

Molecular versus morphological evolution in the moss genus *Echinodium* Jur.

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The Echinodiaceae comprise only one genus, *Echinodium*, with six extant species and a peculiar disjunct distribution pattern. Four species are restricted to the laurel forest (Laurisilva) of the Macaronesian archipelagos, a supposed remnant of the Tertiary flora: *E. prolixum* (Azores, Madeira), *E. spinosum* (Azores, Madeira, Canary Islands), *E. renauldii* (endemic Azores), and *E. setigerum* (endemic Madeira). The other two species are confined to the Australasian region: *E. hispidum* (Eastern Australia, New Zealand, New Caledonia), and *E. umbrosum* (New Zealand, some Pacific islands).

The *Echinodium* species are well-characterised morphologically and ecologically by a number of studies. However, the circumscription of the genus *Echinodium* and its systematic position within the pleurocarpous mosses remains ambiguous.

Based on sequences of the plastid *trnL* intron and the nuclear ribosomal ITS1 and ITS2, we aim to test the monophyly of *Echinodium* and to clarify the systematic relationships of the *Echinodium* species.

The molecular data provide clear evidence for the polyphyly of *Echinodium*. Three molecular groups are observed. The type species *E. spinosum* and the two Macaronesian endemics are closely related and probably represent *Echinodium* sensu stricto. The remaining Macaronesian *E. prolixum* is close to the Lembophyllaceae, whereas the Australasian species are close to *Thamnobryum*.

The present molecular results bear important consequences for the evolutionary history of *Echinodium*, for the significance of morphological characters used to define the genus and for the explanation of the extant distribution pattern, which is discussed.