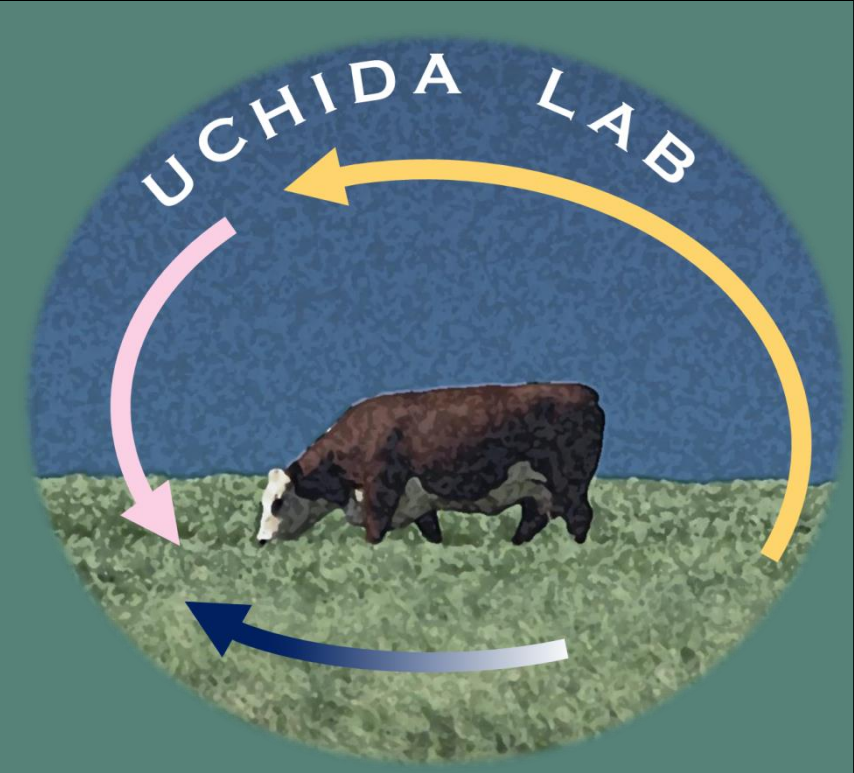




Changes in 16S rRNA bacterial community structures after C and N additions

– comparison of organic farmed and conventionally farmed soils



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Introduction

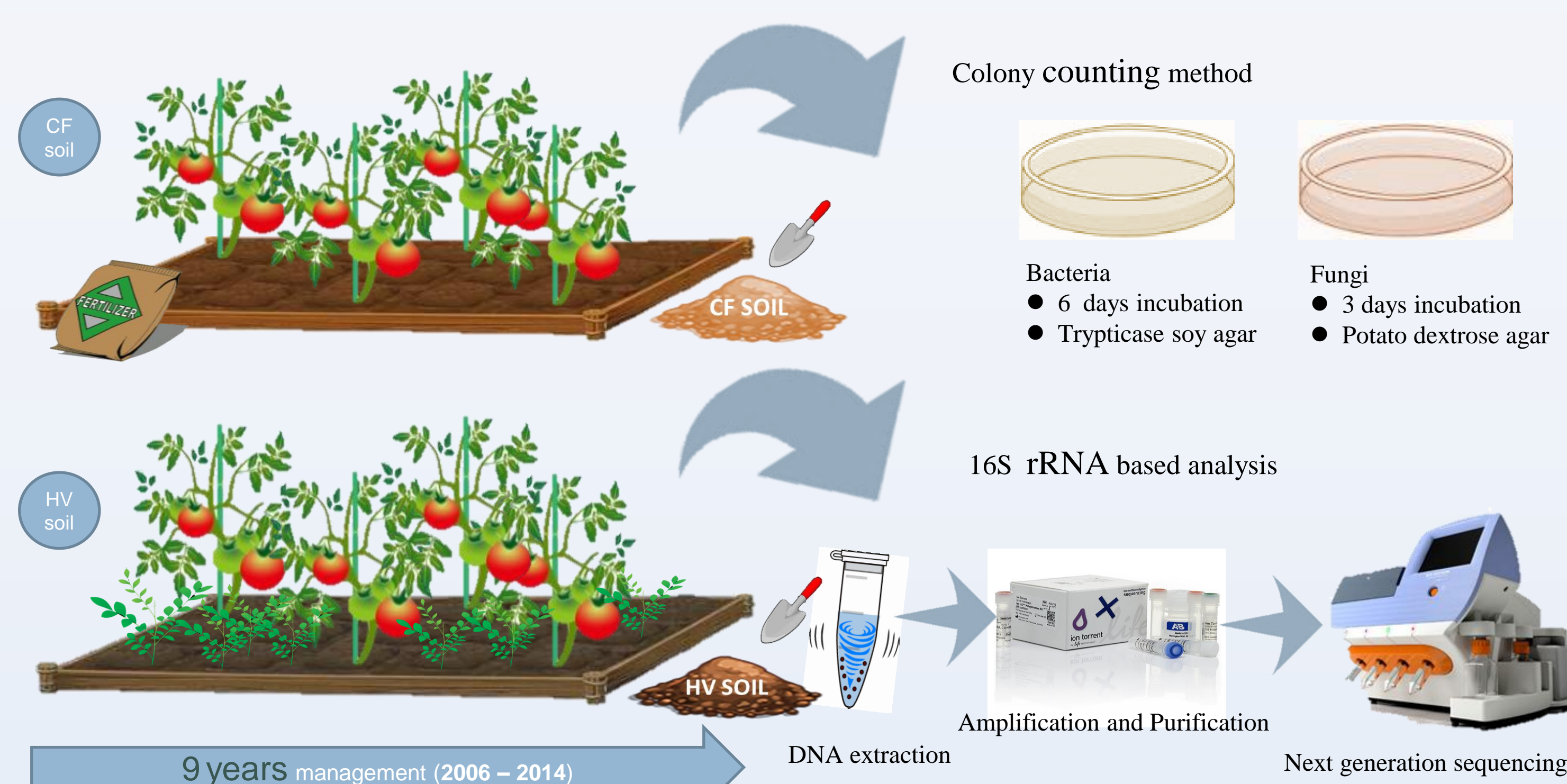
- Green manure legumes are alternatives to chemical fertilizer in organic farming system.
- Green manure legumes supply organic matter to soils as their residues and influence soil microbial community (Mao et al. 2011).
- Microbes can also be sinks for nitrogen (N) and the N within live-microbes (biomass 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

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

Experiment 1.

Materials and Methods



Results

- Colony forming unit of Bacteria ($\times 10^7$): HV (13 ± 5.2) > CF (5.7 ± 2.7) ($p < 0.05$)
- Colony forming unit of Fungi ($\times 10^5$): CF (7.5 ± 1.9) > HV (3.2 ± 3.6) ($p < 0.05$)
- Shannon diversity index at family level: 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

