**DISTINGUISHING SOURCES OF CONFLICT: HYBRIDIZATION IN THE MOST SPECIOSE GENUS OF LICHEN-FORMING FUNGI**

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While advances in high throughput sequencing technologies have been invaluable for understanding evolutionary relationships, increasingly large genomic data sets can still result in conflicting phylogenies. Conflicting signals are often caused by biological processes such as incomplete lineage sorting (ILS) and hybridization. Hybridization has been detected in a variety of organisms, influencing evolutionary processes such as generating reproductive barriers and introducing novel phenotypes. Here, we investigate the role of hybridization in the diversification of the most speciose genus of lichen fungi, *Xanthoparmelia.* Focusing onthe 'Holarctic' *Xanthoparmelia*clade, we used a genome skimming approach to generated 962 single-copy gene regions representing over 2 Mb of the mycobiont genome. From this genome-scale dataset, we inferred evolutionary relationships across using both concatenation and coalescent-based species tree approaches. We also used three independent tests for hybridization to characterize relative contributions of incomplete lineage sorting versus hybridization. Although different species tree reconstruction methods recovered consistent and well-supported trees, there was widespread incongruence among gene trees. Our genome-wide analyses detected multiple hybridization events in the 'Holarctic' *Xanthoparmelia* clade of lichen-forming fungi. Our results suggest that hybridization may have facilitated the transfer of adaptative traits, explaining, in part, the rapid radiation and trait variability in this diverse lineage of lichen fungi. This study highlights the value in using a pluralistic approach for investigating hybridization, even with well-resolved phylogenies.