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Temporal dynamics of fungal DNA assemblages evaluated by eDNA metabarcoding in a forest river water in Japan

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Purpose: Recent studies have shown the usefulness of environmental DNA (eDNA) from river water in understanding both terrestrial and aquatic fungal compositions. However, knowledges on temporal variations in fungal DNA assemblages in river water are still limited. Here, we aimed to describe the fungal DNA assemblages in a forest river water and their temporal dynamics by fungal eDNA metabarcoding.

Methods: The study was conducted in a mixed broad-leaved forest (30-years old secondary forest, c.a., 0.6 ha) in southern Kyoto, Japan. Water samples (in total 3 L) were collected monthly from December 2016 to November 2018 (two-years). Fungal DNA assemblages were detected with MiSeq sequencing of fungal rDNA (ITS1) region.

Results and conclusions: In total, 4388 operational taxonomic units (OTUs) were obtained. Of these, 1680 were assigned as Ascomycota, 732 as Basidiomycota, and 68 as Chytridiomycota. We found that the river water contained divergence in functional groups, including saprotrophic, parasitic, and symbiotic fungi associated with plants and animals in both aquatic and terrestrial habitats. The OTU compositions changed continuously and temporally, and showed a periodic change in the compositions resembling each other by the investigation months regardless of the year. The strength of this periodicity varied among functional groups, being strong in saprophytes and weak in symbionts. Our results indicated that the fungal DNA assemblages in river water were composed of fungal DNA from various taxonomic and functional groups including terrestrial fungi, and suggested that temporal changes of the fungal communities in the riverine forest can be evaluated by examining the eDNA in the river water.