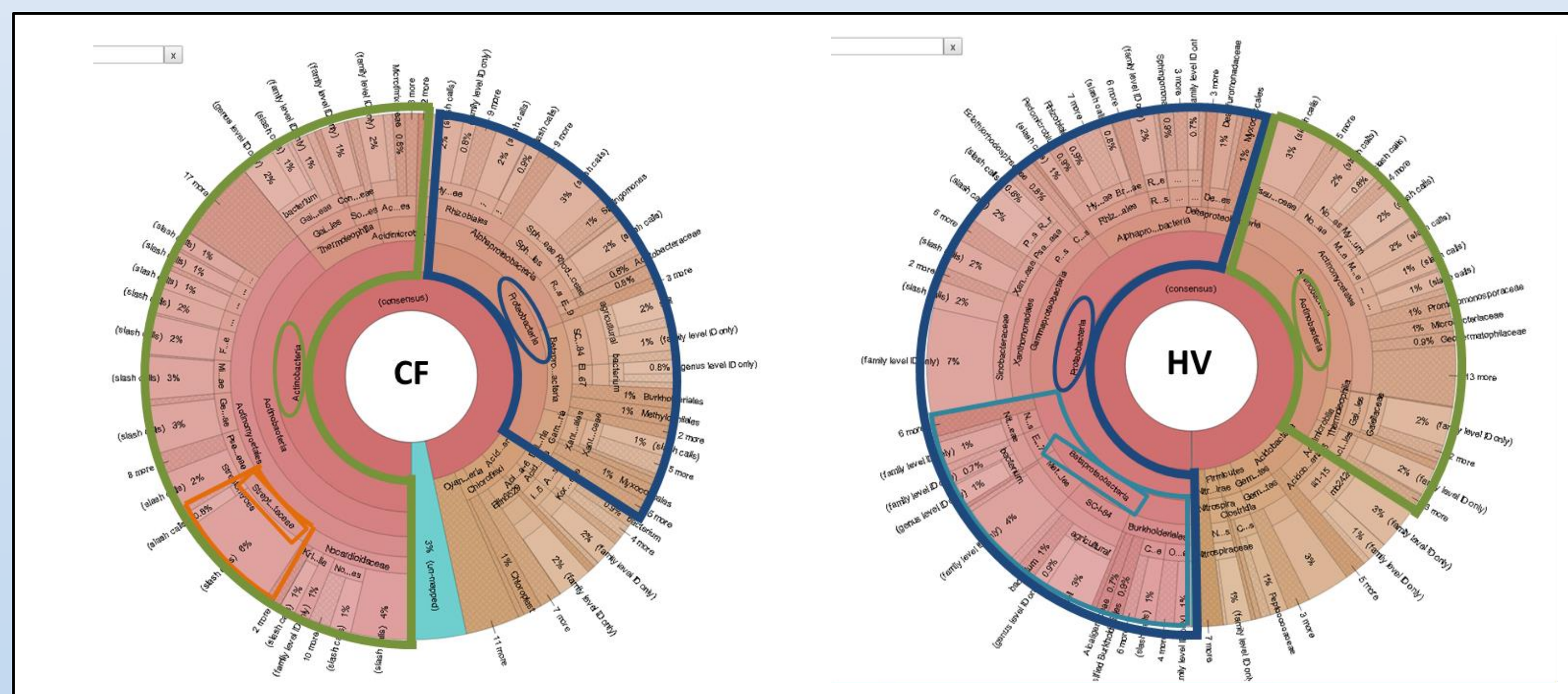


Figure 1. Community composition of soil with the history of chemical fertilizer application (CF) and soil with the history of hairy vetch application (HV) for 9 years (one of representatives). The most dominant phylum and the second dominant phylum (*Actinobacteria* and *Proteobacteria*) were opposite between two soils.

