Abstract

Usually the identification of the Meloidogyne species is based on the morphology of adult females, making it difficult to identify juvenile males and females (J2). Nematodes are considered among the most difficult animals to identify; the use of ribosomal DNA (rDNA)-based diagnostic methods have gained acceptance in applications ranging from quarantine determinations to assessments of biodiversity. Nematodes of the genus Meloidogyne are known for their ability to produce physiological changes in the root system of plants and cause losses in the absorption of nutrients. The objective of this study was to determine if the sequencing of internal transcribed spacer (ITS) regions of rDNA can be used as genetic markers for reliable identification of populations of juvenile males and females (J2) for the main species of the genus Meloidogyne. From samples of diseased tomato roots (Solanum lycopersicum L.), larvae of juvenile females and males of Meloidogyne were collected for the DNA extraction. A rDNA region harboring two ITS regions was amplified. For subsequent sequencing, that region was ligated into pGEM®-T vector. Analysis with the BLASTn program showed that the gene region identified 99.8% with a gene sequence belonging to Meloidogyne incognita Kofoid & White, 1919. This result suggests that the ITS regions can be used as a genetic marker in populations for Meloidogyne species identification.

Keywords

Meloidogyne incognita, ITS, Ribosomal DNA (rDNA).