

EUROPEAN AND MEDITERRANEAN PLANT PROTECTION ORGANIZATION
ORGANISATION EUROPEENNE ET MEDITERRANEENNE POUR LA PROTECTION DES PLANTES
Summary sheet of validation data for a diagnostic test

The EPPO Standard PM 7/98 *Specific requirements for laboratories preparing accreditation for a plant pest diagnostic activity* describes how validation should be conducted. It also includes definitions of performance criteria.

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| Laboratory contact details | Fera Sand Hutton, YO41 1LZ York, United Kingdom |
| Short description of the test | Identification of <i>Meloidogyne enterolobii</i> using barcoding |
| Date, reference of the validation report | 2026-02-09 - Identification of <i>Meloidogyne enterolobii</i> by using JB3-JB5 primers for Molecular Sanger Sequencing in Specimen |
| Validation process according to EPPO Standard PM7/98? | yes |
| Is the lab accredited for this test? | no |
| Was the validated data generated in the framework of a project? | no |
| Description of the test | |
| Organism(s) | <i>Meloidogyne enterolobii</i> (MELGMY) |
| Detection / identification | identification |
| Method(s) | Molecular Extraction DNA RNA Molecular Sanger seq |
| Method: Molecular Extraction DNA RNA | |
| Reference of the test description | |
| Kit | |
| Is a kit used | yes |
| Manufacturer name | QIAGEN |
| Specify the kit used | DNeasy Blood & Tissue Kits |
| Kit used following the manufacturer's instructions? | |
| Other information | |
| Method: Molecular Sanger seq | |
| Reference of the test description | |
| As or adapted from an EPPO diagnostic protocol | yes |
| New test being considered for inclusion in the next version of the EPPO diagnostic protocol? | yes |
| As or adapted from an IPPC diagnostic | no |

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| protocol | |
| Is the test modified compared to the reference test | no |
| Other information | |
| Are the performance characteristics included in the EPPO diagnostic protocol? | no |
| Performance Criteria : | |
| Organism 1.: | Meloidogyne enterolobii(MELGMY) |
| Analytical sensitivity | |
| What is smallest amount of target that can be detected reliably? | PCR reaction not evaluated |
| Diagnostic sensitivity | |
| Proportion of infected/infested samples tested positive compared to results from the standard test, see appendix 2 of PM 7/98 | PCR reaction not evaluated |
| Analytical specificity - inclusivity | |
| Number of strains/populations of target organisms tested | A maximum likelihood (ML) tree was generated including sequences of Meloidogyne enterolobii from EPPO-Q-bank (5) and Fera internal sequences (5). A neighbor joining (NJ) tree was also generated with several sequences from NCBI by using BLAST - Construct Phylogenetic Trees tool. |
| Specificity value | |
| Analytical specificity - exclusivity | |
| Number of non-target organisms tested | A maximum likelihood (ML) tree was generated including 31 sequences from EPPO-Q-bank (18) and Fera Science Ltd. (13), covering the following species: Meloidogyne mali (2), Meloidogyne artiella (3), Meloidogyne dutysi (2), Meloidogyne javanica (2), Meloidogyne incognita (5), Meloidogyne arenaria (2), Meloidogyne naasi (2), Meloidogyne hapla (3), Meloidogyne minor (3), Meloidogyne chitwoodi (3), Meloidogyne fallax (3) and the outgroup Radopholus similis (1) A neighbor joining (NJ) tree was also generated with several sequences from NCBI by using BLAST - Construct Phylogenetic Trees tool. |
| Specificity value | |
| Test performance study | |
| Test performance study? | no |
| Other information | |
| Any other information considered useful | Considering EPPO-Q-bank and NCBI GenBank analysis, there is a 98.26-100% pairwise similarity among all sequences of Meloidogyne enterolobii. Whereas all the other Meloidogyne sp. have <89% pairwise similarity compared with Meloidogyne enterolobii sequences. |

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| The following complementary files are available online: | <ul style="list-style-type: none">• ML tree - M. enterolobii• NCBI-GENBANK M. enterolobii |

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