

CRAIG F. BARRETT, Department of Biology, 53 Campus Drive, West Virginia, University, Morgantown, WV USA 26506 and AARON KENNEDY, Mycology and Nematology Genetic Diversity and Biology Laboratory, USDA-APHIS, Bldg 010a, 10300 Baltimore Blvd., Beltsville, MD USA 20705. **Plastid genome evolution in the mycotrophic orchid genus *Hexalectris* Raf.**

The leafless, terrestrial genus *Hexalectris* Raf. comprises nine species of holomycotrophic orchids native to Mexico and the southern USA. The genus belongs to the tribe Blettiinae, and is closely related to the leafy genera *Basiphyllaea* Schltr. and *Bletia* Ruiz & Pav. Vegetative morphology in Blettiinae follows a trend of reduction, with well-developed, conduplicate leaves in *Bletia*, highly reduced, plicate leaves in *Basiphyllaea*, and absence of leaf laminae in *Hexalectris*. Estimates of relationships among these genera vary among studies. Recent analyses place *Basiphyllaea* as sister to *Hexalectris*, or as nested within *Bletia*; one analysis places *Basiphyllaea* + *Hexalectris* as nested within *Bletia*. Studies in orchid clades containing holomycotrophs and in holoparasitic Orobanchaceae suggest that plastid genome degradation occurs as a result of relaxed selective pressures on photosynthesis, which parallels reduction in vegetative morphology. Thus, Blettiinae serves as a powerful model for comparison with such clades. To test hypotheses of plastid genome reduction in Blettiinae, we sequenced representatives of *Bletia*, *Basiphyllaea*, and *Hexalectris*, focusing primarily on the latter. All species of *Hexalectris* were included, with at least two accessions sampled per species, and more intensive sampling in the widespread *Hexalectris spicata* (Walter) Barnhart, which ranges from Mexico to the eastern USA. Plastid genomes were assembled de novo and annotated, and phylogenetic analyses were conducted based on whole plastomes. Gene losses and pseudogene content were assessed across Blettiinae, as were patterns of selection on individual genes. These patterns are compared with recent mechanistic models of plastome evolution in parasitic lineages.