Diversity of Freshwater Fungal Communities in Wicheon Stream of South Korea

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Purpose: Freshwater is diverse and complex environment for microorganisms. In freshwater ecosystem, fungi are known as a key player in nutrient cycling, especially in organic matter decomposition. Well-known freshwater fungi are a group of polyphyletic fungi that include a high diversity of phyla. However, there are few studies of metagenomics approaches about seasonal dynamics of fungal communities in freshwater.

Methods: In order to investigate structure of fungal community in freshwater environment, we surveyed four spots in Wicheon stream - a branch stream of Nakdonggang River - every three month in 2018, and collected total 48 samples (three type of environmental samples - water, sediment of stream, and soil of hyporheic zone). We performed amplicon-based pyrosequencing using ITS region and taxonomic assignment.

Results and conclusions: A total of 2,200,325 reads with hits for fungi belonging to 3,557 operational taxonomic units (OTUs) were obtained from the total 48 samples. As a result, we presented structure of fungal community at various level - phylum, class, order, family and genus. Mostly fluctuation of diversity index showed reduction in winter and summer compared to spring and fall. The major orders were Pleosporales, Hypocreales, Capnodiales, Sordariales, Helotiales and Xylariales in Ascomycota; Rhizophydiales in Chytridiomycota; and Cystofilobasidiales and Agaricales in Basidiomycota. Interestingly, there are a big difference in construction of fungal communities depending on sample type, sampling site and collection season. Moreover, molecular analysis showed that there are many unknown fungal species in freshwater more than known fungi. These results indicated that environmental factors could be important factors on freshwater fungal community. Based on this study, we will try to evaluate methods of fungal isolation for acquiring of more diverse fungal isolates and investigate of fungal ecological roles in freshwater.