REDUCING UNCERTAINTIES IN THE AFLP ASSESSMENT OF GENETIC RELATIONSHIPS IN ALMOND (*AMYGDALUS COMMUNIS* L.) CULTIVARS FROM APULIA

P. RESTA*, R. CHAABANE*, F. LAMAJ*, M.A. PALASCIANO*, D. DE GIORGIO**

*) Dipartimento di Biologia e Chimica Agro-forestale e Ambientale (DiBCA), Università degli Studi di Bari, Via Amendola 165/A, Bari, Italy
**) Istituto Sperimentale Agronomico, Ministero delle Politiche Agricole e Forestali, Via C. Ulpiani 5, Bari, Italy

cultivar identification, molecular descriptors, multivariate analysis, probability of coincidence, AFLP

Cultivar collections are fundamental for fruit tree breeding and their maintenance and analyses drain significant resources. The employment of DNA comparisons together with the traditional morphophysiological descriptors is a powerful approach for genetic diversity studies and cultivar correspondence analyses. AFLP profiles are widely adopted for their capacity of generating large numbers of descriptors in the absence of previous DNA sequence information. Occasionally, however, spurious bands are amplified, with negative effects on the detection of unbiased estimates of genetic relationships and on the generation of fingerprints. Increasing variables and adopting replications have been proposed in order to improve the detection of the most significant clusters, but these approaches also add up further costs in the analysis of large germplasm collections.

More general research is in progress to evaluate yield stability and the quality of Apulian almond germplasm using the collection gathered and maintained by the MiPAF Experimental Station of Bari. Thus, an AFLP analysis was carried out for estimating genetic relationships on a representative sample of local cultivars (43 denominations). The study was conducted by starting with separate DNA extractions from the leaves of single plants and comparing these results from duplicated profiles, with unreplicated ones, with and without internal controls. Cophenetic correlations, approximate t-test, and matrix correlations were estimated with Mantel’s test. The result indicates that the adoption of internal controls can effectively remove part of the experimental noise from unreplicated profiles.

With regard to the main objective of assessing the genetic relationships among Apulian almonds, strong evidence was obtained that eight denominations, for years maintained separately in the collection, may correspond to just four genotypes. This was based on having obtained identical DNA profiles and on estimating the probability of coincidence among the DNA profiles due to chance. Conversely, an off-type tree in the collection was identified in the cultivar Cosimo di Bari. A trend of aggregation of a few cultivars was also observed, which could provide useful information for the choice of parentals in breeding programs. Finally, a blind study on a DNA sample was included which showed the potential of DNA analyses in making informed decisions in the field of cultivar identification and genetic correspondence. In view of these results, further feasibility tests as
groundwork toward the institution and backing of a network of certified laboratories are proposed and discussed.