

Phylogeny of the genus
Melampodium (Heliantheae, Asteraceae) and the
origins of Polyploids of sect. *Melampodium*

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The genus *Melampodium* (Heliantheae, Asteraceae) comprises 39 species centred in Central America, and exhibits a broad spectrum of basic chromosome numbers ($x = 9, 10, 11, 12$ and 14) and frequent polyploidy. The basic chromosome number change has played an important role in the evolution of the genus and correlates well with its current sectional classification encompassing six sections: *Melampodium* ($x = 10$), *Zarabellia* ($x = 9$), *Serratura* ($x = 12$), *Bibractiaria* ($x = 14$), *Rhizomaria* ($x = 11$), and *Alcina* ($x = 11$). A study of the phylogenetic relationships of the genus based on plastid and nuclear DNA sequence analyses combined with cytogenetic analyses allows us (1) to test the current classification of *Melampodium*, (2) to hypothesise on modes and mechanisms of chromosome number change, and (3) to gain insight into the origin of polyploids. The current sectional classification is supported for four out of the six sections. Two putative sister genera of *Melampodium*, *Acanthospermum* and *Lecocarpus* (both $x = 11$), branch from within a basal polytomy of genus *Melampodium*. $x = 11$ has been inferred as the ancestral basic chromosome number, and two other derived basic chromosome numbers ($x = 9$ and 10) are hypothesised to have originated independently two times each. The analyses of different marker sets (cp *matK*, nr 5S rDNA spacer and nr ITS, low copy nuclear gene *pgiC*) reveal incongruencies which, together with molecular cytogenetic analyses, allow to infer the allopolyploid origin of several species of ser. *Sericea* and ser. *Melampodium* in sect. *Melampodium*.

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