Grasses are colonized by systemic and non-systemic fungal endophytes. Although systemic grass endophytes are well-studied models of mutualism, less is known about the composition of non-systemic fungal endophyte communities.

The effect of sympatry, spatial distribution, and organ specificity were evaluated in fungal endophyte communities associated with 4 wild grasses in Spain: *Ammophila arenaria*, *Dactylis glomerata*, *Elymus farctus*, *Holcus lanatus*.

Endophytes were systematically cultured and identified based on morphology and rDNA sequences.

Endophytes infected 94% of the plants. In total, 356 different species were identified, of which 24% could not be assigned to a known taxon. The mycobiota of each grass was characterized by high inequality in the isolate richness caused by high numbers of unique species, represented by single isolates. Most of the dominant species in each grass were isolated from several organs, and more than one host species. The species richness was similar in leaves and roots or rhizomes. The geographical distance between plants and sampling locations influenced the diversity and composition of the mycobiota of each plant species. Only a small proportion of the fungal species identified on each grass were pathogens. Some endophyte isolates appeared to have alternative ecological functions, e.g., decomposers, entomopathogens, and excretion of mycotoxins and antibiotics.

**Conclusions:**

- Non-systemic endophyte infections are a constant feature of grasses and are characterized by a specific set of consistently present genera.
- The endophytic mycobiota of grasses is very rich in species, with diversity values similar to those observed in other vascular plants.
- Beta diversity is a first order factor governing the richness and distribution of endophytic mycobiota in grasses.
- A large percentage of fungal species could not be fully characterized.

**References:**
