



Phylogenetic Relationship Among Wild and Cultivated Grapevine in Sicily: A Hotspot in the Middle of the Mediterranean Basin

OPEN ACCESS

Edited by:

Rosa Arroyo-García,
Instituto Nacional de Investigación
y Tecnología Agraria y Alimentaria
(INIA), Spain

Reviewed by:

Roberto Bacileri,
Institut National de la Recherche
Agronomique Centre Montpellier,
France

Gabriella De Lorenzis,
University of Milan, Italy

*Correspondence:

Roberto De Michele
roberto.demichela@cnr.it
Francesco Carimi
francesco.carimi@ibbr.cnr.it

†Present Address:

Roberto De Michele,
Institute of Bioscience and
Bioresource (CNR), Palermo, Italy
Francesco Carimi,
Institute of Bioscience and
Bioresource (CNR), Palermo, Italy

‡These authors have contributed
equally to this work

Specialty section:

This article was submitted to
Plant Systematics and Evolution,
a section of the journal
Frontiers in Plant Science

Received: 29 June 2019

Accepted: 29 October 2019

Published: 26 November 2019

Citation:

De Michele R, La Bella F, Gristina AS,
Fontana I, Pacifico D, Garfi G,
Motisi A, Crucitti D, Abbate L
and Carimi F (2019) Phylogenetic
Relationship Among Wild and
Cultivated Grapevine in Sicily:
A Hotspot in the Middle of the
Mediterranean Basin.
Front. Plant Sci. 10:1506.
doi: 10.3389/fpls.2019.01506

Roberto De Michele^{*††}, Francesca La Bella[‡], Alessandro Silvestre Gristina[‡],
Ignazio Fontana, Davide Pacifico, Giuseppe Garfi, Antonio Motisi, Dalila Crucitti,
Loredana Abbate and Francesco Carimi^{*†}

Institute of Biosciences and Bioresources (IBBR), National Research Council of Italy (CNR), Palermo, Italy

Grapevine (*Vitis vinifera* ssp. *sativa*) is a perennial crop especially important for wine and fruit production. The species is highly polymorphic with thousands of different varieties selected by farmers and clonally propagated. However, it is still debated whether grapevine domestication from its wild ancestor (*V. vinifera* ssp. *sylvestris*) has been a single event or rather it occurred on multiple occasions during the diffusion of its cultivation across the Mediterranean. Located in the center of the Basin, Sicily is its largest island and has served as a hotspot for all civilizations that have crossed the Mediterranean throughout history. Hundreds of unique grapevine cultivars are still cultivated in Sicily and its surrounding minor islands, though most of them are menaced by extinction. Wild grapevine is also present with isolated populations thriving along riverbanks. With the aim to evaluate the phylogenetic relationships among Sicilian varieties, and to assess the possible contribution of indigenous wild populations to the genetic makeup of cultivated grapevine, we analyzed 170 domestic cultivars and 125 wild plants, collected from 10 different populations, with 23 SSR markers. We also compared our data with published dataset from Eurasia. Results show that Sicilian wild populations are related to the cultivated Sicilian and Italian germplasm, suggesting events of introgression and/or domestication of local varieties.

Keywords: grapevine, *Vitis vinifera* subsp. *sativa*, *Vitis vinifera* subsp. *sylvestris*, domestication, SSR

INTRODUCTION

Grapevine (*Vitis vinifera* L.) is one of the most widespread and economically important perennial crops on the planet. It was estimated that in 2016 the world vineyard area was 7.4 million hectares, with a production of 76 million tons of fresh grapes and 269 million hectoliters (mhl) of wine (<http://www.oiv.int/>). The cultivation of the domesticated grape (*V. vinifera* L. subsp. *sativa* (DC.) Hegi) is believed to have started at least 7,000–8,000 years ago from its wild progenitor (*V. vinifera* L. subsp. *sylvestris* (Gmel.) Hegi (McGovern, 2003). Archaeological and historical studies evidenced that the primary center of domestication of the grapevine is located between the Near East (Zohary et al., 1996) and the Transcaucasian region (Olmo, 1976), then the grapevine spread around the Mediterranean, following the main civilizations (Carthaginians, Etruscans, Phoenicians, Greeks, and Romans) (McGovern, 2003). During its spreading across the Western Mediterranean regions,

the grapevine increased its genetic variability due to the contribution of multiple genetic pools and progressive human selection (Bacilieri et al., 2013). Different studies support the presence of secondary domestication centers, where spontaneous hybridizations among cultivated forms and local wild plants, or direct selection, generated the pattern of the modern Western European cultivars (Grassi et al., 2003; Arroyo-García et al., 2006; Myles et al., 2011; De Andrés et al., 2012; Riaz et al., 2018). Nowadays, more than 6,000 cultivated varieties are recorded (Lacombe et al., 2013; in OIV, 2017). The genotypes of the cultivated vine are highly heterozygous and most of the modern cultivars are hermaphrodite, self-fertile, and easily crossed (This et al., 2006). Several authors reported a high genetic diversity within the subsp. *sativa*, although it was recently demonstrated that such variability is included within a complex network of close pedigree relationships, derived by crosses among elite cultivars (Myles et al., 2011).

The domestic and the wild vine can be distinguished by morphological differences concerning leaves, flowers, and fruits, although in most cases the distinction of wild grape is hampered by the gene flow between the two subspecies (Di Vecchi-Staraz et al., 2009). The wild grapevine is a dioecious liana that grows in northern Africa, Europe, and the Near and Middle East, in areas between 30° and 50° north latitude. In central and eastern Europe, it thrives in mixed deciduous forests in correspondence with warmer (southern exposure) and humid (valleys of the Rhine, the Loire, the Rhone, the Danube, etc.) microclimates, while in the Mediterranean region it mainly participates in the riparian woodlands (pure or mixed populations dominated by poplars, willows, elms, ash trees, alders in areas with shallow water; pioneer shrub communities with tamarisks and oleanders along the middle-terminal section of the streams; mixed stands with holm and downy oak; shrubby mantle assemblages). At present time wild grapevine has become rather rare due to several forms of human disturbance, such as habitat destruction and fragmentation, silvicultural practices, diffusion of pathogens (e.g., oïdium, phylloxera, mildew, and viruses), improper management of natural environment, and hybridization with domestic forms (Arrigo and Arnold, 2007; Zecca et al., 2010; Garfi et al., 2013; Pacifico et al., 2016; Arnold et al., 2017). Gene flow between wild and cultivated grapevines was confirmed in several countries such as Spain (Arroyo-García et al., 2006; De Andrés et al., 2012), Italy (Zecca et al., 2010) and Georgia (Ekhvaia et al., 2014). In the last years, molecular methods based on the use of microsatellite (SSR) (This et al., 2004; Grassi et al., 2008; Carimi et al., 2011; Lacombe et al., 2013; Emanuelli et al., 2013) and, more recently, on single-nucleotide polymorphism (SNP) markers (Salmaso et al., 2004; Myles et al., 2011; Emanuelli et al., 2013; Laucou et al., 2018; De Lorenzis et al., 2019), as well as on genome sequencing (Zhou et al., 2017) allowed not only to improve the discrimination between wild and cultivated populations, but also to study the relationships among different cultivated varieties and wild accessions.

In Italy, grapevine cultivation is reported since the second half of the 2nd millennium BCE, starting from the Southern regions and then moving northward in the second part of the 1st millennium (Hopf, 1991; Forni, 2012). However, the recent discovery of a large storage jar containing tartaric acid could date

back to the Copper Age (early 4th–3rd millennium BCE) the origin of winemaking in Sicily (Tanasi et al., 2017). Sicily and its satellite islets host a rich vascular flora and due to its central position in the Mediterranean, the island has played and still plays a key role in connecting both plant and human populations of neighboring Mediterranean countries. Among plant species *V. vinifera* subsp. *sylvestris* is also present in the region with isolated populations mainly thriving along riverbanks (Garfi et al., 2013). Moreover, the island boasts a very ancient and rich tradition of viticulture practices and more than 70 different cultivars have been found in mainland Sicily (Carimi et al., 2010; Carimi et al., 2011). In addition, the Sicilian minor islets have recently emerged as a hotspot of genetic diversity for grapevine. Genetic analyses of this germplasm showed that at least 75 different genetic profiles are present in the Aeolian and Pelagie archipelagos, and the isles of Pantelleria and Ustica. Most of these genetic profiles (39) were not listed in national and international grapevine databases (Gristina et al., 2017). Such notable variety may have originated from domestication of wild autochthonous grapevines as well as from introduction of domesticated varieties from different regions during various historical periods.

In order to provide meaningful insights into grapevine evolution and domestication in the Mediterranean Basin, in this work, we compared the unique plant material constituted by the relict populations of Sicilian wild grapevine to the cultivated local germplasm, as well as to grapevine accessions from Western Europe and Central Asia. To evaluate the phylogenetic relationships among Sicilian varieties, and to assess the possible contribution of indigenous wild populations to the genetic makeup of cultivated grapevines, we analyzed with 23 nuclear SSR markers 170 local cultivars (*V. vinifera* spp. *sativa*), from the main Island and surrounding archipelagos, and 125 wild plants (*V. vinifera* spp. *sylvestris*) collected from 10 different Sicilian populations.

MATERIALS AND METHODS

Plant Materials, Study Sites, and Sampling

The list of cultivated and wild accessions analyzed in this study includes all the cultivars that had already been described as traditionally cultivated in Sicily and its minor islands (Carimi et al., 2010; Carimi et al., 2011; Gristina et al., 2017) and all the natural populations identified so far (Garfi et al., 2013), plus other cultivated and wild accessions collected in subsequent surveys.

Most part of the grapevine cultivars and the wild germplasm collected in the field is conserved in the germplasm repository for perennial plants by the Institute of Biosciences and BioResources of the National Research Council of Italy (CNR-IBBR) located in Collesano district (province of Palermo), Italy (37°59'19.9"N, 13°54'55.8"E, 80 m a.s.l.).

Wild *Vitis* germplasm was collected during several surveys between 2007 and 2016 in the main mountainous and protected areas of Sicily (Figure 1). Considering the morphologic resemblance of wild and cultivated grapevines, in order to reduce as much as possible the risk of collecting plants deriving from naturalized grapevine cultivars or rootstocks, the sampling strategy for *V. sylvestris* was based on the main

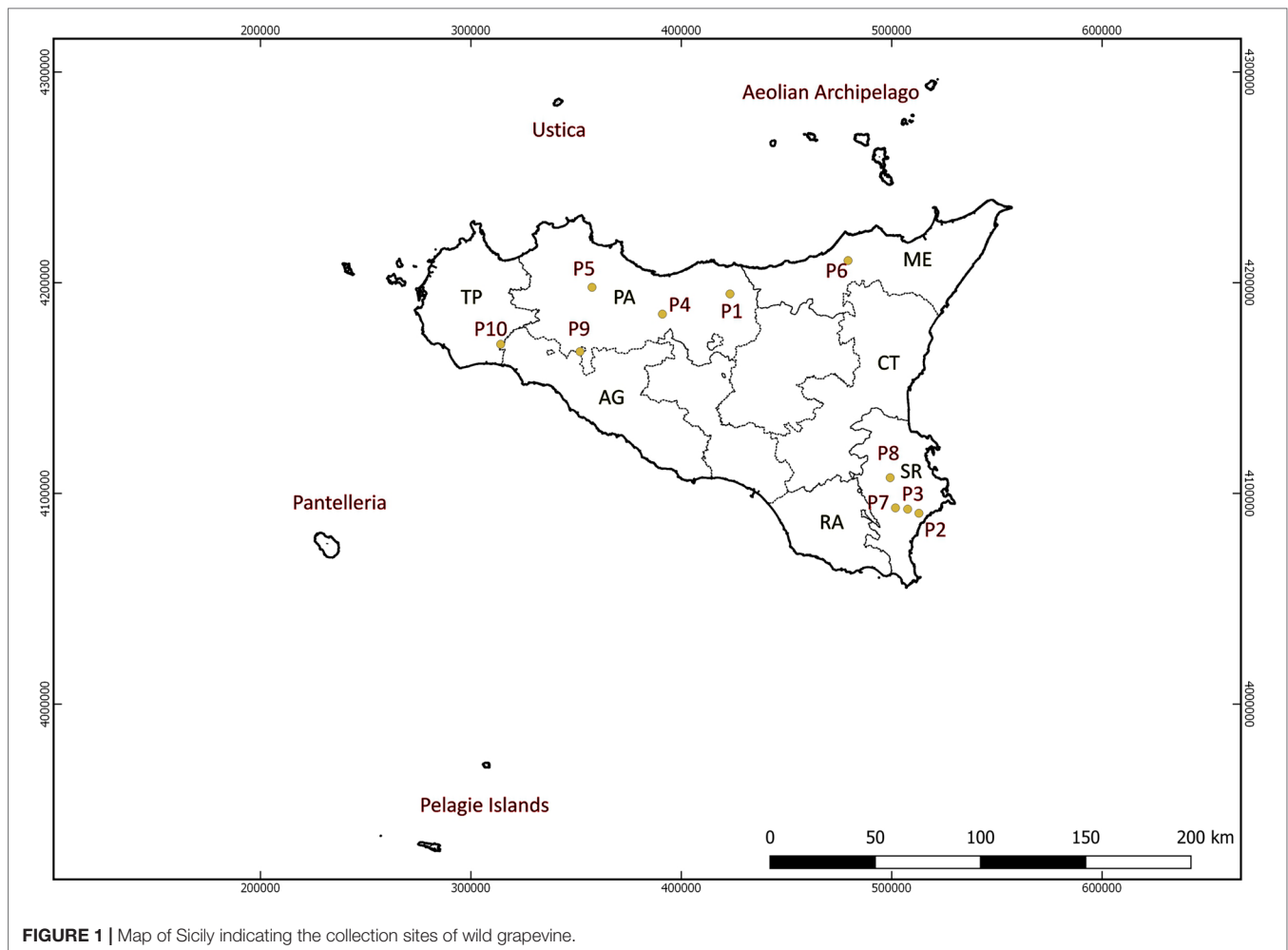


FIGURE 1 | Map of Sicily indicating the collection sites of wild grapevine.

differentiating reference traits used to distinguish wild grapevines from domesticated ones (Olmo, 1976; Garfi et al., 2013). Morphological data acquired *in situ* were integrated by 3–5 years of ampelographic studies carried out on grafted plants at the CNR-IBBR germplasm repository. In total, we collected 131 plants (**Supplementary Table S1**) from 10 different populations (**Supplementary Table S2**). Following molecular screening, four clones (3076 = 3074-P6, 3045 = 3058 = 3059 P4, 3139 = 3140-P10) and two feral forms (3109-P8, 3143-P10) were excluded from further analysis (final wild samples analyzed = 125).

Cultivated germplasm was collected between 2006 and 2017 directly from old vineyards. The cultivated accessions were selected following the indications of farmers and labeled for subsequent analysis and plant propagation. In total, 104 accessions were collected from Sicily and 66 from the surrounding minor islands (**Table 1**).

DNA Extraction and SSR Analysis

Total genomic DNA was extracted from young leaves or inner wood of young cuttings. Tissues were ground into fine powder with liquid nitrogen and stored at -80°C until use. The extraction was carried out following the CTAB method (Doyle and Doyle,

1987). DNA was diluted in water to a final concentration of $10\text{ ng}/\mu\text{l}$, and its quality assessed by spectrophotometric measurements.

Samples were analyzed at 23 SSR loci (Simple Sequence Repeat), i.e., VVS2 (Thomas and Scott, 1993), VVMD5, VVMD6, VVMD7, VVMD17, VVMD21, VVMD24, VVMD25, VVMD27, VVMD28, VVMD32 (Bowers et al., 1996; Bowers et al., 1999), VrZAG62, VrZAG79 (Sefc et al., 1999), VMC1b11 (Zyprian and Töpfer, 2005), VMC4f3.1 (Di Gaspero et al., 2000), VVIb01, VVIh54, VVIIn16, VVIIn73, VVIp31, VVIp60, VVIq52, and VVIv67 (Merdinoglu et al., 2005). Forward primers were labeled with one of four fluorescent dyes: 6-FAM, ATTO550, ATTO565, or Yakima Yellow. SSRs were grouped in six multiplex pools, each comprising three or four SSRs marked by different dyes, and characterized by similar annealing temperatures (**Supplementary Table S3**). Twenty-ng DNA per sample were amplified in 96 wells plates by using either the MyTaq HS (Bioline) or the DreamTaq HS (ThermoFisher) DNA polymerases with the following conditions: 15 min at 95°C (Taq activation step), followed by seven cycles consisting of 30 s at 94°C (denaturation), 90 s at the appropriate annealing temperature (**Supplementary Table S3**; touch-down step, with temperature decreasing by 1°C each cycle), 1 min at 72°C (extension). Additional 25 cycles with the same conditions maintained the final annealing temperature constant (**Supplementary Table S3**). Finally, the final PCR step

TABLE 1 | List of cultivated and wild accessions of *Vitis vinifera* (295) grouped into groups based on their geographic origin and analyzed by 23 SSR markers. The number of samples for each group is presented in brackets.

<i>V. vinifera</i> subsp. <i>sativa</i> (170)	<i>V. vinifera</i> subsp. <i>sylvestris</i> (125)
Sicily main Island (104)	P1 Castelbuono, Madonie Mts., Palermo (16)
Agrigento (8)	P2 Cava Grande Cassibile, Iblei Mts. Syracuse (14)
Catania (19)	P3 Cava Sturia, Iblei Mts. Syracuse (4)
Messina (9)	P4 Riserva Boschi Favara and Granza, Torto Valley Palermo (16)
Palermo (22)	P5 Bosco della Ficuzza, Sicani Mts. Palermo (9)
Ragusa (7)	P6 Stretta di Longi, Nebrodi Mts. Messina (12)
Syracuse (21)	P7 Fiume Manghisi, Iblei Mts. Syracuse (14)
Trapani (18)	P8 Riserva Pantalica and Valle Anapo, Iblei Mts. Syracuse (13)
Circum-Sicilian Islands (66)	P9 Fiume Sosio, Sicani Mts. Agrigento (20)
Aeolian Archipelago (39)	P10 Riserva Zangara, Belice Valley Trapani (7)
Pelagie Islands (3)	
Pantelleria Island (18)	
Ustica Island (6)	

In bold the wild populations code.

was set for 30 min at 60°C. PCR products were size-separated by capillary electrophoresis performed on a genetic analyzer (ABI Data analysis Prism3130, Applied Biosystems, Inc.) by an external service (Eurofins Genomics, Germany). Electropherograms were visually verified by Gene Mapper v. 5.0 software. Allele size was estimated by comparing the fragment peaks with the internal size standard, using the default method for size calling with SSR and the expected repeat size. To correct for amplification shifts among different PCRs, SSR profiles were normalized by including in each amplification run the DNA of standard cultivars Pinot Noir, Sauvignon Blanc, and Zibibbo. For comparison with the published dataset from Riaz et al. (2018), we used a subset of common core of 17 SSRs, excluding VrZAG62, VrZAG69, VVS2, VVMD5, VVMD17, and VVMD6 from our profiles. For normalization among datasets, we used two common varieties, namely Sangiovese (present with the synonym Minutidda in our dataset) and Zibibbo.

Data Analysis

To identify ferals, i.e., wild accessions with at least one cultivated parent, we performed a parentage analysis between Sicilian *sylvestris* and cultivated accessions using Bayes' theorem with the R/Solomon package (Christie et al., 2013). The identified ferals (2) were removed from the set of genotypes on which the analyses were performed.

Several diversity parameters were estimated using GenAlEx 6.5 (Peakall and Smouse, 2012): the number of alleles per locus (N_a), the number of effective alleles per locus (N_e), the observed (H_o) and expected (H_e) heterozygosity (Nei, 1978; Nei, 1987), and the fixation index (F). At population level, pairwise Nei's genetic distances and F_{st} value were calculated. Inbreeding coefficients F_{is} and F_{it} were calculated using Arlequin ver. 3.5.2.2 (Excoffier and Lischer, 2010).

The NJ (Neighbor-Joining) phylogenetic tree was designed by using R/ggtree package (Yu et al., 2017) with Nei's distance. The bootstrap analysis was performed based on 1,000 resamplings.

Genetic relationships among the studied genotypes were investigated by Discriminant Analysis of Principal Components

(DAPC). DAPC, implemented in the R/adeigenet (Jombart, 2008), was performed to infer population subdivision of the analyzed collection, regardless of the geographic origin. The number of principal components (PCs) retained was evaluated using the cross-validation procedure.

Principal coordinates analysis (PCoA) was performed by GenAlEx 6.5 via Covariance matrix with data standardization.

