



Available online at www.sciencedirect.com

ScienceDirect



RESEARCH ARTICLE

Wheat, maize and sunflower cropping systems selectively influence bacteria community structure and diversity in their and succeeding crop's rhizosphere



WEN Xin-ya^{1,2}, Eric Dubinsky³, WU Yao^{1,2}, YU Rong⁴, CHEN Fu^{1,2}

¹ College of Agriculture and Biotechnology, China Agricultural University, Beijing 100193, P.R.China

² Key Laboratory of Farming System, Ministry of Agriculture, Beijing 100193, P.R.China

³ Lawrence Berkeley National Laboratory, Earth Sciences Division, Berkeley, California 94720, USA

⁴ Institute for the Control of Agrochemicals, Ministry of Agriculture, Beijing 100125, P.R.China

Abstract

Wheat and maize are increasingly used as alternative crops to sunflower monocultures that dominate the Hetao Irrigation District in China. Shifts from sunflower monocultures to alternate cropping systems may have significant effects on below-ground microbial communities which control nutrient cycling and influence plant productivity. In this research, rhizosphere bacterial communities were compared among sunflower, wheat and maize cropping systems by 454 pyrosequencing. These cropping systems included 2 years wheat (cultivar Yongliang 4) and maize (cultivar Sidan 19) monoculture, more than 20 years sunflower (cultivar 5009) monoculture, and wheat-sunflower and maize-sunflower rotation. In addition, we investigated rhizosphere bacterial communities of healthy and diseased plants at maturity to determine the relationship between plant health and rotation effect. The results revealed taxonomic information about the overall bacterial community. And significant differences in bacterial community structure were detected among these cropping systems. Eight of the most abundant groups including Proteobacteria, Bacteroidetes, Acidobacteria, Gemmatimonadetes, Chloroflexi, Actinobacteria, Planctomycetes and Firmicutes accounted for more than 85% of the sequences in each treatment. The wheat-wheat rhizosphere had the highest proportion of Acidobacteria, Bacteroidetes and the lowest proportion of unclassified bacteria. Wheat-sunflower cropping system showed more abundant Acidobacteria than maize-sunflower and sunflower monoculture, exhibiting some influences of wheat on the succeeding crop. Maize-maize rhizosphere had the highest proportion of γ -Proteobacteria, Pseudomonadales and the lowest proportion of Acidobacteria. Sunflower rotation with wheat and maize could increase the relative abundance of the Acidobacteria while decrease the relative abundance of the unclassified phyla, as was similar with the health plants. This suggests some positive impacts of rotation with wheat and maize on the bacterial communities within a single field. These results demonstrate that different crop rotation systems can have significant effects on rhizosphere microbiomes that potentially alter plant productivities in agricultural systems.

Received 30 June, 2015 Accepted 30 July, 2015

WEN Xin-ya, E-mail: wxya@cau.edu.cn, Correspondence CHEN Fu, Tel/Fax: +86-10-62733316, E-mail: chenfu@cau.edu.cn

© 2016, CAAS. All rights reserved. Published by Elsevier Ltd.
doi: 10.1016/S2095-3119(15)61147-9

Keywords: bacterial community structure and diversity, rhizosphere, cropping system, 454 pyrosequencing

1. Introduction

In the last decades, many studies have provided evidence that plant-microbe interactions are not only crucial for better understanding of plant growth and health, but also for sustainable agriculture and nature conservation (Philippot *et al.* 2013). Ecologists have been traditionally more concerned about aboveground ecosystem processes, which are much better understood than belowground processes. Recent advances in belowground processes have suggested that understanding the ecology and evolution of rhizosphere has an important significance for enhancing plant productivity and ecosystem functioning (Philippot *et al.* 2013). However, current understanding of the complicated plant-microbe interactions in the rhizosphere is still in its primary stage (Berendsen *et al.* 2012).

