

Molecular diversity of selected *Fragaria* genotypes determined with microsatellite markers

**Anita Kuras, Agnieszka Masny,
Małgorzata Korbin**

Research Institute of Horticulture,
Konstytucji 3 Maja 1/3, 96-100 Skierniewice, Poland,
email: anita.kuras@inhort.pl

Microsatellites markers, consisting tandemly repeated DNA motifs with length from two to five nucleotides, are known as co-dominant and highly polymorphic.

The aim of the presented study was to evaluate diversity of 39 representatives of *Fragaria* genus using microsatellite-based SSR technique. Among 42 primers applied in the PCR tests, 20 generated clear and reproducible polymorphic DNA fragments. Totally, 148 alleles (size range 140–800 bp) were obtained. The mean number of alleles per locus was determined as 6.5.

Cluster analysis by the un-weighted pair-group method with arithmetic averages (UPGMA) allowed evaluating the degree of genetic similarity of analyzed genotypes ranging from 27 to 87 %.

Four clusters of genotypes were revealed. The first one contained wild *Fragaria* genotypes: *Fragaria chiloensis* Yaquina A, *Fragaria chiloensis* Yaquina Y B, *Fragaria chiloensis* Yaquina Chile, *Fragaria chiloensis* Del Norte, *Fragaria chiloensis* subsp. *chiloensis* f. *patagonica*, *Fragaria virginiana* ssp. *glauca*, *Fragaria vesca* subsp. *vesca* Korsic, *Fragaria nubicola*. Remaining three clusters consists cultivated *Fragaria* cultivars: derived from ‘Redgountlet’ and ‘Gorella’ (cluster I), cultivars related to ‘Camarosa’ (cluster II) and cultivars derived from ‘Chandler’ (cluster III).

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