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.

Laboratory contact details	Fera Sand Hutton, YO41 1LZ York, United Kingdom
Short description of the test	Identification of Meloidogyne enterolobii using barcoding
Date, reference of the validation report	2026-02-09 - Identification of Meloidogyne enterolobii 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)	Meloidogyne enterolobii (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

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.

The following complementary files are available online:	• ML tree - M. enterolobii • NCBI-GENBANK M. enterolobii

Creation date: 2026-02-26 13:58:35 - Last update: 2026-03-10 11:10:31