To identify the number of genetic groups in the wild populations and to investigate their relationships with domesticated cultivars we used the software STRUCTURE version 2.3.4 (Pritchard et al., 2000) that employs a model-based Bayesian clustering method. The estimate of the most likely number of genetic groups (K_s) was performed following Pritchard and Wen (2003) and the simulation study by Evanno et al. (2005), which proposed an *ad hoc* statistic, DELTA K . For each K , 20 independent runs (100,000 burn-in, 1,000,000 Markov Chain Monte Carlo) were carried out. All runs were performed with the admixture model. The 20 runs were averaged using the software CLUMPP (CLUSTER Matching and Permutation Program; Jakobsson and Rosenberg, 2007), and shown in histograms using the program Distruct (Rosenberg, 2004). For the hierarchical analysis, samples showing an ancestry value lower than 0.80 to any cluster were removed. The remaining subsets, one for each cluster, were independently subject to a second round of STRUCTURE analysis, as in Emanuelli et al. (2013), following the procedure described above.

RESULTS

Flower Characterization

One of the most obvious traits distinguishing *sativa* vs. *sylvestris* subspecies is the flower structure, since wild grapevine is dioecious whereas flowers of *V. vinifera* subs. *sativa* are usually hermaphroditic. In order to verify that plants collected in putative wild populations showed the dioecious phenotype, we analyzed flower morphology either during collection, or in subsequent years for those plants that had been transferred in the germplasm repository. **Supplementary Table S1** indicates the flower morphology for each plant. As expected, all the 170 cultivated plants had hermaphroditic flowers. Among the wild plants, we could assign a gender only to 122 out of 131 plants (93%), since in nine plants flowers and fruits were not evident at the collection time, and the scions did not survive grafting in the germplasm repository. Among the remainders, 68 plants were clearly females and 54 males, thus allowing us to exclude hermaphrodite plants that are usually considered feral or naturalized forms.

Genetic Diversity in the Sicilian Germplasm

The Sicilian wild and cultivated germplasm was first screened to identify clones and ferals. The four clones and two ferals identified by parentage analysis were then removed from our dataset.

The genetic profiles of the 170 cultivated and 125 wild accessions at 23 nuclear SSR loci are shown in **Supplementary Table S4**, and their statistics in **Table 2**. The total number of alleles (N_a) was 314,

TABLE 2 | Genetic diversity indices calculated for 295 distinct Sicilian genotypes belonging to *sativa* and *sylvestris* accessions.

Locus	N	Na	Ne	Ho	He	F
VWS2	281	14	5.6	0.829	0.821	-0.011
VWMD5	278	17	7.4	0.662	0.865	0.235
VWMD6	284	11	4.8	0.673	0.793	0.151
VWMD7	288	18	5.3	0.823	0.812	-0.014
VWMD17	287	10	3.2	0.408	0.683	0.403
VWMD21	286	15	2.8	0.570	0.646	0.118
VWMD24	283	9	2.9	0.572	0.654	0.124
VWMD25	278	12	4.6	0.705	0.782	0.098
VWMD27	290	13	6.0	0.807	0.833	0.032
VWMD28	262	24	8.8	0.748	0.887	0.156
VWMD32	276	13	5.7	0.783	0.825	0.052
VrZag62	283	11	7.4	0.859	0.865	0.007
VrZag79	281	13	5.2	0.722	0.809	0.107
VMC1b11	285	16	4.5	0.821	0.778	-0.056
VMC4f3.1	291	17	8.7	0.832	0.885	0.061
VVlb01	280	11	2.9	0.639	0.656	0.026
VVlh54	281	16	3.7	0.541	0.727	0.255
VVln16	283	8	3.4	0.640	0.704	0.092
VVln73	295	8	1.4	0.268	0.308	0.131
VVlp31	276	17	7.7	0.793	0.870	0.088
VVlp60	282	15	4.3	0.745	0.769	0.031
VVlq52	284	9	3.5	0.739	0.712	-0.039
VVlv67	284	17	6.5	0.768	0.846	0.092
Mean	282.5	13.7	5.06	0.693	0.762	0.093
Standard Error	1.348	0.809	0.418	0.030	0.026	0.022
Total		314				

Mean value over total samples for each Locus: N, sample size; Na, Number of alleles per locus; Ne, Number of effective alleles; Ho, Observed heterozygosity; He, Expected heterozygosity; F, Fixation index.

with a mean value per locus of 13.7. The marker VVln73 showed the lowest values of Na, effective alleles (Ne), observed and expected heterozygosity (Ho and He), whereas the marker VWMD28 the highest values, with the exception of Ho, where the maximum was present in VrZag62. The F value ranged from -0.056 (VMC1b11) to 0.403 (VWMD17), with a mean value of 0.093.

Genetic diversity analysis at population level shows that the number of alleles (Na) was similar between the cultivated pool (11.8) and the wild pool (10.8 as average), with wild populations ranging from 2.8 (P3, P4) to 7.0 (P9) (Table 3). For the number of effective alleles (Ne), the lowest value was in P4. In the cultivated pool, the observed and expected heterozygosity (Ho and He) were similar (0.697 and 0.741, respectively). The fixation index (F) and the inbreeding coefficient (Fis) were close to zero (0.067 and 0.025, respectively). In wild populations, P1 showed a marked positive F value (0.143), while in the other populations F was negative or close to zero, with P4 showing the lowest value (-0.567). Similarly Fis was strongly negative in P4 showing the lowest Fis value (-0.715).

The pairwise Nei's genetic distances and Fst values for all the wild populations and the cultivated pool is shown in Table 4. Nei's genetic distance ranged from 0.926 (P4-P5) to 0.083 (P8-cultivated). Fst values confirmed the pattern, with the highest value 0.324 for the pair P5-P4 and the lowest value 0.025 for cultivated-P8. Comparing the wild accessions altogether with the cultivated pool, Nei's genetic distance was 0.147, Fst 0.042 ($p < 0.001$), Fis 0.02667 ($p < 0.001$) and Fit 0.07406 ($p < 0.001$).

The genetic diversity of wild and cultivated Sicilian grapevines was first assessed by DAPC analysis of the SSR profiles (Figure

2A). The cultivated samples formed a compact cluster in the upper right part of the graph, whereas the wild samples were scattered along the left and the lower sides of the axes. Populations 4 and 5 were the most divergent along the y and x axes, respectively. P4 formed a separate pool, neither related to the other wild populations nor to the cultivated cluster; P5 was less homogeneous and it was clearly connected to other wild populations, yet it stood the furthest apart from the cultivated pool. Interestingly, three samples from wild populations, from P1, P6, and P8, lied amidst the cluster of *sativa*, possibly indicating cases of genetic introgression. Conversely, few cultivated samples fell close to *sylvestris* pools. These cultivars were: Bracau, Lorisi, Mantonico B, and Tintorè (Supplementary Dataset S1).

Samples were also discriminated by PCoA analysis, that is based on genetic distances (Figure 2B). The distribution pattern closely resembled the one originated by DAPC, with P4 forming an isolated pool, and the cultivated samples clustering on one side of the main axis. Interestingly, the PCoA confirmed that individual plants from P1, P6, and P8 were admixed within the cultivated cluster.

A third independent analysis of the genetic diversity in Sicilian wild and cultivated germplasm was performed by using STRUCTURE. With this method, the most likely sorting indicated two genetic clusters, A and B (Figure 2C, Supplementary Dataset S1). Almost all the cultivated plants (98%) belonged to the cluster B (Figure 2D). Of these, most of them (95%) had an ancestry value higher than 0.65, and 86% higher than 0.80, indicating a strong link to this cluster (Supplementary Dataset S1). Cluster B also included all samples

TABLE 3 | Genetic diversity estimates for wild populations and cultivated grapevines accessions analyzed from Sicily.

Population		N	Na	Ne	Ho	He	F	Fis
P1 - <i>sylvestris</i> (16)	Mean	15.1	5.7	3.5	0.578	0.670	0.143	0.076
	SE	0.3	0.4	0.3	0.043	0.026	0.054	0.054
P2 - <i>sylvestris</i> (14)	Mean	13.9	5.9	3.8	0.684	0.698	0.024	0.054
	SE	0.1	0.4	0.3	0.039	0.025	0.040	0.039
P3 - <i>sylvestris</i> (4)	Mean	3.6	2.8	2.3	0.699	0.527	-0.343	-0.300
	SE	0.1	0.2	0.1	0.056	0.034	0.080	0.092
P4 - <i>sylvestris</i> (16)	Mean	15.7	2.8	2.0	0.739	0.452	-0.567	-0.715
	SE	0.2	0.2	0.1	0.080	0.035	0.105	0.107
P5 - <i>sylvestris</i> (9)	Mean	8.8	4.2	3.0	0.750	0.632	-0.176	-0.122
	SE	0.1	0.2	0.2	0.047	0.027	0.048	0.049
P6 - <i>sylvestris</i> (12)	Mean	12.0	5.7	3.3	0.612	0.653	0.072	0.089
	SE	0.0	0.3	0.3	0.042	0.026	0.044	0.043
P7 - <i>sylvestris</i> (14)	Mean	13.6	4.4	3.1	0.760	0.634	-0.200	-0.233
	SE	0.1	0.3	0.2	0.042	0.027	0.046	0.046
P8 - <i>sylvestris</i> (13)	Mean	12.5	6.0	3.9	0.699	0.710	0.015	-0.006
	SE	0.2	0.4	0.3	0.034	0.026	0.035	0.035
P9 - <i>sylvestris</i> (20)	Mean	19.2	7.0	4.1	0.680	0.691	0.012	-0.037
	SE	0.1	0.6	0.4	0.038	0.035	0.033	0.033
P10 - <i>sylvestris</i> (7)	Mean	7.0	3.8	2.9	0.737	0.627	-0.179	-0.120
	SE	0.0	0.2	0.2	0.052	0.024	0.070	0.070
Total <i>sylvestris</i> (125)	Mean	121.2	10.8	4.6	0.689	0.748	0.082	0.029
	SE	0.7	0.8	0.3	0.029	0.025	0.021	0.020
<i>sativa</i> (170)	Mean	161.3	11.8	4.7	0.697	0.741	0.067	0.025
	SE	1.3	0.6	0.4	0.037	0.028	0.031	0.031
range		3.6–161.3	2.7–11.7	1.9–4.6	0.57–0.76	0.45–0.74	-0.56–0.14	-0.71–0.08

Mean value over loci for each population. N, number of samples; Na, number of alleles per population; Ne, number of effective alleles; Ho, Observed heterozygosity; He, Expected heterozygosity; F, Fixation index; Fis, inbreeding coefficient (within individuals relative to the rest of their subpopulation); SE, standard error. Numbers in brackets represent the number of accessions per group.

TABLE 4 | Estimates of pairwise *F*_{st} values (below the diagonal) and Unbiased Nei's genetic distance (above the diagonal) within overall wild and cultivated Sicilian accessions.

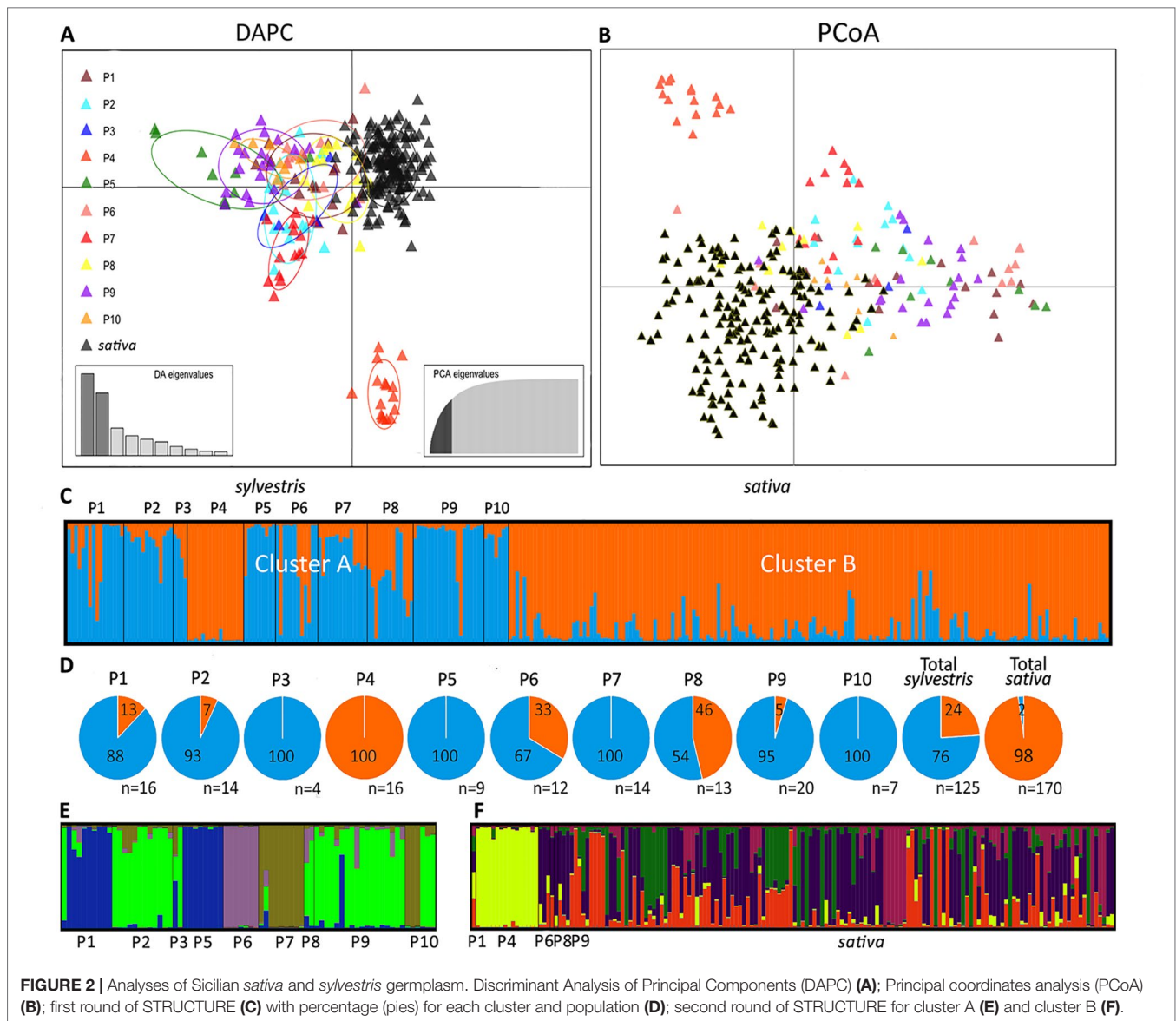
	P1 <i>sylvestris</i>	P2 <i>sylvestris</i>	P3 <i>sylvestris</i>	P4 <i>sylvestris</i>	P5 <i>sylvestris</i>	P6 <i>sylvestris</i>	P7 <i>sylvestris</i>	P8 <i>sylvestris</i>	P9 <i>sylvestris</i>	P10 <i>sylvestris</i>	<i>sativa</i>
P1 <i>sylvestris</i>		0.161	0.319	0.596	0.270	0.285	0.298	0.182	0.202	0.326	0.291
P2 <i>sylvestris</i>	0.054		0.192	0.380	0.423	0.210	0.170	0.112	0.134	0.281	0.225
P3 <i>sylvestris</i>	0.094	0.061		0.592	0.377	0.382	0.393	0.270	0.257	0.397	0.334
P4 <i>sylvestris</i>	0.241	0.191	0.288		0.926	0.635	0.325	0.298	0.606	0.582	0.315
P5 <i>sylvestris</i>	0.093	0.124	0.134	0.324		0.467	0.486	0.452	0.300	0.347	0.575
P6 <i>sylvestris</i>	0.096	0.071	0.125	0.268	0.148		0.377	0.243	0.170	0.415	0.361
P7 <i>sylvestris</i>	0.097	0.062	0.122	0.182	0.155	0.128		0.193	0.268	0.309	0.263
P8 <i>sylvestris</i>	0.049	0.037	0.070	0.172	0.128	0.080	0.068		0.167	0.193	0.083
P9 <i>sylvestris</i>	0.061	0.043	0.072	0.233	0.095	0.059	0.088	0.049		0.221	0.310
P10 <i>sylvestris</i>	0.104	0.090	0.133	0.277	0.125	0.135	0.115	0.066	0.073		0.268
<i>sativa</i>	0.079	0.062	0.081	0.138	0.137	0.100	0.078	0.025	0.080	0.077	

In bold significant *F*_{st} values with $p \leq 0.01$ calculated over 999 permutations.

from wild population P4, all of them with ancestry values higher than 0.80, and few individuals from P1, P6, and P8. Cluster A included the majority (76%) of wild plants. Looking in detail the ancestry values of each population, P3, P5, P7, and P10 had all individuals belonging to cluster A. The remaining populations, with the exception of the above mentioned P4, showed variable degrees of association to cluster A (ranging from 95% of P9 to 54% of P8). The association strength to cluster A was high for all wild populations, with ancestry values higher than 0.80 in most cases. The exceptions were P4, as discussed above, and P8, that was equally mixed between the two clusters, and showed low

ancestry values (<0.65) in most cases. Interestingly, the cluster A also included four cultivated plants (2% of all cultivated). These varieties are Austina bianca, Bracaù, Giugnatica, and Mantónico B. However, the ancestry values were lower than 0.65 for all these plants, indicating a weak association to the cluster.

Since STRUCTURE did not differentiate among the wild populations, except P4, and between P4 and the cultivated pool, we performed a hierarchical STRUCTURE analysis on the outcome of the first round. In the second round, samples from cluster A split into four subclusters (Figure 2E, Supplementary Dataset S1). Only two populations, P3 and P10, were equally



split between two subclusters. Each remaining population belonged exclusively (P2, P5, P6, P7, P8) or predominantly (90% P1; 94% P9) to single subclusters. For cluster B, the second round of STRUCTURE revealed five subclusters (Figure 2F, Supplementary Dataset S1). While the cultivated accessions and the few wild individuals of P1, P6, P8, and P9 (that in the first round grouped in cluster B) showed a very mixed pattern among the five subclusters, all individuals from P4 strongly grouped together in a private subcluster (ancestry value > 0.80 in all cases; Supplementary Dataset S1).

Finally, genetic distances among the Sicilian samples were also visualized in a phylogenetic tree (Supplementary Figure S1). The tree confirmed that most of *sylvestris* populations formed compact branches, indicating that individuals within a population were closely related with each other. The exception was P8 and a small part of P1, P6, and P9, whose individuals were interspersed among the cultivated samples.

Relationship of Sicilian vs. Mediterranean and Central Asian Germplasm

Recently, Riaz et al. (2018) analyzed a large set of cultivated and wild grapevine accessions from across the Mediterranean basin and Central Asia by 20 nuclear SSRs. In order to frame the genetic structure of the Sicilian germplasm within the geographical distribution of the species, we compared the profiles of 17 SSRs, that represented a common set in the two datasets. The genetic parameters for the markers analyzed are shown in Table 5. Overall, ranges and mean values of each parameter were similar to those of the Sicilian germplasm. In the wider survey, we observed a higher number of alleles (N_a and N_e), indicating an increased polymorphism in the largest dataset, as expected, especially since Central Asian populations are characterized by high genetic diversity (Riaz et al., 2018).

Since the dataset by Riaz et al. (2018) contains 289 Italian wild accessions, we first compared our Sicilian wild samples

TABLE 5 | Genetic diversity indices calculated for 1,673 genotypes from Europe to Asia belonging to *sativa* and *sylvestris* accessions.

Locus	Na	Ne	Ho	He	F
VWMD7	20	8.531	0.771	0.883	0.127
VWMD21	21	3.350	0.489	0.702	0.303
VWMD24	13	4.304	0.648	0.768	0.156
VWMD25	23	5.342	0.738	0.813	0.092
VWMD27	22	5.823	0.686	0.828	0.172
VWMD28	32	8.850	0.730	0.887	0.177
VWMD32	19	11.006	0.732	0.909	0.195
VMC1b11	24	6.919	0.702	0.855	0.179
VMC4f3.1	32	8.038	0.796	0.876	0.091
VVlb01	20	3.637	0.635	0.725	0.125
VVlh54	25	5.781	0.653	0.827	0.210
VVln16	14	3.173	0.602	0.685	0.121
VVln73	15	2.170	0.423	0.539	0.216
VMlp31	26	11.012	0.791	0.909	0.130
VVlp60	20	7.152	0.729	0.860	0.152
VVlq52	13	3.927	0.559	0.745	0.250
VVlv67	27	9.553	0.754	0.895	0.158
Mean	21.529	6.387	0.673	0.806	0.168
Standard Error	1.420	0.675	0.026	0.024	0.013
Total	366				

Na, Number of alleles per locus; Ne, Number of effective alleles; Ho, Observed heterozygosity; He, Expected heterozygosity; F, Fixation index.

against this subset. PCoA analysis showed that the two pools were clearly separated, and that the Sicilian samples were characterized by higher diversity along the second axis (**Supplementary Figure S2**). Therefore, the Sicilian wild dataset was not redundant with the Italian dataset, and it could be compared with all the other samples.

