

ANALYSIS OF GENETIC VARIATION IN POPULATIONS OF *MELOIDOGYNE* SPP., FROM TURKEY USING AFLP

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Abstract

Amplified fragment length polymorphisms (AFLP) were used to characterize genetic variation among 29 root-knot nematode populations including *Meloidogyne arenaria*, *M. javanica* and *M. incognita*. These included 22 populations collected from vegetables (tomato, cucumber, eggplant, pepper and melon) in various locations in the Mediterranean Region of Turkey and 7 reference populations. The different species of *Meloidogyne* were differentiated by 11 AFLP primers combinations. Depending on the primer combination used and the nematode genotype analyzed, 15-45 amplified DNA fragments were resolved in a single lane. Intraspecific genetic similarity of *M. arenaria*, *M. incognita* and *M. javanica* ranged from 40 to 67, from 45 to 56 and from 41 to 73, respectively. According to the AFLP patterns, within species, no general correlation could be found between genetic similarity and geographical origin of the populations tested.