

GENETIC CHARACTERIZATION OF SICILIAN FENNEL LANDRACES BY SSR MOLECULAR MARKERS

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genetic diversity, molecular markers, simple sequence repeat

Fennel (*Foeniculum vulgare* Mill. subsp. *vulgare* var. *azoricum* (Mill.) Thell.) is one of the typical crops of the Mediterranean basin. Italy is the greater world-wide and European producer of *grumoli* based on 23700 ha and a production of about 590000 t (ISTAT, 2006).

Fennel is an open pollinated species belongs to the *Apiaceae* family and originated in the Mediterranean region, where it is possible to observe a high genetic variability. In the last few years the interest for a possible industrial use of fennel is growing. Nevertheless, this utilization would allow a diversification of the offer and the introduction of new products. Recently, fennel has become attractive for main international seed companies, which have improved research breeding programs. Moreover, changes of vegetable crops management and in the seed laws may have serious consequences on the maintenance of many local selections.

Considering the outcrossing rate and consequently the high genetic variability of this species more attention should be placed on the characterization of germplasm. The methods based on morphologic features commonly used not always allow the most accurate information due to genotypes-environment interaction; on the contrary it is well reported that genetic methods overcome this problems. Since not many genetic information are available in literature for fennel crop, microsatellites, frequently utilized for this purpose in many plant species, were adopted as molecular technique for fennel genetic characterization.

The aim of this study is the collection and characterization of several Sicilian fennel landraces, by using both morphological and genetic data. Eight fennel genotypes obtained from University of Catania (6 accessions) and from seeds bank of the University of Gatersleben (2 accessions), and one landrace named *finocchio riccio* were analysed. The genetic diversity is estimated and a matrix of presence/absence of DNA fragments is used for the comparison of the accessions in order to obtain the coefficients of genetic similarity. The coefficients are utilized for the UPGMA (Unweighted Pair Group Method Averages) analysis useful for obtaining a dendrogram among accessions.