

COMPARISON BETWEEN AFLP BASED GROUPINGS AND MORPHO-PHYSIOLOGICAL TRAITS IN A COLLECTION OF FIG GENOTYPES (*FICUS CARICA* L.) FROM APULIA

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Since the maintenance of fruit trees cultivar collections drains significant resources, a balance has to be maintained between genetic diversity and agronomic characters of the accessions. DNA comparisons and morpho-physiological descriptors can be used together to estimate the genetic diversity present in reference collections. The adoption of this combined approach to germplasm analysis is more critical when characterizing germplasm for which the cultivar description is incomplete, such as is often the case for minor crops. In fig trees of southern Italy, the high number of local denominations in association with hypotheses of the existence of synonymous denominations of the same genotypes highlights the need of establishing a reference collections of DNA fingerprints associated with traditional descriptors. However, it would be useful to determine the relationship between molecular and morpho-physiological characters before starting large scale genotyping programs. Thus, fruit and leave characters, ripening time, and ostiol appearance of over 38 cultivar denominations have been compared with the result of an AFLP analysis of genetic diversity (UPGMA clustering of simple matching similarities). The studied cultivars were from the fig collection gathered and maintained by the Dipartimento di Scienze delle Produzioni Vegetali of Bari, which includes several denominations with diverse diffusion in the Apulian region.

The result of the comparison with morpho-physiological traits indicated a correspondence only with AFLP based clusters formed at very high similarity levels. Additionally, a second set of AFLP data was produced and compared, which indicated again a perfect agreement in the high similarity range but lack of consistency in the majority of the trends of aggregation within the range of intermediate similarity levels. Furthermore, these results suggest the lack of a strong genetic structure in the fig germplasm analysed. In view of these findings, the possible applications of DNA analyses in the process of establishing core collections are discussed.