

The eFLOWER initiative: A framework for understanding the evolution and diversification of extant and fossil flowers.

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Flowers are central to the biology and evolution of angiosperms (flowering plants). eFLOWER focuses on the history of floral diversification through deep evolutionary time. A comprehensive understanding of global patterns of floral evolution has been prevented so far by the lack of an adequate morphological data set spanning all major angiosperm lineages. Using a new flexible and innovative approach, centered on a multi-user database (PROTEUS), we have built such a data set. Unlike most earlier studies of character evolution at the scale of angiosperms, we have recorded exemplar species instead of higher taxa such as genera or families. This approach allows for explicit reconstructions without assumptions about ancestral states or monophyly of supraspecific taxa, although we acknowledge that it also entails the risk of undersampling morphological variation. Importantly, the exemplar approach allows a direct match with the species sampled in molecular phylogenetic trees, providing the possibility to take branch lengths into account and to explore character evolution with probabilistic models. We report results from a data set of floral traits for 792 species representing all orders and 367 families (87%) of angiosperms, sampled from a recently published timetree calibrated with 136 fossil age constraints. Using this data set and tree, we reconstruct ancestral states for 27 key floral traits using parsimony, maximum likelihood, and Bayesian approaches. These results shed new light on long-standing questions on floral evolution across angiosperms, with important implications for a wide range of disciplines including Evo-Devo, pollination biology, and paleobotany.