Poster Abstract - E.12

THE IDENTIFICATION OF AN UNKNOWN REPLICATED SAMPLE IN A COLLECTION OF CHERRY GENOTYPES (*PRUNUS AVIUM* L.) FROM APULIA

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Cultivar collections are fundamental for fruit tree breeding, and their maintenance drains significant resources. The employment of DNA comparisons together with the traditional morpho-physiological descriptors is a powerful approach for the optimization of collections. Fingerprint analyses are particularly well suited as a rapid and precise tool in the field of genetic correspondence in vegetatively propagated crops. Without taking into account the possibility of spurious bands and/or erroneous subjective interpretations, one significant test is first to identify an unknown sample within a collection based on the fingerprint alone, and second to then establish a conservative estimate of the probability in association with the resulting identity. To this purpose, in a more general research in progress, DNA was isolated from the leaves of a cherry cultivar, whose identity remained unknown throughout the steps of the analysis. The AFLP fingerprints obtained were compared with those corresponding to 28 cherry cultivar genotypes. Based on the presence/absence matrix of only 33 variables, a statistical analysis for estimating the probability of coincidence of the DNA profiles was made. Both the unknown sample and the cultivars analysed originated from the collection gathered and maintained by the Dipartimento di Scienze delle Produzioni Vegetali of Bari. This collection includes numerous denominations with diverse diffusion in the Apulian region and, therefore, the group of 29 genotypes analysed is representative of the cherry population in Apulia.

The unknown sample was correctly attributed as being the cultivar "Stella". This result demonstrates the possibility of identifying a corresponding cultivar on the basis of leaf DNA analysis, without prior information, and in a relatively short time with a few AFLP primer combinations. In addition, an estimate was determined of the probability that the unknown sample and the corresponding cultivar had the same genotype with respect to the alternative hypothesis that casuality led to the obtained result. A conservative estimate, obtained on the basis of the exact probabilities associated with the binomial distribution, favoured 377 times the hypothesis of the unknown sample belonging to the cv Stella vs. the hypothesis of identity by chance. In view of these results the possibile applications of DNA analyses in the field of cultivar identification and genetic correspondence are discussed.