Rhizodeposits account for around 11% of net photosynthetically fixed carbon and 10–16% of total plant nitrogen (Bulgarelli *et al.* 2013). The nutrient allocation vary greatly depending on plant species and age, location along the root system and soil type (Yang and Crowley 2000; Hertenberger *et al.* 2002). Stable isotope probing in combination with microbiota DNA profiling (DNA-SIP) of $^{13}\text{CO}_2$ -labelled plants identified that rhizosphere bacteria assimilate root exudates (Haichar *et al.* 2008). Thus, plants are able to shape the rhizosphere microbiota by active secretion of compounds that facilitate or suppress specific members of the microbial community, establishing a habitat which is favorable for the plant (Doornbos *et al.* 2012). Some plants have their own species-specific organisms in rhizosphere (Lemanceau *et al.* 1995; Berg *et al.* 2002, 2006; Weller *et al.* 2002; Picard and Bosco 2008), bacteria as well as fungi, showing a high degree of host specificity and coevolving with plants (Raaijmakers *et al.* 2009). Some plant species can produce similar communities in different soils (Miethling *et al.* 2000). Different plant species often exhibit different rhizosphere microflorae even if they are growing in the same soil (Viebahn *et al.* 2005; Berg *et al.* 2006; Garbeva *et al.* 2008). As numerous bacterial and fungal groups are found to promote the plant growth and boost their defensive capacity (Zamioudis and Pieterse 2012), plants have even been postulated to actively recruit these beneficial microorganisms in their rhizospheres, for example, to counteract pathogen assault (Cook *et al.* 1995). A recent study further demonstrated that one kind of plant-beneficial rhizobacteria, *Pseudomonas putida*, was recruited to plant roots by

benzoxazinoid secondary metabolites (Neal *et al.* 2012).

With the exploration of the belowground processes, increasing attention is drawn to deep understanding of the structure and the functions of the bacterial communities. Several studies indicate that plants showed strong influence on rhizosphere bacterial community composition (Smalla *et al.* 2001; Kowalchuk *et al.* 2002; Costa *et al.* 2006). In these researches, cultivation and some newer biochemical and molecular analytical tools are used to assay the dominant or special rhizosphere bacteria populations (Smit *et al.* 2001). The new methods include signature fatty acids in cell membranes for phospholipid fatty acid (PLFA) (Nelson *et al.* 2011), fatty acid methyl ester (FAME) profiles (Zelles *et al.* 1992, 1995; Hamel *et al.* 2006), 16S rDNA for denaturing gradient gel electrophoresis (DGGE) (Gu *et al.* 2009) or terminal restriction fragment length polymorphism (T-RFLP) (de Oliveira *et al.* 2006; Donn *et al.* 2015). However, these methods do not provide high resolution taxonomic information to characterize complex soil microbial communities and identify bacteria among different crops (Jansson *et al.* 2012). In the past five years, a paradigm shift in metagenomics have been seen that advances in DNA sequencing, such as pyrosequencing, and high-performance computing enable the application of cross-sectional and longitudinal studies (Knight *et al.* 2012). 454 pyrosequencing has been used to evaluate differences in bacterial communities for its sufficiently sensitive to taxonomic information and highly efficient for mixed samples to be run on the same sequencing run and later binned in a cost-effective and timely manner (Quince *et al.* 2009).

Determining how rhizosphere microbial communities differ among cropping systems is an important step toward understanding how different agricultural strategies can promote beneficial interactions in the rhizosphere. The objective of this study was to characterize the structure and diversity of soil bacterial communities in rhizosphere of wheat, maize, sunflower, and different sunflower rotations in the Hetao Irrigation District in China. We applied 454 pyrosequencing to evaluate differences among these crop rotation systems and provided information about belowground effects on microbial communities that may enhance crop productivity.

2. Materials and methods

2.1. Site and sampling

This study was carried out from March 2011 to September 2012 at Yichang Experimental Station, located in Hetao

Download English Version:

<https://daneshyari.com/en/article/10179939>

Download Persian Version:

<https://daneshyari.com/article/10179939>

[Daneshyari.com](https://daneshyari.com)