Discussion

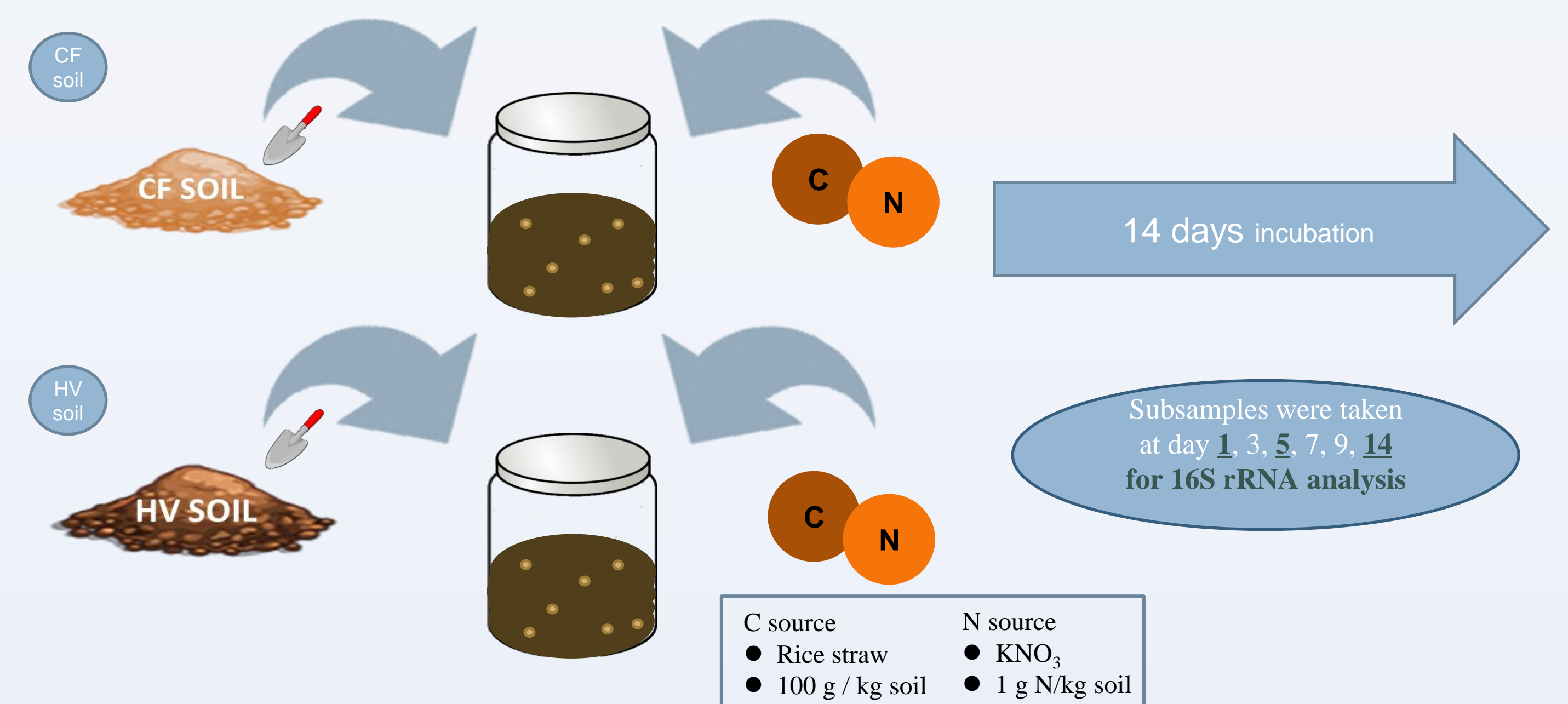
- The ratio of *β -Proteobacteria* was significantly higher in the HV soil compared to CF soil
- The abundance of *β -Proteobacteria* was positively correlated with C mineralization rate thus the phylum is considered to be more favorable to high C condition (Fierer et al. 2007). → the application of HV into soil increased C source in soil and might have increased the abundance of *β -Proteobacteria*.
- The ratio of family *Streptomycetaceae* (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 *Streptomycetaceae*.

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



	CF	HV	P value
Water content (%)	14 ± 2	17 ± 0.5	0.02*
pH (H ₂ O)	6.4 ± 0.8	6.9 ± 0.2	NS
WFPS %	0.23 ± 0.04	0.27 ± 0.04	NS
Total C g kg ⁻¹	39 ± 3	39 ± 2	NS
Total N g kg ⁻¹	3.6 ± 0.3	3.4 ± 0.3	0.03*
NO ₃ ⁻ -N mg kg ⁻¹	279 ± 45	201 ± 167	NS
NH ₄ ⁺ -N mg kg ⁻¹	34 ± 47	4.0 ± 2	NS

Table 1. Basic soil properties for soils sampled at chemical fertilizer (CF) and hairy vetch (HV) soils from a tomato trial (n=3, error = s.d.).

