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**Molecular Systematics of New Zealand skinks of the genus *Cyclodina*.**

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### Abstract.

The taxonomic status, relationships and possible origin(s) of eight skinks from the genus *Cyclodina* were investigated using molecular systematics - one from each of the six recognised and two proposed New Zealand species. DNA sequence data from the mitochondrial 12S ribosomal RNA gene was obtained using the polymerase chain reaction (PCR) and a thermocycling-based sequencing procedure. Phylogenetic analysis was carried out using spectral analysis, which utilizes new and sophisticated algorithms, and the maximum parsimony, minimum evolution and maximum likelihood options of PAUP\* Version 4.0, a new test version of PAUP. New Zealand members of the skink genus *Leiopisma* and three overseas skinks were also included in analyses.

A single resolved tree was not produced, which may indicate that the New Zealand *Cyclodina* diverged rapidly. The eight *Cyclodina* taxa form genetically distinct lineages, supporting the separate taxonomic status of each of the recognised and proposed species. The suggestion that the *C. aenea* population from the Poor Knights Islands is a separate species is well supported, the two *C. aenea* taxa being separated by and/or pairing with other taxa in most trees. However, the possibility of subspecific status cannot be excluded for *C. oliveri* from the Mokohinau Islands (the second proposed new species).

While the eight *Cyclodina* taxa form a closely related group, *L. fallai* pairs with *C. alani* and *L. zelandicum* with the Poor Knights *C. aenea* in many or all of the phylogenies. *L. moco* and the Mauritian skink *L. telfairi* also appear to have links with *Cyclodina*. The level of spectral analysis and bootstrap support is low for most of these relationships; nevertheless a monophyletic origin for *Cyclodina* with regards to the New Zealand *Leiopisma* is not supported under the present taxonomic classification. Longer sequences from additional genes and a larger, more diverse set of skinks are required (in conjunction with other molecular, morphological and ecological information) before the exact relationships of these taxa and the origin(s) and divergence times of the New Zealand *Cyclodina* can be accurately determined. However, the results of this study do suggest that *Cyclodina* is older than previously thought, possibly even Gondwanan in origin.

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