The DAPC analysis of all the cultivated and wild accessions from the Mediterranean and Central Asia, including the Sicilian populations, showed a triangle-shaped distribution (**Figure 3A**). The center of the triangle was populated by the wild samples from Croatia and the cultivated accessions from all the regions. The exceptions were Italy and Sicily, which clustered in the lowest vertex, together with all the Sicilian wild populations. The upper vertex included the *sylvestris* samples from Western Countries (Spain, France, Italy), whereas the rightmost vertex included the Eastern *sylvestris* populations (Armenia, Azerbaijan, Georgia). Similarly, the PCoA graph differentiated the Eastern from the Western wild samples. However, all the cultivated samples, including the Sicilian and the Italian, and the wild Sicilian grouped together in this analysis (**Figure 3B**).

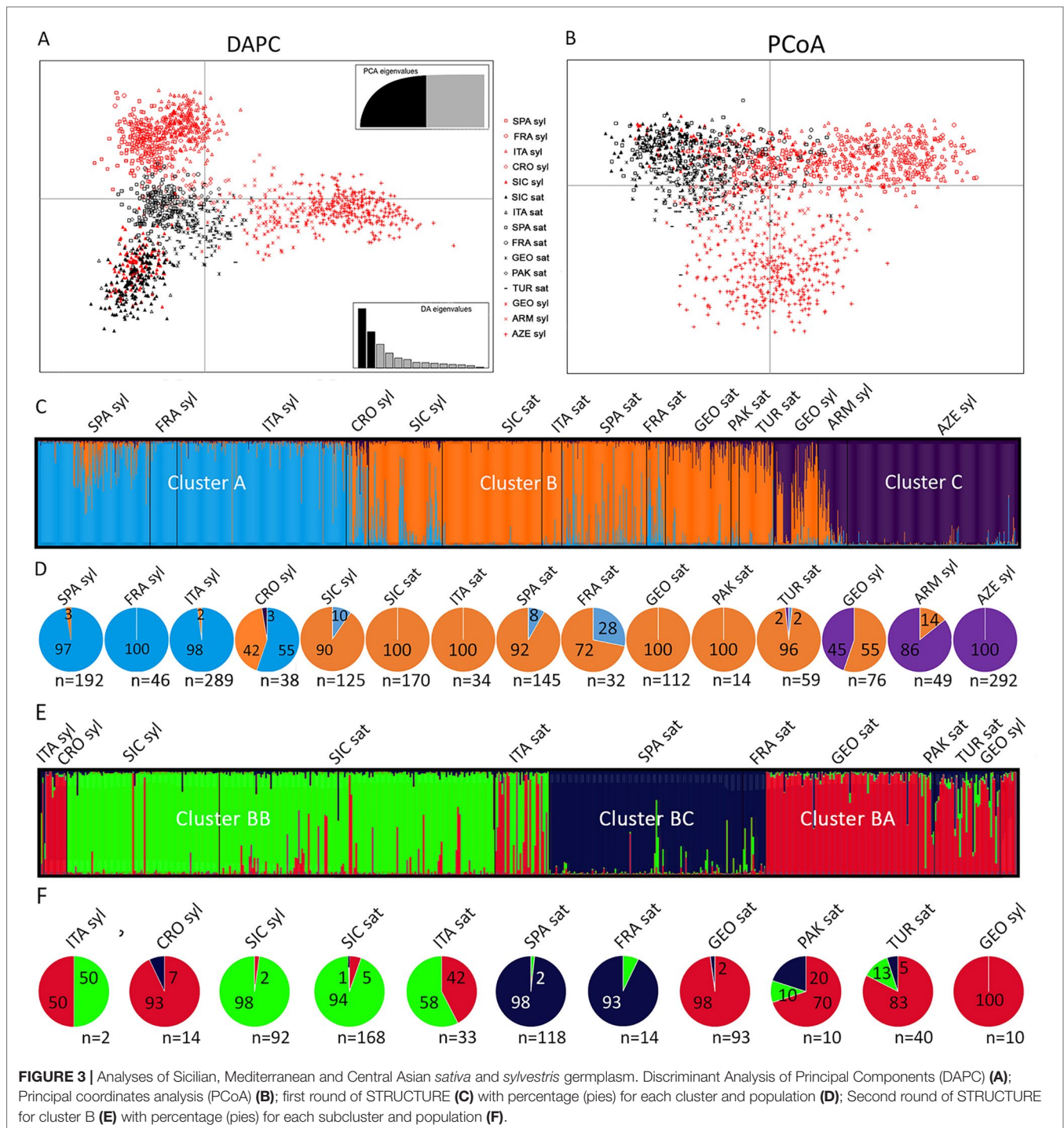
We then analyzed all data by STRUCTURE. The addition of the Sicilian germplasm did not vary the most likely number of clusters compared to the original analyses by Riaz et al. (2018), with $K = 3$ (**Figure 3C**). As in Riaz et al. (2018), one cluster (B) dominated all the cultivated samples, regardless of their origin (**Figure 3D**). A second cluster (C) characterized Asian wild samples. The third cluster (A) was the most abundant for almost all the wild Spanish, French, and Italian samples. The Croatian and Georgian wild samples were especially mixed between cluster A-B and B-C, respectively. A similar situation was observed for the Sicilian wild samples: the major component was cluster B, but many samples showed an important

contribution of cluster A. When the major contribution for each sample was considered, 90% of Sicilian wild samples were dominated by cluster B, and 10% by cluster A. Among the 12 samples belonging to cluster A, seven had an ancestry value higher than 0.65, and three exceeded 0.80 (**Supplementary Dataset S2**). When we looked at the distribution within each Sicilian population, only P5 had a large amount of samples (6 out of 9, 67%) belonging to cluster A; six populations (P3, P4, P6, P7, P8, P10) clustered entirely in cluster B; the remaining populations had a few samples in cluster A. All the cultivated Sicilian samples showed cluster B as major component. Nevertheless, Bracaù also had 22% association with cluster A, Austina bianca 19%, and Giugnatica 18%. For all the other samples, the ancestry value for cluster B was higher than 0.80.

Finally, we run a second round of STRUCTURE on the samples closely associated to cluster B, which included most of the Sicilian germplasm and the *sativa* accessions from all the regions. We identified three subclusters (**Figures 3E, F, Supplementary Dataset S2**). Subcluster BA included most of the Eastern *sativa* (Georgia 98%; Turkmenistan 83%; Pakistan 70%) and the residual Italian, Croatian, and Georgian *sylvestris* that were grouped in cluster B in the first round. Subcluster BB included most of the Sicilian germplasm, both *sylvestris* (98%) and *sativa* (94%), and more than half of the Italian *sativa* accessions (58%). Subcluster BC included almost all the Spanish and French cultivated accessions (98% and 93%, respectively).

DISCUSSIONS

For millennia, grapevine cultivation has been central in the culture and economy of many regions across the Mediterranean Basin and Middle East, with thousands of different varieties



selected. Yet, the exact dynamics of grapevine domestication remains elusive, and subject of a passionate debate among scholars of different fields. In the last decades, molecular techniques have expanded our ability to dig into the genetic signatures left along the history of crossing and migrations. Recent studies have generated genetic profiles for hundreds of cultivated and wild grapevine accessions, though the geographical origin of the

sampled material is generally unequal, with Eastern and Southern populations highly underrepresented. In this study, we compared the genetic structure of wild and cultivated grapevine germplasm from Sicily, a region that has been so far overlooked. Due to its size and its central position in the Mediterranean, bridging between Europe and Africa, Sicily has always played a key role in the migration routes crossing the Mediterranean basin, both for

natural dispersion of species and during human migrations. The recent discovery of a jar containing wine residues dates back the winemaking culture in Sicily to the 4th–3rd millennium BCE, i.e., at approximately the same time of the oldest wine traces found in the Armenia, and about 2,000 years later than the oldest evidence of wine production in Georgia, considered the primary domestication center for grapevine (Areshian et al., 2012; Tanasi et al., 2017; McGovern et al., 2017). For all these reasons, Sicily might have potentially played a major role in the domestication history of grapevine.

We first focused on the comparison between cultivated and wild populations within the Sicilian germplasm. The DAPC and the PCoA distinguished the cultivated from the wild germplasm along the main axis, reflecting major genetic distances between the two groups. Wild samples were especially scattered, indicating a high degree of diversity, probably due to the genetic isolation of most of the populations. The exception was the wild population P4, which separated from the cultivated pool only along the secondary axis, and was not connected with the other wild populations. STRUCTURE confirmed the major divergence between cultivated and wild samples. However, P4 initially grouped together with the cultivated pool, validating the affinity suggested by DAPC and PCoA. Only a second round of STRUCTURE separated P4 from *sativa*, matching the segregation observed along the secondary axis of DAPC and PCoA. These results, together with the *F_{st}* and *Nei* values, that were highest in the pairwise comparisons of P4 with the other wild groups, suggest that P4 is very different from the other Sicilian wild populations, as confirmed by the *F_{is}* value, and that is related to the cultivated accessions. We had already noticed the peculiar genetic makeup of P4 before, though using only six SSR markers (Garfi et al., 2013). It was speculated that the isolation and the unique ecological context of P4 (i.e., a scree-type instead than the usual riparian habitat, **Supplementary Table S2**) likely affected its propagation strategy, relying more on specialized faunal dispersion of seeds than on hydraulic dynamics. In this study, we also observed that P4 was the population showing the highest excess of heterozygosity (*F* and *F_{is}* index), suggesting that it might suffer from genetic introgression from external sources, for example by fertilization of female *sylvestris* plants with pollen from cultivated plants growing nearby, as prompted by the presence of abandoned fields in the surroundings. Intriguingly, all 18 individuals sampled in P4 turned out to be females (**Supplementary Table S1**), a pattern that cannot be explained by random sampling in a natural population of this size. Moreover, we excluded that P4 was a clonal population, spreading by vegetative propagation or apomixy, since genetic analysis revealed that only two plants were clones. All the other individuals were genetically different, though closely related to each other, as evident in the DAPC, PCoA, the second round of STRUCTURE and phylogenetic tree. A possible explanation would be that P4 derives from old dioecious varieties, an uncommon feature in modern cultivated plants, or from hybrids *V. vinifera* × *Vitis* spp., during the early attempts to transfer phylloxera resistance traits to European

grapes. That would explain the dioecious phenotype and the affinity with cultivated varieties. We also have to consider that SSRs are neutral molecular markers, whereas the expression of phenotypic traits can be influenced by environmental conditions. Therefore, it is possible that natural settings (forest or riverbank environment, as opposed to agricultural environment) can favor the expression of a more *sylvestris*-like morphology, while more *sativa*-type traits are masked. Finally, during our collection surveys, we deliberately sought plants possessing all the typical *sylvestris* features, such as a dioecious flower, ignoring those with hermaphroditic flowers, that could randomly appear at each generation in some individuals if a population maintains a significant *sativa* contribution. Yet, P4 forms a compact cluster in all the analyses we have performed, therefore the putative introgression events must have occurred in a common ancestor of all current individuals. Alternatively, P4 might represent the residues of an ancient *sylvestris* population that contributed to the genetic structure of many modern Sicilian and Italian cultivars, as discussed below.

Stronger evidence of introgression from the *sativa* pool characterizes P8, since this population largely mixed with the cultivated pool in all our analyses. Moreover, the STRUCTURE ancestry values of most accessions from P8 were weak, indicating mixed profiles between the *sativa* and *sylvestris* clusters. Confirming this hypothesis, the pairwise genetic distance between P8 and the cultivated pool was very low, and individuals from P8 were dispersed among *sativa* accessions in the phylogenetic tree. Population P8 is located in the Anapo Valley at Pantalica, a site with a large Neolithic necropolis that is known to be actively inhabited since ancient times, and that is currently surrounded by cultivated fields. To a minor extent, we also observed evidence of introgression in single individuals of P1 and P6, since a few samples clustered together with the *sativa* group in the DAPC, PCoA, STRUCTURE, and the phylogenetic tree. The genetic isolation of these populations was also confirmed by the positive inbreeding coefficient value (*F_{is}*). We suspect introgression with cultivated germplasm also for P3, P5, P7, P10 given that the observed heterozygosity (*H_o*) values are higher than the expected (*H_e*). Nevertheless, the negative *F_{is}* value showed by the latter populations, indicating an excess of heterozygosity, could be also due to the following different factors: the small population size, overdominant selection favoring heterozygote survival (heterosis) self-incompatibility system effect, proportion of asexual reproduction and effect of clonal reproduction on the number of heterozygotes (asexuality effect) (Stoeckel et al., 2006). All the other *sylvestris* samples are more isolated, showed different cluster distribution compared to the *sativa* pool and grouped together in the phylogenetic tree, suggesting that their genetic connection with the cultivated pool was weaker. In particular, P5 was the population less related to the *sativa* group, and more similar to the *sylvestris* germplasm from Italy, France, and Spain.

Taking advantage of the extensive study by Riaz et al. (2018), we compared the Sicilian germplasm to cultivated and wild accessions from Western Europe and Central Asia. The dataset

used by Riaz et al. (2018) comprises a large number of Italian *sylvestris* (289 accessions). The exact geographical origin of each accession is not specified in the paper, yet we ascertained that Riaz et al.'s dataset does not comprise any Sicilian sample (De Lorenzis, personal communication), as opposed to the larger collection from which the wild Italian samples from Riaz et al. derived (Biagini et al., 2014). Accordingly, we did not find any clone between our dataset and the one from Riaz et al. (2018). Moreover, DAPC and PCoA showed that the Sicilian *sylvestris* samples were very distantly related to the other wild Italian populations, including also those from the neighboring region Calabria, suggesting that the Sicilian wild populations are genetically isolated from the rest of Italy.

By using the combined dataset, the DAPC, PCoA, and STRUCTURE analyses confirmed what observed by these authors, with three main clusters discriminating: *i*) a Western *sylvestris* pool, *ii*) an Eastern *sylvestris* pool, and *iii*) the cultivated germplasm, regardless of their origin. The latter cluster also contained the wild Croatian samples. The samples falling in the transition zones among these clusters might suggest events of gene flow between wild populations and the cultivated germplasm in these regions, as previously reported from several investigations (Arroyo-García et al., 2006; Myles et al., 2011; De Andrés et al., 2012; Riaz et al., 2018). In addition to these three main pools, the DAPC also showed a fourth cluster which included most of the Sicilian *sylvestris* plants and all the Sicilian and Italian cultivated samples, suggesting that Sicilian and Italian cultivars are closely related, as expected due to the close geographical proximity, the deep historical connections between the two areas, and the intense commercial exchanges. Moreover, the Sicilian and Italian cultivars were more related with each other, and with the Sicilian *sylvestris*, than with other cultivars worldwide, suggesting events of genetic isolation and/or local secondary domestication, with introgression of genetic material from the Sicilian wild germplasm (possibly, from populations related to current P4) into the cultivated Italian pool. The latter hypothesis is consistent with the assumption that grapevine cultivation in Italy spread from the Southern regions northward since the second part of the 1st millennium BCE (Hopf, 1991; Forni, 2012).

The two-step analysis through STRUCTURE provided some additional information. In the first round of STRUCTURE, the cultivated Sicilian germplasm clustered together with most of the other *sativa* accessions; on the contrary, the wild populations showed a mixed distribution, clustering in part with the cultivated accessions and in part with the Western *sylvestris* pool, a situation similar to what observed in Croatia and, as for the Eastern cluster, in Georgia and Armenia. The different results obtained from STRUCTURE in the analysis of the Sicilian germplasm alone (where the cultivated pool clearly differed from the wild populations) and the wide scale analysis, might depend on the number of SSR markers used (23 in the first analysis and 17 in the second) and on the larger genetic diversity present in the world dataset, that may hinder the smaller differences within the Sicilian accessions. However, the second round of STRUCTURE clearly distinguished a cluster

including nearly all the Sicilian germplasm, both *sylvestris* and *sativa*, and more than half of the Italian cultivated accessions, thus confirming the affinity among these groups, already observed in the DAPC analysis. The hierarchical STRUCTURE also separated the cultivated accessions from other regions of the world in two additional clusters. One included almost all samples from Western Europe (Spain and France); a third cluster included the Eastern *sativa* accessions (Georgia, Pakistan, Turkmenistan) plus *sylvestris* from Georgia, Croatia and Italy. Interestingly, about half of the Italian (42%) cultivated accessions also showed affinity for this cluster. Therefore, the Italian cultivars are very different from the rest of Western Europe, and appear as mix between the Eastern group and the Sicilian pool. Accordingly, the list of Italian *sativa* accessions grouping together with the Sicilian germplasm consists predominantly (15 out of 18) of cultivars from Southern regions (Aglanico, Aglianicone, Catarratto Foglia tonda, Frappato, Grillo, Magliocco, Malvasia, Malvasia del Lazio, Malvasia nera di Brindisi, Montonico, Nerello cappuccio, Primitivo, Sangiovese, Sciacarello, Zibibbo) with the exception of three cultivars that are from Northern Italian regions (Glera, Ribolla gialla, and Schiava lombarda), pointing to a close relationship of this group with the Sicilian germplasm. Conversely, the remaining Italian cultivars, which show affinity with the Eastern pool, are varieties mostly cultivated in the Northern regions (Albarola, Barbera, Brugnola, Butascera, Croatina bianca, Croatina int. corto, Luglienga bianca, Marzemino, Merlina, Moradella di Montalto, Rossara, Rossola, Schiava grossa, Sirica).

The close relationship between the Sicilian *sylvestris* and the Sicilian and Italian *sativa* pools, observed in the wide DAPC, PCoA, and STRUCTURE analyses, is intriguing and can be explained by two different hypotheses. First, it is possible that many Sicilian wild populations suffer from introgression of *sativa* germplasm. This scenario is plausible, considering many different factors, such as the relatively small extension of the island, its millennial history of exploitation, the ancient reduction of its original forest cover, the importance of viticulture in the local economy with extensive fields, and the diffusion of recent diseases threatening the natural populations (Pacífico et al., 2016). We especially found strong evidence for this situation in population P8. Alternatively, it is possible that the current wild Sicilian populations are phylogenetically related to a *sylvestris* group that has not been identified yet, or is even extinct, and that contributed to the early domestication of grapevine. In that case, the residual current Sicilian wild populations maintain a close link to the cultivated germplasm or even directly contributed to the development of some local *sativa* varieties. For its genetic homogeneity, separation from the other *sylvestris* populations and its relation to the cultivated Sicilian and Italian pool, P4 represents an intriguing candidate.

In agreement with this hypothesis, our analyses indicated a few Sicilian cultivated varieties as closely related to the Sicilian wild germplasm, namely Austina bianca, Bracaù, Giugnatica, Lorisi, Mantonico, and Tintorè. Unfortunately, we could retrieve very little historical information for these varieties. Austina bianca

is a white grape variety cultivated in the province of Palermo, it was traditionally used for table and wine production. Bracaù, also known as Grecaù, is not mentioned in ancient literature. It is a black berry vine grown in the province of Catania, traditionally used for wine production (Carimi et al., 2010). Giugnatica is a red table grape grown in the Aeolian archipelago. It is considered an early grape that ripens in June. The first citation of Lorisì dates back to the beginning of the nineteenth century. Geremia (1836) mentioned Lorisì, also known as Visparu (Geremia, 1839) in a review of wine varieties found in the vineyards of Etna valley, province of Catania. It was used to make good quality sweet white wines and for the production of raisins. In the second half of the nineteenth century, Caruso (1869) mentions two forms of Lorisì (white and black berry) grown in the area of Cefalù, province of Palermo. Mantonico, existing as white and black berry versions, has been described in Sicily under different names: Muntonicu, Montonico nero femminino, Mantonicu niuru fimmineddu, Montonico nero and Mantonicu niuru for the black berry version, and Montonico bianco, Mantonicu vranco, Mantonicu masculu for the white berry version. The first citations of this vine dates back to the early 1500s (Venuti, 1516), and later on it was also mentioned by Cupani (1696), Sestini (1812) and Minà Palumbo (1891). In the Aeolian archipelago, where our accession was collected, the red grape form is considered a traditional local variety and is used to produce sweet wines (Gristina et al., 2017). The Tintorè grape, of unknown origin, was found in the province of Agrigento and used to darken the wine. There is no historical information on this grape variety in Sicily. Our results show that Sicilian wild populations are related to the cultivated Sicilian and Italian germplasm, suggesting events of introgression and/or domestication of local varieties. It is thus intriguing to speculate that these ancient Sicilian varieties may derive from local *sylvestris* germplasm.

