



Responses of soil microbial communities and their network interactions to saline-alkaline stress in Cd-contaminated soils

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ABSTRACT

Land degradation by salinization and sodification changes soil function, destroys soil health, and promotes bioaccumulation of heavy metals in plants, but little is known about their fundamental mechanisms in shaping microbial communities and regulating microbial interactions. In this study, we explored the impact of saline-alkaline (SA) stress on soil bacterial and fungal community structures in different Cd-contaminated soils of Dezhou, Baoding, Xinxiang, Beijing and Shenyang cities from the North China Plain, China. Increased soil salinity and alkalinity enhanced Cd availability, indicated by significant increases in available Cd²⁺ in soil solution of 34.1%–49.7%, soil extractable Cd of 32.0–51.6% and wheat root Cd concentration of 24.5%–40.2%, as well as decreased activities of antioxidative enzymes of wheat root when compared with CK (no extra neutral or alkaline salts added). Soil bacteria were more active in response to the SA stress than fungi, as the significant structural reorganization of soil bacterial microbiota rather than fungal microbiota between SA and CK treatments was illustrated by principal component analysis. Adding neutral and alkaline salts enriched oligotrophic and haloalkaliphilic taxa in the Sphingobacteriaceae, Cellvibrionaceae, and Caulobacteraceae bacterial families, but decreased some Acidobacteria such as subgroup 6_norank, which was a sensitive biomarker that responded only to Cd contamination in CK-treated soils. Conversely, fungi were more sensitive to soil differences than bacteria: the composition of the fungal community was significantly different among different soil types. Phylogenetic molecular ecological network (pMEN) analysis further indicated that the microbial community structure and network interactions were altered to strengthen the adaptability of microorganisms to SA stress; the changes in structure and network interactions were proposed to contribute to competitive interactions. Most of the keystone genera identified in SA-treated soils, such as *Blastococcus*, *Gemmatimonas*, RB41, or *Candida*, had relatively low abundances (<1%), indicating their disproportionate ecological roles in triggering resistance or tolerance to SA stress and Cd toxicity.

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1. Introduction

Land degradation by salinization and sodification is a significant problem for agriculture especially in the arid or semi-arid regions of the world. In the North China Plain (NCP), there are large arid or semi-arid areas, and water is in short supply. However, the NCP is an important grain base in China, and it provides about one fourth of the country's total cereal crops (Zhang et al., 2015; Xu et al.,

2018). To maintain proper agricultural production in the NCP, agricultural irrigation with treated or even untreated wastewater is common. Thereby, salt-affected soils are typical in these regions, because intensive irrigation of cropped soil can cause saline groundwater at shallow levels with salt concentrations of 3–5 g/L in the NCP (Ma et al., 2015; Singh, 2016; Haj-Amor et al., 2017).

Soil salinization and alkalization always happen concurrently in sodic soils. Frequent ionic exchange of Na⁺ with H⁺ causes the dissociation of water in soil solution, resulting in increased levels of NaOH in the medium and potentially increasing the soil pH above 10.5 (Sou/Dakouré et al., 2013). In the NCP, neutral and alkaline salts in the soil including NaCl, Na₂SO₄, NaHCO₃, and Na₂CO₃ are the

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