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## ‘Sangiovese’ and ‘Garganega’ are two key varieties of the Italian grapevine assortment evolution

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### Summary

Two synonymous cases have been found using a set of 11 SSR markers: ‘Garganega’ and ‘Grecanico dorato’; ‘Catarratto bianco comune’, ‘Catarratto bianco lucido’ and ‘Catarratto bianco extra lucido’. Molecular data at 36 SSR loci showed that ‘Sangiovese’ and ‘Garganega’ represent two key varieties in the Italian ampelographic assortment evolution, as they both have a first degree relationship with numerous wine varieties. ‘Sangiovese’ showed this link with ten varieties: ‘Foglia tonda’, ‘Frappato’, ‘Gaglioppo’, ‘Mantonicone’, ‘Morellino del Casentino’, ‘Morellino del Valdarno’, ‘Nerello mascalese’, ‘Susumaniello’, ‘Tuccanese di Turi’ and ‘Vernaccia nera del Valdarno’. Seven varieties resulted closely related to ‘Garganega’: ‘Trebiano toscano’ *alias* ‘Ugni blanc’, ‘Albana’, ‘Empibotte’, ‘Malvasia bianca di Candia a sapore semplice’, ‘Marzemina bianca’, ‘Catarratto’ and ‘Greco del Pollino’. However, being ‘Sangiovese’ parents disputed and those of ‘Garganega’ still unknown, it was not possible to determine the univocal direction of the various crosses. Identification of the “missing” parents would allow these genealogical trees to be drawn up with greater precision.

**Key words:** Catarratto, Trebbiano toscano, Grecanico dorato, pedigree, SSR, synonyms.

### Introduction

Researches on grapevine varieties pedigree determination have been increased in the last years by means of microsatellite markers (SSR) (SEFC *et al.* 2001), contributing to clarify the evolution of the current ampelographic assortment. One of the most interesting examples is the discovery of the origin of dozens of French varieties from a single pair of parents, ‘Pinot’ and ‘Gouais’ (BOWERS *et al.* 1999 a, BOURSIQUOT *et al.* 2004). This explains why they have less allelic variability than groups of varieties in other countries with strong viticultural traditions and, using specific tests, they can be precisely assigned to their corresponding geographical region of origin (SEFC *et al.* 2000).

‘Sangiovese’ and ‘Garganega’ are ancient and renowned wine varieties, the former being widely cultivated throughout Italy, the latter in Veneto region, mainly in the

provinces of Verona and Vicenza. ‘Sangiovese’ is better known than ‘Garganega’ and was mentioned for the first time by SODERINI (1590) as ‘Sangiogheto’; actually it is the most commonly cultivated black grape variety in Italy and is the basis for the production of famous wines, such as Chianti and Brunello di Montalcino. ‘Garganega’ is probably less known but perhaps even older than ‘Sangiovese’, as it was cited under this name as one of the grapes in the province of Padova by Pier de’ Crescenzi in the 13th century (CALÒ and COSTACURTA 2004). It is famous for the excellent Soave and Gambellara wines and its origins are still unknown.

As a consequence, the hypothesis is plausible that they could have generated progenies over the centuries or could be related to other cultivars growing in the same area. Many possible close kinships emerged from the comparison of ‘Sangiovese’ and ‘Garganega’ molecular profiles with those of hundreds of genotypes collected in the database of Centro di Ricerca per la Viticoltura. These indications were further investigated by increasing the molecular analyses up to 36 SSR loci. Many varieties showed to be involved in a parent-offspring link, some of them having economic or historical importance, such as ‘Trebiano toscano’ *alias* ‘Ugni blanc’, ‘Catarratto’, ‘Albana’, ‘Frappato’, ‘Gaglioppo’, ‘Nerello mascalese’ and ‘Marzemina bianca’. These results trace out the role played by ‘Sangiovese’ and ‘Garganega’ in the appearance of many and well known Italian varieties.

### Material and Methods

**Plant material:** More accessions belonging to 22 varieties were used for genotyping (Tab. 1). They came from the Centro di Ricerca per la Viticoltura collections of Conegliano (Treviso), Arezzo and Turi (Bari), and also from private vineyards in Tuscany and Sicily.

