Abstract Detail

Systematics Section/ASPT

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A molecular framework phylogeny for *Ptilotus* R.Br. (Amaranthaceae): Implications for classifications within the Aervoids.

Ptilotus R.Br. (Amaranthaceae) comprises over 100 species, which are endemic to Australia except for one species (*P. conicus* R.Br.) that has a distribution extending to Timor and adjacent islands. The center of diversity for the genus is the arid Eremean Province of Western Australia, with smaller numbers of species found in open mesic temperate areas and wet-dry tropics. Family-wide studies have placed *Ptilotus* within the monophyletic Aervoid clade, consisting of *Aerva* Forssk. (16 spp.), *Nothosaerva brachiata* (Linn.) Wight and *Ptilotus*. A lack of extensive sampling within this clade has made it difficult to discern the relationships between the genera. To date, no robust infrageneric classification has been proposed for *Ptilotus*, in part due to the lack of consistent morphological differences between the major groups of taxa. ITS nrDNA and *matK* cpDNA were amplified by PCR and sequenced from all major informally recognized groups within *Ptilotus* and several outgroup taxa. Sequences were edited with Geneious 6.0, aligned using webPRANK, and analyzed using Bayesian inference (MrBayes 3.2.2) and maximum likelihood (GARLI 2.01). The current study provides the first framework phylogeny for *Ptilotus*, provides evidence for the monophyly of the genus, clarifies phylogenetic relationships within the genus and the Aervoids, allows assessment of congruence of robust clades with morphological variation, and identifies characters to aid in an infrageneric classification. This study will provide the framework for further studies into character evolution, physiology and ecology in the genus; in addition, *Ptilotus* is likely to provide useful insights into the evolution and adaptation of the arid Australian biota.

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