Changes in 16S rRNA bacterial community structures after C and N additions – comparison of organic farmed and conventionally farmed soils

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Introduction

- Green manure legumes are alternatives to chemical fertilizer in organic farming system.
- Green manure legumes supply organic matter to soils as their residues and influence soil microbial community (Mao et al. 2013).
- Microbes can also be sinks for nitrogen (N) and the N within live-microbes (biomass N) cannot be utilized by plants resulting in the competition between plant and microbe for available N.
- The use of green manure legumes may lead to increased available N in soils but it may influence on soil microbial N assimilation (N immobilization) potential.

Key Questions
1. Does the long-term legume application change soil microbial community structure? → Exp 1.
2. Does soil microbial community with the history of legume application affect microbial N immobilization potential? → Exp 2.

Experiment 1.

Materials and Methods

- Colony forming unit of Bacteria (x10^7): HV (13 ± 5.2) > CF (5.7 ± 2.7) (p < 0.05).
- Colony forming unit of Fungi (x10^7): CF (7.5 ± 1.9) > HV (3.2 ± 3.6) (p < 0.05).
- Shannon diversity index at family revel: HV (5.94 ± 0.1) > CF (5.54 ± 0.24) (p < 0.05).
- Different soil microbial structures after 9 years of organic vs conventional farming

Results

- The ratio of β-Proteobacteria was significantly higher in the HV soil compared to CF soil.
- The abundance of β-Proteobacteria was positively correlated with C mineralization rate thus the phylum is considered to be more favorable to high C condition (Fierer et al. 2007).
- The application of HV into soil increased C source in soil and might have increased the abundance of β-Proteobacteria.
- The ratio of family Streptomyces (family Actinobacteria, genus Streptomyces) was significantly higher in the CF soil compared to HV soil.
- Genus Streptomyces utilizes sulfate as sulfur sources (Fischer et al. 2012).
- The application of chemical fertilizer (Ammonium sulfate) into CF soil increased available S source and might have increased the abundance of Streptomyces.

Discussion

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Conclusion

- Exp1. Long term use of legume plants in organic farming system changed the structures of bacterial community and increased their diversity when compared to those of conventionally farmed system.
- Exp2. Microbial community structures became similar within 14 days with addition of excess C and N.
- No difference was observed in decrease rates of N and changes in microbial biomass C during 14 days incubation.
- The long term use of hairy vetch in soils might not change the soil function in terms of short-term N immobilization process when C and N source is applied into soil.

Experiment 2.

Materials and Methods

- Decreasing NO₃⁻ - N concentration
- KCl extraction with colorimetry
- Increasing microbial biomass carbon
- Chloroform fumigation method
- 16S rRNA gene analyses
- Same as Exp 1.

Results

- No difference in decrease of NO₃⁻ and increase of microbial biomass carbon

Discussion

- In both soil, Proteobacteria and Bacteroidetes dominated in the end whereas Firmicutes disappeared over time.
- Firmicutes was dominant 3 days after organic matter addition but it was replaced by proteobacteria at 14 and 60 days (Pascault et al. 2013).
- Changing pattern looked very similar in two soils
- Proteobacteria and Firmicutes increased with organic matter addition (Van et al. 2014) and Bacteroidetes increased its abundance with high C availability (Fierer et al. 2007).
- Bacterial community structure was affected by C addition.