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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.