Genetics of wild cherry (*Prunus avium* L.) in Greece

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A breeding program on wild cherry (*Prunus avium* L.) in Greece aimed at wood production has led to the selection of 10 natural populations from entire species natural distribution in the country. Population evaluation was based on the phenotypic quality of individuals within populations (tree height, diameter, stem form, strength of apical meristem, absence of insect or disease problems, absence of frost related problems, lateral branch angle and diameter, etc), and on selected plus-tree amenability to macro and micropropagation. Based on the above criteria four populations from northern Greece (Nymphaea, Vathytopos, Xanthi, and Polydendri) have been selected for further evaluation. Selected plus trees from these populations were macropropagated and established in a clonal gene bank in Xyloupolis, Greece. The genetic diversity and relationships of 35 selected *Prunus avium* plus trees of this collection was investigated based on 17 microsatellite loci (SSR). Notable amounts of genetic diversity were observed. Percent polymorphic loci was 82,4. Heterozygosity and Shannon information index presented generally high values (H_{exp}=0,472; H_{obs}=0,399; I=0,272). The allelic variation observed was sufficient for unambiguous DNA fingerprinting. Average probability of identity (P_{ID}) and polymorphic information content (PIC) were 0,473 and 0,292 respectively. A principal coordinate analysis showed the formation of four groups that generally correspond to the four natural populations of origin.

The wild cherry clonal collection was compared to a collection of five widely used sweet cherry cultivars in northern Greece. A total of 12 microsatellite loci were used. Allelic numbers ranged from two to seven, while most private alleles occurred in the wild cherry individuals. Expected heterozygosity and Shannon information index were higher in the wild cherry material. An analysis of molecular variance indicated that a significant amount (32%) of the total variation resided among groups. Results from a principal coordinate analysis indicated the diverse origin of this material. Sweet cherry cultivars formed a short independent cluster, which was conspicuously differentiated from all wild cherry individuals that formed a large widely dispersed group in a graph of the first two principal coordinates.

Key words: *Prunus avium*, microsatellites, DNA fingerprinting

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