

Bacterial community in melon/cowpea intercropping systems with reduced nitrogen application

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INTRODUCTION

Intercropping systems consist of simultaneous growth of two or more crop species on the same area and at the same time (Brooker et al., 2015). It can effectively improve the mobilization and uptake of nitrogen, phosphorous, potassium, and micronutrients through interspecific interactions in rhizosphere (Zuo and Zhang, 2008). Most recent research has focalized on the use of grain legumes like cowpea (*Vigna unguiculata* L. Walp) adapted to stressful environments, associated with high temperatures, drought or low fertility, that can improve legume nitrogen uptake by enhanced nodulation of legumes (Li et al., 2007). Soil microorganisms play an important role in soil biogeochemical processes, decomposition of organic matter and suppression of soil-borne pathogens (Li et al., 2012). The changes in soil microbial communities may be both a cause and reflection of the better performance in the intercropping systems. The purpose of this study was to explore the responses of microbial communities to different combinations of intercropping (melon (*Cucumis melo*)/cowpea (*Vigna unguiculata*)), with decrease of external fertilizer inputs in a Mediterranean semiarid farm during one year.

MATERIALS AND METHODS

This study was carried out in Cartagena, SE Spain, with semiarid Mediterranean climate. The field experiment was designed as a randomized block with three replications, and each plot had 150 m². We compared a melon monocrop (M) and different melon-cowpea intercropping systems (one-year time): Mixed intercropping (MC1) and row intercropping 1:1 (melon:cowpea) (MC2), row intercropping 2:1 (melon:cowpea) (MC3). A cowpea monocrop was also established (C). All crops were drip irrigated and grown under organic management. The fertilizer rate was reduced by 30% in the intercropping compared to melon monocropping.

Melon and cowpea were simultaneous harvested from 31 July to 10 August. Soil DNA from each treatment was extracted using the DNeasy Power Soil Kit (Qiagen). Ion 16STM Metagenomics kit from Thermo Fisher Scientific® was used to analyse bacterial community using the Ion Torrent™ semiconductor sequencing workflow. Two pair of primers from 16S rDNA regions (V2-4-8 and V3-6, 7-9) was used. The *amoA*, *nirK* and *narG* gene of the nitrogen cycle was investigated by qPCR in all treatments based on the ISO standard 17601 (ISO, 2016). The Shannon diversity index (H) and Inverse of Simpson index (1-D) was calculated using the Vegan package (Oksanen et al., 2013) respectively in R.

MAIN RESULTS

The increase in crop yield with melon and cowpea intercropping systems was confirmed. Interspecific competition for nutrients resources and belowground interactions is well known to affect crop growth and grain yield in intercropping systems (Corre-Hellou et al., 2006). The Shannon index of bacterial community was similar in all cultivation systems. The overall microbial community composition significantly differed between monocrop and intercropping systems (Fig. 1) in agreement with Alvey et al. (2003). Dominant phyla found in this study was in line with previous studies investigating plant-associated bacterial and fungal communities (Bulgarelli et al., 2013). Also, in intercropping systems, higher members of the genera *Pseudomonas* and *Shingomonas*, which are well-known as plant growth-promoting bacteria and/or for the production of secondary metabolites (Lodewyckx et al., 2002) (Fig. 1).

Moreover, effective use of nitrogen is considered the most important factor with respect to the advantages of intercropping. Abundance of genes related to N-cycling, in nitrification (*amoA*) and denitrification (*nirK*, *NarG*) genes, indicated no differences between monocrop and intercropping systems (Fig. 2), but trending to be lower in the last; this fact could indicate the effectiveness of legume (cowpea) in the intercropping compared to monocropping, that it could fix nitrogen, reducing the functional genes of soil microbial communities to N uptake.

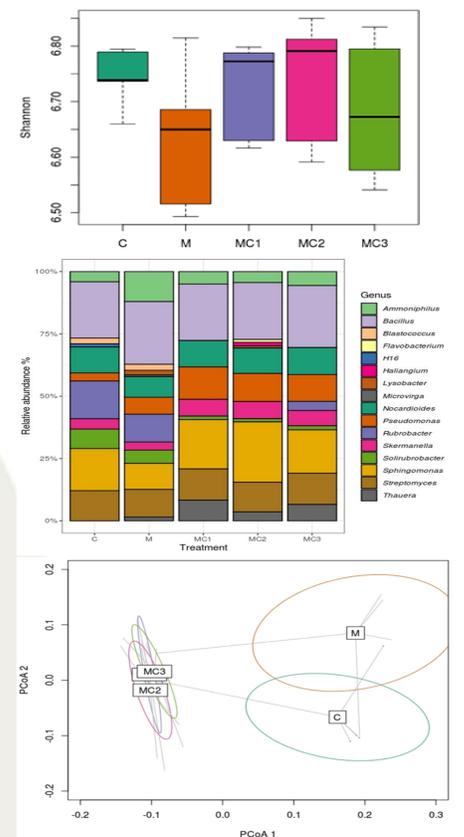


Fig. 1 Shannon diversity index (a) PCoA of the bacterial community (b) and relative abundance (>1%) of bacterial genus (c) of the different cropping systems.

Melon monocrop (M); Cowpea monocrop (C); Mixed intercropping (MC1); Intercropping 1:1 (melon:cowpea) (MC2); Intercropping 2:1 (melon:cowpea) (MC3).

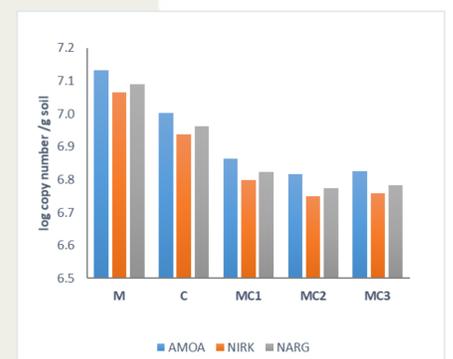


Fig 2. Abundance of N-genes markers of cultivation systems.

Melon monocrop (M); Cowpea monocrop (C); Mixed intercropping (MC1); Intercropping 1:1 (melon:cowpea) (MC2); Intercropping 2:1 (melon:cowpea) (MC3).

The preliminary results of the study show that intercropping (melon/cowpea) can contribute to multiple agroecosystem services by increased yield, reduce the use of chemical fertilizer and change bacterial community to increase soil quality, increasing plant growth-promoting bacteria and the nitrogen efficiency use in the agroecosystem.

