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Species delimitation and the population genetics of rare plants: A case study using the New Zealand native pygmy forget-me-not group (*Myosotis*; Boraginaceae)

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Abstract

Myosotis L., the forget-me-nots, is a genus of about 100 species distributed in the Northern and Southern Hemispheres. There are two centres of diversity, Eurasia and New Zealand. The New Zealand species are a priority for taxonomic revision, as they comprise many threatened species and taxonomically indeterminate entities. This thesis includes a taxonomic revision of the native New Zealand *Myosotis pygmaea* subgroup, followed by an exploration of the genetic effects of rarity, and implications for conservation management.

Species delimitation follows the general lineage model, in which multiple lines of evidence are analysed to identify evolutionary lineages. The morphological data collected from herbarium specimens and live plants grown in a common garden were used to delineate the *M. pygmaea* group and identify several groups within it that nearly matched the current taxonomy. High levels of plasticity were also uncovered. Microsatellite loci were developed as polymorphic markers for the *M. pygmaea* group for species delimitation and conservation genetics. Over 500 individuals were genotyped, mostly focusing on the *M. pygmaea* group but including several outgroup species for comparison. Several genetic clusters were identified showing morphological or geographic patterns. Considering both the genetic and morphological data, as well as novel ecological niche modelling, there is evidence for three main lineages within the *M. pygmaea* group which are formally recognised as *M. antarctica*, *M. brevis* and *M. glauca*. *M. antarctica* is further subdivided into two subspecies based on allopatry and morphology, namely subsp. *antarctica* and subsp. *traillii* (formerly *M. drucei* + *M. antarctica* and *M. pygmaea*, respectively).

Using this new taxonomic framework to explore genetic variation relative to rarity shows very little difference among species. This is most likely due to the confounding effect of high levels of self-fertilization and low dispersal, which means that the majority of genetic variation within these species is partitioned between, rather than within populations. The implication for conservation is that each population is equally important in terms of their contribution to the genetic diversity of each species. This thesis represents a major increase in our knowledge of the evolution, systematics, taxonomy, rarity and conservation of New Zealand native forget-me-nots.

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