Conservation Biology of Threatened Native Olives (Genus *Notelaea*) in Southern Queensland

Royal Society of Queensland Research Project, 2018

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Background to Project

The genus *Notelaea* (family Oleaceae) is endemic to Australia and consists of 12 species. One of these species, *Notelaea lloydii*, is listed as vulnerable under the *Environment Protection and Biodiversity Conservation Act 1999* (Cth) (EPBC Act, 1999) and the Queensland *Nature Conservation Act 1992* due to its restricted distribution encompassing approximately 3700 km^2 in South East Queensland (Conservation Advice for *Notelaea lloydii*, 2008; *Nature Conservation (Wildlife Management) Regulation 2006*, 2017). *Notelaea lloydii* occurs in about five small disjunct populations, each with fewer than 30 individuals, together with a few other individuals scattered along roadsides (Queensland Herbarium records and personal observations). Given the high degree of urbanisation and vegetation clearance in South East Queensland, it is possible that intra-specific gene flow is limited between these small and isolated populations and inbreeding may be a significant risk. Consequently, it is essential that an evaluation of the levels of genetic diversity within populations and the genetic differentiation and gene flow among populations is undertaken to inform conservation management strategies.

Furthermore, *N. lloydii* occurs in sympatry at the only site where the critically endangered *N. ipsviciensis* is found. *Notelaea ipsviciensis* exhibits intermediate morphology between *N. lloydii* and *N ovata*, raising speculation that it is a natural hybrid of the two (Beyleveld, 2006; Harris, 2004). Both *N. lloydii* and *N. ovata* have overlapping flowering periods, further increasing the possibility of inter-species gene flow. Such hybridisation can place a rare species at an increased risk of extinction through genetic swamping (Ellstrand & Elam, 1993; Levin et al., 1996). If hybrids do not exhibit reduced fitness relative to parental taxa, they may ultimately displace pure populations of one or both parental taxa. Therefore, it is of critical conservation importance to evaluate the levels of genetic diversity and genetic structure of *N. lloydii* population at the site where it is sympatric with *N. ipsviciensis*, to determine whether it is at risk of extinction due to displacement by this potential hybrid.

Genetic data (SNPs) have been obtained for a small number of samples and populations of *N. lloydii*, and preliminary results indicate little genetic structure among *N. lloydii* populations. Further sampling is required to improve resolution, and a comparative population genetics study with a common *Notelaea* species is required to understand the relative genetic diversity and inbreeding among the *N. lloydii* populations, Furthermore, the inclusion of other *Notelaea* species will allow systematic uncertainties to be resolved.

Project Significance

When a rare plant species is known to exist only in small and isolated populations threatened by urban development and land clearing, it is critical to have a good understanding of the levels of genetic diversity and gene flow to enable effective conservation management strategies to be developed. In such situations, protecting only the habitat may not ensure the long-time survival of the species. It may be

necessary to intervene through strategies such as augmentation, re-introduction and translocation to ensure the viability of *N. lloydii* into the future, and this should be undertaken only once a thorough understanding of the conservation genetics of the species has been obtained.

Objectives of the Research

The aim of this project is to examine the levels and patterns of genetic diversity within and among the remnant populations of rare *N. lloydii* and common *N. longifolia*, as well as resolving taxonomic uncertainties within the genus *Notelaea*.

Research Outcomes

Our genome-wide SNP data does not support *N. ipsviciensis* as a distinct species but a natural hybrid, raising doubts whether it should be given conservation priority. Also, the SNP phylogeny which includes all the known *Notelaea* spp. indicates that *N. lloydii* forms a monophyletic clade including *N. microcarpa*, suggesting that the two taxa may constitute a single species. Nevertheless, our comparative population genetic analysis has revealed a high degree of genetic structure among the fragmented *N. lloydii* populations and high levels of inbreeding compared to the more common *N. longifolia*, emphasising the necessity of a broad conservation approach going beyond the species level.

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