



# First report of the root-knot nematode *Meloidogyne mali* infecting elm trees in Belgium

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*Meloidogyne mali* is an EPPO A2 listed pest. It has been recently recorded in the UK at a site where, in the early 1980's, elm trees were imported from The Netherlands as part of a breeding programme against Dutch elm disease (DED) (Prior *et al.*, 2019). *M. mali* has also been reported from sites in France and Italy where elm trees from the DED breeding programme were planted. Belgium received potentially infected elm trees (*Ulmus* spp.) from the same programme via The Netherlands (EPPO, 2017) which were planted at one experimental site of the Research Institute for Nature and Forest (INBO). In April 2018, root samples of elm trees taken from this site were found to be infected with *M. mali*.

The root samples exhibited irregularities of the root pattern, appearing as a 'string-of-beads', typical of infection by *M. mali* (Fig. 1). To identify nematodes to species level, morphological and molecular characterisation was conducted. For morphological identification, second-stage juveniles and perineal patterns of females dissected from root galls were used (Fig. 2). Morphological observations revealed close similarity in the perineal pattern to the descriptions of Araki (1988). Likewise, most morphometric values were in accordance to previously reported measurements. Second-stage juvenile measurements (n=21) were as follows (mean±SD (range)): length 354.4±19.5 (321.03-392.93) µm, width 14.5±2.2 (10.94-18.33) µm, width at anus 8.8±1.4 (6.27-10.83) µm, stylet length 10.6±1.2 (8.26-12.81) µm, tail length 31.1±4.8 (22.54-43.72) µm and tail terminus length 9.8±0.9 (7.21-10.82) µm.

The diagnosis was confirmed using PCR of genomic DNA (gDNA) isolated from individual nematodes. gDNA of *M. mali* was amplified with different pairs of primers, namely JB3/JB5 for the cytochrome oxidase subunit I gene (Derycke *et al.*, 2010), 28-81for/28-1006rev for the 28S ribosomal DNA gene (Holterman *et al.*, 2009) and LAMP-inner primers (Mma-F3/Mma-B3) for the ITS-5.8S ribosomal DNA gene (Zhou *et al.*, 2017). The PCR amplification products were purified and sequenced (GenBank Accession No. MN047286). Nucleotide sequences were compared with those from related *Meloidogyne* species and shared the closest identity (99%; 100% coverage) with an accession of *M. mali* (KM887145.1) from Japan. To our knowledge, this is the first report of *M. mali* in Belgium.

## Acknowledgements



Figure 1

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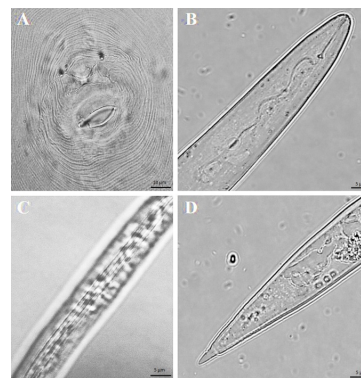


Figure 2

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