

Distribution of fungal endophyte genotypes in doubly infected host grasses

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Abstract

Fungal endophytes of the genus *Epichloë* live intercellularly in above ground plant parts of many pooid grasses of the temperate regions. The associations are characterized by single genotype entities since a given host individual normally contains a single endophyte genotype. They can persist over the life span of the hosts. This study examines whether two fungal genotypes can coexist within a host plant, and how fungal genotypes are distributed within a host in the case of double infections. We selected four *Epichloë bromicola* strains that we identified as unique genotypes through RAPD analysis. Young *Bromus erectus* plants, derived from callus cultures, were artificially inoculated with all possible double-strain mixtures of these fungal genotypes. For identification of fungal genotypes *in planta*, we designed genotype specific primer pairs that flanked size-variable loci in the fungal genomes. Diagnostic PCR revealed that only one fungal genotype was present in most inoculated plants, but double infections were also observed with a frequency of 8% of all infected plants. Subsequent analyses of individual tillers of doubly infected plants revealed that in a given tiller, both the leaf-blade and the leaf-sheath were colonized with only one endophyte genotype. Tillers without any detectable fungal DNA were observed as well. Thus, coexistence of multiple endophyte genotypes within a single host plant is governed by mutual exclusion at the tiller level.