



Evolutionary history of Australian *Chenopodium* alliance.

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Covering approximately 70% of the continent, Australia's arid zone is among the largest and least investigated regions globally. One of the most ubiquitous and surprisingly diverse floral components of the Australian arid zone includes members of the *Chenopodium* alliance (*Chenopodium*, *Einadia* and *Rhagodia* of the family Amaranthaceae), which are known for their drought and salinity tolerance and thus suitability for land restoration. Despite a recent generic reclassification, the evolutionary history of this taxonomic group remains unclear. We aimed to test the littoral connection hypothesis, which postulates that contemporary desert floras arose via dispersal and diversification from coastal ancestors, as one mechanism to explain the diversity within this taxon. We conducted a phylogenetic analysis of all currently accepted species using a targeted sequencing approach with a custom-designed bait set. Our initial results indicate that the most recent common ancestor of this clade arrived in Australia by a long-distance dispersal event from continental Eurasia at the onset of the Pliocene. Subsequently, the alliance rapidly diversified inland without extensive polyploidisation, with the continuous aridification of the Australian interior during the Pleistocene and Holocene likely facilitating this process. Our findings also provide new insights into the recent nomenclatural revisions within this alliance.

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