CONCLUSIONS

The comparison of the genetic structure of Sicilian *sylvestris* populations with the cultivated local germplasm and the grapevine accessions across Western Europe and Central Asia confirms the genetic separation between the Western and Eastern *sylvestris* pools, and their connections with the cultivated germplasm. The Sicilian wild populations appeared closely related to the local cultivated germplasm, probably due to gene flow between the two pools, for either hybridization or early events of introgression of the *sylvestris* germplasm into *sativa* accessions. Considering the archeological evidences that point to Sicily among the oldest centers in grapevine

REFERENCES

- Areshian, G. E., Gasparyan, B., Avetisyan, P. S., Pinhasi, R., Wilkinson, K., Smith, A., et al. (2012). The chalcolithic of the Near East and south-eastern Europe: discoveries and new perspectives from the cave complex Areni-1, Armenia. *Antiquity* 86, 115–130. doi: 10.1017/s0003598x00062499
- Arnold, C., Bachmann, O., and Schnitzler, A. (2017). Insights into the *Vitis* complex in the Danube floodplain (Austria). *Ecol. Evol.* 7, 7796–7806. doi: 10.1002/ece3.3187
- Arrigo, N., and Arnold, C. (2007). Naturalised rootstocks in Europe and consequences to native wild grapevine. *PLoS One* 2, e251. doi: 10.1371/journal.pone.0000521

cultivation (Copper Age, early 4th–3rd millennium BCE), it is plausible that the genetic affinity among current Sicilian *sylvestris* and *sativa* germplasms derives from early domestication events occurred in this region. The data set and the results presented here, in a region of primary interest for understanding domestication, migration, and expansion of grape around the Mediterranean basin, may contribute to facilitate future investigations to further unravel the phylogenetic history and population dynamics of grapevine.

DATA AVAILABILITY STATEMENT

All datasets for this study are included in the article/Supplementary Files.

AUTHOR CONTRIBUTIONS

RM and FC conceived and supervised the project. RM, AG, LA, AM, GG and FC contributed to collect plant materials. RM, DC and FB performed the genetic characterization of the plant material. RM, AG and IF analysed the data. RM, AG, IF, and FC analysed and interpreted data. RM, AG, DP and FC wrote the first draft. All authors made a substantial, direct and intellectual contribution to this work. All of the author approve the final version of the manuscript.

FUNDING

This research was supported by Regione Siciliana (PSR Sicilia 2007–2013, Sottomisura 214/2A-Preservazione della biodiversità: Centri pubblici di conservazione, Grant No. 94750767637).

ACKNOWLEDGMENTS

We are grateful to Mr. Giacomo and Alessandro Mannone of 'Mannone Nurseries' in Petrosino (district of Trapani) for helping us to the identification of main Sicilian grapevines and for supplying nursery plants.

SUPPLEMENTARY MATERIAL

The Supplementary Material for this article can be found online at: <https://www.frontiersin.org/articles/10.3389/fpls.2019.01506/full#supplementary-material>

- Arroyo-García, R., Ruíz-García, L., Bolling, L., Ocete, R., López, M. A., Arnold, C. et al. (2006). Multiple origins of cultivated grapevine (*Vitis vinifera* L. ssp. *sativa*) based on chloroplast DNA polymorphisms. *Mol. Ecol.* 15, 3707–3714. doi: 10.1111/j.1365-294X.2006.03049.x
- Bacilieri, R., Lacombe, T., Le Cunff, L., Di Vecchi-Staraz, M., Laucou, V., Genna, B., et al. (2013). Genetic structure in cultivated grapevines is linked to geography and human selection. *BMC. Plant Biol.* 13, 25. doi: 10.1186/1471-2229-13-25
- Biagini, B., De Lorenzis, G., Imazio, S., Failla, O., and Scienza, A. (2014). Italian wild grapevine (*Vitis vinifera* L. subsp. *sylvestris*) population: insights into

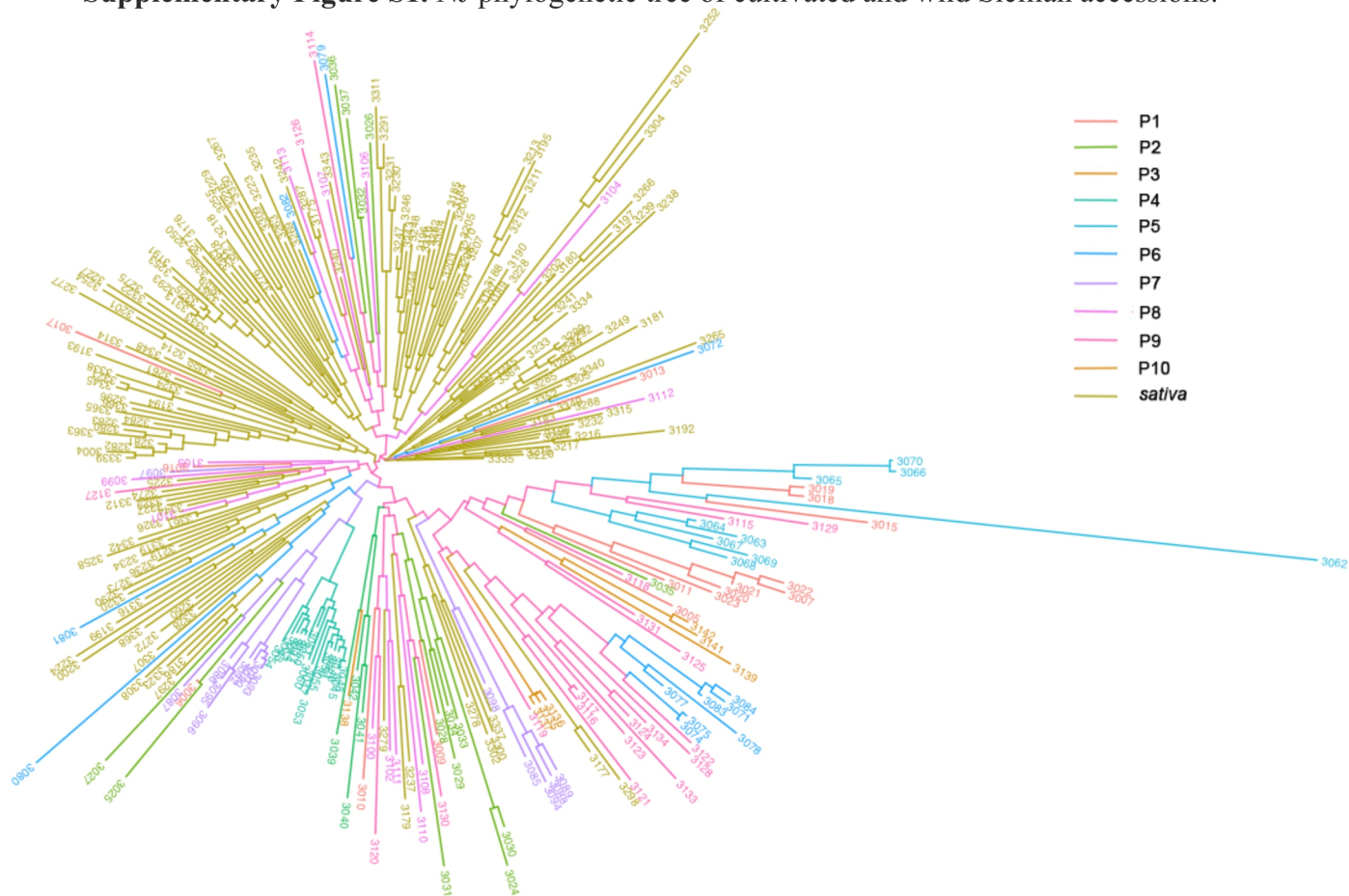
- eco-geographical aspects and genetic structure. *Tree Genet. Genomes* 10 (5), 1369–1385. doi: 10.1007/s11295-014-0767-4
- Bowers, J. E., Dangl, G. S., Vignani, R., and Meredith, C. P. (1996). Isolation and characterization of new polymorphic simple sequence repeat loci in grape (*Vitis vinifera* L.). *Genome* 39, 628–633. doi: 10.1139/g96-080
- Bowers, J. E., Dangl, G. S., and Meredith, C. P. (1999). Development and characterization of additional microsatellite DNA markers for grape. *Am. J. Enol. Viticult.* 50, 243–246.
- Carimi, F., Mercati, F., Abbate, L., and Sunseri, F. (2010). Microsatellite analyses for evaluation of genetic diversity among Sicilian grapevine cultivars. *Genet. Resour. Crop Ev.* 57 (5), 703–719. doi: 10.1007/s10722-009-9506-3
- Carimi, F., Mercati, F., De Michele, R., Fiore, M. C., Riccardi, P., and Sunseri, F. (2011). Intra-varietal genetic diversity of the grapevine (*Vitis vinifera* L.) cultivar 'Nero d'Avola' as revealed by microsatellite markers. *Genet. Resour. Crop Ev.* 58 (7), 967–975. doi: 10.1007/s10722-011-9731-4
- Caruso, G. (1869). *Trattato di viticoltura e vinificazione. ovvero il presente e l'avvenire enologico dell'Italia meridionale*. Stamperia di Giovanni Lorusnaider: Palermo.
- Christie, M. R., Tennessen, J. A., and Blouin, M. S. (2013). Bayesian parentage analysis with systematic accountability of genotyping error, missing data and false matching. *Bioinformatics* 29 (6), 725–732. doi: 10.1093/bioinformatics/btt039
- Cupani, F. (1696). *Hortus Catholicus seu illustrissimi, and excellentissimi principis Catholicae*. Neapoli: Ed. Benzi.
- De Andrés, M. T., Benito, A., Pérez-Rivera, G., Ocete, R., Lopez, M. A., Gaforio, L. et al. (2012). Genetic diversity of wild grapevine populations in Spain and their genetic relationships with cultivated grapevines. *Mol. Ecol.* 21 (4), 800–816. doi: 10.1111/j.1365-294X.2011.05395.x
- De Lorenzis, G., Mercati, F., Bergamini, C., Cardone, M. F., Lupini, A., and Maucri, A. et al. (2019). SNP genotyping elucidates the genetic diversity of Magna Graecia grapevine germplasm and its historical origin and dissemination. *BMC Plant Biol.* 19 (1), 7. doi: 10.1186/s12870-018-1576-y
- Di Gaspero, G., Peterluner, E., Testolin, R., Edwards, K. J., and Cipriani, G. (2000). Conservation of microsatellite loci within the genus *Vitis*. *Theor. Appl. Genet.* 101, 301–308. doi: 10.1007/s001220051483
- Di Vecchi-Staraz, M., Laucou, V., Bruno, G., Lacombe, T., Gerber, S., Bourse, T., et al. (2009). Low level of pollen-mediated gene flow from cultivated to wild grapevine: consequences for the evolution of the endangered subspecies *Vitis vinifera* L. subsp. *silvestris*. *J. Hered.* 100, 66–75. doi: 10.1093/jhered/esn084
- Doyle, J. J., and Doyle, J. L. (1987). A rapid DNA isolation procedure from small quantities of fresh leaf tissue. *Phytochem. Bull.* 19, 11–15.
- Ekhvaia, J., Gurushidze, M., Blattner, F. R., and Akhalkatsi, M. (2014). Genetic diversity of *Vitis vinifera* in Georgia: relationships between local cultivars and wild grapevine, *V. vinifera* L. subsp. *silvestris*. *Genet. Resour. Crop Ev.* 61, 1507–1521. doi: 10.1007/s10722-014-0125-2
- Emanuelli, F., Lorenzi, S., Grzeskowiak, L., Catalano, V., Stefanini, M., Troggio, M., et al. (2013). Genetic diversity and population structure assessed by SSR and SNP markers in a large germplasm collection of grape. *BMC Plant Biol.* 13, 39. doi: 10.1186/1471-2229-13-39
- Evanno, G., Regnaut, S., and Goudet, J. (2005). Detecting the number of clusters of individuals using the software structure: A simulation study. *Mol. Ecol.* 14, 2611–2620. doi: 10.1111/j.1365-294x.2005.02553.x
- Excoffier, L., and Lischer, H. E. (2010). Arlequin suite ver 3.5: A new series of programs to perform population genetics analyses under Linux and Windows. *Mol. Ecol. Resour.* 10, 564–567. doi: 10.1111/j.1755-0998.2010.02847.x
- Forni, G. (2012). "The origin of "old world" viticulture," in *Caucasus and Northern Black Sea region ampelography*. Eds. Maghradze, L., Rustioni, A., Scienza, J., Turok, O., and Failla, D. *Vitis*, special issue. (VITIS, The Journal of Grapevine Research.), 27–38.
- Garfi, G., Mercati, F., Fontana, I., Collesano, G., Pasta, S., Vendramin, G. G., et al. (2013). Habitat features and genetic integrity of wild grapevine *Vitis vinifera* L. subsp. *silvestris* (C.C. Gmel.) Hegi populations: a case study from Sicily. *Flora* 208, 538–548. doi: 10.1016/j.flora.2013.08.005
- Geremia, G. (1836). Vertunno Etneo ovvero Stafulegrafia, storia delle varietà delle uve che trovansi nel dintorno dell'Etna. *Atti. dell'Accademia Gioenia. Catania.* 11, 313–340.
- Geremia, G. (1839). Vertunno Etneo ovvero Stafulegrafia, storia delle varietà delle uve che trovansi nel dintorno dell'Etna. *Atti. dell'Accademia Gioenia. Catania.* 14, 3–5557–68.
- Grassi, F., Labra, M., Imazio, S., Spada, A., Sgorbati, S., Scienza, A., et al. (2003). Evidence of a secondary grapevine domestication centre detected by SSR analysis. *Theor. Appl. Genet.* 107, 1315–1320. doi: 10.1007/s00122-003-1321-1
- Grassi, F., Mattia, F. D., Zecca, G., Sala, F., and Labra, M. (2008). Historical isolation and Quaternary range expansion of divergent lineages in wild grapevine. *Biol. J. Linn. Soc.* 95, 611–619. doi: 10.1111/j.1095-8312.2008.01081.x
- Gristina, A. S., De Michele, R., Garfi, G., La Mantia, T., Fontana, I., Spinelli, P., et al. (2017). Urgent need for preservation of grapevine (*Vitis vinifera* L. subsp. *vinifera*) germplasm from small circum-Sicilian islands as revealed by SSR markers and traditional use investigations. *Genet. Resour. Crop Ev.* 64 (6), 1395–1415. doi: 10.1007/s10722-016-0444-6
- Hopf, M. (1991). "South and Southwest Europe", in *Progress in old world palaeoethnobotany*. Eds. Van Zeist, K., Wasylikowa, K. E., and Behre, W. (Balkema: Rotterdam-Brookfield), 241–277.
- Jakobsson, M., and Rosenberg, N. A. (2007). CLUMPP: a cluster matching and permutation program for dealing with label switching and multimodality in analysis of population structure. *Bioinformatics* 23, 1801–1806. doi: 10.1093/bioinformatics/btm233
- Jombart, T. (2008). adegenet: a R package for the multivariate analysis of genetic markers. *Bioinformatics* 24 (11), 1403–1405. doi: 10.1093/bioinformatics/btn129
- Lacombe, T., Boursiquot, J. M., Laucou, V., Di Vecchi-Staraz, M., Peros, J. M., and This, P. (2013). Large-scale parentage analysis in an extended set of grapevine cultivars (*Vitis vinifera* L.). *Theor. Appl. Genet.* 126, 401–414. doi: 10.1007/s00122-012-1988-2
- Laucou, V., Launay, A., Bacilieri, R., Lacombe, T., Adam-Blondon, A. F., Bérard, A., et al. (2018). Extended diversity analysis of cultivated grapevine *Vitis vinifera* with 10K genome-wide SNPs. *PLoS One* 13 (2), e0192540. doi: 10.1371/journal.pone.0192540
- McGovern, P., Jalabadze, M., Batiuk, S., Callahan, M. P., Smith, K. E., and Hall, G. R. (2017). Early Neolithic wine of Georgia in the South Caucasus. *Proc. Natl. Acad. Sci.* 114 (48), E10309–E10318. doi: 10.1073/PNAS.1714728114
- McGovern, P. E. (2003). *Ancient wine: the search for the origins of viniculture*. Princeton: Princeton University Press.
- Merdinoglu, D., Butterlin, G., Bevilacqua, L., Chiquet, V., Adam-Blondon, A.F. and Decroocq, S. (2005). Development and characterization of a large set of micro satellite markers in grapevine (*Vitis vinifera* L.) suitable for multiplex PCR. *Mol. Breed.* 15, 349–366. doi: 10.1007/s11032-004-7651-0
- Minà Palumbo, F. (1891). *Viticultura Sicula. Cenni storici. Atti e Rendiconti Acc. Zelaniti in Acireale. vol. III, 71–82*. Acireale, Italy: Vincenzo Micale.
- Myles, S., Boyko, A. R., Owens, C. L., Brown, P. J., Grassi, F., Aradhya, M. K., et al. (2011). Genetic structure and domestication history of the grape. *Proc. Natl. Acad. Sci.* 108, 3530–3535. doi: 10.1073/pnas.1009363108
- Nei, M. (1978). Estimation of average heterozygosity and genetic distance from a small number of individuals. *Genetics* 89, 583–590.
- Nei, M. (1987). *Molecular evolutionary genetics*. (New York: Columbia University Press).
- OIV. (2017). *Vitiviniculture Situation. OIV Statistical Report on World Vitiviniculture*. Paris: International Organisation of Vine and Wine. <http://www.oiv.int/>.
- Olmo, H. P. (1976). "Grapes," in *Evolution of crop plants*. Eds. Simmonds, N. W. (London: Longman), 294–298.
- Pacifico, D., Stigliano, E., Sposito, L., Spinelli, P., Garfi, G., Gristina, A. S., et al. (2016). Survey of viral infections in spontaneous grapevines from natural environments in Sicily. *Eur. J. Plant Pathol.* 145, 189–197. doi: 10.1007/s10658-015-0785-6
- Peakall, R., and Smouse, P. E. (2012). GenAlEx 6.5: genetic analysis in Excel. Population genetic software for teaching and research—an update. *Bioinformatics* 28, 2537–2539. doi: 10.1093/bioinformatics/bts460
- Pritchard, J. K., and Wen, W. (2003). *Documentation for STRUCTURE Software: Version 2*. Chicago: University of Chicago Press.
- Pritchard, J. K., Stephens, M., and Donnelly, P. (2000). Inference of population structure using multilocus genotype data. *Genetics* 155, 945–959.
- Riaz, S., De Lorenzis, G., Velasco, D., Koehmstedt, A., Maghradze, D., Bobokashvili, Z., et al. (2018). Genetic diversity analysis of cultivated and wild grapevine (*Vitis vinifera* L.) accessions around the Mediterranean basin and Central Asia. *BMC Plant Biol.* 18, 137. doi: 10.1186/s12870-018-1351-0
- Rosenberg, N. A. (2004). DISTRUCT: a program for the graphical display of population structure. *Mol. Ecol. Notes* 4, 137–138. doi: 10.1046/j.1471-8286.2003.00566.x

- Salmaso, M., Faes, G., Segala, C., Stefanini, M., Salakhutdinov, L., Zyprian, E., et al. (2004). Genome diversity and gene haplotypes in the grapevine (*Vitis vinifera* L.), as revealed by single nucleotide polymorphisms. *Mol. Breed.* 14, 385–395. doi: 10.1007/s11032-004-0261-z
- Sefc, K. M., Regner, F., Turetschek, E., Glössl, J., and Steinkellner, H. (1999). Identification of microsatellite sequences in *Vitis riparia* and their applicability for genotyping of different *Vitis* species. *Genome* 42, 367–373.
- Sestini, D. (1812). *Dei vini in generale della Sicilia*. Firenze, Manuscript 11c: Accademia dei Gorgofili.
- Stoeckel, S., Grange, J., Fernández-Manjarres, J. F., Bilger, I., Frascaria-Lacoste, N., and Mariette, S. (2006). Heterozygote excess in a self-incompatible and partially clonal forest tree species — *Prunus avium* L. *Mol. Ecol.* 5, 2109–2118. doi: 10.1111/j.1365-294X.2006.02926.x
- Tanasi, D., Greco, E., Di Tullio, V., Capitani, D., Gulli, D., and Ciliberto, E. (2017). 1H-1H NMR 2D-TOCSY, ATR FT-IR and SEM-EDX for the identification of organic residues on Sicilian prehistoric pottery. *Microchem. J.* 135, 140–147. doi: 10.1016/j.microc.2017.08.010
- This, P., Jung, A., Boccacci, P., Borrego, J., Costantini, L., Crespan, M., et al. (2004). Development of a common set of standard varieties and standardized method of scoring microsatellites markers for the analysis of grapevine genetic resources. *Theor. Appl. Genet.* 109, 1448–1458. doi: 10.1007/s00122-004-1760-3
- This, P., Lacombe, T., and Thomas, M. R. (2006). Historical origins and genetic diversity of wine grapes. *Trends Genet.* 22, 511–519. doi: 10.1016/j.tig.2006.07.008
- Thomas, M. R., and Scott, N. S. (1993). Microsatellite repeats in grapevine reveal DNA polymorphisms when analyzed as sequence tagged sites (STSs). *Theor. Appl. Genet.* 86, 985–990. doi: 10.1007/bf00211051
- Venuti, A. (1516). *De agricultura opusculum*. Napoli, Italy: Sigismondo Mayer Alemanno.
- Yu, G., Smith, D. K., Zhu, H., Guan, Y., and Lam, T. T.-Y. (2017). ggtree: an R package for visualization and annotation of phylogenetic trees with their covariates and other associated data. *Methods Ecol. Evol.* 8, 28–36. doi: 10.1111/2041-210x.12628
- Zecca, G., De Mattia, F., Loviou, G., Labra, M., Sala, F., and Grassi, F. (2010). Molecular grapevine: *Sylvestris*, hybrids or cultivars that escaped from vineyards? Molecular evidence in Sardinia. *Plant Biol.* 12, 155–162. doi: 10.1111/j.1438-8677.2009.00226.x
- Zhou, Y., Massonnet, M., Sanjak, J. S., Cantu, D., and Gaut, B. S. (2017). Evolutionary genomics of grape (*Vitis vinifera* ssp. *vinifera*) domestication. *Proc. Natl. Acad. Sci.* 114 (44), 201709257. doi: org/10.1073/pnas.1709257114
- Zohary, D. (1996). "Domestication of the Grapevine *Vitis vinifera* L. in the Near East," in *The origins and ancient history of wine*. Eds. McGovern, S., Fleming, S., and Katz, P. (New York: Gordon and Breach), 23–30.
- Zyprian, E., and Töpfer, R. (2005). *Development of microsatellite-derived markers for grapevine genotyping and genetic mapping*. GeneBank: NCBI.

