The Wild Origins of *Clianthus* Cultivars and Their Value for Ex Situ Conservation[®]

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Clianthus is an endangered genus endemic to New Zealand. Random amplified polymorphic DNA (RAPD) analysis, followed by hierarchical cluster analysis, showed that *Clianthus* cultivars are not representative of the remaining range of wild populations. As such, they constitute minimal value for the ex situ conservation of *Clianthus* diversity. Cultivar 'White Heron' probably comes from close to the most north-easterly extremity of the distribution of *C. maximus* in the wild (near East Cape). Cultivars Kaka King® (Naturally Native New Zealand Plants Ltd.), 'Maximus', and 'Red Cardinal' are very closely related (or indistinguishable), and also originate from the north-eastern range of this species. Cultivar 'Flamingo' associates with the more south-westerly populations of this species.

INTRODUCTION

Plants in the genus *Clianthus* (kowhai ngutukaka, or kaka beak) make outstanding garden specimens with their arching branches and pendulous sprays of large scarlet, pink, or white pea-like flowers. In recognition of this, a number of *Clianthus* selections have been made from wild populations; these are available as named cultivars in nurseries worldwide. However, *Clianthus* was not common when the first botanical specimens were collected by Banks and Solander in 1769 (Colenso, 1885), and it is now listed as an endangered plant in the wild (de Lange et al., 1999).

Following on from earlier molecular work (Gardiner, 1991; Gardiner et al., 1993), genetic variation within and amongst all wild *Clianthus* populations was measured to assist conservation efforts. Known cultivars were also screened to determine their likely origins, and to assess if they constituted a useful conservation resource for ex situ conservation.

MATERIALS AND METHODS

Clianthus maximus is currently found in small populations within 50 km of the eastern coast of the North Island of New Zealand. A second species, *C. puniceus*, occurred until recently on a small island north of Auckland (Moturemu Island in Kaipara Harbour) (Shaw and Burns, 1997). The random amplified polymorphic DNA (RAPD) technique was used to detect genetic variation within and amongst these wild populations. The same technique was applied to five named *Clianthus* cultivars ('Flamingo'), Kaka King[®] [Naturally Native New Zealand Plants Ltd.], 'Maximus', 'Red Cardinal', and 'White Heron'. Genetic distance was estimated between all possible pairs of populations, and used to perform a hierarchical cluster analysis.

RESULTS AND DISCUSSION

There was a strong effect of geographic location on genetic composition of wild *Clianthus* populations, the more distant populations were from each other, the more distantly related they were genetically. Such a simple relationship was not expected because kaka beak has been cultivated by Maori for centuries, and the seeds have been transported from place to place around New Zealand (Colenso, 1885; Shaw and Burns, 1997).

There was a distinction between more north-easterly populations (closer to East Cape), and the more south-westerly ones (at and south-west of Lake Waikaremoana). This genetic structure allowed the likely origins of cultivars to be identified. Cultivar 'White Heron' probably comes from close to the most north-easterly extremity of the distribution of *C. maximus* in the wild (near East Cape). Cultivars Kaka King[®], 'Maximus', and 'Red Cardinal' are very closely related (or indistinguishable), and also originate from the north-eastern range of this species. Cultivar 'Flamingo' associates with the more south-westerly populations of this species.

While the analysis indicated that cultivated material had been sourced from different wild populations, the overall low level of genetic diversity in the cultivated samples relative to the wild populations suggested that domesticated stock does not broadly represent the genetic base of *Clianthus* in the wild. Further sampling from the wild to introduce new breeding stock into cultivation should be structured to take account of the strong geographical trends in inter-population genetic differentiation.

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