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GENETIC VARIABILITY OF AN ITALIAN APPLE GERMPLASM COLLECTION

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Breeding apple varieties of high quality, merging grower demands and consumer satisfaction requests, is a challenging task. In this species, strict self-incompatibility, slow growth and long juvenile period of seed-derived plants hamper the efficient crossing and selection of desired genotypes. The long generation cycles make the marker-assisted selection strategic in apple breeding. By this approach molecular markers, linked to genes of desired traits are used instead of the traditional phenotypic based selection. The genetic variability among apple varieties and germplasm accessions represents the basis for association studies.

In this work, a panel of apple simple sequence repeats (SSRs) markers was chosen to study the extent and distribution of genetic variability in a collection of more than 400 apple accessions of the Italian germplasm maintained in the experimental fields of the Dept. of Fruit Tree and Woody Plant Science, University of Bologna. The cluster analysis allowed to solve practical doubts between synonymy and homonymy of genotypes with a similar phenotype and to describe the relationships among the Italian apple germplasm varieties that represent a wide source of genetic diversity in which discover allelic forms of functional genes useful for breeding purposes. This analysis made also possible the identification of various triploid genotypes. Moreover, the same set of cultivars was phenotyped for fruit quality traits.

This work was carried out within the framework of the 'Fruit Breedomics EU project' and represents a preliminary step in the definition of an Italian apple 'core collection'. The wide panel of selected genotypes will be used to improve the knowledge of genetic variability distribution by exploring the phenotypic and allelic diversity available in the apple germplasm and it allows the identification of the genomic regions involved in the genetic control of major horticultural traits through genome-wide analyses.