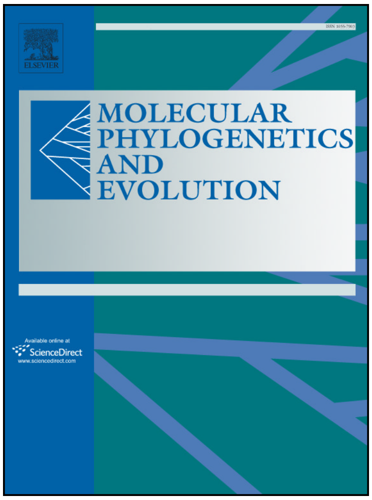

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Abstract:

The number of species recognized in section *Asperae* of the flowering plant genus *Hydrangea* differs widely between subsequent revisions. This variation is largely centered around the *H. aspera* species complex, with numbers of recognized species varying from one to nearly a dozen. Despite indications of molecular variation in this complex, no sequence-based species delimitation methods have been employed to evaluate the primarily morphology-based species boundaries. In the present study, a multi-locus coalescent-based approach to species delimitation is employed in order to identify separate evolutionary lines within *H.* sect. *Asperae*, using four chloroplast and four nuclear molecular markers. Eight lineages were recovered within the focal group, of which five correspond with named morphotypes. The other three lineages illustrate types of conflict between molecular species delimitation and traditional morphology-based taxonomy. One molecular lineage comprises two named morphotypes, which possibly diverged recently enough to not have developed sufficient molecular divergence. A second conflict is found in *H. strigosa*.