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AMF assemblages in biocrusts from a Neotropical savanna are not related to the perennial Trachypogon

The mycorrhizal symbiosis plays an important role in nutrient uptake by plants. The AMF act as a bridge, connecting the soil and plant roots. The mycorrhizal fungi help their plant hosts by taking up and transferring soil mineral nutrients. Soil mycelial networks and mycorrhizal hyphal connections between neighboring plants may pass through the biocrusts, which would provide a mechanism for the direct transfer of nutrients and carbon among co-occurring plants, as has been reported for other semiarid ecosystems. The relationship of mycorrhizal fungi with the biocrust and plants in the *Trachypogon* savanna is completely unknown. This aspect is important due to the fact that mycorrhizal symbiosis is a key ecological mechanism in the soil of the *Trachypogon* savanna, since plant growth in these ecosystems is strongly limited by soil resources such as mineral nutrients (P and N) and water. Thus, the study of the assemblages of AMF in these ecosystems is very important to a better understanding of the ecological processes mediated by this soil microbial group that affects multiple ecosystem functions.

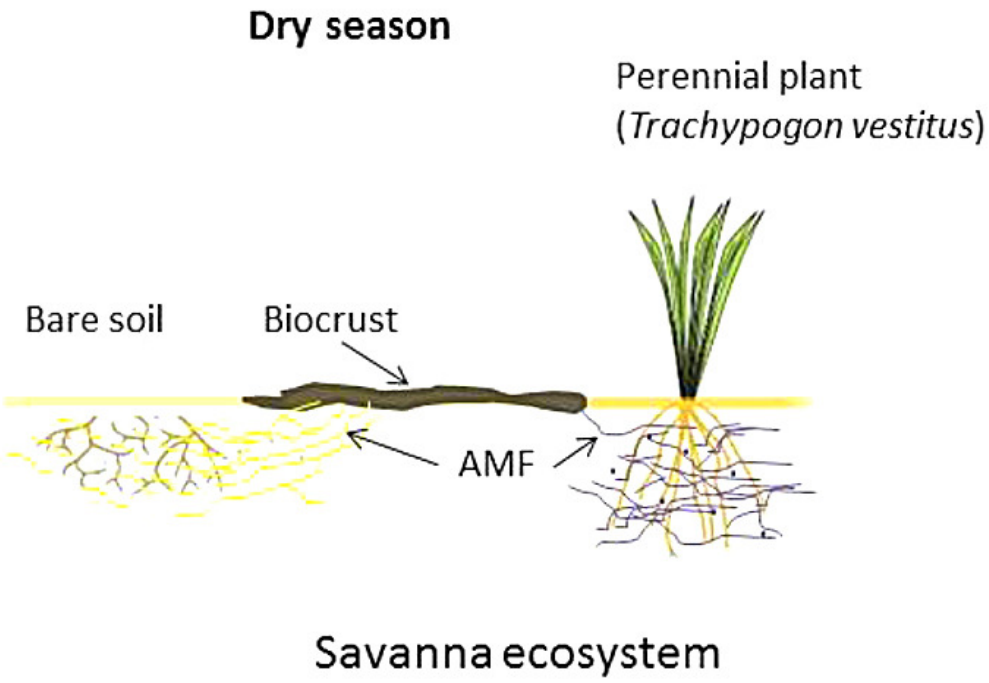

Fig. 1. The biocrusts in the Trachypogon savanna are colonized by AMF. Biocrusts are colonized by a characteristic AMF community that differs significantly from the community hosted by the roots of the surrounding plants of *T. vestitus*.

Considering the hypothesis that the biocrusts can be linked to vegetation through the mycelial network of arbuscular fungi, we would expect a greater similarity between the assemblages of mycorrhizal fungi of the rhizosphere of dominant plants (patch zone) and those present in the biocrusts than with the assemblages in the bare soil zones. In order to resolve these aspects, our objectives were to determine (i) whether there are

AMF in the biocrusts, (ii) whether the assemblages of AMF are linked to the *Trachypogon* patches, and (iii) whether the composition of the assemblages is related to soil properties affected by microbiological activity.

