes may greatly influence the ecological functions of wetlands. Many studies have investigated microbial community assembly of wetlands at local scale (Dedysh et al., 2006; Foulquier et al., 2013; Hartman et al., 2008; Peralta et al., 2010;

Serkebaeva et al., 2013). However, few studies provide comprehensive understandings on the bacterial community assemblages and driving factors at regional scale (Wu et al., 2013).

Although ecologists have made great progresses in understanding the mechanisms shaping biogeographical patterns of macroorganism community, the community assembly of microorganisms is still not fully understood. The high-throughput sequencing technique makes it available to survey the microbial biogeographic patterns at large spatial scales without culturing, and to test the applications of ecological theories on microbial communities (Barberán et al., 2014; Kirchman et al., 2010; Marsh, 1999; Muyzer et al., 2004; Muyzer et al., 1993; Prosser et al., 2007; Riesenfeld et al., 2004; Schmidt et al., 1991; Tringe et al., 2005).

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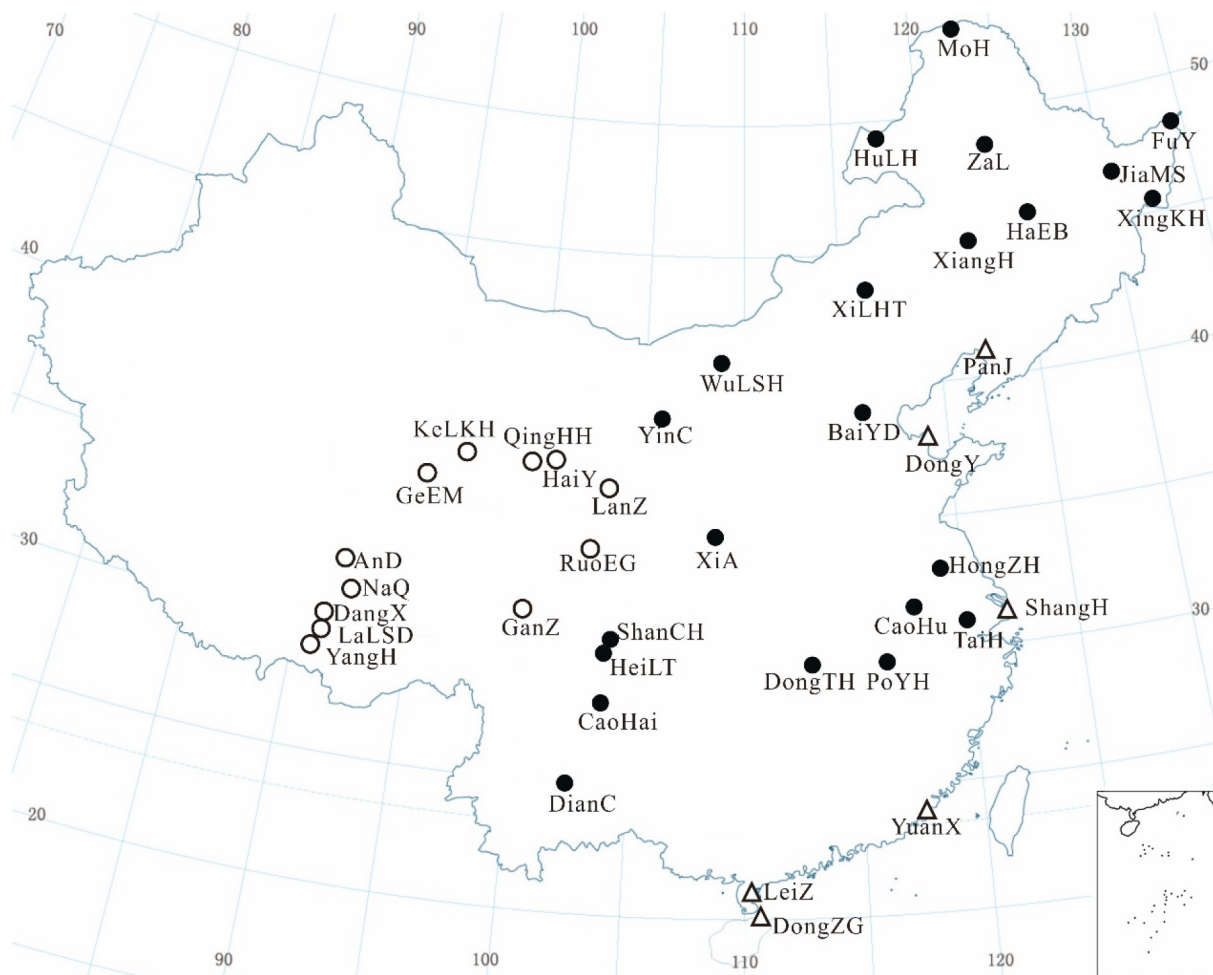


