MARKER ASSISTED SELECTION IN TOMATO FOR ROOT-KNOT NEMATODE RESISTANCE BREEDING

ANTAL SZŐKE[1], KITTI LENCSÉS[1], DIÁNA DEBRECENI[1], ERZSÉBET KISS[1], PÉTER MILOTAY[2], LÁSZLÓ HESZKY[1]

[1]Szent István University, Institute of Genetics and Biotechnology
2100 Gödöllő, Páter Károly u. 1.
Szoke.Antal@mkk.szie.hu
[2]Vegetable Crops Research Institute Corporation
6000 Kecskemét, Mészöly Gyula u. 6.

The the root-knot nematodes (Meloidogyne spp.) are the most dangerous pests of the tomato (Lycopersicon esculentum Mill.). The easiest, cheapest and the most environmentally friendly way of protection is the breeding and production of resistant hybrids. The resistance gene, Mi, originating from the wild tomato species L. peruvianum, confers effective resistance in cultivated tomato against root-knot nematode species. Mapping markers closely linked to the resistance gene makes possible an early and cheap selection of genotypes.

In our work, molecular markers were used to determine the genotypic constitution of Mi gene in breeding lines of ZKI Zrt. Kecskemét, F_1 hybrids and 18 foreign varieties. Previously these breeding lines and hybrids were tested for nematode resistance by artificial infection.

Presence or absence of the Mi gene was examined with gene-specific PCR primers. Amplification of a 500 bp fragment indicated the existence of the Mi gene in the resistant genotypes, while its lack from sensitive cultivars showed, that dominant Mi gene is not present. A CAPS marker, REX provides a possibility to discriminate the homo- and heterozygous genotypes within the resistant lines. REX primer pairs amplified a 720 bp fragment in all genotypes independently of their resistance characters. TaqI restriction enzyme digested only the PCR product amplified in the resistant genotypes, resulting in two fragments (554 bp and 166 bp) in homozygous lines. Due to the indigestibility of marker-allele present in the susceptible plants three DNA fragments (720 bp, 554 bp, 166 bp) were detected in heterozygous genotypes. The separation of the three different genotypes became easier with the PMiF primers designed for the promoter of the Mi gene, since the application of this marker does not require restriction digestion. A 350 and a 550 bp fragment was amplified in the sensitive and in the resistant homozygous genotype, respectively, while in the heterozygote both DNA fragments (350 and 550 bp) appeared.

To confirm the marker-treat cosegregation, artificial infection was performed in F_2 population. Extent of damage was determined by counting the female and egg masses. Checking with artificial infection, the molecularly predicted resistance means real resistance in provocative environment.

Our results indicated that the uses of molecular markers linked to the root-knot nematode resistance gene are reliable and successfully adaptable in tomato breeding programs.