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Effect of soil microbial diversity on maize decomposition and on *Fusarium graminearum*

土壌微生物の多様性がとうもろこし残渣の分解と病原菌 *Fusarium graminearu* に与える影響

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1. Introduction

Decomposition of plant residue is an important process in agricultural soils, which recycles soil nutrients. The processes are driven by microbes colonizing plant surfaces as well as in soil. However, the interaction among microbiomes from plant and soil during residue decomposition remains unknown. Also, the importance of microbial diversity on soil nutrition cycling, including residue decomposition, has been suggested in relation to soil fertility but quantitative research are few.

2. Methods

I aimed to manipulate soil microbial diversities by preparing three soils, namely “x1”, “x162” and “sterile soil”. For “x1” and “x162”, autoclaved soil was mixed with differently diluted inoculants containing microbial cells extracted from the original soil. For “sterile soil”, sterilized water was added instead of microbial inoculants. “Original soil” which had not been sterilized was included as a control. We incorporated litter bags with fresh/autoclaved maize leaves into these soils. During 6 weeks incubation, the weight of the litter bags as well as soil C contents were measured. Soil microbial DNA was extracted from the soils and from the litter, used for 16S rRNA gene quantification and community analyses.

3. Results

As expected, the reduction of soil microbial diversity led to slower decomposition rates of the litter in soils. This effect was not apparent when sterile litter was added to soils with reduced diversity. These results suggest that soil microbial diversity as well as the interaction of microbiomes from soil and those from plant would control litter decomposition rates. Meanwhile, a marked increase of DOC was occurred in soils after autoclaving.

4. Conclusion

Our results emphasize the importance of soil microbial diversity on litter decomposition processes. Soil microbiome with high diversity tend to promote litter degradation. Moreover, it is positively influenced by plant microbiome, resulting in active nutrient cycling.