**Supplementary data**

**File 1.** Development of sequence-characterized amplified region (SCAR) primers.

Amplification reactions were carried out in volumes of 50 µl containing 5 ng of total DNA, 200 µM each dNTP, 100 nM each primer, 1 unit of *Taq* DNA polymerase and 1x *Taq* buffer (Biolabs, France). Amplification was performed on a PTC-100 MJ Research thermal cycler (MJ Research Inc., Waltham, Mass., USA). Sixty-seven Random Amplified Polymorphic DNA (RAPD) primers were tested on different *Meloidogyne* spp. gDNA including *M. incognita, M. arenaria*, *M. javanica*, *M. exigua*, *M. paranensis* and *M. graminicola*. The 40 primers OPA-01 to OPA-40 were synthesised by Operon Technologies (Alameda, CA, USA). The 27 remaining primers (A02, A04, C02, C09, C16, D05, D13, D15, E07, F06, J20, K01, K04, K06, K07, K09, K14, K19, K20, L08, M10, M20, N07, N10, P01, P02 and P05; [53]) were synthesised by Eurogentec (Seraing, Belgium). The cycling program was 1 min at 95°C; 40 cycles of 30 s at 95°C, 30 s at 36°C, and 2 min at 68°C followed by a final incubation of 10 min at 68°C. Only five of 67 RAPD primers tested (OPA-4, OPA38, K19, K20 and N10) allowed specific amplification of 200 to 1,000 bp DNA fragments of *M. graminicola* populations previously isolated from rice plants in the Philippines and Brazil (data not shown). Primer N10 allowed a strong and specific single amplification of a 655-bp fragment from these two *M. graminicola* populations while no similar amplification was found on *M. incognita*, *M. arenaria*, *M. javanica, M. exigua* and *M. paranensis*. Consequently, the 655-bp RAPD amplification product from primers (N10: 5’-ACAACTGGGG-3’) was purified from 1.5% agarose gel, cloned into the pGEM®-T Easy Vector (Promega) and sent for sequencing using standard procedures and M13 primers (Cogenics, UK) and deposited in the GenBank database (under accession number KF499563). Specific SCAR primer sequences (SCAR-MgFW: 5'-GGGGAAGACATTTAATTGATGATCAAC-3' and SCAR-MgRev: 5'-GGTACCGAAACTTAGGGAAAG-3') were designed inside the RAPD amplicon and synthesised by Eurogentec (Seraing, Belgium). Amplifications using the SCAR primers were performed as described for the RAPD analysis, using the following conditions: 1 min at 95°C; 30 cycles of 30 s at 95°C, 30 s at 60°C and 1 min at 68°C followed by a final extension step of 10 min at 68°C. DNA extraction and PCR from single J2 was performed according to the protocol described for “ITS amplification and sequencing” with the “Phusion High-Fidelity DNA Polymerase” (Thermo Fisher Scientific Inc.) and the following conditions: 98°C for 30 s; 35× (98°C, 10 s; 60°C, 30 s; 72°C, 40 s); 72°C for 10 min.

**File 2.** Host range test performed with all Vietnamese *M. graminicola* populations. Level of infection is based on number of root galls and presence of nematodes confirmed by acid fuchsine staining: - non infected (no gall); + very low infection (1 gall); ++ mild infection (2 to 10 galls); +++ heavy infection (more than 10 galls).

|  |  |
| --- | --- |
| **Host plant** | **Level of infection** |
| Tomato cv. Money Maker | - |
| Tomato cv. Rutgers | - |
| Tobacco  | - |
| Maize cv. MX2 | - |
| Ricecv. IR64 | + + + |
| Welsh onion  | + + + |
| Common onion  | + + + |
| Garlic  | + + + |
| Peanut cv. V5 | - |
| Green bean  | - |
| Mung bean  | - |
| Soybeancv*.* DT84 | - |

**File 3.** CLUSTAL O (1.2.0) multiple sequence alignment between the 640-bp DNA SCAR fragment generated from The Philippines *M. graminicola* isolate and Contig MiV1ctg921 from *M. incognita*. The annealing locations of oligonucleotide primers and their orientations are indicated by arrows.



**File 4**. CLUSTAL O (1.2.0) multiple sequence alignment of a 386-bp DNA region including a portion of the 18S rDNA gene, the complete ITS-1 and part of the 5.8S rDNA gene from 36 *M. graminicola* isolates*.*

>DQ909046.1

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>KJ572383.1

CTGCCCGGGACTGAGCCATTTCGAGAAATTTGGGGACCGTTGATTAAACATTTATTTGTTTTTTTGATGGAAACCAATTTAATCGCAGTGGCTTGAACCGGGCAAAAGTCGTAACAAGGTAGCTGTAGGTGAACCTGCTGCTGGATCATTACTTTTTATGTAATGCTTTACATTTGAATTTATCGCATCATTTCATATGATGTGTAACGGCTCTCACTGGTGTCTAGGTGTTGCTGATTCAGCTGTCTTCGTCCGTGGCTGAATATGAGG-TGACATGTTAGGATTCTATTGAATCGTAAGACTTAATGAGCCT-CTTAAG-TGAGGAC--GCCAGCAATTTTTTTTTT---CAAT-AAA-TTTTTTTTTAAAAGACATTAA---TAAAAATTAA-C

>JQ724108.1

CTGCCCGGGACTGAGCCATTTCGAGAAATTTGGGGACCGTTGATTAAACATTTATTTGTTTTTTTGATGGAAACCAATTTAATCGCAGTGGCTTGAACCGGGCAAAAGTCGTAACAAGGTAGCTGTAGGTGAACCTGCTGCTGGATCATTACTTTTTATGTAATGCTTTACATTTGAATATATCGCATCATTTCATATGATGTGTAACGGCTCTCACTGGTGTCTAGGTGTTGCTGATTCAGCTGTCTTCGTCCGTGGCTGAATATGAGG-TGACATGTTAGGATTCTATTGAATCGTAAGACTTAATGAGCCT-CTTAAG-TGAGGAC--GCCAGCAATTTTTTTTTT---CAAT-AAA-TTTTTTTTTAAAAGACATTAA---TAAAAATTAA-C

**File 5**. List of ITS haplotypes and nucleotide polymorphisms used for the construction of the network (Fig. 6).

ITS sequences were generated in this study and downloaded from GenBank*.* Genebank accession number of each haplotype is given. The position of each nucleotide polymorphism is indicated based on the sequence alignment given in File 4. As Haplotype 1 is represented by the highest number of accessions, it was considered as the consensus sequence. When polymorphism is observed, the nucleotide is highlighted in yellow.

