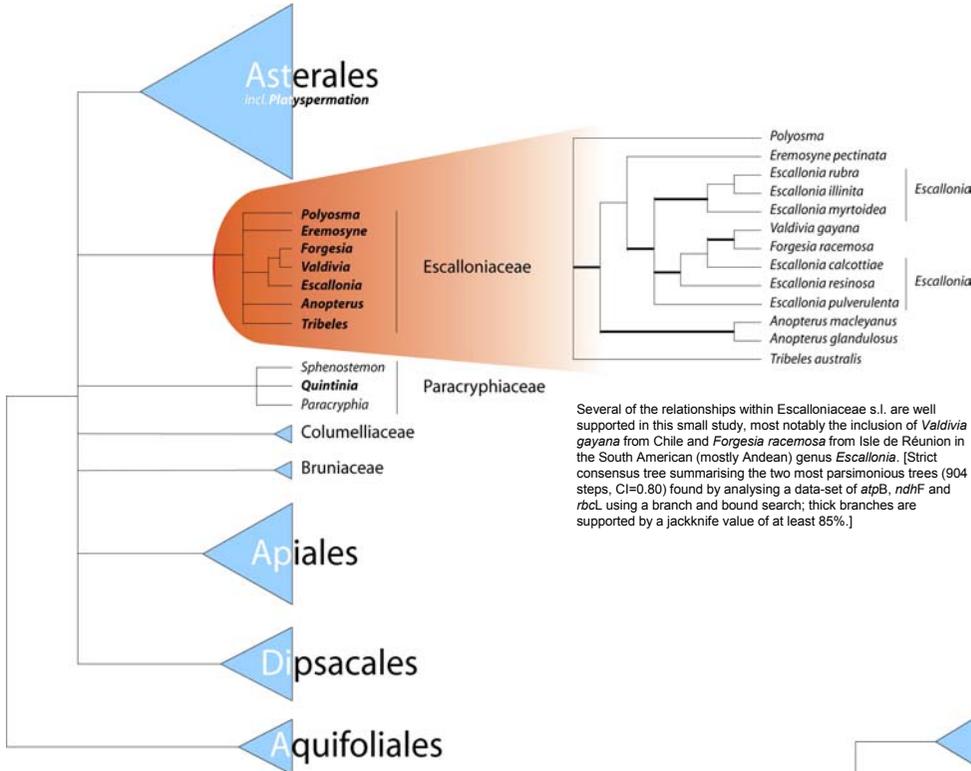




What—if anything—is Escalloniaceae?

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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, *Platyspermatium*, 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.

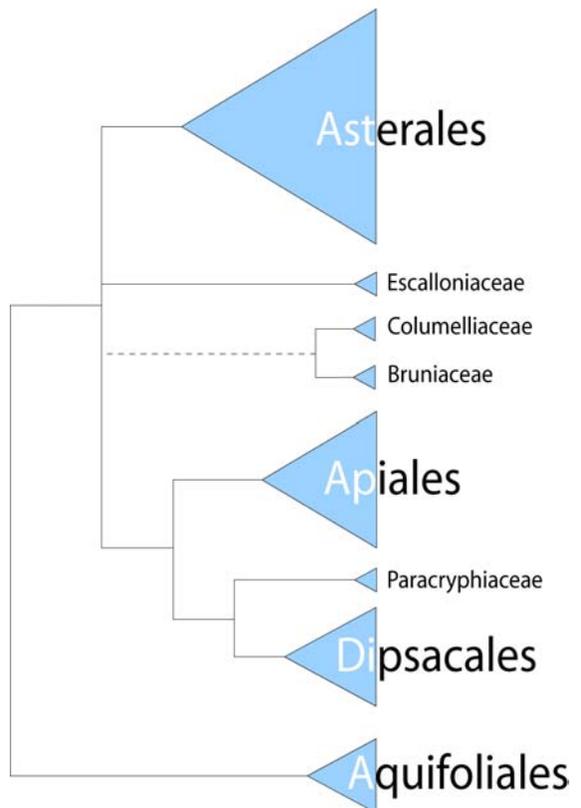


Unplaced families in the campanulids in the latest APG-system

Paracryphiaceae	1 sp	New Caledonia
Sphenostemonaceae	c 10 spp in 1 genus	South-East Asia, Australasia
Columelliaceae	2 spp in 2 genera	Andes
Bruniaceae	75 spp in 12 genera	South Africa
Eremosynaceae	1 sp	Australia
Polyosmaceae	c 90 spp in 1 genus	South-East Asia, Australasia
Tribelaceae	1 sp	South America
Escalloniaceae		
Anopterus	2 spp	Australia
Escallonia	c 39 spp	South America
Forgesia	1 sp	Réunion
Quintinia	c 25 spp	Australasia
Valdivia	1 sp	South America
Platyspermatium	1 sp	New Caledonia

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 racemosa* 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 analysing 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%.]

A Bayesian analysis of a three-gene dataset (*atpB*, *ndhF* and *rbcl*) for 50 campanulid taxa support a close relationship between the small families Polyosmaceae, Tribelaceae, Eremosynaceae and most members of Escalloniaceae, all previously on morphological grounds suggested to be related. A close relationship between *Platyspermatium* and Aiseuosmiaceae (Asterales) is also strongly supported, as is the exclusion of *Quintinia* from Escalloniaceae. Together with *Paracryphia* (Paracryphiaceae) and *Sphenostemon* (Sphenostemonaceae), *Quintinia* is strongly supported to be included in an expanded Paracryphiaceae. It is also suggested that Escalloniaceae is (again) expanded to include its former members *Polyosma*, *Tribelaceae* and *Eremosyne*. With these changes, the number of campanulid families unplaced as to order in the latest APG-system can be reduced from eight to four. Although both Escalloniaceae and Paracryphiaceae in their new circumscriptions are quite heterogeneous, they are not more so than many other recognised families. They also share a south-hemispheric distribution, and there are several possible but badly known morphological synapomorphies for both families. [Bayesian analysis with MrBayes; each marker in its own partition, all under the GTR+I+I-model.]



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 Bruniaceae-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. [Nine molecular markers with more than 17600 characters including gaps and 59 taxa in a Bayesian analysis with MrBayes and the GTR+I+I-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.]



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