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Conservation implications of the genetic structure and mycorrhizal diversity in a rare and threatened terrestrial orchid

Over the last two decades there is a growing body of evidence of highly specialised and dynamic associations between orchids and their mycorrhizal partners. We hypothesize that mycorrhizal interactions may have contributed to the evolutionary diversification of species within the *Caladenia* complex. This study for the first time, integrates plant and mycorrhizal genetics to deliver conservation outcomes for a rare and threatened species. Thus a detailed understanding of mycorrhizal specificity and diversity may be critical in conservation planning. Through previous studies investigating *in situ* and *in vitro* germination, a highly specific fungal association was found to exist between *Caladenia huegelii* and its symbiont (Swarts *et al.*, unpub). Here PCR based methods were used to investigate the fungal diversity associated with *C. huegelii* endophytes in a multidimensional scaling context, integrating micro – macro scales of geographic distribution. Sequencing of the highly variable internal transcribed spacer (ITS) region of *C. huegelii* endophytes isolated from germinated protocorms and adult plants indicated no variation over the known geographical range of the species. Microsatellite markers were developed for *C. huegelii* to investigate the level of genetic variation in all extant populations and sub-populations. Paternity assignment on seedlings germinated *in vitro* from naturally pollinated capsules was carried out to investigate pollinator activity within sites. This study shows the importance of integrating orchid and fungal genetics for effective conservation strategies for orchid species, in particular rare and threatened orchids.