Genetic variation of S-alleles in wild and sweet cherry population of Czech Republic

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Abstract

Sweet cherry is an important and valuable crop to Czech Republic. A number of wild cherry cultivars have been developed for fruit production and therefore numerous genetic studies have been conducted for the species to understand genetic self-incompatibility mechanism. Gametophytic self-incompatibility is controlled by multi allele S-locus where two tightly linked genes, S-RNase and SFB (S haplotype-specific F-box), determine the specificity of the pollen and the style. As part of this objective we investigated the S-genotype of 91 cheery cultivars i.e. 50 wild and 41 sweet cherry. S-locus analysis was carried out by PCR analysis of S-RNase and SFB genes. PCR was done using conserved primers and fragments detection was carried out by capillary electrophoresis. The genotypes where the length of amplicon had similarity with other alleles were confirmed with the appropriate allele-specific primers for the known alleles. We identified 16 different S haplotypes: S1, S2, S3, S4, S5, S6, S9, S12, S13 and S16 (Sweet cherry) and S7, S14, S18, S19, S21, S22 (wild cherry) and cultivars were assigned to 24 incompatibility groups. Ten new incompatible group varieties were determined for wild cherry which could serve as universal pollinator. S-haplotypes for sweet cherry S1, S3 and S4 were the most frequent and S2 was less frequent in Czech Republic. Other S-haplotypes that were common in northern and central Europe are S5 and S6. The wild cherry populations differed significantly with respect to allelic frequencies from sweet cherry cultivars; alleles S1, S3 and S4, which are more frequent in sweet cherry, were less frequent in the wild cherry collections. S-haplotypes S14, S16 and S22 were the most frequent and S18 was less frequent in wild populations of cherry in Czech Republic. The results evidently provide cross-compatibility information for cross design and orchard management. The results also reveal the S-locus diversity of this plant material.

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Key words: Prunus avium, S-allele, S-RNase, F-box

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