Abstract

Real-time PCR in nuclear ribosomal DNA (nrDNA) is becoming a well-established tool for the quantification of arbuscular mycorrhizal (AM) fungi, but this genomic region does not allow specific amplification of closely related genotypes. The large subunit of mitochondrial DNA (mtDNA) has a higher resolution power, but mtDNA-based quantification has not been previously explored in AM fungi. We applied real-time PCR assays targeting the large subunit of mtDNA to follow the DNA dynamics of two isolates of *Glomus intraradices* s. l. coexisting in the roots of medic (*Medicago sativa*). The mtDNA-based quantification was compared to quantification in nrDNA.

The ratio of copy numbers determined by the nrDNA and mtDNA based assays consistently differed between the two isolates. Within isolate, copy numbers of the nuclear and the mitochondrial gene were closely correlated. Both quantification approaches revealed similar trends in the dynamics of both isolates, depending on whether they were inoculated alone or together. After twelve weeks of cultivation, competition between the two isolates was observed as a decrease in the mtDNA copy numbers of one of them. The coexistence of two closely related isolates, which cannot be discriminated by nrDNA-based assays, was thus identified as a factor influencing the dynamics of AM fungal DNA in roots. Altogether, the results of the study show that real-time PCR assays targeted to the large subunit of mtDNA may become useful tools for the study of coexisting AM fungi.