

Conservation genetics of *Notelaea lloydii* (Oleaceae) in south-eastern Queensland, Australia

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Abstract

Habitat fragmentation can increase the chance of population bottlenecks and inbreeding, and may ultimately lead to reduced fitness and local extinction. *Notelaea lloydii* is a native olive species endemic to Australia and listed as vulnerable due to its restricted distribution. A recent molecular systematics study has revealed there might be some geographic structuring among the *N. lloydii* populations. Therefore, we undertook a genome wide Single Nucleotide Polymorphism (SNP) analysis to determine levels and patterns of genetic diversity, inbreeding and gene flow within and among *N. lloydii* populations in south-eastern Queensland (SE-QLD). Furthermore, as the reproductive phase of a plant's life history has a profound influence on genetic diversity, life history reproductive traits were also studied. Our SNP analysis revealed low genetic diversity, inbreeding and significant genetic structuring even among proximate populations. Results of a flower and fruit bagging experiment in two consecutive seasons revealed that *N. lloydii* produced many flowers but only a few fruits survived to maturity. There were no differences in bagged and un-bagged flowering and fruiting rates and therefore, we conclude that the high fruit abortion rate was probably due to inbreeding depression and/or suboptimal conditions, rather than pollinator availability and insect attack. Overall, results of this study indicate that the populations of *N. lloydii* are small, inbred and genetically isolated and represent unique management units that require local conservation management due to ongoing threats associated with urbanisation.

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