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What—if anything—is Escalloniaceae?

Some groups of angiosperms have been treated as veritable dustbins, where various unrelated but somewhat similar taxa have been placed. One of the more notorious has been the Escallonia-alliance. Its status as well as circumscription has been quite variable, variously treated as subfamilies under Saxifragaceae (sensu Engler), a family of its own, or included in Grossulariaceae (e.g., Cronquist). Recently, the alliance has been extensively splitted, and in the latest APG-system it now finds its members in several parts of the eudicots, mostly in various families of Asterales. Of the genera still considered somewhat closely related to Escallonia, three have been erected to monogeneric families (i.e., Eremosynaceae, Polyosmaceae and Tribelaceae), while Escalloniaceae itself consists of five genera (Anopterus, Escallonia, Forgesia, Quintinia and Valdivia). A sixth, thoroughly neglected genus, Platyspermation, has also sometimes been placed in Escalloniaceae. These families are in the APG-system included among the campanulids (Euasterids II) but unplaced as to order, together with the small families Bruniaceae, Columelliaceae, Paracryphiaceae and Sphenostemonaceae. The relationships between these families, as well as between most of the orders of the campanulids, have so far not been known with any certainty.

Several of the relationships within Escalloniaceae s.l. are well supported in this small study, most notably the inclusion of Valdivia gayana from Chile and Forgesia rozeniae from Isle de Réunion in the South American (mostly Andean) genus Escallonia. [Strict consensus tree summarising the two most parsimonious trees (904 steps, CI=0.80) found by analyzing a data-set of atpB, ndhF and rbcL using a branch and bound search; thick branches are supported by a jackknife value of at least 85%.]

Some molecular markers with more than 17600 characters including gaps and 59 taxa in a Bayesian analysis with MrBayes and the GTR+Γ-model for the nine nucleotide partitions and coding=informative for the gaps; several of the markers are not sequenced for some or several of the taxa.

Future prospects: By adding a larger amount of data to the data-set it was possible to receive high posterior probability (PP) values for an already suspected sister-group relationship between Dipsacales and Paracryphiaceae, as well as for a sister-group relationship for Apiales and the Dipsacales-Paracryphiaceae clade. The support for a Bruniae-Columelliaceae clade is still low (dotted line, PP=0.87), but hopefully this and other unsupported relationships can be solved by sampling more markers and, for some clades, a denser sampling of taxa.