Conflict of Interest: The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

Copyright © 2019 De Michele, La Bella, Gristina, Fontana, Pacifico, Garfi, Motisi, Crucitti, Abbate and Carimi. This is an open-access article distributed under the terms of the Creative Commons Attribution License (CC BY). The use, distribution or reproduction in other forums is permitted, provided the original author(s) and the copyright owner(s) are credited and that the original publication in this journal is cited, in accordance with accepted academic practice. No use, distribution or reproduction is permitted which does not comply with these terms.

Supplementary Figure S1. NJ phylogenetic tree of cultivated and wild Sicilian accessions.



Supplementary Table S1. List of 301 *V. vinifera* subsp. *sativa* and *sylvestris* grapevine samples analysed.

Accessions ID	Species	Population Code	Source District / Area (Population Code)	Name	Sex
3089	<i>V. vinifera</i> subsp. <i>sylvestris</i>	P7	Fiume Manghisi, Iblei Mts. SR (P7)		♂
3090	<i>V. vinifera</i> subsp. <i>sylvestris</i>	P7	Fiume Manghisi, Iblei Mts. SR (P7)		♀
3091	<i>V. vinifera</i> subsp. <i>sylvestris</i>	P7	Fiume Manghisi, Iblei Mts. SR (P7)		♀
3092	<i>V. vinifera</i> subsp. <i>sylvestris</i>	P7	Fiume Manghisi, Iblei Mts. SR (P7)		♀
3093	<i>V. vinifera</i> subsp. <i>sylvestris</i>	P7	Fiume Manghisi, Iblei Mts. SR (P7)		♀
3094	<i>V. vinifera</i> subsp. <i>sylvestris</i>	P7	Fiume Manghisi, Iblei Mts. SR (P7)		♂
3095	<i>V. vinifera</i> subsp. <i>sylvestris</i>	P7	Fiume Manghisi, Iblei Mts. SR (P7)		♂
3096	<i>V. vinifera</i> subsp. <i>sylvestris</i>	P7	Fiume Manghisi, Iblei Mts. SR (P7)		♂
3097	<i>V. vinifera</i> subsp. <i>sylvestris</i>	P7	Fiume Manghisi, Iblei Mts. SR (P7)		♀
3098	<i>V. vinifera</i> subsp. <i>sylvestris</i>	P7	Fiume Manghisi, Iblei Mts. SR (P7)		♂
3099	<i>V. vinifera</i> subsp. <i>sylvestris</i>	P8	Riserva Pantalica e Valle Anapo, Iblei Mts. SR (P8)		♂
3100	<i>V. vinifera</i> subsp. <i>sylvestris</i>	P8	Riserva Pantalica e Valle Anapo, Iblei Mts. SR (P8)		♂
3101	<i>V. vinifera</i> subsp. <i>sylvestris</i>	P8	Riserva Pantalica e Valle Anapo, Iblei Mts. SR (P8)		nd
3102	<i>V. vinifera</i> subsp. <i>sylvestris</i>	P8	Riserva Pantalica e Valle Anapo, Iblei Mts. SR (P8)		nd
3104	<i>V. vinifera</i> subsp. <i>sylvestris</i>	P8	Riserva Pantalica e Valle Anapo, Iblei Mts. SR (P8)		♀
3105	<i>V. vinifera</i> subsp. <i>sylvestris</i>	P8	Riserva Pantalica e Valle Anapo, Iblei Mts. SR (P8)		♂
3106	<i>V. vinifera</i> subsp. <i>sylvestris</i>	P8	Riserva Pantalica e Valle Anapo, Iblei Mts. SR (P8)		♀
3107	<i>V. vinifera</i> subsp. <i>sylvestris</i>	P8	Riserva Pantalica e Valle Anapo, Iblei Mts. SR (P8)		♂
3108	<i>V. vinifera</i> subsp. <i>sylvestris</i>	P8	Riserva Pantalica e Valle Anapo, Iblei Mts. SR (P8)		♀
3109	<i>V. vinifera</i> subsp. <i>sylvestris</i>	P8	Riserva Pantalica e Valle Anapo, Iblei Mts. SR (P8)		♀
3110	<i>V. vinifera</i> subsp. <i>sylvestris</i>	P8	Riserva Pantalica e Valle Anapo, Iblei Mts. SR (P8)		♀
3111	<i>V. vinifera</i> subsp. <i>sylvestris</i>	P8	Riserva Pantalica e Valle Anapo, Iblei Mts. SR (P8)		♂
3112	<i>V. vinifera</i> subsp. <i>sylvestris</i>	P8	Riserva Pantalica e Valle Anapo, Iblei Mts. SR (P8)		♀
3113	<i>V. vinifera</i> subsp. <i>sylvestris</i>	P8	Riserva Pantalica e Valle Anapo, Iblei Mts. SR (P8)		♀
3114	<i>V. vinifera</i> subsp. <i>sylvestris</i>	P9	Fiume Sosio, Sicani Mts. AG (P9)		♂
3115	<i>V. vinifera</i> subsp. <i>sylvestris</i>	P9	Fiume Sosio, Sicani Mts. AG (P9)		♂
3116	<i>V. vinifera</i> subsp. <i>sylvestris</i>	P9	Fiume Sosio, Sicani Mts. AG (P9)		♂
3117	<i>V. vinifera</i> subsp. <i>sylvestris</i>	P9	Fiume Sosio, Sicani Mts. AG (P9)		♀
3118	<i>V. vinifera</i> subsp. <i>sylvestris</i>	P9	Fiume Sosio, Sicani Mts. AG (P9)		♂
3119	<i>V. vinifera</i> subsp. <i>sylvestris</i>	P9	Fiume Sosio, Sicani Mts. AG (P9)		♀
3120	<i>V. vinifera</i> subsp. <i>sylvestris</i>	P9	Fiume Sosio, Sicani Mts. AG (P9)		♂
3121	<i>V. vinifera</i> subsp. <i>sylvestris</i>	P9	Fiume Sosio, Sicani Mts. AG (P9)		♂
3122	<i>V. vinifera</i> subsp. <i>sylvestris</i>	P9	Fiume Sosio, Sicani Mts. AG (P9)		♀
3123	<i>V. vinifera</i> subsp. <i>sylvestris</i>	P9	Fiume Sosio, Sicani Mts. AG (P9)		♀
3124	<i>V. vinifera</i> subsp. <i>sylvestris</i>	P9	Fiume Sosio, Sicani Mts. AG (P9)		♂
3125	<i>V. vinifera</i> subsp. <i>sylvestris</i>	P9	Fiume Sosio, Sicani Mts. AG (P9)		♂
3126	<i>V. vinifera</i> subsp. <i>sylvestris</i>	P9	Fiume Sosio, Sicani Mts. AG (P9)		nd
3127	<i>V. vinifera</i> subsp. <i>sylvestris</i>	P9	Fiume Sosio, Sicani Mts. AG (P9)		♀
3128	<i>V. vinifera</i> subsp. <i>sylvestris</i>	P9	Fiume Sosio, Sicani Mts. AG (P9)		♂
3129	<i>V. vinifera</i> subsp. <i>sylvestris</i>	P9	Fiume Sosio, Sicani Mts. AG (P9)		♂
3130	<i>V. vinifera</i> subsp. <i>sylvestris</i>	P9	Fiume Sosio, Sicani Mts. AG (P9)		♀
3131	<i>V. vinifera</i> subsp. <i>sylvestris</i>	P9	Fiume Sosio, Sicani Mts. AG (P9)		♂
3133	<i>V. vinifera</i> subsp. <i>sylvestris</i>	P9	Fiume Sosio, Sicani Mts. AG (P9)		♂
3134	<i>V. vinifera</i> subsp. <i>sylvestris</i>	P9	Fiume Sosio, Sicani Mts. AG (P9)		♀
3135	<i>V. vinifera</i> subsp. <i>sylvestris</i>	P10	Riserva Zangara, Belice Valley TP (P10)		♂
3136	<i>V. vinifera</i> subsp. <i>sylvestris</i>	P10	Riserva Zangara, Belice Valley TP (P10)		♂
3137	<i>V. vinifera</i> subsp. <i>sylvestris</i>	P10	Riserva Zangara, Belice Valley TP (P10)		nd
3138	<i>V. vinifera</i> subsp. <i>sylvestris</i>	P10	Riserva Zangara, Belice Valley TP (P10)		nd
3139	<i>V. vinifera</i> subsp. <i>sylvestris</i>	P10	Riserva Zangara, Belice Valley TP (P10)		♀
3140	<i>V. vinifera</i> subsp. <i>sylvestris</i>	P10	Riserva Zangara, Belice Valley TP (P10)		♀
3141	<i>V. vinifera</i> subsp. <i>sylvestris</i>	P10	Riserva Zangara, Belice Valley TP (P10)		nd
3142	<i>V. vinifera</i> subsp. <i>sylvestris</i>	P10	Riserva Zangara, Belice Valley TP (P10)		♂
3143	<i>V. vinifera</i> subsp. <i>sylvestris</i>	P10	Riserva Zangara, Belice Valley TP (P10)		♀
3175	<i>V. vinifera</i> subsp. <i>sativa</i>	SR	Syracuse (SR)	Albanello	♀♂
3176	<i>V. vinifera</i> subsp. <i>sativa</i>	CT	Catania (CT)	Alzano	♀♂
3177	<i>V. vinifera</i> subsp. <i>sativa</i>	PA	Palermo (PA)	Austina bianca	♀♂
3178	<i>V. vinifera</i> subsp. <i>sativa</i>	PA	Palermo (PA)	Barbarossa	♀♂
3179	<i>V. vinifera</i> subsp. <i>sativa</i>	CT	Catania (CT)	Bracàù (Grecàù)	♀♂
3180	<i>V. vinifera</i> subsp. <i>sativa</i>	SR	Syracuse (SR)	Bruntisi nero	♀♂
3181	<i>V. vinifera</i> subsp. <i>sativa</i>	CT	Catania (CT)	Calabrese	♀♂
3183	<i>V. vinifera</i> subsp. <i>sativa</i>	ME	Messina (ME)	Carnuffino	♀♂
3184	<i>V. vinifera</i> subsp. <i>sativa</i>	CT	Catania (CT)	Carricante A	♀♂
3185	<i>V. vinifera</i> subsp. <i>sativa</i>	CT	Catania (CT)	Carricante C	♀♂
3186	<i>V. vinifera</i> subsp. <i>sativa</i>	PA	Palermo (PA)	Catanese nero	♀♂
3187	<i>V. vinifera</i> subsp. <i>sativa</i>	TP	Trapani (TP)	Catarratto D	♀♂
3188	<i>V. vinifera</i> subsp. <i>sativa</i>	AG	Agrigento (AG)	Catarratto A	♀♂
3189	<i>V. vinifera</i> subsp. <i>sativa</i>	TP	Trapani (TP)	Catarratto B	♀♂
3190	<i>V. vinifera</i> subsp. <i>sativa</i>	PA	Palermo (PA)	Catarratto C	♀♂
3191	<i>V. vinifera</i> subsp. <i>sativa</i>	PA	Palermo (PA)	Catarratto nero	♀♂
3192	<i>V. vinifera</i> subsp. <i>sativa</i>	PA	Palermo (PA)	Catarratto Termini	♀♂
3193	<i>V. vinifera</i> subsp. <i>sativa</i>	SR	Syracuse (SR)	Cessalà	♀♂
3194	<i>V. vinifera</i> subsp. <i>sativa</i>	AG	Agrigento (AG)	Cirriaciò	♀♂
3195	<i>V. vinifera</i> subsp. <i>sativa</i>	ME	Messina (ME)	Coda di volpe	♀♂
3196	<i>V. vinifera</i> subsp. <i>sativa</i>	EO	Aeolian archipelago (EO)	Corinto A	♀♂
3197	<i>V. vinifera</i> subsp. <i>sativa</i>	EO	Aeolian archipelago (EO)	Corinto B	♀♂
3198	<i>V. vinifera</i> subsp. <i>sativa</i>	TP	Trapani (TP)	Damaschino A	♀♂
3199	<i>V. vinifera</i> subsp. <i>sativa</i>	PA	Palermo (PA)	Diretta bianca	♀♂
3200	<i>V. vinifera</i> subsp. <i>sativa</i>	PA	Palermo (PA)	Diretta bianca (Uva di Francia)	♀♂

Supplementary Table S1. List of 301 *V. vinifera* subps. *sativa* and *sylvestris* grapevine samples analysed.

Accessions ID	Species	Population Code	Source District / Area (Population Code)	Name	Sex
3201	<i>V. vinifera</i> subps. <i>sativa</i>	PA	Palermo (PA)	Diretta nera A	♀♂
3202	<i>V. vinifera</i> subps. <i>sativa</i>	CT	Catania (CT)	Dolcetta	♀♂
3203	<i>V. vinifera</i> subps. <i>sativa</i>	RG	Ragusa (RG)	Frappato C	♀♂
3204	<i>V. vinifera</i> subps. <i>sativa</i>	RG	Ragusa (RG)	Frappato 2	♀♂
3205	<i>V. vinifera</i> subps. <i>sativa</i>	RG	Ragusa (RG)	Frappato 3	♀♂
3206	<i>V. vinifera</i> subps. <i>sativa</i>	RG	Ragusa (RG)	Frappato A	♀♂
3207	<i>V. vinifera</i> subps. <i>sativa</i>	RG	Ragusa (RG)	Frappato B	♀♂
3208	<i>V. vinifera</i> subps. <i>sativa</i>	RG	Ragusa (RG)	Frappato F	♀♂
3210	<i>V. vinifera</i> subps. <i>sativa</i>	SR	Syracuse (SR)	Gamay	♀♂
3211	<i>V. vinifera</i> subps. <i>sativa</i>	AG	Agrigento (AG)	Grecanico A	♀♂
3212	<i>V. vinifera</i> subps. <i>sativa</i>	AG	Agrigento (AG)	Grecanico B	♀♂
3213	<i>V. vinifera</i> subps. <i>sativa</i>	TP	Trapani (TP)	Grecanico C	♀♂
3214	<i>V. vinifera</i> subps. <i>sativa</i>	CT	Catania (CT)	Grecaù (Bracau)	♀♂
3215	<i>V. vinifera</i> subps. <i>sativa</i>	TP	Trapani (TP)	Grillo A	♀♂
3216	<i>V. vinifera</i> subps. <i>sativa</i>	TP	Trapani (TP)	Grillo C	♀♂
3217	<i>V. vinifera</i> subps. <i>sativa</i>	TP	Trapani (TP)	Grillo D	♀♂
3218	<i>V. vinifera</i> subps. <i>sativa</i>	PA	Palermo (PA)	Jala bianca	♀♂
3219	<i>V. vinifera</i> subps. <i>sativa</i>	ME	Messina (ME)	Inzolia A	♀♂
3220	<i>V. vinifera</i> subps. <i>sativa</i>	AG	Agrigento (AG)	Inzolia C	♀♂
3221	<i>V. vinifera</i> subps. <i>sativa</i>	PA	Palermo (PA)	Inzolia imperiale A	♀♂
3223	<i>V. vinifera</i> subps. <i>sativa</i>	CT	Catania (CT)	Inzuccherato	♀♂
3224	<i>V. vinifera</i> subps. <i>sativa</i>	SR	Syracuse (SR)	Inzuccherato di Noto	♀♂
3225	<i>V. vinifera</i> subps. <i>sativa</i>	AG	Agrigento (AG)	Lacrima di Maria A	♀♂
3226	<i>V. vinifera</i> subps. <i>sativa</i>	SR	Syracuse (SR)	Leanfurtisi	♀♂
3227	<i>V. vinifera</i> subps. <i>sativa</i>	PA	Palermo (PA)	Lorisi (Orisi)	♀♂
3228	<i>V. vinifera</i> subps. <i>sativa</i>	ME	Messina (ME)	Lucignola	♀♂
3229	<i>V. vinifera</i> subps. <i>sativa</i>	SR	Syracuse (SR)	Malvagia	♀♂
3230	<i>V. vinifera</i> subps. <i>sativa</i>	EO	Aeolian archipelago (EO)	Malvasia di Lipari C	♀♂
3231	<i>V. vinifera</i> subps. <i>sativa</i>	EO	Aeolian archipelago (EO)	Malvasia di Lipari A	♀♂
3232	<i>V. vinifera</i> subps. <i>sativa</i>	PA	Palermo (PA)	Marsala (Mareschino)	♀♂
3233	<i>V. vinifera</i> subps. <i>sativa</i>	AG	Agrigento (AG)	Marsigliana	♀♂
3234	<i>V. vinifera</i> subps. <i>sativa</i>	PA	Palermo (PA)	Minna di vacca B	♀♂
3235	<i>V. vinifera</i> subps. <i>sativa</i>	ME	Messina (ME)	Minnavacchina	♀♂
3236	<i>V. vinifera</i> subps. <i>sativa</i>	SR	Syracuse (SR)	Minnella bianca (Passulana)	♀♂
3237	<i>V. vinifera</i> subps. <i>sativa</i>	SR	Syracuse (SR)	Monteleone	♀♂
3238	<i>V. vinifera</i> subps. <i>sativa</i>	SR	Syracuse (SR)	Moscato di Noto B	♀♂
3239	<i>V. vinifera</i> subps. <i>sativa</i>	SR	Syracuse (SR)	Moscato bianco	♀♂
3240	<i>V. vinifera</i> subps. <i>sativa</i>	SR	Syracuse (SR)	Moscato di Noto C	♀♂
3241	<i>V. vinifera</i> subps. <i>sativa</i>	SR	Syracuse (SR)	Muscatedda	♀♂
3242	<i>V. vinifera</i> subps. <i>sativa</i>	SR	Syracuse (SR)	Muscatidduni	♀♂
3243	<i>V. vinifera</i> subps. <i>sativa</i>	CT	Catania (CT)	Nerello Mascalese B	♀♂
3244	<i>V. vinifera</i> subps. <i>sativa</i>	CT	Catania (CT)	Nerello Mascalese C	♀♂
3245	<i>V. vinifera</i> subps. <i>sativa</i>	CT	Catania (CT)	Nerello cappuccio A	♀♂
3246	<i>V. vinifera</i> subps. <i>sativa</i>	CT	Catania (CT)	Nerello Mascalese D	♀♂
3247	<i>V. vinifera</i> subps. <i>sativa</i>	CT	Catania (CT)	Nerello Mascalese E	♀♂
3248	<i>V. vinifera</i> subps. <i>sativa</i>	CT	Catania (CT)	Nerello Mascalese A	♀♂
3249	<i>V. vinifera</i> subps. <i>sativa</i>	TP	Trapani (TP)	Nero d'Avola A	♀♂
3250	<i>V. vinifera</i> subps. <i>sativa</i>	PA	Palermo (PA)	Nero grosso	♀♂
3251	<i>V. vinifera</i> subps. <i>sativa</i>	EO	Aeolian archipelago (EO)	Nivureddu	♀♂
3252	<i>V. vinifera</i> subps. <i>sativa</i>	CT	Catania (CT)	Nivuro Bronte	♀♂
3253	<i>V. vinifera</i> subps. <i>sativa</i>	PA	Palermo (PA)	Nucera nera (Perricone)	♀♂
3254	<i>V. vinifera</i> subps. <i>sativa</i>	SR	Syracuse (SR)	Nzuccherato	♀♂
3255	<i>V. vinifera</i> subps. <i>sativa</i>	ME	Messina (ME)	Oriddu	♀♂
3258	<i>V. vinifera</i> subps. <i>sativa</i>	SR	Syracuse (SR)	Oso nivuro	♀♂
3259	<i>V. vinifera</i> subps. <i>sativa</i>	TP	Trapani (TP)	Perricone A	♀♂
3260	<i>V. vinifera</i> subps. <i>sativa</i>	PA	Palermo (PA)	Pizzutella	♀♂
3261	<i>V. vinifera</i> subps. <i>sativa</i>	SR	Syracuse (SR)	Precoce	♀♂
3262	<i>V. vinifera</i> subps. <i>sativa</i>	ME	Messina (ME)	Preventivo	♀♂
3263	<i>V. vinifera</i> subps. <i>sativa</i>	SR	Syracuse (SR)	Racignola bianca	♀♂
3265	<i>V. vinifera</i> subps. <i>sativa</i>	EO	Aeolian archipelago (EO)	Racina di vento	♀♂
3266	<i>V. vinifera</i> subps. <i>sativa</i>	CT	Catania (CT)	Racinedda	♀♂
3267	<i>V. vinifera</i> subps. <i>sativa</i>	SR	Syracuse (SR)	Recunu (Bufania)	♀♂
3269	<i>V. vinifera</i> subps. <i>sativa</i>	EO	Aeolian archipelago (EO)	Rucignola	♀♂
3270	<i>V. vinifera</i> subps. <i>sativa</i>	SR	Syracuse (SR)	Russetto	♀♂
3271	<i>V. vinifera</i> subps. <i>sativa</i>	SR	Syracuse (SR)	Sparo virdisi	♀♂
3272	<i>V. vinifera</i> subps. <i>sativa</i>	PA	Palermo (PA)	Sultanina	♀♂
3273	<i>V. vinifera</i> subps. <i>sativa</i>	PA	Palermo (PA)	Tallone nero	♀♂
3274	<i>V. vinifera</i> subps. <i>sativa</i>	AG	Agrigento (AG)	Tintorè (Ibisu)	♀♂
3275	<i>V. vinifera</i> subps. <i>sativa</i>	PA	Palermo (PA)	Triboti nera	♀♂
3276	<i>V. vinifera</i> subps. <i>sativa</i>	PA	Palermo (PA)	Tripolina bianca	♀♂
3277	<i>V. vinifera</i> subps. <i>sativa</i>	PA	Palermo (PA)	Uva francisi	♀♂
3278	<i>V. vinifera</i> subps. <i>sativa</i>	CT	Catania (CT)	Visparola	♀♂
3279	<i>V. vinifera</i> subps. <i>sativa</i>	ME	Messina (ME)	Vitraruolo	♀♂
3004	<i>V. vinifera</i> subps. <i>sativa</i>	PT	Pantelleria island (PT)	Zibibbo A	♀♂
3280	<i>V. vinifera</i> subps. <i>sativa</i>	PT	Pantelleria island (PT)	Zibibbo augustano	♀♂
3281	<i>V. vinifera</i> subps. <i>sativa</i>	PT	Pantelleria island (PT)	Zibibbo B	♀♂
3282	<i>V. vinifera</i> subps. <i>sativa</i>	PT	Pantelleria island (PT)	Zibibbo carricante	♀♂
3283	<i>V. vinifera</i> subps. <i>sativa</i>	PT	Pantelleria island (PT)	Zibibbo grosso	♀♂