**Nuclear SSR loci analysis:** Genotyping was performed with 11 SSR loci (basic set) routinely employed at the Centro di Ricerca per la Viticoltura of Conegliano for cultivar identification (VVS2, THOMAS and SCOTT 1993; VVMD5, VVMD7, VVMD27 and VVMD28, BOWERS *et al.* 1996 and 1999 b; VtZAG62 and VtZAG79, SEFC *et al.* 1999; ISV2, ISV3, ISV4 and VMCNG4b9, CRESPIAN 2003). Since two groups of synonymous varieties were found (‘Grecanico dorato’ and ‘Garganega’; ‘Catarratto

Table 1

List of 22 analysed varieties

Sangiovese
Ciliegiolo
Foglia tonda
Morellino del Casentino
Morellino del Valdarno
Tuccanese di Turi
Gaglioppo di Cirò
Vernaccia nera del Valdarno
Nerello mascalese
Mantonicone
Susumaniello
Garganega
Grecanico dorato
Marzemina bianca
Catarratto bianco comune
Catarratto bianco lucido
Catarratto bianco extra lucido
Trebbiano toscano
Malvasia bianca di Candia a sapore semplice
Empibotte
Albana
Greco del Pollino

bianco comune', 'Catarratto bianco lucido' and 'Catarratto bianco extra lucido'), only one sample for each cultivar was used and the analysis was continued for 19 varieties with 25 nSSR loci, making totally 36 nSSR loci: VVS1 and VVS29 (THOMAS and SCOTT 1993); VVMD17, VVMD21, VVMD24, VVMD25, VVMD26, VVMD31, VVMD32 and VVMD36 (BOWERS *et al.* 1996 and 1999 b); VrZAG21, VrZAG64 and VrZAG83, SEFC *et al.* 1999; VMC1e12, VMC4g6, VMC2h9, VMC3d7, VMC2g2, VMC6e10, VMC4h6, VMC4c6, VMC2h4 and VMC5g6.1 (Vitis Microsatellite Consortium); scu05, SCOTT *et al.* 2000; UCH11, LEFORT *et al.* 2002.

Multiplex PCR of two or three SSR loci were suitably arranged based on expected allele lengths. The PCR reaction mixture (25 µl final volume) contained 20 ng total DNA, 10 µl Eppendorf HotMasterMix (2.5 x) and 5 pmoles of each primer. The PCR was performed in an AB 9700 thermal cycler with the following steps: 1 min 30 s at 94 °C; 35 cycles at 94 °C for 30 s, 55 °C for 30 s, 65 °C for 30 s; 65 °C for 7 min and a final step of at least 10 min at 8 °C to stop the reaction. Five µl of the PCR product were tested on 2 % agarose gel; on the basis of signal intensity, 0.75-1.5 µl of amplified DNA were used for electrophoresis onto a sequencing gel (5 % polyacrylamide, 1 x TBE, 7 M urea). Amplification products of cultivars with alleles of known molecular size were used as references for allele sizing. Allele bands were revealed by silver staining and visually scored at least twice, as reported in CRESPIAN and MILANI (2001).

**Statistical analyses:** The molecular database used for data elaboration encompassed the SSR profiles of 668 wine and table cultivars. Two different approaches were applied: the Kingroup v2 software (KONOVALOV *et al.* 2004) and the haplotype probability (HP).

Kingroup v2 program was used to calculate the likelihoods of the hypothesized pedigree relationships and their significance *versus* alternative relations. The kinship relatedness estimator was applied; parent-offspring relation as primary hypothesis and unrelated as null hypothesis.

The haplotype probability, *i.e.* the expected frequency of an *i* allele at a particular locus was calculated, given the Hardy and Weinberg law assumptions and basing on the third Mendel's law, with the following formula:

$$HP = 2p_i - p_i^2$$

where  $p_i$  is the frequency of allele *i*, computed with Cervus 3.0.3 software ([www.fieldgenetics.com](http://www.fieldgenetics.com)). The loci non in HW equilibrium, as calculated by Cervus, were discarded (VVMD7, VrZAG62 and ISV3). The SSR loci localized on the same linkage group (ADAM-BLONDON *et al.* 2004, MERDINOGLU *et al.* 2005) were considered as a single locus (15 LGs were used) and the allele univocally shared with 'Sangiovese' or 'Garganega' having the lowest frequency was chosen for HP computation; when the common allele was not univocally identifiable, that with greater frequency was selected, consequently the corresponding estimate may be biased in excess. The calculations were done with Excel computation sheet. The total haplotype probability, therefore the probability to find a particular allele combination, obtainable from the supposed parentage relationship, was computed as the product of the HPs at all LGs considered.

## Results and Discussion

**Synonyms:** Genotyping results with the basic set of SSR markers revealed two synonymies (probability of identity:  $7.3 \times 10^{-15}$ ). Firstly, 4 accessions of 'Garganega' and 4 of 'Grecanico dorato' showed the same molecular profile, confirming what previously pointed out by VANTINI *et al.* (2003) on just 2 samples. 'Garganega' has been known in Veneto since at least 1200 and has great morphological variability (COSMO and POLSINELLI 1960, CALÒ and COSTACURTA 2004). The first citation relating to 'Grecanico dorato', growing in Sicily, dates back to the end of 17th century (PASTENA 1969) and different phenotypes were described also in this case.

