

GENETIC AND PLOIDY DIVERSITY OF PEAR GERMPLASM OF LAZIO REGION, ITALY

DRAGA S.*, PALUMBO F.*, BARBAGIOVANNI MIRACOLO I.***, PATI F.***,
BARCACCIA G.*

*) University of Padua

**) Arsial

germplasm collection, molecular markers, ploidy, synonymy, molecular diversity

Pear (*Pyrus Communis*) is an important temperate fruit with high nutritional and economic value. Italy, as the largest pear producer in EU and second in the world, represents a particularly rich germplasm characterised by hundreds of local varieties. Despite this vast genetic variability, very few research studies have been concentrated on the local varieties present in Italy. In this study, we attempted to genetically characterize a collection of 311 pear accessions, collected from the five provinces of the Lazio region. By means of nine SSR markers, we searched for cases of synonymy and homonymy among the accessions, and we investigated the genetic structure of the entire germplasm. The microsatellites set showed a high polymorphism information content (mean PIC=0.77) and resulted particularly efficient both in the production of molecular profiles useful for the study of genetic diversity, and in the prediction of the degree of ploidy. The SSR analysis revealed 23 genotypes with 100% of genetic similarity (i.e. in each case from two to eight samples proved identical molecular profiles), as expected since the accessions also shared the same nomenclature. Moreover, synonymy cases were observed in sixteen accessions with different names, but identical molecular profiles. On the contrary, cases of homonymy were also present, predominantly with higher frequency among the 'Spina' pear accessions. Noteworthy, one hundred and fifty samples (out of 311) displayed triallelic profiles whilst the remaining were diploids. These results were further confirmed by flow cytometry data analysis.

According to the Bayesian model-based analysis, the highest ΔK values were

observed by setting the ancestral population size to 2 and 12. However, both cases did not support the hypothesis of a common triploid ancestor, being the triploid accessions randomly distributed throughout the clusters. This scenario would therefore suggest the occurrence of repeated and spontaneous triploidization events over the years, probably because of hybridization phenomena. For further genetic investigations, a DNA barcoding analysis was necessary to construct a reliable ancestry tree, shedding light on the diversification process within the pear germplasm. Triploids, as sustained with data from literature, have the tendency to show more preferable traits for the market demand and this phenotypical selection can explain their high frequency and distribution.