Supplementary Table S1. List of 301 *V. vinifera* subsp. *sativa* and *sylvestris* grapevine samples analysed.

Accessions ID	Species	Population Code	Source District / Area (Population Code)	Name	Sex
3284	<i>V. vinifera</i> subsp. <i>sativa</i>	PT	Pantelleria island (PT)	Zibibbo nero	♀♂
3285	<i>V. vinifera</i> subsp. <i>sativa</i>	TP	Trapani (TP)	Nero d'Avola B	♀♂
3286	<i>V. vinifera</i> subsp. <i>sativa</i>	TP	Trapani (TP)	Nero d'Avola C	♀♂
3287	<i>V. vinifera</i> subsp. <i>sativa</i>	TP	Trapani (TP)	Nero d'Avola D	♀♂
3292	<i>V. vinifera</i> subsp. <i>sativa</i>	TP	Trapani (TP)	Nero d'Avola F	♀♂
3294	<i>V. vinifera</i> subsp. <i>sativa</i>	TP	Trapani (TP)	Nero d'Avola G	♀♂
3299	<i>V. vinifera</i> subsp. <i>sativa</i>	TP	Trapani (TP)	Nero d'Avola E	♀♂
3304	<i>V. vinifera</i> subsp. <i>sativa</i>	CT	Catania (CT)	Alicante, Licante	♀♂
3307	<i>V. vinifera</i> subsp. <i>sativa</i>	EO	Aeolian archipelago (EO)	Inzolia imperiale B	♀♂
3308	<i>V. vinifera</i> subsp. <i>sativa</i>	EO	Aeolian archipelago (EO)	Cantaro	♀♂
3309	<i>V. vinifera</i> subsp. <i>sativa</i>	EO	Aeolian archipelago (EO)	Trummana	♀♂
3310	<i>V. vinifera</i> subsp. <i>sativa</i>	EO	Aeolian archipelago (EO)	Minutidda	♀♂
3311	<i>V. vinifera</i> subsp. <i>sativa</i>	EO	Aeolian archipelago (EO)	Malvasia B	♀♂
3312	<i>V. vinifera</i> subsp. <i>sativa</i>	EO	Aeolian archipelago (EO)	Livedda	♀♂
3313	<i>V. vinifera</i> subsp. <i>sativa</i>	EO	Aeolian archipelago (EO)	Mascarisi	♀♂
3314	<i>V. vinifera</i> subsp. <i>sativa</i>	EO	Aeolian archipelago (EO)	Racina i mustu B	♀♂
3315	<i>V. vinifera</i> subsp. <i>sativa</i>	EO	Aeolian archipelago (EO)	Nuciddara	♀♂
3316	<i>V. vinifera</i> subsp. <i>sativa</i>	EO	Aeolian archipelago (EO)	Moscato nero	♀♂
3317	<i>V. vinifera</i> subsp. <i>sativa</i>	EO	Aeolian archipelago (EO)	Diretta nera B	♀♂
3319	<i>V. vinifera</i> subsp. <i>sativa</i>	EO	Aeolian archipelago (EO)	Minnilottina	♀♂
3320	<i>V. vinifera</i> subsp. <i>sativa</i>	EO	Aeolian archipelago (EO)	Mantonico A	♀♂
3321	<i>V. vinifera</i> subsp. <i>sativa</i>	EO	Aeolian archipelago (EO)	Cornicchiola A	♀♂
3322	<i>V. vinifera</i> subsp. <i>sativa</i>	EO	Aeolian archipelago (EO)	Lacrime di Maria B	♀♂
3323	<i>V. vinifera</i> subsp. <i>sativa</i>	EO	Aeolian archipelago (EO)	Inzolia nera A	♀♂
3324	<i>V. vinifera</i> subsp. <i>sativa</i>	EO	Aeolian archipelago (EO)	Fiore d'arancio (Trunzu)	♀♂
3325	<i>V. vinifera</i> subsp. <i>sativa</i>	EO	Aeolian archipelago (EO)	Lugliatica (Luglienga)	♀♂
3326	<i>V. vinifera</i> subsp. <i>sativa</i>	EO	Aeolian archipelago (EO)	Lacrime di Maria C	♀♂
3327	<i>V. vinifera</i> subsp. <i>sativa</i>	PT	Pantelleria island (PT)	Greca	♀♂
3328	<i>V. vinifera</i> subsp. <i>sativa</i>	PT	Pantelleria island (PT)	Caleu	♀♂
3329	<i>V. vinifera</i> subsp. <i>sativa</i>	PT	Pantelleria island (PT)	Minna di vacca C	♀♂
3333	<i>V. vinifera</i> subsp. <i>sativa</i>	PE	Pelagie Islands (PE)	Funcia chiatia	♀♂
3335	<i>V. vinifera</i> subsp. <i>sativa</i>	PE	Pelagie Islands (PE)	Catarratto E	♀♂
3337	<i>V. vinifera</i> subsp. <i>sativa</i>	US	Ustica island (US)	Inzolia nera B	♀♂
3338	<i>V. vinifera</i> subsp. <i>sativa</i>	US	Ustica island (US)	Alivedda nera	♀♂
3339	<i>V. vinifera</i> subsp. <i>sativa</i>	US	Ustica island (US)	Damaschino B	♀♂
3340	<i>V. vinifera</i> subsp. <i>sativa</i>	US	Ustica island (US)	Albanella bianca	♀♂
3342	<i>V. vinifera</i> subsp. <i>sativa</i>	US	Ustica island (US)	Menna vacca A	♀♂
3343	<i>V. vinifera</i> subsp. <i>sativa</i>	US	Ustica island (US)	Zu Manuele	♀♂
3344	<i>V. vinifera</i> subsp. <i>sativa</i>	PT	Pantelleria island (PT)	Centoruotoli	♀♂
3345	<i>V. vinifera</i> subsp. <i>sativa</i>	EO	Aeolian archipelago (EO)	Cornicchiola B	♀♂
3348	<i>V. vinifera</i> subsp. <i>sativa</i>	RG	Ragusa (RG)	Cutrera	♀♂
3349	<i>V. vinifera</i> subsp. <i>sativa</i>	CT	Catania (CT)	Zu Matteo	♀♂
3350	<i>V. vinifera</i> subsp. <i>sativa</i>	TP	Trapani (TP)	Catanese bianca	♀♂
3351	<i>V. vinifera</i> subsp. <i>sativa</i>	TP	Trapani (TP)	Dunnuni	♀♂
3352	<i>V. vinifera</i> subsp. <i>sativa</i>	TP	Trapani (TP)	Fumusa	♀♂
3354	<i>V. vinifera</i> subsp. <i>sativa</i>	ME	Messina (ME)	Nocera	♀♂
3355	<i>V. vinifera</i> subsp. <i>sativa</i>	EO	Aeolian archipelago (EO)	Prunesta	♀♂
3361	<i>V. vinifera</i> subsp. <i>sativa</i>	PT	Pantelleria island (PT)	Inzolia Tunisina A	♀♂
3362	<i>V. vinifera</i> subsp. <i>sativa</i>	PT	Pantelleria island (PT)	Nero nostrale	♀♂
3363	<i>V. vinifera</i> subsp. <i>sativa</i>	PT	Pantelleria island (PT)	Zibibbo con i seni	♀♂
3364	<i>V. vinifera</i> subsp. <i>sativa</i>	PT	Pantelleria island (PT)	Garignano	♀♂
3365	<i>V. vinifera</i> subsp. <i>sativa</i>	PT	Pantelleria island (PT)	Zibibbo minna di vacca	♀♂
3366	<i>V. vinifera</i> subsp. <i>sativa</i>	PT	Pantelleria island (PT)	Zibibbo maschulune	♀♂
3367	<i>V. vinifera</i> subsp. <i>sativa</i>	PT	Pantelleria island (PT)	Pionastro	♀♂
3368	<i>V. vinifera</i> subsp. <i>sativa</i>	PT	Pantelleria island (PT)	Inzolia Tunisina B	♀♂
3288	<i>V. vinifera</i> subsp. <i>sativa</i>	EO	Aeolian archipelago (EO)	Racina i mustu A	♀♂
3289	<i>V. vinifera</i> subsp. <i>sativa</i>	EO	Aeolian archipelago (EO)	Cuda i vulpe	♀♂
3290	<i>V. vinifera</i> subsp. <i>sativa</i>	EO	Aeolian archipelago (EO)	Pirricone raspo rosso (3°Tipo)	♀♂
3291	<i>V. vinifera</i> subsp. <i>sativa</i>	EO	Aeolian archipelago (EO)	Malvasia A	♀♂
3293	<i>V. vinifera</i> subsp. <i>sativa</i>	EO	Aeolian archipelago (EO)	Nerello Mascarisi	♀♂
3296	<i>V. vinifera</i> subsp. <i>sativa</i>	EO	Aeolian archipelago (EO)	Cappuccio	♀♂
3297	<i>V. vinifera</i> subsp. <i>sativa</i>	EO	Aeolian archipelago (EO)	Perricone B	♀♂
3298	<i>V. vinifera</i> subsp. <i>sativa</i>	EO	Aeolian archipelago (EO)	Giugnatica	♀♂
3300	<i>V. vinifera</i> subsp. <i>sativa</i>	EO	Aeolian archipelago (EO)	Putrisa	♀♂
3302	<i>V. vinifera</i> subsp. <i>sativa</i>	EO	Aeolian archipelago (EO)	Mantonico B	♀♂
3305	<i>V. vinifera</i> subsp. <i>sativa</i>	EO	Aeolian archipelago (EO)	Mantonico C	♀♂
3334	<i>V. vinifera</i> subsp. <i>sativa</i>	PE	Pelagie Islands (PE)	Bertuccio	♀♂

nd: Sex not determined.

Supplementary Table S2. Wild grapevine populations analysed: habitat conditions and vegetation patterns.

Population name and Geographical districts	Population code	Habitat	Anthropic evidences	Vegetation patterns and dominant trees/shrubs
Castelbuono, Madonie Mts., Palermo	P1	Temporary river banks	Sporadic drafted, aged olive trees along the track to the sampling area	Riparian forest, canopy cover 100%, h = 5-8 m. <i>Salix pedicellata</i> , <i>Populusnigra</i> , <i>Laurusnobilis</i> , <i>Quercus ilex</i> , <i>Clematis cirrhosa</i> , <i>Hedera helix</i> , <i>Smilax aspera</i>
Cava Grande Cassibile, Iblei Mts. Syracuse	P2	Permanent river banks	Small cultivated patches inside the sampling area; Large abandoned and active cultivations in the surroundings	Riparian forest, canopy cover 60%, h = 6-8 m. <i>Quercus ilex</i> , <i>Fraxinusornus</i> , <i>Salix pedicellata</i> , <i>Ficuscarica</i> , <i>Platanusorientalis</i> , <i>Ailanthus altissima</i> , <i>Pistacialentiscus</i> , <i>Nerium oleander</i> , <i>Erica multiflora</i> , <i>Phlomisfruticosa</i> , <i>Clematis cirrhosa</i>
Cava Sturia, Iblei Mts. Syracuse	P3	Temporary river banks	Abandoned and active cultivations in the surroundings	Maquis, canopy cover 100%, h = 6-8 m. <i>Quercus ilex</i> , <i>Q. virgiliana</i> , <i>Ficuscarica</i> , <i>Olea europaeavar.sylvestris</i> , <i>Fraxinusornus</i> , <i>Ailanthus altissima</i> , <i>Pistacialentiscus</i> , <i>P. terebinthus</i> , <i>Rhamnusalaternus</i> , <i>Phillyrealatifolia</i> , <i>Smilax aspera</i> , <i>Hedera helix</i>
Riserva Boschi Favara and Granza, Torto Valley Palermo	P4	Scree-type deposits	Sporadic small patches of abandoned fields along the track to the sampling area	Pioneer communities, canopy cover 40%, h = 2-4 m. <i>Ficuscarica</i> , <i>Rubus</i> sp., <i>Clematis cirrhosa</i> , <i>Quercusvirgiliana</i> (along the external border)
Bosco della Ficuzza, Sicani Mts. Palermo	P5	Temporary river banks	Sporadic small patches of abandoned fields and charcoal areas along the stream banks	Riparian forest, canopy cover 100%, h = 15-20 m. <i>Quercusvirgiliana</i> , <i>Acer campestris</i> , <i>Q. ilex</i> , <i>Fraxinusornus</i> , <i>F. oxyphylla</i> , <i>Q. suber</i> , <i>Salix pedicellata</i> , <i>Populusnigra</i> , <i>Ficuscarica</i> , <i>Crataegusmonogyna</i> , <i>Cytisustriflorus</i> , <i>Rubus</i> , sp., <i>Smilax aspera</i> , <i>Hedera helix</i> , <i>Clematis cirrhosa</i> , <i>Ruscusaculeatus</i>
Stretta di Longi, Nebrodi Mts. Messina	P6	Permanent river banks	Grazing-disturbance evidences	Riparian forest, canopy cover 100%, h = 8-10 m. <i>Salix pedicellata</i> , <i>Ficuscarica</i> , <i>Fraxinusangustifolia</i> , <i>Celtisaustralis</i> , <i>Clematis cirrhosa</i> , <i>Hedera helix</i> , <i>Rubus</i> sp.
Fiume Manghisi, Iblei Mts. Syracuse	P7	Permanent river banks	Abandoned and active cultivations in the surroundings	Riparian forest, canopy cover 80%, h = 8-12 m. <i>Salix pedicellata</i> , <i>Ficuscarica</i> , <i>Platanusorientalis</i> , <i>Quercus ilex</i> , <i>Clematis cirrhosa</i> , <i>Hedera helix</i>
Riserva Pantalica and Valle Anapo, Iblei Mts. Syracuse	P8	Permanent river banks	Small cultivated patches inside the sampling area; Large abandoned and active cultivations in the surroundings	Riparian forest, canopy cover 80%, h = 10-15 m. <i>Salix pedicellata</i> , <i>Populusnigra</i> , <i>Ficuscarica</i> , <i>Platanusorientalis</i> , <i>Quercus ilex</i> , <i>Fraxinusornus</i> , <i>Rhamnusalaternus</i> , <i>Nerium oleander</i> , <i>Clematis cirrhosa</i>
Fiume Sosio, Sicani Mts. Agrigento	P9	Permanent river banks	Sporadic small patches of abandoned fields along the track to the sampling area	Riparian forest, canopy cover 100%, h = 8-15 m. <i>Salix pedicellata</i> , <i>Quercus ilex</i> , <i>Q. virgiliana</i> , <i>Crataegusmonogyna</i> , <i>Prunusspinosa</i> , <i>Pistaciaterebinthus</i> , <i>Viburnum tinus</i> , <i>Rhamnusalaternus</i> , <i>Hedera helix</i>
Riserva Zangara, Belice Valley Trapani	P10	Permanent river banks	Large vineyard in the surroundings. Small abandoned olive patches inside the sampling area	Riparian forest, canopy cover 70%, h = 8-12 m. <i>Ulmuscanescens</i> , <i>Salix pedicellata</i> , <i>Populusnigra</i> , <i>Ficuscarica</i> , <i>Tamarix</i> sp., <i>Nerium oleander</i> , <i>Myrtuscommunis</i> , <i>Hedera helix</i>

Supplementary Table S3. SSR marker and PCR multiplex conditions used. The set of six highly reproducible microsatellites suggested by the European group working within the grape GENRES projects is indicated in bold.

