Poster Presentation 3

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Rapid characterization of wood-decaying fungal communities using the nanopore sequencing system

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Purpose: Detection and identification of tree pathogenic fungi are essential for forest pest management and tree protection, especially of hidden wood decay without fruiting body. Conventional molecular diagnostic methods to detect and identify are reliable but laborious and time-consuming. Recent high-throughput DNA sequencing technologies potentially provide efficient tools for characterizing the ecology and functioning of pathogenic fungi. Here, we examined the applicability of a portable nanopore-based sequencing system to the detection and identification of wood-decaying fungi in the field.
Methods: Healthy and decayed wood samples were collected from *Chamaecyparis pisifera* wood, and genomic DNA was extracted from those samples. Based on the samples, a short-read Illumina amplicon sequencing of the rDNA ITS2 was conducted. Then, the qualitative (taxonomic richness) and quantitative (taxonomic relative abundance) recovery of taxa by long-read amplicon sequencing of fungal rDNA and shotgun metagenomics were tested using the Oxford Nanopore MinION platform.
Results and conclusions: The short-read sequencing found that OTUs of the genus *Serpula* dominated in fungal communities of decayed wood. The nanopore sequencing also succeeded in detecting dominant OTUs affiliated in the genus *Serpula*, although taxonomic richness was low and taxonomic relative abundance was biased in comparison with the results from the short-read sequencing. These results show that the portable nanopore sequencing system is potentially applicable to characterizing the significant components of wood-decaying fungi, implying an advantage for routine diagnosis of forest pathogens.