Fig. 1. Sampling sites of the wetland soils in China. Hollow circle: samples from Tibet plateau wetland (TP), solid circle: samples from inland wetland (IW), hollow triangle: samples from coastal wetland (CW).

Many evidences support that microbial assemblages show obvious biogeographic patterns which are determined by multiple biotic and abiotic factors, such as pH (Fierer and Jackson, 2006; Lauber et al., 2009), temperature (Barcenas-Moreno et al., 2009; Hoj et al., 2007), phosphorus (Allison et al., 2007; Andersson et al., 2010), carbon availability (Drenovsky et al., 2004; Hu et al., 2014), salinity (Lozupone and Knight, 2007; Wang et al., 2011) and vegetation (Saetre, 1999). However, the driving factors that determine biogeographical patterns within a single habitat may be different from that in a region or a biome (Fierer, 2008; Ganderton and Coker, 2005).

From the view point of ecological processes, both deterministic and stochastic processes are recognized to contribute to microbial community assembly (Dumbrell et al., 2009; Langenheder and Székely, 2011; Ofițeru et al., 2010; Stegen et al., 2012b; Wang et al., 2013). At large temporal or spatial scale, historic factors are also important for the community assembly pattern (Hanson et al., 2012; Liu et al., 2017; Vellend, 2010). The niche-based deterministic processes (including abiotic and biotic selections) imply that microbial community assemblage patterns reflect the effects of contemporary environmental conditions, and similar environments may harbor similar compositions. Stochastic processes (dispersal and ecological drift) also strongly shape microbial community patterns, as indicated for animals and plants (Caruso et al., 2011; Stegen et al., 2012a; Van Der Gast et al., 2008). Many studies indicate that the variations in communities are primarily influenced by dispersal limitation (Caruso et al., 2011; Dumbrell et al., 2009; Lekberg et al., 2012; Martiny et al., 2011; Martiny et al., 2006). In most cases, microbial community assembly is simultaneously

influenced by deterministic and stochastic processes (Chase and Myers, 2011; Fierer, 2008; Green et al., 2008; Liu et al., 2017). Deciphering the effects of deterministic and stochastic factors often depend on the complex calculating approaches, such as variance partitioning and null models (Vellend et al., 2014). Fierer et al. indicate that the most robust approach for quantifying the effects of dispersal limitation on microbial biogeography is to compare microbial communities across identical habitats at various geographic scales (Fierer, 2008).

Local environmental conditions and spatial factors have been extensively considered to be the major competitive elements driving microbial biogeography (Bokulich et al., 2014; Langenheder and Ragnarsson, 2007; Lindström and Langenheder, 2012). Many studies demonstrate that the relative contributions of environmental and spatial factors in microbial distribution patterns are likely scale-dependent (Martiny et al., 2011; Martiny et al., 2006). Environmental variables have stronger effects on the variations in microbial communities at small spatial scales, while geographic distance can better explain the variations at larger spatial scales (Hollister et al., 2010; Horner-Devine et al., 2004; Kou et al., 2017; Yao et al., 2017).

China has various types of wetlands. In Tibet plateau, wetlands are mainly associated to lakes with high salinity water. In the inland areas except Tibet plateau, wetlands mainly distribute along with lakes and rivers. Large areas of wetlands also distribute among the Chinese coastline. The commons and differences of microbial communities in these wetlands at large spatial scale are not revealed. Previous studies have shown that the Tibet Plateau has distinctive soil microbial community structure (Yang et al., 2014; Yun et al., 2014). Coastal wetlands

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