SSR marker	Forward primer	Reverse primer	Reference	Core repeat	Annealing T °C (max-min)	Dye	PCR multiplex
VVS2	CAG CCC GTA AAT GTA TCC ATC	AAATTCAAAATTCTAATTCAACTGG	Thomas and Scott (1993)	(GA) _n	57-50	YAKYE	3
VVMD5	CTAGAGCTACGCCAATCCAA	TATACCAAAAATCATATTCCTAAA	Bowers et al. (1996)	(CT) _n AT(CT) _n ATAG(AT) _n	62-55	AT565	2
VVMD6	ATCTCTAACCCCTAAAACCAT	CTGTGCTAAGACGAAGAAGA	Bowers et al. (1996)	(CT) _n C(CT) _n TTAG(CT) _n TAAT-(CT) _n C(CT) _n C(CT) _n	63-56	AT565	1
VVMD7	AGAGTTGCGGAGAACAGGAT	CGAACCTTCACACGCTTGAT	Bowers et al. (1996)	(CT) _n	62-55	AT550	2
VVMD17	TGACTCGCCAAAATCTGACG	CACACATATCATACCACACGG	Bowers et al. (1999)	(CT) _n	57-50	AT565	3
VVMD21	GGTTGTCTATGGAGTTGATGTTGC	GCTTCAGTAAAAAGGGATTGCG	Bowers et al. (1999)	(CT) _n GAGAAGG(A) _n	62-55	YAKYE	4
VVMD24	GTGGATGATGGAGTAGTCACGC	GATTTTAGGTTTCATGTTGGTGAAGG	Bowers et al. (1999)	(CT) _n	61-54	YAKYE	6
VVMD25	TTCCGTTAAAGCAAAAAGAAAAAGG	TTGGATTGAAAATTTATTGAGGGG	Bowers et al. (1999)	(CT) _n	57-50	AT550	3
VVMD27	GTACCAGATCTGAATACATCCGTAAGT	ACGGGTATAGAGCAAAACGGTGT	Bowers et al. (1999)	(CT) _n	62-55	FAM	2
VVMD28	AACAATTCATGAAAAGAGAGAGAGAGA	TCATCAATTCGTATCTCTATTGCTG	Bowers et al. (1999)	(CT) _n	62-55	YAKYE	2
VVMD32	TATGATTTTTAGGGGGTGAGG	GGAAAGATGGGATGACTCGC	Bowers et al. (1999)	(CT) _n	63-56	AT550	1
VrZAG62	GGTGAATGGGCACCGAACACACGC	CCATGTCTCTCCTCAGCTTCTCAG	Sefc et al. 1999	(GA) _n	63-56	YAKYE	1
VrZAG79	AGATTGTGGAGGAGGGAACAAACCG	TGCCCCATTTTCAAACCTCCCTTCC	Sefc et al. 1999	(GA) _n	63-56	FAM	1
VMC1b11	CTTTGAAAATTCCTTCCGGGTT	TATTCAAAAGCCACCCGTTCTCT	Zyprian and Töpfer (2005)	(GA) _n	62-55	FAM	4
VMC4f3.1	AAAGCACTATGGTGGGTGTAATA	TAACCAATACATGCATCAAGGA	Di Gaspero et al. (2000)	(CT) _n TT (CT) _n	60-53	FAM	5
VV1b01	TGACCCTCGACCTTAAAATCTT	TGGTGAGTGCAATGATAGTAGA	Merdinoglu et al. (2005)	(CT) _n	60-53	AT565	5
VV1h54	CCGCACTTGTGTTGAATTTTACAG	CAAACCGTTTTTACACCCAGCAG	Merdinoglu et al. (2005)	(GA) _n	61-54	FAM	6
VV1n16	ACCTCTATAAGATCCTAACCTG	AAGGGAGTGTGACTGATATTTT	Merdinoglu et al. (2005)	(CA) _n CG (CA) _n	62-55	AT565	4
VV1n73	TACTTCACCTAACCAATACAGCT	AATACATAAGGTGAAGATGCCT	Merdinoglu et al. (2005)	(CA) _n	60-53	AT550	5
VV1p31	TATCCAAGAGACAAAATTCACC	TTCTCTGTTTCTCTGCAAAATGG	Merdinoglu et al. (2005)	(GA) _n	61-54	AT550	6
VV1p60	GGGGAATAACTAAAATTGAGGAT	GTATGAATGCGGATAGTTTGTG	Merdinoglu et al. (2005)	(TG) _n A(GT) _n (GA) _n	57-50	FAM	3
VV1q52	TAAAAGGATGGTAGATGACAGA	ACAGGAAAAGTGTCAATGGTTA	Merdinoglu et al. (2005)	(CT) _n	62-55	AT550	4
VV1v67	TATAACTTCTCATAGGGTTTCC	TTGGAGTCCATCAAATTCATCT	Merdinoglu et al. (2005)	(CA) _n AT(CA) _n (GA) _n TT(GA) _n (AG) _n	61-54	AT565	6

SSR markers with the same PCR multiplex number were amplified in a single PCR mix, all primers being pooled in the PCR mix and analyzed in the same sequencer run

Supplementary Table S4. Genetic profiles of cultivated and wild Sicilian accessions.

Accession code	Population / Sample name	VVIp60	VVMD28	VVib01	VVMD27	VViv67	VVMD32	VVin16	VVMD21	VVMD24	VVMD7	VVC1b11	VVin73	VVIp31	VVih54	VVIq52	VVC4f3_1	VVMD25	VrZag79	VrZag62	VVMD17	VVMD5	VVMD6	VVS2	
3005	P1	302 302	227 235	290 294	185 185	356 362	0 0	149 151	247 253	206 210	251 253	167 181	257 263	0 0	0 0	80 80	166 178	0 0	243 243	192 192	214 222	231 231	209 209	128 134	
3006	P1	314 314	227 243	290 294	179 185	0 0	0 0	151 151	245 245	210 210	243 253	165 167	255 263	182 182	165 165	76 80	182 204	238 254	0 0	0 0	0 0	227 233	209 209	138 138	
3007	P1	312 320	235 257	290 290	189 191	356 362	253 255	149 151	253 253	210 212	251 269	181 187	257 263	174 178	163 165	74 74	166 178	238 238	247 247	192 192	214 220	233 233	201 209	128 148	
3009	P1	316 316	227 257	288 290	179 179	352 362	251 271	149 151	247 253	206 210	237 243	167 167	263 263	176 186	165 177	74 80	182 202	238 248	245 249	186 198	214 222	233 233	211 211	128 152	
3010	P1	314 318	0 0	292 294	181 185	354 358	257 257	151 157	247 255	206 210	263 269	165 187	263 263	182 186	165 165	76 80	170 202	248 262	243 251	192 198	214 224	0 0	201 201	128 130	
3011	P1	302 312	235 235	290 290	189 191	352 364	243 255	151 151	247 247	206 210	253 265	165 187	263 263	178 182	149 163	74 74	172 188	240 266	247 247	192 194	222 222	233 233	209 209	128 148	
3013	P1	314 314	235 235	294 298	185 189	352 366	251 251	149 149	247 253	206 206	243 253	165 165	263 263	188 188	167 167	74 80	178 188	262 262	247 251	186 200	220 220	233 233	209 211	128 148	
3015	P1	302 312	227 249	292 292	181 191	364 364	255 255	149 149	247 247	204 216	253 259	181 187	257 263	182 182	163 163	74 74	166 172	238 238	247 259	194 194	222 222	233 233	201 209	128 148	
3016	P1	318 318	227 235	290 290	185 185	0 0	0 0	251 251	149 149	247 247	206 210	253 253	165 173	263 263	188 188	163 177	74 80	0 0	248 254	245 249	186 198	214 222	231 231	209 211	128 138
3017	P1	314 318	245 245	290 290	189 193	352 358	239 271	157 157	247 247	210 210	247 253	165 183	261 263	180 192	163 165	76 80	172 172	238 238	251 257	184 186	220 220	227 227	207 207	128 128	
3018	P1	312 312	235 235	290 290	189 189	362 364	255 255	149 151	245 245	210 214	253 257	165 181	263 263	180 194	163 163	74 74	172 172	238 248	245 245	194 194	222 222	233 233	201 209	128 148	
3019	P1	312 312	235 235	290 290	189 191	362 364	255 255	149 151	245 245	210 214	253 257	181 181	263 263	182 194	163 163	74 80	172 172	238 248	245 245	194 194	222 222	233 233	201 209	128 148	
3020	P1	312 320	227 235	290 290	179 189	356 362	0 0	149 149	253 253	210 212	243 251	165 181	257 263	174 178	163 163	74 74	166 178	238 238	0 0	0 0	0 0	233 233	201 201	128 128	
3021	P1	312 320	235 257	290 290	189 191	356 362	0 0	149 151	253 253	210 212	251 269	181 187	257 263	174 178	163 165	74 74	166 178	238 238	0 0	0 0	0 0	233 233	201 209	128 148	
3022	P1	312 320	235 257	290 290	189 191	356 362	255 255	149 151	253 253	210 212	251 269	181 187	257 263	174 178	163 165	74 74	166 178	238 238	245 245	192 192	214 222	233 233	201 209	128 148	
3023	P1	312 312	235 257	290 290	189 191	356 356	255 255	149 151	247 253	206 206	251 269	181 187	257 263	174 188	165 167	74 74	178 206	238 254	247 247	192 192	214 220	227 233	209 209	128 148	
3024	P2	302 320	233 271	290 294	185 185	352 366	249 259	147 157	245 245	210 210	237 253	173 181	263 265	182 192	163 163	74 80	202 202	248 254	251 251	194 200	222 222	233 243	209 211	128 134	
3025	P2	314 322	227 271	290 294	185 191	362 370	255 271	147 151	245 245	210 210	253 263	165 167	255 265	182 182	165 169	76 80	182 204	238 254	251 251	192 200	214 222	227 233	209 209	138 152	
3026	P2	302 318	227 259	290 290	179 189	362 362	251 251	157 157	247 245	206 214	253 257	167 183	257 263	182 186	165 177	74 76	188 188	254 254	247 251	194 198	214 224	227 241	191 209	148 152	
3027	P2	314 320	257 257	290 294	181 185	358 362	255 259	151 151	245 253	210 210	257 267	167 187	263 261	182 186	165 165	74 80	172 204	248 248	243 247	198 198	214 224	233 233	201 211	130 138	
3028	P2	316 318	227 253	290 290	191 191	352 362	249 255	149 151	247 247	206 210	237 247	165 167	263 263	176 186	165 177	74 80	182 202	238 248	247 247	186 194	222 222	233 233	211 211	128 152	
3029	P2	302 318	227 235	288 288	183 185	352 362	251 255	151 151	247 247	206 210	253 253	165 181	263 263	176 182	167 177	74 78	182 188	248 248	251 251	186 200	224 224	233 243	191 211	128 128	
3030	P2	302 320	231 241	290 294	185 185	352 352	249 259	147 157	247 247	210 210	237 253	173 181	263 265	182 192	163 163	74 80	202 202	248 248	251 251	194 200	222 222	233 243	207 211	128 134	
3031	P2	302 318	227 227	288 294	185 191	356 366	251 255	157 157	241 253	206 210	243 267	169 183	263 265	172 186	149 149	74 80	170 172	262 262	251 251	192 200	222 222	233 233	207 207	128 128	
3032	P2	312 314	233 241	290 294	179 189	362 362	251 255	147 151	247 247	0 0	253 253	0 0	263 263	182 186	163 165	74 74	182 170	238 254	247 251	192 198	222 224	227 239	201 201	0 0	
3033	P2	302 328	227 235	290 294	185 185	352 366	251 255	149 151	247 247	206 210	247 253	167 181	263 263	182 188	163 177	74 76	172 202	248 248	247 251	186 198	222 222	227 241	211 211	152 152	
3034	P2	318 318	225 241	290 290	185 187	352 362	251 255	147 151	247 247	206 210	247 253	167 181	263 263	182 188	163 177	74 78	166 182	248 254	251 251	186 200	214 224	233 243	191 211	128 138	
3035	P2	312 314	235 235	294 294	179 189	352 362	239 255	149 151	247 253	210 210	243 269	165 183	263 263	182 182	149 163	72 80	176 178	248 262	247 251	184 192	222 222	227 227	201 209	128 148	
3036	P2	302 328	227 227	292 294	179 189	352 362	253 257	149 149	247 255	206 214	257 267	167 181	263 263	182 192	163 163	80 78	170 182	248 254	251 251	192 198	224 224	229 229	207 211	148 152	
3037	P2	312 314	235 259	292 294	179 189	362 362	253 257	147 151	247 247	206 210	253 253	181 193	263 263	182 186	163 163	74 74	170 182	238 254	247 251	192 198	224 224	227 241	201 201	138 138	
3039	P3	0 0	235 235	288 288	189 189	356 356	251 255	147 149	247 247	206 208	243 253	165 183	263 263	174 188	163 177	0 0	166 204	238 238	251 251	186 192	214 222	229 241	0 0	0 0	
3040	P3	312 312	235 257	288 294	185 185	352 362	251 255	147 147	241 247	210 210	253 253	165 183	263 263	174 182	163 163	74 80	174 186	248 262	251 251	198 198	214 222	227 241	191 211	148 152	
3041	P3	312 318	233 257	288 288	185 189	352 362	251 255	149 151	241 247	206 210	243 253	165 183	263 263	182 182	165 167	74 80	172 174	240 248	247 251	198 198	214 222	229 241	191 211	148 148	
3042	P3	312 318	257 257	0 0	185 189	352 362	0 0	149 151	239 247	206 210	253 255	165 183	263 263	0 0	0 0	74 80	172 174	0 0	243 247	186 198	212 222	239 241	191 211	148 148	
3043	P4	314 318	243 257	290 290	181 185	352 358	251 271	149 151	247 247	206 210	253 253	169 183	263 263	186 188	163 175	78 80	182 188	254 254	247 251	198 202	222 222	235 249	209 211	130 138	
3044	P4	314 318	243 257	290 290	181 185	352 360	251 271	149 151	247 247	206 210	253 253	169 183	263 263	186 186	165 177	80 80	182 188	254 254	247 251	198 202	222 222	235 249	209 211	130 138	
3045	P4	314 318	243 257	290 290	181 185	352 360	253 271	149 151	247 247	206 210	251 253	169 183	263 263	186 186	165 177	80 80	182 188	254 254	247 251	198 202	224 224	235 247	209 211	130 138	
3046	P4	314 318	243 257	290 290	181 185	352 360	251 271	149 151	247 247	206 210	251 253	169 183	263 263	186 188	165 177	80 80	182 188	252 254	247 251	198 202	224 224	235 247	209 211	130 138	
3047	P4	314 318	243 257	290 290	181 185	352 360	255 263	149 151	247 253	206 210	251 253	169 183	263 263	186 186	165 177	80 78	182 188	254 254	247 251	192 198	214 224	235 247	209 211	130 138	
3048	P4	314 318	243 257	290 290	181 185	352 360	251 271	149 151	247 247	206 210	251 253	169 183	263 263	186 186	165 177	80 80	182 188	254 254	247 251	198 202	224 224	235 247	209 211	130 138	
3050	P4	0 0	243 257	290 290	181 185	352 358	251 271	149 151	247 247	206 210	251 253	169 183	263 263	186 186	165 177	0 0	182 188	254 254	243 247	198 202	224 224	233 235	0 0	0 0	
3051	P4	0 0	235 243	290 290	181 185	352 360	251 271	149 151	247 253	20															

Supplementary Table S4. Genetic profiles of cultivated and wild Sicilian accessions.

Accession code	Population / Sample name	VVIp60	VVMD28	VVib01	VVMD27	VViv67	VVMD32	VVin16	VVMD21	VVMD24	VVMD7	VVC1b11	VVin73	VVIp31	VVih54	VVIq52	VVC4f3_1	VVMD25	VrZag79	VrZag62	VVMD17	VVMD5	VVMD6	VVS2																							
3095	P7	0	0	233	257	290	294	179	191	354	362	239	255	147	151	253	253	210	210	253	265	165	169	263	263	186	190	165	177	0	0	188	206	254	266	247	251	192	198	232	224	233	235	0	0	0	0
3096	P7	312	318	233	257	290	294	179	191	354	362	239	255	147	151	253	253	210	210	253	265	165	169	263	263	186	190	165	175	78	80	188	206	254	266	247	251	192	198	222	224	233	235	201	201	138	148
3097	P7	318	318	227	235	290	290	185	185	362	370	249	251	149	151	247	253	210	210	243	253	165	183	263	263	176	186	165	165	74	72	202	202	254	254	247	251	192	200	222	222	231	231	207	211	128	128
3098	P7	314	320	235	257	290	290	179	185	352	362	249	271	149	151	247	247	206	206	253	255	181	183	263	265	178	182	165	165	80	78	172	202	248	254	251	251	192	200	214	222	227	227	201	201	128	130
3099	P8	312	312	227	235	290	294	185	185	360	366	251	255	149	151	247	247	210	210	243	269	165	169	263	263	186	188	165	173	74	76	188	206	238	254	239	247	192	192	214	222	231	231	209	211	128	138
3100	P8	312	318	227	235	294	294	185	185	354	354	239	251	151	157	247	247	206	210	243	253	165	169	263	263	186	186	165	173	74	80	182	188	240	248	235	239	192	198	222	222	225	245	209	211	128	152
3101	P8	318	318	227	235	290	306	185	193	366	384	0	0	149	151	247	253	206	210	237	243	165	183	263	263	188	188	167	175	76	80	188	206	248	254	0	0	0	0	0	0	231	231	209	211	132	146
3102	P8	302	318	235	257	294	294	185	191	354	356	251	255	151	151	241	247	206	210	243	253	169	183	263	263	172	186	165	165	74	80	182	206	248	248	243	251	200	200	214	224	241	241	209	209	152	152
3104	P8	316	318	235	243	290	290	185	193	352	362	249	261	151	157	241	253	210	214	243	265	187	193	255	263	174	178	149	163	74	80	188	206	240	240	243	257	186	192	214	214	227	233	209	211	128	140
3105	P8	318	318	227	227	0	0	179	189	362	362	239	255	149	151	247	247	206	210	243	253	165	183	263	263	0	0	0	0	74	76	178	206	0	0	245	257	186	192	222	222	227	233	211	211	138	138
3106	P8	312	318	227	245	290	294	181	191	354	360	249	271	149	157	241	247	206	214	253	259	183	183	263	265	182	186	163	173	74	80	168	188	240	254	247	251	198	198	222	224	227	229	209	209	128	138
3107	P8	314	318	227	235	290	290	183	191	354	362	249	271	151	151	241	247	206	210	251	265	165	181	263	263	174	182	165	165	76	76	188	204	240	254	249	249	192	202	214	224	227	229	209	209	128	138
3108	P8	302	302	227	227	290	290	191	191	352	354	0	0	149	157	247	253	210	210	243	253	165	183	263	263	174	186	173	173	76	80	168	172	238	238	247	251	186	192	212	222	227	233	201	209	128	148
3110	P8	302	318	235	247	292	292	189	191	352	352	251	251	149	179	247	249	206	206	265	267	165	183	261	265	174	186	165	165	74	76	168	172	238	266	247	251	192	194	214	222	233	233	201	209	128	128
3111	P8	302	318	247	247	294	294	185	195	352	356	0	0	147	147	247	247	206	210	243	253	183	183	263	263	172	186	165	165	74	74	188	206	248	248	245	249	0	0	214	224	235	241	201	211	132	152
3112	P8	314	318	243	257	294	298	179	179	354	366	249	251	149	151	245	245	206	210	253	253	169	169	263	263	174	186	167	177	74	80	178	186	240	248	0	0	192	200	212	222	241	241	209	211	128	138
3113	P8	302	300	259	259	290	294	191	195	352	370	251	271	151	151	247	247	206	206	243	243	169	183	263	263	174	182	167	167	76	74	170	170	248	254	247	257	184	194	224	224	227	235	209	211	138	148
3114	P9	302	312	227	259	292	294	189	191	352	366	257	261	147	149	247	257	210	214	237	243	165	165	257	257	174	188	149	163	74	80	172	172	238	254	251	259	192	202	214	222	233	241	207	211	138	148
3115	P9	312	320	227	243	288	290	185	189	362	366	0	0	149	157	247	247	214	214	253	265	165	181	263	263	174	178	149	175	76	80	172	204	248	254	0	0	214	222	233	233	201	201	148	152		
3116	P9	302	314	259	263	290	290	185	185	362	370	241	251	147	149	247	247	206	210	253	267	165	193	263	263	182	194	149	163	74	80	182	206	248	248	251	251	192	194	214	222	223	233	201	211	148	152
3117	P9	302	314	225	257	290	290	185	185	362	370	241	251	147	149	247	247	206	210	253	267	165	193	263	263	182	194	149	163	74	80	182	206	248	248	251	251	192	194	214	222	223	233	201	211	148	152
3118	P9	302	322	227	235	290	294	179	185	352	362	255	255	0	0	247	247	0	0	253	253	165	167	257	263	0	0	163	163	76	80	178	178	0	0	247	251	186	192	214	222	227	241	201	209	138	138
3119	P9	316	318	227	243	288	290	181	191	0	0	257	259	147	149	247	247	206	210	261	265	165	165	263	263	194	194	147	165	74	80	178	178	248	266	247	259	192	194	214	222	0	0	201	209	128	148
3120	P9	312	318	235	263	294	294	185	191	354	354	239	249	147	157	247	255	206	206	253	265	165	181	263	263	186	186	149	163	74	80	172	186	240	248	251	251	192	192	214	214	231	231	201	211	128	152
3121	P9	0	0	257	257	290	290	185	189	356	362	239	255	147	157	247	247	206	210	243	253	165	165	257	257	178	182	149	159	0	0	182	206	248	248	251	259	194	194	214	214	239	241	0	0	0	0
3122	P9	302	312	217	235	288	290	185	189	352	362	249	251	157	157	247	247	210	214	265	265	165	165	263	265	186	188	163	181	76	80	172	204	240	262	251	251	192	192	214	222	227	227	201	201	152	152
3123	P9	314	314	227	263	290	294	189	191	364	366	251	255	149	157	247	247	214	214	251	255	165	165	263	263	174	178	165	175	74	74	178	204	238	252	251	251	192	192	214	222	223	241	201	207	150	152
3124	P9	312	312	227	235	290	290	179	181	362	362	249	249	157	157	247	247	206	214	261	265	165	165	263	263	186	186	165	181	74	74	172	172	238	266	251	259	186	192	214	222	225	231	201	207	128	148
3125	P9	318	322	235	257	294	294	179	181	354	362	249	255	149	157	247	253	206	214	253	265	165	193	263	263	182	182	161	167	74	80	172	188	262	266	257	259	192	198	212	212	233	241	201	211	128	148
3126	P9	318	318	255	255	288	306	179	189	362	370	251	255	149	149	247	247	206	210	243	261	173	179	263	263	188	188	149	173	76	80	178	202	248	254	259	259	192	194	214	224	227	233	209	209	132	152
3127	P9	318	322	243	257	290	290	181	191	352	360	263	263	149	149	247	247	206	208	243	247	165	189	263	263	188	188	163	175	80	80	188	206	248	252	243	247	186	194	222	224	227	239	211	211	130	152
3128	P9	320	328	225	251	290	290	185	189	352	366	249	249	149	157	247	247	210	210	261	265	165	16																								

Supplementary Table S4. Genetic profiles of cultivated and wild Sicilian accessions.

