

Simple sequence repeat-based assessment of genetic relationships among *Prunus* rootstocks

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ABSTRACT. Ten SSR loci, previously developed for *Prunus*, were analyzed to examine genetic relationships among 23 rootstock candidates for sweet and sour cherries, of the species *P. avium*, *P. cerasus*, *P. mahaleb*, and *P. angustifolia*. Five genotypes of *P. laurocerasus*, not used as rootstock, were included in the molecular analysis. The number of alleles per locus ranged from 8 to 12, with a mean of 9, while the number of microsatellite genotypes varied from 8 to 17, indicating that the SSRs were highly informative. The degree of heterozygosity (0.61) was high. Clustering analysis resulted in two main clusters. The first cluster was divided into two subclusters; the first subcluster consisted of *P. avium* and *P. cerasus*, and the second subcluster consisted of *P. laurocerasus*. The second cluster was divided into two subclusters. The first subcluster consisted of *P. mahaleb* genotypes and the second consisted of *P. angustifolia* genotypes. The reference rootstocks also clustered with their associated botanical species. Unweighted pair-group method with arithmetic mean analysis demonstrated that *P. laurocerasus*

genotypes had less genetic variation and that *P. avium* genotypes were more closely related to *P. cerasus*. The SSR-based phylogeny was generally consistent with *Prunus* taxonomy information, suggesting the applicability of SSR analysis for genotyping and phylogenetic studies in the genus *Prunus*.

Key words: *Prunus*; SSR; Genotyping; Diversity; Rootstock