

Evaluating the performance of anchored hybrid enrichment generated nuclear, plastid and mitochondrial markers in the species-rich genus *Lepanthes* (Orchidaceae: Pleurothallidinae)

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Most of the phylogenetic studies in Orchidaceae are based on inferences obtained from the sequencing of few molecular markers. However, these inferences usually do not solve recalcitrant nodes in phylogenies. To tackle this problem, new sequencing techniques such as Anchored Hybrid Enrichment (AHE) allow the obtaining of ~ 500 orthologous loci, thus increasing the amount of information analyzed. This technique has been evaluated in several plant groups, including Arecaceae, Fabaceae, Lamiaceae, Oxalidaceae, Pinaceae, Proteaceae, Serraceniaceae and Zingiberales yielding better resolution to recalcitrant nodes in phylogenies. However, these phylogenetic studies on multi-locus datasets found high levels of discordance and conflicting topologies due to biological phenomena such as hybridization, gene duplication or deep coalescence or noise derived from systematic or stochastic errors. In order to test the performance of the AHE datasets in a species complex of the genus *Lepanthes*, we conducted gene/species tree and network inferences together with phylogenetic informativeness analyses with concatenated and coalescent-based methods. We obtained a fully resolved phylogeny but also found high discordance in the topology of the individual gene trees and paraphyly in the grouping of alleles of one species, *Lepanthes horrida*. This might indicate that ancient hybridization, polyploidy and/or incomplete lineage sorting may have contributed to speciation in *Lepanthes*. These analyses also revealed two undescribed species that were not previously disclosed based on inferences from ITS and matK datasets. Our study shows that only with a large number of phylogenetic markers it is possible to disentangle cryptic species and morphological traits evolving in parallel or convergently.