

GENETIC MARKERS

– THE PROGRESSIVE TRENDS IN PLANT BREEDING

Genetické markery – současný trend ve šlechtění rostlin

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Souhrn, klíčová slova

Metody molekulárních markerů dnes patří k dynamicky se rozvíjejícím nástrojům moderních šlechtitelů. Tento příspěvek shrnuje možnosti využití molekulárních markerů v domácím šlechtění odrůd rajčat, jabloní a brambor na rezistenci vůči nejproblematičtějšímu škodlivému organismům těchto plodin. Geny rezistence uvedených plodin byly detekovány a charakterizovány vybranými DNA markery. Byla ověřena segregace markerů ve vybraných potomstvech.

Rajče, jabloň, brambor, DNA markery, rezistence, *Venturia inaequalis*, *Meloidogyne incognita*, *Globodera rostochiensis*

Summary, keywords

At the present time, methods of molecular markers belong to progressively developed tools of modern breeders. This paper summarises capability of using of molecular markers in autochthonous breeding of tomato, apple and potato for resistance against the most pestilential pests of these crops. Genes of resistance of the crops were detected and characterised by elected DNA markers. There was verified segregation of markers in elected progenies, as well.

Tomato, apple, potato, DNA markers, resistance, *Venturia inaequalis*, *Meloidogyne incognita*, *Globodera rostochiensis*

Introduction

Resistance of preponderance present-day cultivars is conditioned by major genes. In tomato (*Lycopersicon esculentum*) is the resistance against to parasitic soil nematode *Meloidogyne incognita* determined by *Mi* gene. In apple (*Malus x domestica* BORKH.) exists gene *Vf* that is responsible for resistance to apple scab (*Venturia inaequalis* CKE.). The basic gene of potato resistance against to Ro1 pathotype of potato cyst nematode (*Globodera rostochiensis*) is dominant allele of *H1* gene.

Methods

For DNA analysis of tomato were used F₂ progenies of cultivars Nema F₁ and Petopride F₁. The both cultivars have genotype *Mimi* - are resistant. For bulked analysis of F₂ progeny was used a co-dominant CAPS marker according to WILLAMSON *et al.* (1994). Experiment with apple was realised with collected resistant cultivars with dominant allele *Vf* (Otava, Rajka, Resista, Rosana, Rubinola, Selena, Topaz) and cultivars with recessive allele *vf* (Angold, Gloster, Golden Delicious, Idared, Mac Intosh, Oldenburg Red, Spartan, Zuzana). For detection of *Vf* was used modified method according to TARTARINI *et al.* (1999). For DNA analysis of segregation of *H1* allele in potato were used F₁ progenies of hybridisation between cultivars Ornella x Mira and Tábor x Mira. Cultivar Mira is resistant against to Ro1, cultivars Ornella and Tábor are susceptible. Here was applied modified PCR marker according to NIEWÖHNER *et al.* (1995). DNA of all plants was isolated by GenElute Plant Genomic DNA Kit[™] (Sigma, SRN). All markers were applied according to cited authors.

Results - discussion

The said modifications of methods are results of optimisation that is necessary for the flawless function of the method. More of information about the optimisation is possible to read in relevant articles in this book. The all of results have corresponded with results of said authors. Nema F₁ and Petopride F₁ were heterozygous in *Mi* gene. In F₂ progeny of tomatoes were identified all possible genotypic combinations in correspondence with presumptive segregation ratio (1:2:1). Results were in congruence with greenhouse tests. Roots of susceptible plants were by *Meloidogyne incognita* affected. In apples were identified heterozygous and recessively homozygous genotypes. It corresponded with declared resistance or susceptibility respectively of cultivars. In F₁ progenies of the said hybrid combinations was detected dominant allele of *H1* gene in congruence with provocation greenhouse tests provided by VÚB Havl. Brod. Next statistical analyse proved, that the genotype of cultivar Mira is H1h1h1h1, thus simplex.

References

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