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**ABSTRACTS** - Oral Presentations

**Community composition, structure, and function of submerged detritus-inhabiting fungi across temperate peatland and stream habitats**

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Freshwater fungi play a key role in plant debris decomposition, are pivotal in transferring energy and nutrients to higher trophic levels, and are essential for removing toxic heavy metals and degrading xenobiotics. Using both culture-dependent and culture-independent techniques, we examined how habitat, geography, and phylogeny influence the structure of detritus-inhabiting fungal communities within temperate peatland and alkaline stream habitats. Isolate function was determined using qualitative agar based assays in conjunction with modern quantitative assays. Results indicated that all sites contain numerous unidentified, abundant taxa but that stream communities contain more species, have greater phylogenetic diversity, and possess greater phylogenetic distinctiveness as compared to peatlands. In addition, analysis of the nine most abundant fungal classes indicated that phylogenetic clustering was more prominent within peatland habitats as compared to stream habitats. Lastly, site variation had the greatest impact on community structure, followed by habitat, and region. Functional results indicated that all culturable fungi demonstrated beta-glucosidase activity, while some fungi tested positive for starch degradation, overall cellulase activity, and tannase activity. Starch degradation was common within the Eurotiomycetes and overall cellulase and tannase activity was common within the Dothideomycetes and Sordariomycetes. Fluorometric analyses indicated that environmental pH alters the overall environmental function of Dothideomycetes species, while environmental pH did not alter the overall environmental function of Sordariomycetes species. Lastly, peatland and stream habitat species clusters demonstrate variable enzymatic capabilities suggesting niche partitioning as a mechanism to reduce intra-generic competition.