

GENETIC DIVERSITY OF SICILIAN LEMON GERMPLASM IDENTIFIED BY MOLECULAR MARKERS

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Citrus limon, genetic diversity, ISSR, RAPD

The lemon cultivation (*Citrus limon* L.) is spread in the Southern Italy, specially in Sicily, the first Italian region for lemon production. Whereas in the other Citrus growing countries, one cultivar prevails on the others ('Eureka' in U.S.A., 'Genoa' in Argentina, 'Galego' in Brasil and 'Berna' in Spain), on the contrary, in Italy, each lemon cultivated area (Palermo, Catania, Syracuse, Messina, Reggio Calabria, Salerno and Naples) has a wide range of genotypes mostly derived from bud mutation from 'Femminello' cultivar.

Over the past century, also the Italian lemon has suffered a dramatic reduction in the gene pool, because of 'malsecco' disease, that imposed the tolerance as necessary feature. So, some genotypes getting interesting breeding characters risk to disappear because of this disease. Currently, in Sicily, there are yet several lemon varieties with interesting agronomical traits.

In the last years, the collection and the characterization of fruit crop germplasm is becoming a common concern among geneticists and breeders, to identify and preserve the genetic diversity of a specie for setting up new breeding programmes for genetic improvement.

In the present study, 35 phenotypically diverse genotypes, including 'Femminello', 'Monachello' and 'Lunario' varieties, were collected from different parts of Sicily and used in the investigation. Polymerase Chain Reaction (PCR)-based molecular markers techniques have been used to characterize the phenotypic-based selection of Sicilian lemon and to analyse their genetic variability. Twenty RAPD primers and twenty ISSR primers were used to detect genetic polymorphisms. Twenty four genotypes were discriminated and the relative Nei's genetic distance (GD) estimates were used to carry out a cluster analysis by unweighted pair-group method using an arithmetic averaging (UPGMA) algorithm.

The accessions analysed could be clustered in two principal groups, including indistinctly plants coming from different collecting areas. Several phenotypically-different but genetically-similar plants belonged to the same subgroup, representing the Sicilian base 'Femminello' genotype.

The Nei's analysis of genetic diversity showed a low grade of variability ($H_T = 0.02$). Higher genetic variability was identified in genotypes of Palermo zone, having a tighter relationship with the genotypes of Messina zone. Data obtained from this study have been also used to provide several other information about genetic relationships among the cultivars examined. This information, with morphological and phenological descriptors, could be useful for assessing the basis of breeding programmes aimed at the genetic improvement of lemon.