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ABSTRACTS - Oral Presentations

Detecting polyploidy and its role in diversification across Hydnum (Cantharellales)
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Whole genome duplication and gene-loss events leading to changes in ploidy levels are well-characterized in plants and animals. However, the frequency of ploidy changes and subsequent effects on diversification are poorly understood in mushroom-forming fungi. Previous research on the genus Hydnum (Cantharellales) has suggested that some species vary in ploidy level and differ by as much as a four-fold increase in chromosome sets. If so, ploidy level could correlate with changes in morphology observed across the phylogeny of Hydnum. Here, we present a framework to estimate ploidy levels in Hydnum and discuss hypotheses regarding the effect of polyploidy on morphology and diversification in the genus. To estimate ploidy levels in Hydnum, we collected dense basidiospore deposits from a range of species to compare relative gene content using flow cytometry. To study the phylogenetic distribution of ploidy level and other characters, we constructed a three-gene (ITS, rbp2, tef1) phylogeny from more than 50 samples of Hydnum, which provides a robust evolutionary framework for comparative analysis.