Accession code	Population / Sample name	VVIp60	VVMD28	VVib01	VVMD27	VViv67	VVMD32	VVin16	VVMD21	VVMD24	VVMD7	VVC1b11	VVin73	VVIp31	VVih54	VVIq52	VVC4f3_1	VVMD25	VrZag79	VrZag62	VVMD17	VVMD5	VVMD6	VVS2
3213	Grecaico C	322 328	235 247	290 294	179 193	356 370	249 257	149 149	247 247	206 206	253 257	169 183	255 263	174 188	167 167	72 72	186 202	240 254	249 249	186 198	224 224	227 233	201 209	128 138
3214	Grecaù (Bracau)	314 318	227 233	290 294	179 181	360 360	251 255	149 149	247 253	206 208	247 251	165 169	263 263	180 186	163 163	74 80	172 188	236 246	249 253	186 202	222 222	227 227	207 211	128 138
3215	Grillo A	318 318	0 0	290 298	179 195	370 384	251 271	149 155	247 263	206 210	243 253	165 183	263 263	174 190	165 165	74 74	172 180	248 254	247 251	184 200	222 222	225 227	207 211	138 144
3216	Grillo C	318 318	233 239	290 298	179 193	370 384	251 271	149 151	247 263	206 210	247 249	165 183	263 263	174 190	165 167	76 76	172 180	248 254	245 249	184 200	222 222	225 227	207 211	138 144
3217	Grillo D	318 318	233 241	290 298	179 195	370 384	251 271	149 151	247 263	206 210	243 253	165 183	263 263	174 190	165 165	74 80	172 180	248 254	247 251	184 200	220 220	227 227	191 211	138 146
3218	Jala bianca	318 318	267 267	290 294	179 185	352 358	239 249	155 157	241 247	206 206	251 257	169 183	263 263	178 186	165 177	80 80	170 182	238 254	249 255	198 202	224 224	227 233	201 209	134 138
3219	Inzolia A	314 318	243 247	294 306	185 195	370 370	251 257	149 151	247 247	206 206	237 243	179 183	263 263	178 188	165 165	76 80	202 206	238 254	245 249	186 200	222 222	0 0	209 209	132 134
3220	Inzolia C	314 318	227 257	290 298	183 193	352 360	251 257	0 0	0 0	206 206	243 251	0 0	263 263	174 194	165 165	74 76	172 188	240 254	247 249	188 200	222 222	227 227	207 209	130 138
3221	Inzolia imperiale A	314 318	0 0	290 298	179 179	352 366	251 271	149 155	241 247	204 206	0 0	165 183	255 263	184 186	165 165	76 80	166 186	254 254	249 257	184 198	224 224	0 0	207 207	134 138
3223	Inzuccherato	318 326	227 227	0 0	179 193	328 384	257 271	149 149	253 253	206 208	0 0	165 183	263 263	0 0	0 0	74 76	172 188	0 0	241 251	188 188	224 224	225 225	207 207	140 148
3224	Inzuccherato di Noto	318 322	235 245	290 294	185 195	334 366	251 255	149 149	247 253	206 210	253 255	181 183	255 255	178 186	165 165	76 80	166 174	254 254	251 257	184 192	220 220	239 243	209 215	130 130
3225	Lacrima di Maria A	318 318	243 247	0 0	179 193	352 368	249 255	149 149	247 253	206 208	237 243	165 183	263 263	0 0	0 0	78 82	188 206	0 0	249 249	186 198	222 222	227 241	207 211	132 144
3226	Leanfurtisi	314 318	255 255	0 0	179 185	352 370	251 257	151 157	241 247	206 212	241 249	167 171	263 263	0 0	0 0	82 82	172 190	0 0	251 251	188 196	214 224	225 227	191 211	130 146
3227	Lorisi (Orisi)	318 324	235 257	0 0	181 195	362 362	251 257	151 151	241 249	212 212	243 235	165 171	263 263	0 0	165 173	74 76	170 186	238 238	243 251	186 196	214 222	235 243	201 209	132 138
3228	Lucignola	318 322	233 235	290 298	179 179	352 370	249 271	0 0	0 0	0 0	243 243	0 0	263 263	174 190	163 173	74 80	172 172	240 254	241 249	192 200	214 224	227 227	207 207	128 138
3229	Malvasia	318 326	255 255	292 300	179 179	352 352	249 251	151 157	247 253	206 206	241 249	165 169	263 263	174 188	165 165	82 82	172 188	254 254	243 251	188 200	224 224	225 225	191 207	138 146
3230	Malvasia di Lipari C	302 318	233 255	290 294	179 183	348 362	251 271	149 155	247 247	206 214	247 253	165 183	257 263	172 182	157 163	76 80	172 182	240 254	243 247	186 200	222 222	227 227	191 207	138 138
3231	Malvasia di Lipari A	318 326	241 255	290 294	183 183	348 362	251 271	149 155	247 247	206 214	247 253	165 183	257 263	172 182	157 163	76 80	172 182	240 254	243 247	186 200	222 222	227 227	191 207	128 138
3232	Marsala (Mareschino)	314 318	0 0	290 298	179 195	352 366	251 257	151 151	247 253	208 216	243 247	181 183	263 263	174 188	165 165	74 80	166 166	240 254	245 249	186 200	222 222	0 0	191 207	128 140
3233	Marsigliana	314 318	0 0	290 306	183 185	352 356	249 251	149 151	241 247	206 212	243 243	173 183	263 263	188 188	165 165	74 80	172 206	238 254	249 257	184 186	222 222	225 225	191 207	128 128
3234	Minna di vacca B	314 318	249 249	300 310	185 195	370 370	249 251	0 0	0 0	0 0	237 243	0 0	263 263	178 188	163 165	76 80	202 206	238 254	249 255	184 202	222 224	229 239	207 209	132 134
3235	Minnavacchina	318 324	233 255	294 308	191 193	352 370	251 255	149 151	247 247	204 206	241 249	167 183	263 263	182 188	165 175	76 76	206 206	246 252	245 249	186 200	222 224	239 249	209 209	136 138
3236	Minnella bianca (Passulana)	314 318	241 241	294 306	185 195	366 370	249 251	151 153	247 247	206 206	237 243	179 183	263 263	178 188	165 165	76 80	202 206	238 254	251 257	184 202	220 222	229 241	209 211	132 134
3237	Monteleone	302 314	245 245	288 294	189 195	352 370	251 257	149 151	247 247	206 206	251 267	169 181	263 263	176 182	179 173	76 80	172 186	240 248	249 251	192 194	212 224	233 239	191 207	128 138
3238	Moscato di Noto B	314 314	247 267	294 300	179 193	358 370	263 271	147 147	247 263	208 214	237 253	183 187	261 263	182 186	165 165	76 76	166 206	240 248	251 255	184 194	220 222	229 229	207 211	128 138
3239	Moscato bianco	318 324	235 257	290 294	179 193	358 358	263 263	147 147	261 263	206 206	243 253	183 187	261 263	182 188	165 165	74 76	166 206	238 254	255 255	194 194	220 222	241 241	201 209	132 138
3240	Moscato di Noto C	318 318	0 0	290 294	0 0	352 352	251 271	0 0	263 263	0 0	0 0	0 0	263 263	174 188	165 165	74 80	0 0	240 254	249 249	184 200	224 224	0 0	209 209	138 138
3241	Muscatedda	314 318	235 245	290 294	179 179	352 370	257 271	147 157	253 253	206 214	243 253	165 183	263 263	182 182	165 179	74 76	166 182	240 254	247 255	184 186	214 224	229 243	209 209	128 138
3242	Muscaticiduni	302 318	257 257	290 294	189 195	352 370	249 251	153 153	247 247	206 206	241 243	169 183	263 263	174 182	167 173	76 76	170 172	248 254	247 257	184 194	224 224	227 235	209 211	138 146
3243	Nerello Mascalese B	314 318	227 241	290 298	179 179	352 352	251 255	149 151	241 247	206 212	243 253	165 169	263 263	172 182	163 163	74 80	172 178	240 240	251 259	194 200	212 222	225 225	191 209	128 138
3244	Nerello Mascalese C	314 318	0 0	290 298	179 179	352 354	251 255	0 0	0 0	0 0	243 253	0 0	263 263	188 194	163 165	80 80	172 178	240 240	251 259	194 200	214 222	225 225	191 209	128 138
3245	Nerello cappuccio A	314 322	247 257	290 294	181 185	352 352	249 251	0 0	0 0	0 0	243 243	0 0	263 263	174 176	165 165	74 76	0 0	240 254	251 259	184 186	222 222	227 229	191 207	128 138
3246	Nerello Mascalese D	314 318	225 241	290 298	179 179	352 354	251 255	151 151	241 247	206 212	243 253	167 171	263 263	188 194	163 163	80 80	172 178	240 240	251 259	194 200	214 222	227 237	191 209	128 138
3247	Nerello Mascalese E	314 318	225 241	290 298	179 179	352 354	251 255	151 153	241 247	206 212	243 253	165 183	263 263	186 188	163 163	74 80	172 178	240 240	251 259	194 200	212 222	227 237	191 209	128 138
3248	Nerello Mascalese A	314 318	241 241	290 298	179 179	352 354	251 255	149 149	241 247	206 206	243 253	165 183	263 263	188 194	163 163	76 82	172 178	240 240	249 257	194 200	212 222	227 239	191 209	128 138
3249	Nero d'Avola A	312 314	235 235	298 298	179 181	354 366	251 251	147 149	247 253	206 210	243 253	169 183	263 263	174 188	165 165	78 80	186 186	240 254	251 251	184 200	220 220	227 227	209 211	138 146
3250	Nero grosso	318 326	231 241	290 290	185 193	352 352	249 271	149 155	241 247	206 210	243 243	167 173	263 263	190 194	165 165	74 78	180 190	248 254	251 255	188 188	224 224	233 233	191 207	130 138
3251	Nivureddu	318 326	233 257	0 0	183 185	352 352	251 257	149 155	241 247	206 206	243 243	165 165	263 263	0 0	165 165	76 76	178 190	0 0	243 247	186 194	214 222	229 237	191 191	128 130
3252	Nivuro Bronte	314 318	0 0	288 290	195 193	358 358	239 239	151 157	241 241	208 208	243 247	187 193	255 263	174 182	167 167	74 80	166 186	240 240	257 257	186 186	212 236	225 225	207 211	138 138
3253	Nucera nera (Perricone)	318 328	233 257	292 292	183 185	352 352	251 257	149 155	241 247	206 206	243 247	165 165	263 263	190 190	165 165	74 76	178 190	240 254	243 247	186 194	212 222	229 237	191 191	128 130
3254	Nzuccherato	318 326	241 255	290 290	179 195	328 328	251 271	151 151	257 257	206 210	247 255	165 165	263 263	190 194	165 175	74 76	172 188	240 244	243 243	186 186	222 222	227 235	207 207	140 150
3255	Oriddu	318 322	0 0	294 298																				

Supplementary Table S4. Genetic profiles of cultivated and wild Sicilian accessions.

Accession code	Population / Sample name	VVIp60	VVMD28	VVib01	VVMD27	VViv67	VVMD32	VVin16	VVMD21	VVMD24	VVMD7	VMC1b11	VVin73	VMIp31	VVih54	VVIq52	VMC4f3_1	VVMD25	VrZag79	VrZag62	VVMD17	VVMD5	VVMD6	VVS2																							
3298	Giugnatica	0	0	231	255	290	290	185	189	356	356	239	239	157	157	247	263	206	210	243	251	173	173	263	263	164	180	163	167	0	0	178	178	240	240	251	259	192	202	214	214	229	237	0	0	0	0
3299	Nero d'Avola E	314	314	235	241	298	298	179	181	354	366	249	251	147	149	247	253	206	210	243	253	169	183	263	263	174	188	165	165	78	80	186	188	240	254	247	247	184	200	222	222	227	227	209	211	138	148
3300	Putrisa	314	320	247	259	290	294	181	185	346	360	249	257	149	151	245	247	206	210	243	257	181	183	263	263	172	188	165	175	80	80	166	186	240	254	247	255	188	188	222	222	227	239	201	201	128	128
3302	Mantonico B	314	318	243	257	290	294	179	193	0	0	255	255	149	149	241	255	212	214	243	253	165	167	257	263	172	186	165	177	76	80	166	178	240	248	247	247	192	192	214	222	227	233	191	209	128	128
3304	Alicante, Licante	318	318	241	241	288	290	193	193	352	358	241	249	151	157	241	247	208	214	243	247	187	193	255	263	174	182	163	167	74	80	170	186	240	254	257	257	186	186	214	238	227	241	209	209	132	142
3305	Mantonico C	0	0	227	227	290	294	179	189	356	360	0	0	151	151	247	255	206	206	243	257	169	183	255	263	182	188	163	165	0	0	188	188	240	254	243	247	194	200	222	222	227	233	0	0	0	0
3307	Inzolia imperiale B	314	314	0	0	290	294	185	185	352	352	257	271	149	149	255	255	206	206	253	251	187	187	263	263	172	182	165	177	74	76	172	206	238	248	243	251	184	186	224	224	225	225	209	209	128	128
3308	Cantaro	314	316	241	255	290	294	179	179	352	384	249	271	149	151	241	253	206	206	235	249	169	187	263	263	190	190	165	175	74	76	182	188	238	244	245	245	186	200	220	224	233	245	209	211	128	138
3309	Trummana	316	318	0	0	290	294	179	179	356	358	249	251	149	149	247	253	204	210	243	241	165	171	263	263	186	188	165	165	74	74	178	188	240	254	245	249	186	200	224	224	225	225	191	191	148	134
3310	Minutidda	318	318	233	243	288	290	179	185	352	352	251	255	149	149	241	247	206	212	243	265	165	165	263	263	190	194	165	173	74	80	172	178	240	240	243	257	186	192	214	222	227	237	191	209	128	128
3311	Malvasia B	318	328	233	253	290	294	179	183	348	362	251	271	149	155	245	245	206	214	243	249	165	183	257	263	172	182	157	163	76	80	172	182	240	254	239	243	186	200	224	224	225	225	191	209	138	140
3312	Livedda	318	318	235	247	290	294	181	193	352	356	239	251	147	147	247	253	206	206	237	243	173	183	263	263	180	182	163	163	74	80	186	188	248	254	0	0	186	194	224	224	227	229	211	211	132	148
3313	Mascaris	318	328	233	257	290	290	183	185	352	352	251	257	149	155	241	247	206	206	243	243	165	165	263	263	190	190	165	165	74	76	178	190	240	254	241	245	186	194	214	222	229	237	191	191	128	130
3314	Racina i mustu B	314	318	233	235	290	290	179	189	360	360	0	0	147	151	247	255	210	210	251	257	177	183	255	263	178	186	165	175	74	76	172	172	238	248	245	251	194	198	222	222	227	229	191	209	128	140
3315	Nuciddara	314	318	241	241	290	294	185	185	352	352	251	251	147	147	247	247	206	210	253	251	165	169	263	263	174	188	165	179	76	80	172	178	248	254	237	243	198	200	222	222	241	241	207	207	138	138
3316	Moscato nero	314	318	235	243	294	294	179	185	366	384	269	271	149	155	247	253	210	210	251	253	165	171	263	263	178	186	165	165	74	78	172	206	248	254	239	255	184	190	222	222	233	239	209	211	130	146
3317	Diretta nera B	318	318	235	243	290	298	179	193	352	358	251	251	149	151	247	253	206	210	243	253	165	183	263	263	174	188	165	165	76	80	188	206	240	254	251	251	184	200	222	222	227	233	209	211	132	138
3319	Minnilotina	314	318	243	247	0	0	185	193	368	370	251	251	149	151	247	253	206	206	237	243	179	183	263	263	0	0	0	0	76	80	206	206	238	238	251	251	184	200	222	222	229	239	211	213	132	134
3320	Mantonico A	318	322	243	243	294	294	185	185	352	366	251	271	149	149	247	247	206	210	253	259	165	173	255	263	186	186	163	165	74	76	166	206	238	254	239	251	184	202	220	220	227	239	191	211	128	130
3321	Cornicchiola A	312	314	243	257	290	290	179	181	342	352	257	261	147	151	247	263	206	210	251	253	165	183	263	263	180	194	159	165	80	84	166	202	238	248	251	251	194	202	222	224	237	249	191	211	140	146
3322	Lacreme i Maria B	316	318	241	241	290	290	179	195	358	384	0	0	149	149	247	255	204	210	239	249	165	171	263	263	188	190	163	163	74	76	180	188	244	248	0	0	0	0	0	0	223	229	191	209	146	150
3323	Inzolia nera A	312	314	231	245	290	306	169	183	352	354	0	0	149	151	241	247	206	206	241	249	165	169	263	263	186	190	165	177	76	80	188	190	238	244	243	247	186	196	224	224	239	239	209	211	128	152
3324	Fiore d'arancio (Trunzu)	314	328	235	243	290	294	179	185	352	352	271	271	151	151	253	263	206	206	237	243	165	169	263	263	174	184	165	175	74	80	188	206	248	254	251	257	194	202	222	222	227	233	191	211	128	148
3325	Lugliatica (Luglienga)	318	328	233	257	290	290	183	185	352	352	251	257	149	155	241	247	206	206	243	243	165	165	263	263	190	190	165	165	74	76	178	190	240	254	243	247	186	194	214	224	229	237	191	191	128	130
3326	Lacreme i Maria C	318	318	243	247	290	306	185	193	368	384	249	251	149	151	247	253	206	210	237	243	165	183	263	263	188	188	167	175	76	80	188	206	248	254	251	257	186	202	224	224	227	241	209	211	132	146
3327	Greca	314	318	247	257	290	306	185	185	356	366	251	257	149	149	247	253	206	206	237	243	183	183	263	263	188	200	165	175	74	80	202	206	248	254	247	253	188	202	222	224	239	239	209	211	132	138
3328	Caleu	314	322	257	257	290	294	183	193	352	356	261	271	149	151	247	253	206	206	237	247	183	183	263	263	182	188	165	165	76	80	186	188	238	248	247	257	186	202	224	224	239	241	209	211	128	148
3329	Minna di vacca C	318	318	0	0	290	294	179	185	352	358	239	251	149	149	253	253	204	206	243	247	165	183	263	263	188	190	163	163	76	80	188	202	248	254	0	0	186	194	224	224	233	239	207	211	132	146
3333	Funcia chiatta	314	318	241	241	290	290	179	193	358	366	249	271	149	151	251	253	210	214	243	241	165	183	263	263	174	190	165	167	74	80	166	188	248	254	251	257	184	186	222	222	227	227	209	209	138	146
3334	Bertuccio	314	322	0	0	290	294	181	185	0	0	249	251	149	151	247	251	206	212	243	243	173	183	263	263	176	188	165	165	74	76	178	178	240	254	251	259	184	186	220	220	225	225	207	207	138	140
3335	Catarratto E	0	0	227	235	290	294	179	179	352	368	251	251	149	149	247	253	206	210	243	253	165	183	263	263	174	178	165	165	0	0	0	0	240	254	243	247	194	198	222	222	227	227	0	0	0	0
3337	Inzolia nera B	314	320	243	257	290	294	185	193	356																																					