ABILITY OF EFFECTIVE DNA MARKERS APPLICATION IN APPLETREE BREEDING

Možnosti efektivního využití DNA markerů ve šlechtění jabloní

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Souhrn, klíčová slova

Aktuálním trendem šlechtění jabloní jsou programy zaměřené na získání odrůd s rezistencí vůči strupovitosti (Venturia inaequalis CKE.). V tomto příspěvku je prezentována možnost využití kodominantních multi-PCR markerů pro detekci dominantního majorgenu Vf, který tuto rezistenci podmiňuje. Pro experimenty byla použita potomstva několika hybridních kombinací, u kterých byla studována segregace těchto markerů

jabloně, Malus x domestica BORKH., strupovitost, Venturia inaequalis CKE., rezistence, DNA, PCR, markery

Summary, keywords

Programmes, that are oriented to getting of new cultivars resistant to apple scab (Venturia inaequalis CKE.), are progressive trends in appletree breeding. This paper presented the ability of co-dominant multi-PCR markers for detection of dominant Vf allele of gene for qualitative resistance against to apple scab. For realisation of experiments were used progenies of some hybride combinations, where was studied the segregation of these markers

Apple, Malus x domestica BORKH., apple scab, Venturia inaequalis CKE., resistance, DNA, PCR, markers

Introduction

At present time are in breeding processes increasingly used genetic markers based on nucleic acids polymorphism. This paper presents the scope of detecting alleles of the major V_f gene that controls the resistance of apple against to apple scab (*Venturia inaequalis* CKE.). This gene was transferred to the genome of the current cultivars of apple from the botanical species *Malus floribunda*. Dominantly homozygous and heterozygous sets of the V_f gene control the resistance of apple against to scab (DAYTON *et al.,* 1970). GIANFRANCESCHI *et al*. (1996) have got two RAPD markers for detection of genes of resistance against to apple scab of *Malus* species. One of those markers was able to detect the main gene of resistance, V_f *gene.* This gene was detected in all of analysed resistant cultivars of appletree. TARTARINI *et al*. (1999) used the combination of dominant and co-dominant PCR markers for detection of the gene.

Methods

There were analysed three hybrid combinations (forty individual seedlings in each hybrid combination): A (HL149-V_fv_f x HL1816-V_fv_f, B (HL1705-V_fv_f x HL1909-V_fv_f and C (HL1761-V_fv_f x Rezista-V_fv_f).

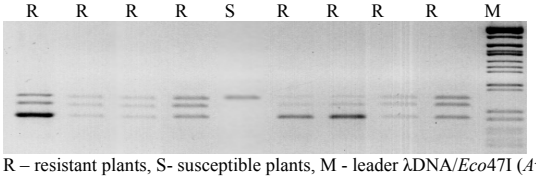
DNA was isolated by GenElute Plant Genomic DNA Kit" (Sigma, SRN). For detection of V_f was the modified multi-PCR method according to TARTARINI *et al*. (1999) used. For amplification of co-dominant marker were oligonucleotide sequences ALO7F (5' TGA AAG AGA GAT CCA GAA AGT G 3') and ALO7R (5' CAT CCC TCC ACA AAT GCC 3') used. Primers, AM19F (5' CGT AGA ACG GAA TTT GAC AGT G 3') and AM19R (5' GAC AAA GGG CTT AAG TGC TCC 3'), represent dominant marker.

Results - discussion

Analyse by multi PCR was proved in all parents and their progenies. All parental genotypes were detected as heterozygous.

At figure 1 is showed electrophoreogram of segregated hybrid combination progeny A. All resistant seedlings at the figure 1 have got genotype V_fv_f the susceptible plant has genotype v_fv_f.

Figure 1: Bulked analysis of multi-PCR markers in crossing combination A



R – resistant plants, S- susceptible plants, M - leader λDNA/*Eco*47I (*Ava*II)

Notional genotype ratio of segregation of the made crosses was 1:2:1. In the table 1 is proved statistical evaluation of real ratio of segregation by χ^2- test.

Table 1: Statistical evaluation of multi-PCR markers segregation by χ^2 test

Crossing	Marker segregation			χ^2	Expectation
	V_fV_f	V_fv_f	v_fv_f		
A	8	20	12	0,80	0,50-0,70
B	6	19	15	4,15	0,10-0,30
C	4		9	4,10	0,10-0,30

It was verified experimentally, that the modified method according to TARTARINI *et al*. (1999) is useful for application in practical breeding.

References

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