Endophytic fungi diversity in two *Begonia* species found in the tropical rainforest

Authors: Correia, A.M.L.[1], Lira, S.P.[2], Assis, M.A.[3], Rodrigues, A.[1]

Institutions: [1]Department of Biochemistry and Microbiology, UNESP – Univ. Estadual Paulista (Av. 24-A, 1515, Bela Vista, Rio Claro, SP, Brazil), [2]Department of Exact Sciences, USP – Univ. São Paulo (Av. Pádua Dias, 11, Piracicaba, SP, Brazil) [3] Department of Botany, UNESP – Univ. Estadual Paulista (Av. 24-A, 1515, Bela Vista, Rio Claro, SP, Brazil).

Abstract

Endophytic fungi live within plant tissues without causing any apparent symptoms of disease. Such fungi represent an intriguing group which diversity and distribution are not yet understood. Using culture dependent methods coupled with a polyphasic approach for fungal identification, we evaluated the diversity of endophytic fungi associated with *Begonia fischeri* and *Begonia* sp. both found in a fragment of tropical rainforest (Ubatuba-SP). Five mature individuals of each plant species were sampled and four leaves of each individual were surface disinfected. Five 0.8 cm leaf fragments were plated in potato dextrose agar and malt agar 2% both supplemented with antibiotics. Plates were incubated at 28 °C for up to ten days. After incubation, morphotypes were identified using DNA barcoding (sequencing of the ITS region). Operational taxonomic units (OTUs), Chao1 and Shannon indices were generated at a 97% sequence similarity. A total of 269 isolates were obtained comprehending 120 of *B. fischeri* and 149 of *Begonia* sp. After morphotyping and ITS sequencing, we obtained a total of 34 OTUs compreending 14 genera. Five out of 34 OTUs were identified only above order level. *Colletotrichum* and *Diaphorte* were the prevalent genera representing 55% and 15% of the isolates, respectively. In addition, other genera with lower frequency such as *Xylaria* (3.3%), *Neopestalotiopsis* (3.3%) and *Nigrospora* (3%) were observed. The Shannon index indicated that fungal communities of *B. fischeri* (H'= 2.77) were more diverse than in *Begonia* sp. (H'= 1.77). Correspondence analysis demonstrated that the plant host explains 28.81% of the differences between communities. Such differences are also supported by SIMPER analysis (index of 74.12%). However, nine OTUs were shared between fungal communities of both plant species. Such OTUs corresponded to 198 isolates (73% of the isolates), comprehending the prevalent genera found in the study. Our results suggest that fungal communities are structured according to the plant host, however, the high number of isolates shared between communities reveal that environmental factor (such as the proximity of the collection sites) may also explain structuring of the fungal communities.

Keywords: Endophytes, Fungal Community, Barcoding.

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