TITLE: CHANGING IN FUNGAL COMMUNITY ASSOCIATED WITH ORCHIDS ROOTS MAINTAINED IN THE NURSERY AFTER HAVE BEEN REMOVED FROM IRON ORE MINING AREAS

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ABSTRACT:

Orchidaceae is the largest family along monocotyledons displaying widespread and endemic species. Nevertheless, many of them are vulnerable to extinction due to human activities like logging, illegal harvesting and mining. A successful orchid conservation program requires the presence of suitable mycorrhizal fungi, since orchids depend on them for seed germination. The Anglo American company keeps a native plant nursery, in Serra do Espinhaço (Minas Gerais, Brazil), to preserve orchid species that are removed from iron ore exploration area. This work aimed to evaluate the whole fungal community profile in the radicular system of five orchid species kept in this nursery: Bulbophyllum ariane, Cattleya bicolor, Campylocentrum micranthum, Encyclia patterns, and Polystachya concreta. To assess the fungal community, samples of roots of these orchids were collected from the orchids roots kept in nursery, during two distinct periods: (a) two months and (b) four years. Total DNA were extracted, and ITS1 region of fungi were sequenced by Illumina MiSeq. For B. ariane and C. micranthum fungal species richness were greater in orchids kept during two months while for *P. concreta* this value was higher for four-year period. The richness for C. bicolor and E. patterns did not differ between the period of evaluation, maybe due to the high percentage of shared fungi for both period, 33.3 % and 47.8 %, respectively. The ascomycetes were the dominant fungi in both periods except in C. micrathum, which keep for four years. The well-known mycorrhizal fungi Ceratobasidium and the fungi of Sebacinales were detected only in P. concreta and E. patterns. These results show that the species richness and fungal community change during the period of time the orchids are kept in the nursery, however these modifications depend on the orchid species.

KEYWORDS: Mycorrhizal fungi, second generation sequencing, *Bulbophyllum* ariane, Cattleya bicolor, Campylocentrum micranthum, Encyclia patterns, Polystachya concreta

DEVELOPMENT AGENCY: ANGLO AMERICAN IRON ORE BRAZIL, FAPEMIG, CAPES, CNPq,