Results

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

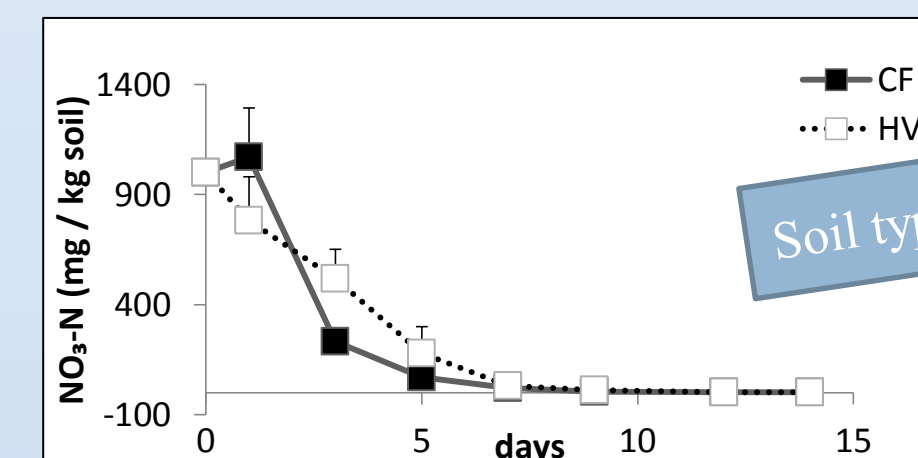


Figure 2. Change in NO₃⁻ of soils with the history of chemical fertilizer application (CF) and soil with the history of hairy vetch application (HV) with C and N input during 14 days incubation.

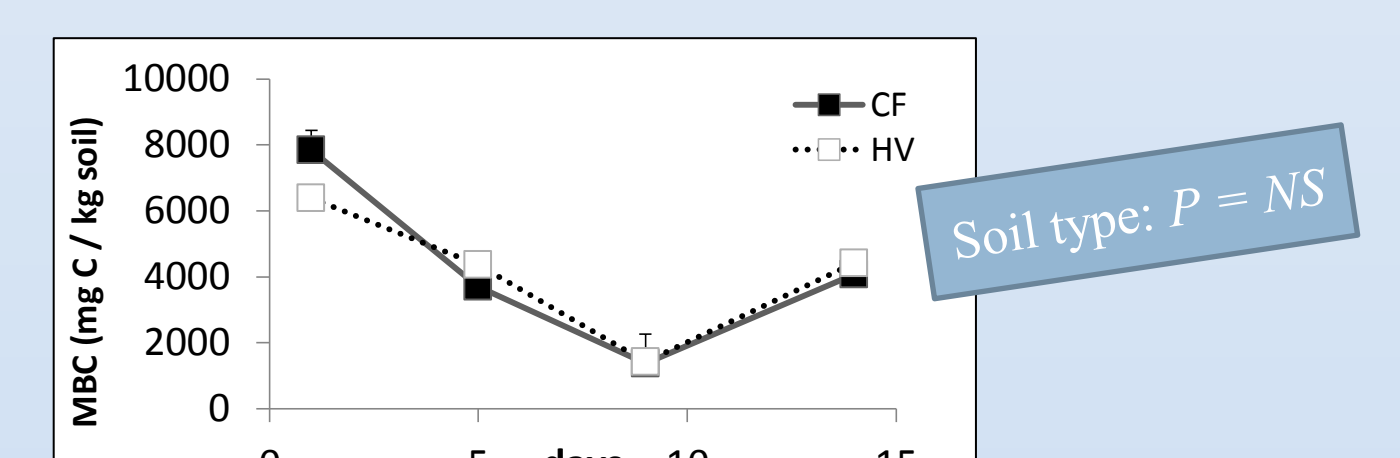


Figure 2. Change in microbial biomass carbon of soils with the history of chemical fertilizer application (CF) and soil with the history of hairy vetch application (HV) with C and N input during 14 days incubation.

