

Lineage and ‘role’ in integrative taxonomy of a heterotrophic orchid complex

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Abstract

Lineage-based species definitions applying coalescent approaches to species delimitation have become increasingly popular. Yet, the application of these methods and the recognition of lineage-only definitions have recently been questioned. Species delimitation criteria that explicitly consider both lineages and evidence for ecological ‘role’ shifts provide an opportunity to incorporate ecologically meaningful data from multiple sources in studies of species boundaries. Here, such criteria were applied to a problematic group of mycoheterotrophic orchids, the *Corallorhiza striata* complex, analyzing genomic, morphological, phenological, reproductive-mode, niche, and fungal host data. A recently developed method for generating genomic polymorphism data—ISSRseq—demonstrates evidence for four distinct lineages, including a previously unidentified lineage in the Coast Ranges and Cascades of California and Oregon, USA. There is divergence in morphology, phenology, reproductive mode, and fungal associates among the four lineages. Integrative analyses, conducted in population assignment and redundancy analysis frameworks, provide evidence of distinct genomic lineages and a similar pattern of divergence in the ‘extended’ data, albeit with weaker signal. However, none of the ‘extended’ datasets fully satisfy the condition of a significant ‘role’ shift, which requires evidence of fixed differences. The four lineages identified in the current study are recognized at the level of variety, short of comprising different species. This study represents the most comprehensive application of ‘lineage+role’ to date and illustrates the advantages of such an approach.

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