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Anchored Hybrid Enrichment generated nuclear, plastid and mitochondrial markers resolve the *Lepanthes horrida* (Orchidaceae: Pleurothallidinae) species complex

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ABSTRACT

Phylogenetic relationships in species complexes and lineages derived from rapid diversifications are often challenging to resolve using morphology or standard DNA barcoding markers. The hyper-diverse genus *Lepanthes* from Neotropical cloud forest includes over 1200 species and many recent, explosive diversifications that have resulted in poorly supported nodes and morphological convergence across clades. Here, we assess the performance of 446 nuclear-plastid-mitochondrial markers derived from an anchored hybrid enrichment approach (AHE) coupled with coalescence- and species network-based inferences to resolve phylogenetic relationships and improve species recognition in the *Lepanthes horrida* species group. In addition to using orchid-specific probes to increase enrichment efficiency, we improved gene tree resolution by extending standard angiosperm targets into adjacent exons. We found high topological discordance among individual gene trees, suggesting that hybridization/polyploidy may have promoted speciation in the lineage via formation of new hybrid taxa. In addition, we identified ten loci with the highest phylogenetic informativeness values from these genomes. Most previous phylogenetic sampling in the Pleurothallidinae relies on two regions (ITS and *matK*), therefore, the evaluation of

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