学位論文内容の要旨

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学位論文題名

Understanding the dynamics of soil microbial communities and gas emissions under different soil amendments

（異なる土壌改良資材施用が土壌微生物叢ダイナミクスとガス排出量に及ぼす影響評価）

Soil microbes play important roles in regulating the soil health. The addition of organic materials to soils can improve the activities of the microbes. Specifically, soil microbes utilize carbon (C) from the applied organic materials to increase their abundance and activities. Contrastingly, soil microbes decompose the added materials and emit the C to the atmosphere as carbon dioxide (CO_2). Studies have shown that charred organic materials like biochar can store C in the soil and improve the microbial activities. However, research to verify the impact of biochar on microbial community under different biochar applications is needed. Also, compared to biochar, manure can support microbial activities but the factors regulating the variabilities in manure decomposition are underexplored. First study investigated the effects of different biochar materials on the bacterial community. Second study examined microbial community using network analysis. Third experiment examined the decomposition of cow dung and gas emissions.

1. Response of bacterial diversity to different application methods of charred organic materials on sandy soil

A pot study was conducted to investigate the effects of different materials (chicken manure CM, rice straw RS, and rice husk RH) used to produce biochar on soil microbiome. The biochar was applied as single (CM, RS, and RH), combined form CM+RS, or CM+RH as mixed or surface under a dent corn. In results, surface applications increased the microbial diversity in the soil. This is because of the increased numbers of OTU such as *Actinobacteria*

and *Proteobacteria* at the phylum level. Also, RS treatments impacted the microbial richness, and evenness under surface application. This study showed that biochar materials and application methods should be considered when interpreting its impact on the microbial community.

2. Revealing the effects of different biochar feedstocks on the microbial communities using network analysis

The study aimed to investigate the microbial community interactions among different biochar materials using network analysis. The analysis was performed in R software and the network visualizations carried out in Gephi software. The results showed dominate phyla to be *Proteobacteria*, *Actinobacteria*, and *Chloroflexi* within the biochar materials. Rice husk biochar increased *Euryarchaeota*, while chicken manure biochar increased *Planctomycetes* in the soil. Therefore, biochar feedstocks should be considered when choosing biochar for soil amendment due to their interactions with microbes.

3. Bacterial communities and soil properties influencing the variations in dung decomposition and gas emissions among Japanese dairy farms

An incubation study was set-up with the dung and soil sampled from 15 different farms in Hokkaido. Gas emissions and changes in soil microbiomes were measured. In results, *Firmicutes* and *Bacteroidetes* were significantly decreased while *Proteobacteria* and *Actinobacteria* increased during dung decomposition. Higher numbers of OTUs were found in soils with low CO_2 (3750) compared to the high CO_2 (3438). Also, soil properties such as soil C, nitrogen, and CEC strongly influenced the emissions pattern based on the positive correlation with the high CO_2. These results indicated the impact of soil properties on dung decomposition and gas emissions.