



Distinct responses of soil bacterial and fungal communities to changes in fertilization regime and crop rotation

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ARTICLE INFO

Handling Editor: Yvan Capowiez

Keywords:

Bacteria

Crop rotation

Enzyme activity

Fungi

Long-term fertilization

PLS-PM

ABSTRACT

Nutrient availability and plant diversity are two important factors determining crop productivity in agricultural ecosystems, but little is known about the underlying mechanisms shaping microbial communities and their regulatory roles in soil biological activity and function. Here, we explored the impacts of fertilization regimes and crop rotations on soil physicochemical properties, crop yield and bacterial and fungal community structures in a 26-year field experiment. The critical determinants for regulating soil enzyme activity profiles involved in carbon (C), nitrogen (N) and phosphorus (P) cycling were identified by the partial least squares path model (PLS-PM). Long-term inorganic or organic fertilization significantly increased soil total N by 27%–77% and crop yield by 237%–419% and decreased soil pH by an average of 0.4 units when compared with non-fertilized control. Soil bacteria were more sensitive than fungi to the fertilization practices. Nutrient additions enriched copiotrophic taxa affiliated to the *Pseudomonadaceae* and *Cytophagaceae* bacterial families, but reduced some Acidobacteria such as subgroup 4 RB41, which was the most sensitive biomarker responding to no fertilization. Conversely, fungi were more active in response to crop conversion from wheat-maize to wheat-soybean rotation, leading to a 3-fold enhancement of an unclassified Sordariomycetes family in soybean-based rotation. PLS-PM revealed that fertilization-induced increases in soil enzyme activities were regulated by the bacterial community, while plant-driven alterations in yield, organic C input and soil aggregate-size distribution played an important role for fungal development, which, however, had no significant link to soil enzyme activity profiles. Our results suggest that different response patterns of soil bacteria and fungi to agricultural practices might have consequences for ecosystem function.

1. Introduction

Anthropogenic activities, especially agricultural production practices, strongly impact soil microbial ecosystems by changing the physicochemical properties of soil in the short- (Fernandes et al., 2011) and in the long-term (Hartmann et al., 2015), resulting in significantly altered soil processes (Ai et al., 2015; Qu et al., 2014). Fertilizer inputs (chemical or organic), pesticide application, planting diversity (e.g., crop rotations), and tillage practices affect soil microorganisms in different ways (Álvarez-Martín et al., 2016; Mbuthia et al., 2015). Among them, the influences of fertilization on soil microbiota are of great importance, as microorganisms have been identified as the key drivers of soil nutrient turnover and are therefore closely linked to soil fertility and crop yield (Mäder et al., 2002). Since 1998, the consumption of nitrogen (N), phosphorus (P) and potassium (K) fertilizers in China has increased by 49%, 19%, and 33%, respectively (Wu and Ma, 2015), resulting in a marked increase in soil nutrient content in numerous

agricultural lands. In north-central China, 3 years of N fertilizer application (300 kg N hm^{-2}) increased soil nitrate ($\text{NO}_3\text{-N}$) concentration by 8-fold and decreased soil pH by nearly 0.31 units (Zhao et al., 2014). However, the ecosystem-level influences of these fertilizer-induced alterations on the activity and function of various microbial taxa are unclear.

Crop rotation such as diversification with legume crops is an alternative strategy to maintain soil quality and crop productivity when compared with monocultural cropping patterns (Tiemann et al., 2015). Crops impact the soil microbiota by shaping their composition and diversity through root exudates, plant residues and symbiotic association, or directly altering soil carbon (C) input, nutrient availability and soil structure (e.g., texture and aggregates distribution) (Ai et al., 2015; Graaff et al., 2010; Su et al., 2017; Trivedi et al., 2015). Legumes with their high N content and enhanced ecosystem N inputs associated with biological N fixation are regarded as a preferential alternative to rotate with other crop species (Murugan and Kumar, 2013). However, the

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