



Tropentag, September 16-18, 2015, Berlin, Germany

“Management of land use systems for enhanced food security:
conflicts, controversies and resolutions”

Molecular Characterisation of Root-Knot Nematodes Obtained from African Nightshades in Western Kenya

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Abstract

African nightshades are in focus of an interdisciplinary and international research project. Root-knot nematodes (RKN) of the genus *Meloidogyne* spp. are polyphagous phytopathogens of global importance infecting the African nightshades. Diagnosis of RKN species is the first step for effective pest management. This study represents the first molecular characterisation of a RKN species from Kenya based on partially sequenced 18S of rDNA cistron. A total of 250 root samples were collected from five agro-ecological zones (AEZs) in Uasin Gishu, Bungoma and Kakamega counties. Polymerase chain reaction (PCR) was used to amplify a specific 1.8 kb sequence of the ribosomal RNA of single females from 22 populations of RKN. Sequencing was performed using six primers and SSU rDNA was amplified as two partially overlapping fragments using three universal (988F, 1096F and 1813F) and one nematode specific primer (1912R). Primer 988F or 1096F was used in combination with primer 1912R. The second fragment was amplified with primers 1813F and 2646R. Preliminary results from 22 RKN isolates subjected to PCR reaction and sequencing revealed that isolates from the study areas were most closely related to *M. javanica*, *M. incognita*, *M. ethiopica*, *M. cruciani*, *M. arenaria* and *M. hapla*. *Meloidogyne javanica* was identified in Upper midlands (UM)1, UM2 and UM3 agro-ecological zones while *M. arenaria* was found in UM1 and Lower midlands area 1 (LM1). *Meloidogyne incognita* predominantly occurred in UM2, UM3 and UM4 zones while *M. hapla* was found in farms from UM4 and LM1. Both *M. ethiopica* and *M. cruciani* were identified in farms from UM4. The isolates identity to GenBank references ranged from 91 % to 99 % with *M. javanica* and *M. incognita* predominantly occurring in 80 % of the AEZs, followed by *M. arenaria* and *M. hapla* with 40 % and *M. ethiopica* and *M. cruciani* distributed in UM4. Mixed populations of RKN occurred in a single farm hence causing different unspecific symptoms on AFNS. All the isolates were distantly related to *Coslenchus cancellatus*. These results contribute to the understanding of the variability of RKN species and provide data on the identification of RKN on AFNS lines from Kenya.

Keywords: African nightshades, diagnostics, *Meloidogyne* spp., phylogeny, ribosomal DNA, SSU