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GENETIC DIVERSITY AMONG GRAPEVINE CULTIVARS FROM THE IONIAN COAST OF REGGIO CALABRIA

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Simple Sequence Repeat, local genotypes, synonymies and homonymies, Vitis vinifera L.

Grapevine (*Vitis vinifera* L.) is one of the oldest agricultural crops cultivated to produce mainly table fruits and wine. The number of different varieties held in worldwide germplasm collections is estimated to be 10.000 (Alleweldt and Dettweiler, 1994 – The genetic resources of *Vitis*: world list of grapevine collections, 2^ edn. Geilweilerhof, Siebeldingen). This wide genetic diversity is probably due to several mechanisms such as multiple domestication events from wild vines and the old practice of growing seedling from spontaneous or controlled crossing. The vegetative propagation of grapevine frequently produces clones genetically identical to the parental plant, but spontaneous mutations can occur in the regenerative cells that give rise to different clones.

A total of fifty-six grapevine genotypes were sampled from several sites of the Ionian areas of Reggio Calabria Province from Calabria, considered an important casket of biodiversity, where old vineyards are widely spread. The grapevine collection was selected as a representative sample of genetic variability from that area. Total genomic DNA was extracted from young fresh leaves and genetic characterization was performed using twelve of the most utilized microsatellite markers (VVS2, VVS5, VVMD5, VVMD7, VVMD25, VVMD27, VVMD28, VVMD6 VrZAG62, VrZAG64, VrZAG67 and VrZAG79) for grapevine. The goal of this work is to evaluate the level of biodiversity and to clarify proposed cases of synonymies and homonimies, in order to safeguarding the still existing diversity. Several varieties sampled in the present study had their names quoted in historical and literary sources, while others found and sampled in old vineyards had their names not reported in ancient literature. According to their genetic profiles at SSR loci, 33 different genetic profiles were found, in which several cases of synonymies (Nerello Sculli, Nerello Lamezia, and among different presumed clones of Magliocco Dolce and Malvasia) and cases of homonymy (Olivella and Marcigliana) were discovered. Several genetic parameters, such as expected (H_e) and observed (H_o) heterozygosities, polymorphic information content (PIC) and probability of identity (PI) were evaluated to assess the efficacy of the chosen loci for the analyses. Pairwise genetic distances between all genotypes analyzed were calculated. A dendrogram representing the genetic similarities among genotypes was obtained using the UPGMA method to investigate their relationships, explaining them from an historical point of view. The genetic analysis confirmed the supposed high level of diversity in this Mediterranean area. The cluster distribution of varieties did not reflect their geographic distribution, suggesting different and successive introductions of cultivars in this area of Calabria region from different areas of origin.