The community structure of the AMF, using a molecular approach and soil properties (Total N, available P, pH, CE, Organic C, Water soluble carbon, Dehydrogenase, Urease, Protease-BAA, Acid phosphatase, β-glucosidase) were investigated in three habitats: rhizospheric soil and roots of *Trachypogon vestitus* (0-20 cm), biological soil crusts (BSCs. 0-2 mm), and bare soil (without vegetation and biocrusts, 0-20 cm).

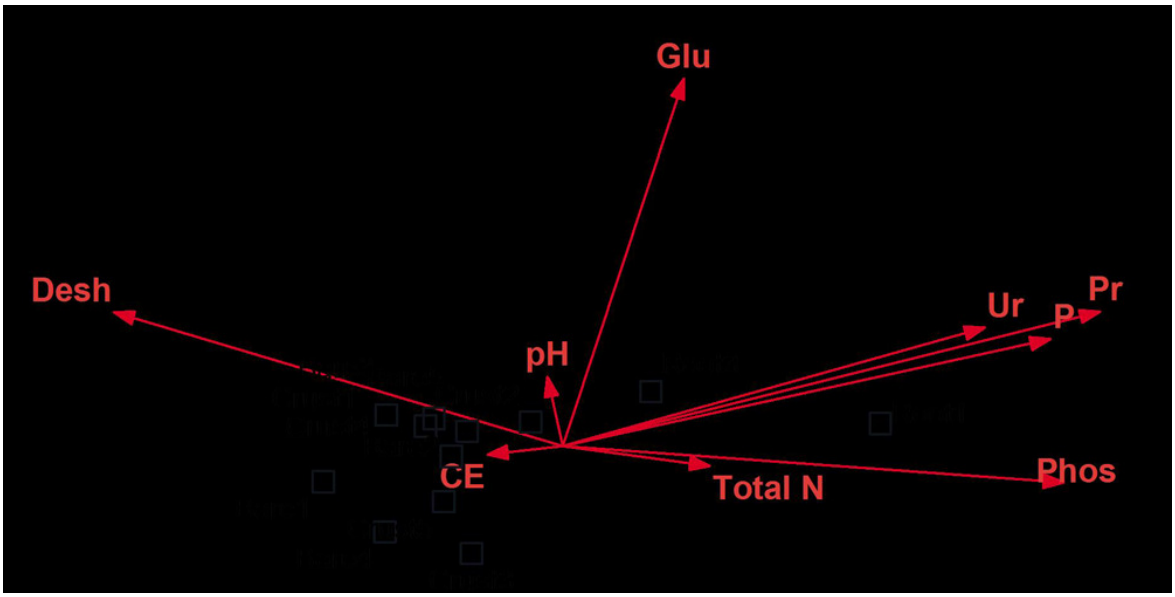

FIg. 2. Canonical correspondence analysis (CCA) showing the influence of soil properties on the AM fungal community composition in bare soil, biological soil crusts and roots of T. vestitus. The first two axes explained 52.8% of the total variance (80.7% for the model). Abbreviations: Desh: Dehydrogenase; Glu: β-glucosidase; Ur: Urease; P:available P; Pr: Protease-BAA; Phos: Acid phosphatase; Bare: Soil bare; Crust: biological soil crusts; Root: roots of *T. vestitus*.

The multivariate analysis showed that, among the soil properties taken into consideration in our study, the protease and glucosidase activities (related to enzymatic activity) had a significant relationship with the distribution of the AM fungal community. The biocrusts in the Venezuelan savanna are colonized by an AM fungal community linked to that of bare soil and significantly different ($P<0.05$) from that hosted by the roots of the surrounding plants of *T. vestitus*, a dominant perennial species of this ecosystem. This suggests that the assemblages of AMF in biocrusts are related more closely to those of annual plant species appearing in favorable conditions. This research opens new and interesting questions on the assemblages and role of AMF in annual plant species growing in biocrusts.

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