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Phylogenetic affinities, species delimitation and adaptive radiation of New Zealand *Ranunculus*

A thesis presented in partial fulfilment of the requirements for the degree of

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ABSTRACT

*Ranunculus* is the largest genus in the Ranunculaceae family and comprises c. 600 species. Its distribution is almost worldwide and the largest number of species occurs in temperate zones of North and South America, Europe, Asia, Australia, New Zealand, and in the alpine regions of New Guinea. In New Zealand the genus *Ranunculus* contains about 41 species and is found both in lowland and alpine environments. This thesis reports a phylogentic analysis of lowland and alpine New Zealand *Ranunculus*, an assessment of morphological variation and species boundaries among complex alpine species and examines evidence suggesting adaptive radiation of the alpine *Ranunculus* lineage.

Phylogenetic analysis suggests that New Zealand species of *Ranunculus* are not a monophyletic group. For some New Zealand species the closest affinities inferred from the analysis of nrDNA and cpDNA sequences are to species from other land masses such as Australia, the Northern Hemisphere, southern South America and islands in the southern Oceans. Contrary to Fisher’s hypothesis (1965), the Andean South American *Ranunculus* in the section *Trollianthoideae* are not closely related to the New Zealand alpine group. The *Trollianthoideae* section was not monophyletic and the Peruvian-Ecuadorian species in it form a lineage sister to European alpine species. Instead, aquatic and sub-aquatic species from the Euro-Mediterranean region and southern South America and the Kerguelen Island were inferred as the closest relatives to the New Zealand alpine *Ranunculus*; albeit this relationship was weakly supported. Findings from this study suggest that colonisation of *Ranunculus* into the Southern Hemisphere has been a dynamic process and several long distance dispersal events and different colonisation routes have been used. Dispersal from New Zealand to Australia and vice versa, has also been inferred. Bird transportation and oceanic currents are speculated as being the most likely vectors for long dispersal for this group.

Morphological variability at the species level is a feature of several species of *Ranunculus* worldwide. In New Zealand, the alpine species *R. insignis* and *R. enysii* are characterised by extensive morphological variability across their distribution range. Currently, these two species include a number of geographically restricted forms that in earlier taxonomic treatments were considered as separate species. Analysis of qualitative and quantitative morphological characters using parametric and non-parametric statistical tests and multivariate analysis, habitat characterisation using environmental variables from the GIS database LENZ and molecular analyses of nrDNA and cpDNA sequences have provided a
framework for interpreting and understanding the nature of this phenotypic variation. An argument based on morphological, genetic and ecological support for the reinstatement of the species *R. insignis*, *R. lobulatus* and *R. monroi* is presented here. The last two species may correspond to lineages of recent origin. Hybridisation and introgression between *R. insignis* and *R. lobulatus* are suggested as being responsible for intermediate phenotypes found in areas where their distribution overlaps. Morphological variability in *R. enysii* is inferred to have had a complex origin. The species has a disjunct distribution and events of hybridisation and/or introgression with *R. monroi* and *R. gracilipes* seems to have occurred in some of the northern and southern populations, respectively. These hybrid lineages may have swamped out pure lineages of *R. enysii* and eliminated the ancestral phenotype. Studies including assessment of gene flow using microsatellites, phenotypic stability under common garden condition and pollination experiments will be necessary to further test these hypotheses.

Contrary to the latter two species, *R. lyallii* is morphologically uniform across its distribution range but genetically diverse (11 haplotypes, one of them shared with *R. buchananii*). Morphological stability in this species is probably explained by morphological stasis and habitat specialisation.

The alpine *Ranunculus* group is outstanding in the New Zealand flora in terms of its great phenotypic and ecological diversity of its members. These two features plus the monophyletic nature of the group and its recent origin have suggested to previous researchers that the radiation of this group has been adaptive. Phylogenetic analysis of 20 taxa in this group using nrDNA and cpDNA sequences has shown that the group includes four lineages and that genetic diversity between the species forming each lineage is low. This confirms findings from earlier studies by Lockhart *et al.* (2001). Cluster Analysis, multidimensional scaling analysis and histological and scanning microscopy observations of morphological and anatomical vegetative and reproductive characters were used to quantify the extent of morphological diversity in the group. Habitat diversity of this group was characterised using 16 environmental variables available from the GIS database LENZ and analysed using Canonical variates analysis. Although four habitat types were identified, there was no correlation between habitat and phenotype as predicted for an adaptive radiation. A number of alternative explanations for this lack of correspondence are discussed. The conclusion drawn from this study was that available data layers and resolution of LENZ limit the use of GIS databases for testing hypotheses of adaptation in the New Zealand Alps.
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