



Soil water content drives non-symbiotic nitrogen fixation in peatlands on the Zoige Plateau in China

Xiaodong Zhang (1,2), Xiaoming Kang (1,2), Haidong Wu (1,2), Jinzhi Wang (1,2), Liang Yan (1,2), Yong Li (1,2)

(1) Institute of Wetland Research, Chinese Academy of Forestry, Beijing, China (zhangxiaod@caf.ac.cn), (2) Sichuan Zoige Wetland Ecosystem Research Station, Tibetan Autonomous Prefecture of Aba, China

Peatlands cover 16.8% (4605 km²) of the Zoige Plateau, making it the largest peatland area in China. This area has been affected by intensive human activities since the 1960s, especially artificial drainage of peatlands for creating pastures. Drainage has caused dramatic declines in water table in Zoige in recent decades. Non-symbiotic nitrogen (N) fixation is one of the main pathways through which N enters ecosystems, and plays a critical role in N cycling in peatlands. However, it remains unclear how changes in water table may influence the community structure of N fixers and their N-fixing ability. We carried out a field investigation at ten sites along a water table gradient from pristine to degraded peatlands in Zoige in July, 2017 to examine how variations in water table may affect N fixation. The potential N fixation rate (R_{nfix}), soil water content (SWC), and ¹⁵N abundance in topsoil (1-10 cm) were measured at each site. The community composition of diazotrophs was analyzed with *nifH* genes, which encode dinitrogenase reductase. The results showed that R_{nfix} in top soils ranged from 0.14-36.16 nmol g⁻¹ (dry soil) day⁻¹ across the sites, and was correlated closely with SWC. The highest R_{nfix} (30.06±4.78 nmol g⁻¹ day⁻¹) was observed in sedge marsh with high SWC (> 45%, w/w), while the lowest R_{nfix} (0.18±0.03 nmol g⁻¹ day⁻¹) was found in degraded land with low SWC (< 5%, w/w). The abundance of soil *nifH* genes varied from 1.50 × 10⁴ to 5.93 × 10⁷ copies g⁻¹ dry soil, and was positively correlated with R_{nfix} . In addition, the *nifH* sequences over the ten sites tended to be phylogenetically clustered into three groups at the genus level, corresponding to three soil moisture levels. Furthermore, Both the R_{nfix} and the abundance of *nifH* genes were positively correlated with soil N content, but negatively correlated with soil ¹⁵N abundance, indicating that the N fixed by diazotrophs contributed significantly to the N pools of topsoil. We concluded that soil R_{nfix} and diazotrophic communities were primarily driven by SWC in Zoige peatlands. This study revealed the responses of non-symbiotic N fixation to variations in water table, and contributes to a better understanding of the mechanisms underlying human impacts on nitrogen cycling.