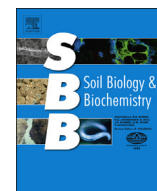




Contents lists available at ScienceDirect

## Soil Biology &amp; Biochemistry

journal homepage: [www.elsevier.com/locate/soilbio](http://www.elsevier.com/locate/soilbio)

## Influence of 34-years of fertilization on bacterial communities in an intensively cultivated black soil in northeast China

Jing Zhou<sup>a, b</sup>, Dawei Guan<sup>a</sup>, Baoku Zhou<sup>c</sup>, Baisuo Zhao<sup>d</sup>, Mingchao Ma<sup>a, d</sup>, Jie Qin<sup>a</sup>, Xin Jiang<sup>a, d</sup>, Sanfeng Chen<sup>b</sup>, Fengming Cao<sup>a, d</sup>, Delong Shen<sup>d</sup>, Jun Li<sup>a, d, \*</sup>

<sup>a</sup> Institute of Agricultural Resources and Regional Planning, Chinese Academy of Agricultural Sciences, Beijing 100081, PR China

<sup>b</sup> College of Biological Sciences, China Agricultural University, Beijing 100094, PR China

<sup>c</sup> The Institute of Soil Fertility and Environmental Sources, Heilongjiang Academy of Agricultural Sciences, Harbin 150086, PR China

<sup>d</sup> Laboratory of Quality & Safety Risk Assessment for Microbial Products (Beijing), Ministry of Agriculture, Beijing 100081, PR China

## ARTICLE INFO

## Article history:

Received 17 December 2014

Received in revised form

29 May 2015

Accepted 10 July 2015

Available online xxx

## Keywords:

Bacterial community

Soil properties

Nitrogen and phosphorus fertilization

Wheat yield

Illumina Miseq

## ABSTRACT

Although the effects of chemical fertilization management on microbial communities in soils have been well studied, few studies have examined such impacts of long-term chemical fertilizations on the microbial community in black soils common to northeast China. We applied high-throughput pyrosequencing and quantitative PCR of the 16S rRNA gene to investigate bacterial communities in a long-term fertilizer experiment started in 1980. The following fertilizer treatments were compared with control plots (no fertilizer): N<sub>1</sub> (low nitrogen fertilizer), N<sub>2</sub> (high nitrogen fertilizer), N<sub>1</sub>P<sub>1</sub> (low nitrogen plus low phosphorus fertilizers) and N<sub>2</sub>P<sub>2</sub> (high nitrogen plus high phosphorus fertilizers). All fertilization treatments resulted in decreases in soil pH and increases in wheat yield and concentrations of total nitrogen, organic matter and KCl-extractable NO<sub>3</sub><sup>-</sup> and NH<sub>4</sub><sup>+</sup>. Fertilization also led to a significant decrease in total 16S rRNA gene abundance and bacterial diversity. The phyla Proteobacteria, Acidobacteria and Actinobacteria dominated in all fertilized treatments. There was an increase in relative abundance of Actinobacteria, Proteobacteria, TM7 and Verrucomicrobia across all fertilized treatments compared to unfertilized controls, whereas phyla Acidobacteria and Nitrospirae decreased. The bacterial communities in unfertilized controls and lower-mineral fertilizers (i.e. N<sub>1</sub> and N<sub>1</sub>P<sub>1</sub>) were predominantly composed of Acidobacteria, Actinobacteria and Proteobacteria, and separated from the communities where more concentrated fertilizer regimes were used (i.e. N<sub>2</sub> and N<sub>2</sub>P<sub>2</sub>) based on principal coordinates analysis. Soil pH and NO<sub>3</sub><sup>-</sup> concentration appeared to be the most important factors in shaping bacterial communities. Our findings suggested that long-term inorganic fertilizer regimes reduced the biodiversity and abundance of bacteria. The influence of more concentrated fertilizer treatments was greater than that of lower concentrations.

© 2015 Elsevier Ltd. All rights reserved.

## 1. Introduction

The interaction between plants, soil and microorganisms is considered to be the major driver of ecosystem functions (Suleiman et al., 2013) and microorganisms respond quickly to any modification of vegetation or soil properties (Hallin et al., 2009; Zhao et al., 2014). The diversity and abundance of bacteria community

in agroecosystems is critical to maintaining soil quality, productivity and ecological balance in cropland areas (C.H. Li et al., 2014; Y. Li et al., 2014). Over the past 100 years, extensive agricultural intensification has been implemented by high inputs of chemical fertilizers which, in turn, are resulting in serious degradation of soil physicochemical properties (Singh et al., 2014). The nutrient-based alteration and associated microbiota were not surprisingly reflected in significant shifts in nitrogen-fixing bacteria (Berthrong et al., 2014), ammonia-oxidizing bacteria (Ai et al., 2013), methanotrophs (Dai et al., 2013) and denitrifiers (Tang et al., 2010). Understanding the shifts in microbial community structure and composition following long-term fertilization may have significant implications for the development of better fertilizer regimes for

\* Corresponding author. Institute of Agricultural Resources and Regional Planning, Chinese Academy of Agricultural Sciences, Beijing 100081, PR China. Tel.: +86 10 82106208.

E-mail address: [lijun01@caas.cn](mailto:lijun01@caas.cn) (J. Li).

<http://dx.doi.org/10.1016/j.soilbio.2015.07.005>

0038-0717/© 2015 Elsevier Ltd. All rights reserved.