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Quantitative detection of foliar nematodes (*Aphelenchoides* spp.) in complex DNA backgrounds

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Foliar nematodes, a subset of species within the genus *Aphelenchoides*, are plant parasites causing considerable economic damage to a number of important food (rice, strawberry) and ornamental (flower bulbs) plants. However, they constitute only a (numerical) minor group among a majority of fungivorous species. Distinction between (mostly harmless) fungal feeding *Aphelenchoides* species and high impact plant parasites such as the quarantine organism *A. besseyi*, and *A. fragariae, A. ritzemabosi* and *A. subtenuis* is severely hampered by the scarcity of informative morphological characters. Only taxonomic experts can distinguish between the foliar and harmless environmental species. Therefore, based on (nearly) full-length small subunit ribosomal DNA (SSU rDNA) sequences (≈1,700 bp), a phylogenetic tree was generated, and the four target species appeared as distinct, well-supported groups. As the use of the ITS regions for species detection purposes requires a thorough inventory of the intraspecific variation, we preferred to use SSU rDNA, a relatively conserved coding region within the ribosomal DNA cistron with a – for these four *Aphelenchoides* species– low intraspecific variation. PCR primers were developed with high, identical annealing temperatures (63°C). None of the close non-target species tested gave a significant PCR signal after 60 cycles. These primers can be used for the rapid screening of plant material and soil for the presence of one or multiple foliar nematode species and will be used by the Dutch Plant Protection Service (NVWA).
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