

Posters – Abstracts

Molecular identification of fungal endophytes in *Dipodium roseum* roots

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Abstract. *Dipodium* or hyacinth orchids are large, fleshy, terrestrial orchids commonly seen in summer in Australian woodlands. Most species have limited chlorophyll, appear to be non-photosynthetic and rely on mycorrhizal fungi for their nutrition. Previous molecular investigations of the endophytic fungi of roots of *Dipodium variegatum* and *Dipodium hamiltonianum* have shown that the orchids are largely colonised by members of the ectomycorrhizal basidiomycete family, the Russulaceae. The fact that these plants consistently grew close to the base of *Eucalyptus* and *Callitris* trees suggested that the orchids acquire carbon and minerals from the tree host via an ectomycorrhizal connection. In the current project the fungal endophytes of *Dipodium roseum* were investigated for the first time. Orchid roots were sampled from multiple sites over two seasons in southern Queensland, Australia. DNA was extracted from colonised roots and isolated pellets of the orchid. PCR amplification was conducted using ITS1F and ITS4 primers and following DNA purification, sent for Sanger sequencing at the Australian Genome Research Facility. BLAST searches of returned sequences against the GenBank database revealed a variety of fungi colonising the roots of *D. roseum*. This included a number of fungi not previously found as root endophytes of Orchidaceae species.

Keywords. *Dipodium*, Russulaceae, endophytic fungi.