- Microbial structure getting similar over time with added excess C and N

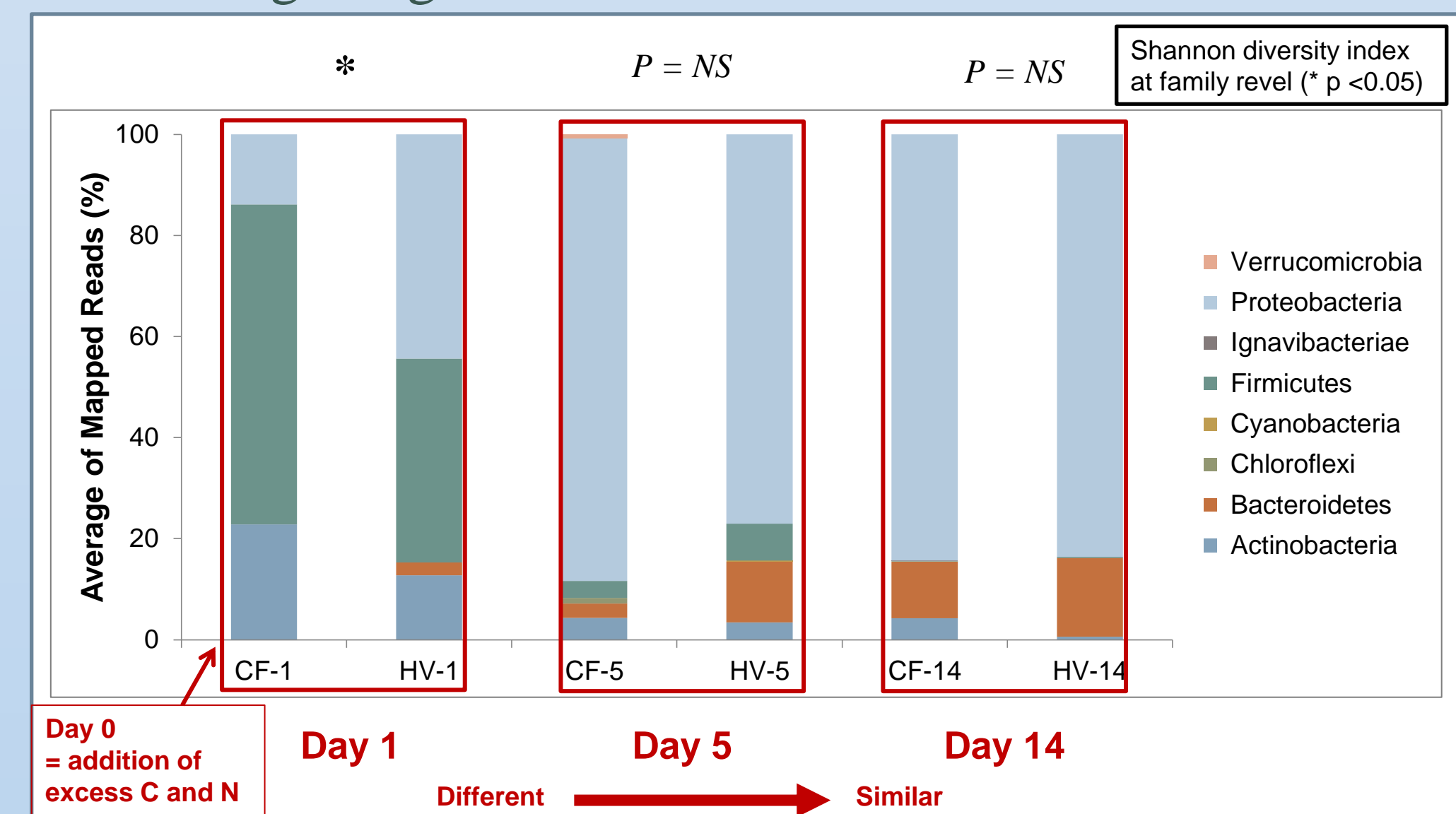


Figure 4. Change of bacterial community composition with the history of chemical fertilizer application (CF) and soil with the history of hairy vetch application (HV) with C and N input during 14 days incubation. The changing pattern seemed to be similar between two soils.

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.