

Community analysis of fungi and bacteria related to tree root decomposition in Japanese forest soil

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Purpose: The tree root play various roles, such as nutrient source for underground ecosystem, carbon stock and so on. These roles will retain until the tree root are completely degraded. Wood degradation above the ground is caused by termites and wood rot fungi, however, it is not clear yet what kinds of organisms degrade tree root under the ground, and its period. We analyzed fungal and bacterial communities which degrade buried in forest soil to search for wood degrader.

Methods: Wood species of *Cryptomeria japonica* were buried in five forest in Japan. They were buried at three kinds of level, on the ground, 5-10 cm, and 20-30 cm depth. Some of them were collected half or one year after and total DNAs were extracted. 16s rDNA and Internal transcribed spacer (ITS) region was amplified from extracted DNA by PCR, respectively. These PCR products were sequenced by using Miseq (illumina) and result sequences were searched using NCBI/DDBJ/EMBL database.

Results: The microbial communities in the sample specimens from the test sites were similar diverse between the depth of ground level and experimental periods, except for one site, in which the community had lower diversity of the community mainly consisted of *Megacollybia* and *Bacilli*.

Conclusions: In the early degradation, microbial communities are rich in variety. We have to study the succession of the communities along with the progress of further decomposition, as a future work. This work was supported by JSPS KAKENHI Grant Number JP12345678Grant-in-Aid for Scientific Research B (19H03012).