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Orchid mycorrhizal colonization in *Rhyncostylis retusa* (L.) blume

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Introduction

The family Orchidaceae is the most species-rich plant family in the world, with an estimated 17 500 to 35 000 species, and a circum global distribution (Dressler 1993). It is also one of the most advanced plant families with many adaptations that enable long-term survival. All orchids have an obligate relationship with mycorrhizal symbionts during seed germination, with most of the symbionts being *Rhizoctonia*-like fungi (Arditti 1992). Reliance on mycorrhizal interactions is an adaptive mechanism that has allowed orchids to persist in relatively less ideal habitats, and has led to their occurrence worldwide.

Understanding mycorrhizal symbiosis is of great importance, as the fungal symbionts may play a key role in determining orchid distribution and diversity. The relationship of orchids with fungi is relatively unique in the plant kingdom. Orchid species vary in their fungal specificity, both among genera and over the course of their life cycle. Orchid mycorrhizal fungi are found intracellularly in cells of the cortex, and are

confined to the roots (Hadley 1982). Within the cells, the mycorrhizae form dense coils of mycelium called pelotons, which are considered as adaptations to the host cell (Hadley 1982). Ecologically, orchid mycorrhizae are important in that they allow the plant to have two possible sources of nutrition, and the plant may use fungal carbohydrates to supplement, replace or alternate with its own photosynthetic activity. Since the fungal partner is generally able to break down complex organic materials, the orchids that grow with them are able to tap unusual substrate for nutrients, including bog peat, highly calcareous soils, and dust debris or tree branches.

Rhyncostylis retusa (L.) Blume, commonly known as foxtail orchid, is a medium-sized species, found in deciduous and dry lowland forests, and savanna-like woodlands with stout, repent, short stem, curved, fleshy, ligulate, deeply channelled, and apically retuse leaves. It blooms on a 60-cm long axillary pendant called racemose, and is densely flowered (100–140), with small, magenta and white flowers (2 cm in diameter) with spots, in cylindrical inflorescence. In

the present paper, orchid mycorrhizal colonization is reported in *R. retusa*.

Methodology

Epiphytic orchid *R. retusa* (L.) Blume collected from Mollem area (North Goa) was brought to the laboratory, and velamen roots were processed for mycorrhizal colonization. The roots of the orchid plant species were washed thoroughly in water, cut into 1-cm fragments, and analysed for mycorrhizal association, using the method described by Phillips and Hayman (1970). The presence of mycorrhizal fungi in the cortical cells was examined under Leica compound microscope.

Observations and discussion

The roots of the epiphytic orchid *R. retusa* are consistently and heavily colonized by pelotons (Figure 1), representing a potentially substantial source of carbon and other nutrients. Within the cells, hyphae form coils called pelotons, which greatly increase the interfacial surface area between orchid and fungi. A membrane and an interfacial matrix material surround these pelotons (Peterson, Uetake, and Zelmer 1998). Each intracellular peloton has a short life span, lasting only a few days, before it degenerates and is digested by the orchid cell. In fact, hyphae have short life span; the older hyphae develop large vacuoles and thick cell walls, and the cytoplasm degenerates. The hyphal cells eventually collapse, and are consumed by the orchid cell. During this process, the plant cell remains functional, and can be recolonized by any surviving hyphae, or by fungi invading from adjacent cells.

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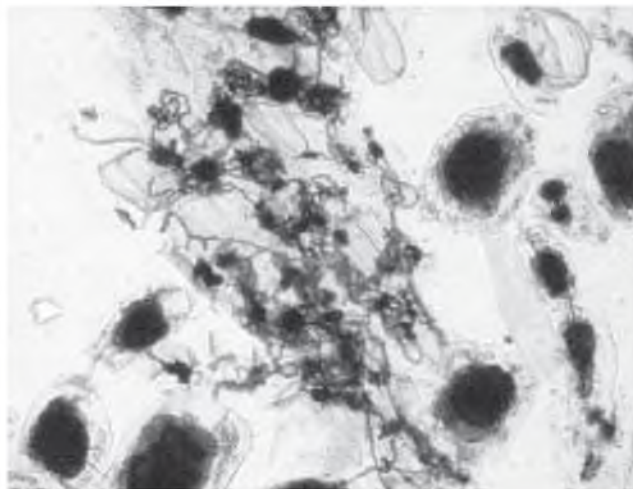


Figure 1 Orchid mycorrhizal fungi in *Rhyncostylis retusa* with pelotons in the cortical cells of the roots (400×)

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