

Floral evolution in *Echinopsis* s.l. and implications on the taxonomy of the genus

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The genus *Echinopsis* s.l. in its current circumscription is one of the largest and least under-stood genera in the Cactaceae. It comprises, amongst others, such formerly independent genera as *Trichocereus* with mostly columnar growth and large, white flowers, *Echinopsis* s.str. with white, funnel-shaped flowers, and *Lobivia* with small, colourful flowers. As gradual transitions between these taxa make clear delineations impossible, they are nowadays lumped as *Echinopsis* s.l. but are still in use to distinguish intrageneric groups. Such groups — as well as species — are often characterized by floral traits and by their supposed pollination syndrome. However, real knowledge on pollination biology is lacking for almost the entire genus, and phylogenetic studies based on molecular data are needed to understand the taxonomic value of floral characters.

Ongoing studies on pollination biology show that solitary bees and hawkmoths are the main pollinators in *Echinopsis*, but inferring potential pollinators on the base of floral characters can be misleading. Molecular phylogenetics indicate that certain floral trait combinations (syndromes) not only evolved several times within the genus as adaptations to the same pollinator groups, but also can switch rapidly. Therefore, the use of floral characters for systematics is misleading and may only be used with extreme care. A preliminary phylogeny based on chloroplast markers is presented, with its focus on groups with potential shifts in pollination ecology. Apparent rapid evolution in some clades hinders their resolution and makes additional methods like DNA fingerprinting necessary to fully understand such young groups. As hybridization events are supposed, the additional use of nuclear markers is needed to fully understand the evolution and systematics of *Echinopsis* s.l.