MOLECULAR GENETIC DETECTION OF MI GENE ALLELIC CONFIGURATION IN VARIOUS TOMATO GENOTYPES

Molekulárněgenetická detekce alelické sestavy genu *Mi* u různých genotypů rajčete

Sylva SKUPINOVÁ, Pavel VEJL, Petr SEDLÁK, Martina BARDOVÁ, Marta ANDRLOVÁ, Jana ISCHIOVÁ
KGOZ AF ČZU

Souhrn, klíčová slova

*Metodou CAPS (Cleaved Amplified Polymorphic Sequence) markerů bylo studováno 15 genotypů rajčte (*Lycopersicon esculentum*). Do experimentu byly zařazeny 2 odrůdy s deklarovanou rezistencí, 1 odrůda s deklarovanou senzitivitou a 12 novošlechtění s neznámou sestavou genu* Mi. *Metodou CAPS po restrikčním štěpení enzymem* Taq *I. byly jednoznačně určeny alelické série v genu* Mi. *Byla potvrzena heterozygotní sestava genu Mi u odrůd s deklarovanou rezistencí vůči háďátkům rodu Meloidogyne (Nemá F_1, Petopride F_1) a recesivně homozygotní se stava u odrůdy Rio Grande s deklarovanou senzitivitou. U testovaných novošlechtění byly nalezeny všechny možné sestavy genu* Mi.

CAPS markery, Meloidogyne incognita, PCR, Mi gen, rezistence, rajče, Lycpersicon esculentum

Summary, keywords

Using CAPS (Cleaved Amplified Polymorphic Sequence) markers were studied 15 genotypes of tomato (Lycopersicon esculentum), 2 varieties with declared resistance, 1 variety with declared susceptible to nematodes of Meloidogyne genus and 12 in Mi *gene unknown genotypes in Mi gene. The CAPS method confirms that varieties Nema F_1 and Petopride F_1 are heterozygous in Mi gene, variety Rio Grande is recessive homozygous and in other tested genotypes were found all of possible genotypes in Mi gene.*

CAPS markers, Meloidogyne incognita, PCR, Mi gene, resistance, tomato, Lycpersicon esculentum

Introduction

The application of molecular genetics has been progressively more and more concerned also with the process of creating new varieties. Genetic markers based on the polymorphism of nucleic acids allow the detection of specific allelic sets of a number of significant genes. Although these analyses are from the laboratory and financial point of view demanding, they allow the gene to be unequivocally characterised, are quick, non-destructive towards the plant material, and the results are not effected by the external environment.

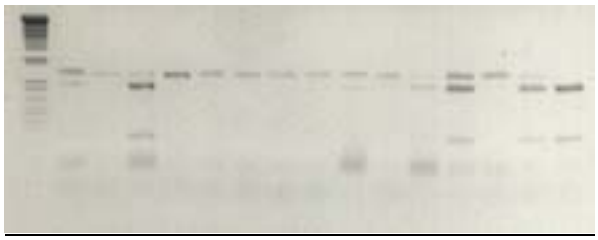
This paper presents the scope of using co-dominant DNA markers in the detection of *Mi* gene of the *Lycopersicon esculentum*, resistant against parasitic soil nematodes of the *Meloidogyne incognita*.

Methods

DNA was isolated from seedlings using plant „GenElute Plant Genomic DNA Kit“ (Sigma, SRN). For moleculargenetics analysis was used method CAPS markers according to Williamson *et al.* 1994. In 25 µl reaction mix were used 0,5µM of both primers REX – F1 5´- TCGGACCCTTGGTCTGAATT – 3´, REX – R2 5´- GCCAGAGATGATTCGTGAGA – 3´. The 750 bp PCR product was digested with *Taq* I. Amplification products were resolved on a 1.5% agarose gel.

Results - discussion

In the following electrophoreogram are results of digested PCR products



Evaluation of CAPS markers – detection of genotype in *Mi* gene:
1 – 144/2 – D, 2 – 310/2 – H, 3 - 132/3 – R, 4 - 310/3 – H, 5 - N3 – H, 6 - 68/3 – R, 7 - N1 – H, 8 - 48/1 – R, 9 - 133/4 – R, 10 - 43/4 – R, 11 - 132/1 – R, 12 - 281/1 – R, 13 - Nema F_1 – H, 14 - Rio Grande – R, 15 – Petopride F_1 – H, S - leader
D- dominant homozygous, H – heterozygous, R – recessive homozygous

References

Willamson, V. M., Ho, J. Y., Wu, F. F., Miller, N., Kaloshian, I.: Theoretical and Applied Genetics, 87: 757 – 763,1994.

This paper is result of grants FRVŠ 1102/2002, MSM: 412100002, ČZU 21190/1312/213110