Microsatellite based assessment of genetic distances within *Prunus* genus

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Introduction

Molecular markers - like microsatellites (SSR) - provide objective possibility for estimating genetic diversity. Microsatellite markers are used not only for cultivar identification but also for the verification of synonyms and homonyms (Testolin et al., 2000; Cheng and Huang, 2009; Wünsch, 2009; Bodor et al., 2014).

Our the aim was to determine genetic distances within 5 members of *Prunus* genus using 6 SSR markers (BPPCT 002, BPPCT030, BPPCT 041, UDP 96 001, UDP 96 005, UCDCH 17) (Cipriani et al., 1999; Dirlewanger et al., 2002; Struss et al., 2003).

Material and methods

This research was carried out with 51 peach (*Prunus persica* L.), 15 apricot (*Prunus armeniaca* L.), 38 sweet cherry (*Prunus avium* L.), 29 sour cherry (*Prunus cerasus*) and 37 plum genotypes from National Food Chain Safety Office (Hungary) and from NARIC, Cegléd using the same 6 SSR primer pairs.

The DNA was extracted from leaves using E.Z.N.A OMEGA DNA extraction kit.

The amplified products were separated on 6% polyacrylamide gel. The precise size of the amplified SSR regions were detected by Cy-5 fluorescently labeled primers and determined by ALFwin Fragment Analyser 1.0 software.

Results and discussion

The SSR allele sizes in the case of all genotypes are summarized according to the species in *Table 1.* Out of the 6 *Prunus* SSRs BPPCT 041 did not amplify any alleles in apricots.

In the case of peach 13, sweet cherry 12, sour cherry 21, apricot 10 and plum 41 polymorphic alleles were observed (*Table 1*).

In general out of the 6 *Prunus* microsatellites UDP 96 005 was that locus where the highest number of alleles was amplified and BPPCT 030 produced the least.

Conclusions

Our result showed for instance that peach cultivars can not be discriminated with UCDCH 17 primer pair but as *Table 1* demonstrates it was one of the most variable loci in plum genotypes. In general, UDP 96 005 locus gave the highest allele number in the analyzed varieties.

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Table 1: Observed allele sizes in base pair on the tested Prunus varieties

Varieties	BPPCT41	BPPCT30	BPPCT002	UDP96-005	UDP96-001	UDC-CH017
peach	219, 221	158, 170, 176	229, 231	156, 172	121, 129	138
sweet cherry	201	140	179, 183	110, 118, 120, 136	110, 125	188, 198
sour cherry	201, 229	140, 158, 162	167,179,183	106, 110, 118, 120, 136	101, 115, 125	178, 182, 188, 198, 200
apricot	-	140, 148	187,189	94, 110, 120, 156	110	128
plum	197, 201, 205, 207 211, 215, 219, 221	130, 144, 148	177, 179, 183, 187, 189, 193, 207, 219	94, 100, 106, 110, 112, 114, 136, 150, 156	99, 101, 113,125,138	130, 138, 140, 142, 144, 152, 154, 160

Our hypothesis was that with SSR markers we are able to determine the genetic distances regarding these varieties. In the case of BPPCT 030 and UDP 96 005 amplifies a 140 bp long and a 110 bp long fragment, respectively in apricot, sweet cherry and sour cherry, thus there could be an ancestral relationship between them.

In conclusion, our results suggest that within the *Prunus* genus we could be able to determine not only the intervarietal, but the interspecific genetic distances, as well.

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