Genomic Tools to Reconstruct the Grapevine Domestication and Evolution in the Western Mediterranean Basin

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Italy is one of the major wine producers, with the area under vine cultivation reaching 690,000 hectares in 2016. The most ancient archeological evidence of grape consumption in Italy dates back to the Epigravettian and Mesolithic periods, in Grotta del Romito (Cosenza, Calabria) and Grotta dell'Uzzo (Trapani, Sicilia), respectively, where seeds of wild grapevines have been identified.[1] Sicily, together with the other regions of southern Italy (Calabria, Campania, Basilicata and Puglia), played a key role in the introduction of new forms of viticulture to Italy during Greek colonization. The aim of this work was to identify the genetic relationships among southern Italy and eastern Mediterranean Sea countries germplasm by a SNP genotyping.

A total of 187 grapevine accessions, originating from Italy, Greece and the Eastern Mediterranean Sea were genotyped by Vitis18kSNP chip array (Illumina Inc., San Diego, California), containing 18 071 SNPs. The SNP polymorphisms have been used to identify synonymies/homonymies, calculate the genetic distances among the cultivars (clustering analysis), the genetic relationships (Principal component analysis, PCA), structure analysis and parentage analysis.

The SNP genotyping of 187 grapevine accessions from Italy, Greece and the Eastern Mediterranean Sea countries produced a dataset of polymorphic loci counting 11023 SNP loci. A dendrogram was built to investigate the genetic relationships among the genotypes. The range of similarity varied from 100 to about 83%. A total of 158 unique genotypes were detected, with the higher number of synonymies identified among Italian genotypes. Other synonymies were also noticed between genotypes from Italy and the Eastern Mediterranean Sea. Cluster analysis was not able to define groups based on the geographic origin. Indeed, samples coming from different Italian regions were clustered together with genotypes originated from the other countries. Nevertheless, the Greek genotypes were clustered in a group including the most part of the Eastern Mediterranean Sea samples.

PCA identified two main clusters: Cluster 1 grouped together mainly samples from eastern Mediterranean Sea countries (97%) and southern Italy (59%), together with northern Italy, and Cluster 2 comprised only samples coming from the south of Italy (31%). The first two principal components, representing the first uncorrelated variables in which the correlated variables (SNPs) were transformed, explained the 39% of total variability. The genetic clusters were not geographically restricted.

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Structure analysis identified two as the most likely number of ancestral genetic groups (K = 2). Only the 8% of genotypes showed a percentage of membership > 80%. Although the high number of admixed genotypes, the spatial interpolation of ancestry proportions inferred assigned genotypes from the Eastern Mediterranean Sea countries and southern Italy to the same cluster. In the second cluster, samples belonging to northern Italy were mainly included.

The grouping of Italian and Greek samples together in the same clusters are in agreement with the historical events joining these two areas.[2] These results supported the hypothesis that during Greek colonization, Calabria and Sicilia played an important role for evaluating the potential of varieties coming from the eastern Mediterranean and their spreading firstly in southern Italy and afterwards in Etruscan Italy (Central Italy) and France.[3]

The first (parent-offspring) relationships were detected to define a proposed pedigree of southern Italian samples. Up to 52 genotypes from southern Italy shared almost one PO relationship. Most relationships were identified between southern Italian genotypes. Interpopulation relationships were also identified. The cultivars with the highest number of relationships were Sangiovese (13) and Mantonico Bianco (10). Other genotypes showing a well-defined pedigree-network were Bombino bianco (7 PO relationships) and Aglianico (6). These results revealed the use of elite cultivars in grape breeding programs. These cultivars have shaped the grapevine ampelographic platform of southern Italy. The elite cultivars (such as Sangiovese and Aglianico) were varieties widespread in many important winegrowing areas or minor varieties but with large local interest (such as Mantonico Bianco and Bombino bianco).[4]

In conclusion, a significant degree of gene flow was observed in agreement with historical and socio-eco-political events that occurred in the Mediterranean Basin. These results highlighted the central role of southern Italian germplasm in the spread of grapevine through Western Europe. The uniqueness of this ampelographic platform was mainly an outcome of complex natural or human-driven crosses involving elite cultivars.

Notes

[1] Costantini 1982; Cattani et al. 2004.

[2] Buono – Vallariello 2002.

[3] Collesano 1998; Buono – Vallariello 2002.

[4] Cipriani et al. 2010.

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