In order to detect possible synonymies, suggested by the Sicilian name of this cultivar reminding to a hypothetical Greek origin, its molecular profile was compared with those of the *Vitis* microsatellite databases of Centro di Ricerca per la Viticoltura of Conegliano (Italy), University of California, Davis (USA) and University of Crete, Heraklion (Greece) <http://www.biology.uoc.gr/gvd/> as well as with genotypes from various references in literature. 'Garganega'/'Grecanico dorato' showed to be different from all previously described varieties.

The second case of synonymy regarded 'Catarratto', the most widely white wine variety actually growing in Sicily. Three phenotypes were selected in the course of time: 'Catarratto bianco comune', 'Catarratto bianco lucido' and 'Catarratto bianco extra lucido'; the first two are registered in the Italian National Catalogue as distinct varieties. Nevertheless, all the accessions analyzed with the basic set of SSR markers showed identical profile. 'Catarratto bianco comune', 'Catarratto bianco lucido' and 'Catarratto bianco extra lucido' were registered in the Italian National Catalogue as distinct varieties. Nevertheless, all the accessions analyzed with the basic set of SSR markers showed identical profile. 'Catarratto bianco comune', 'Catarratto bianco lucido' and 'Catarratto bianco extra lucido' were registered in the Italian National Catalogue as distinct varieties. Nevertheless, all the accessions analyzed with the basic set of SSR markers showed identical profile.

ratto' is an ancient variety with historical presence on the island and not cultivated elsewhere, to our knowledge. The type with glossy clusters was first reported by the Ampelographic Commission of Palermo (1883), who distinguished it from 'Catarratto bianco comune', characterized by very pruinose berries. 'Catarratto extra lucido', showing clusters completely without bloom, was selected by PASTENA (1971) among 'Catarratto lucido' vines and our data confirmed what this ampelographer stated *i.e.* the 'Catarratto's are variants obtained by massal selection exploiting the intravarietal variability, therefore the three typologies are somatic mutants derived from vegetative propagation from the same original seedling (Fig. 1).



Fig. 1: From left to right: clusters of 'Catarratto bianco comune', 'Catarratto bianco lucido' and 'Catarratto bianco extra lucido'.

**P e d i g r e e :** 'Sangiovese' displayed first degree relationships with the following black skinned wine varieties (in brackets the percentage of shared alleles): 'Foglia tonda' (0.611), 'Frappato' (0.625), 'Gaglioppo' (0.653), 'Mantonicone' (0.667), 'Morellino del Casentino' (0.722), 'Morellino del Valdarno' (0.625), 'Nerello mascalese' (0.639), 'Susumaniello' (0.625), 'Tuccanese di Turi' (0.625) and 'Vernaccia nera del Valdarno' (0.570), sharing with them at

least one allele at each of the 36 SSR loci analysed (Tab. 2). 'Foglia tonda' and 'Morellino del Casentino' were also linked by a first degree relationship, but for only one allele at VMC 5g6.1 locus. The 'Sangiovese' parents 'Ciliegiolo' and 'Calabrese di Montenuovo' detected by VOULLAMOZ *et al.* (2007) were disputed by DI VECCHI STARAZ *et al.* (2007), since their molecular data indicated a different pedigree for 'Ciliegiolo' as an offspring of 'Sangiovese' and no reliable parent pair could be identified for 'Sangiovese' among the very large number of individuals they tested. The varieties closely related to 'Sangiovese' included cultivars growing in different areas: some were minor Tuscan cultivars, *i.e.* 'Foglia tonda', 'Morellino del Casentino', 'Morellino del Valdarno' and 'Vernaccia nera del Valdarno', this last different from 'Vernaccia' of Marche region (central Italy). Among these, only 'Foglia tonda' is listed in the Italian Catalogue of Vine Varieties and has a certain notoriety, whereas the others have been identified recovering local germplasm and are currently undergoing characterisation (CRESPIAN *et al.*, 2004). Others were typical varieties of Sicily and Calabria, forming part of the viticultural tradition of southern Italy, *i.e.* 'Frappato', 'Gaglioppo', 'Nerello mascalese' and 'Mantonicone'. Lastly there were two varieties from Apulia: 'Susumaniello', registered in the Italian Catalogue, and the unacknowledged 'Tuccanese di Turi' (Bari) (Fig. 2). 'Sangiovese' cannot be generated by any pair of these cultivars, not even taking into account 'Ciliegiolo', nor by selfing of one of them, because it shows alleles absent in each one SSR profile considered.

Similarly to 'Sangiovese', 'Garganega' also exhibited close relationships with many varieties, having at least one allele in common at each of the 36 SSR loci used (Tab. 3); most of them are well-known and fully described. They were 'Trebbiano toscano' *alias* 'Ugni blanc' (0.653), 'Albana' (0.667), 'Empibotte' (0.667) and 'Malvasia bianca di Candia a sapore semplice' (0.639), all spread in central Italy; 'Marzemina bianca' (0.639), an ancient cultivar of

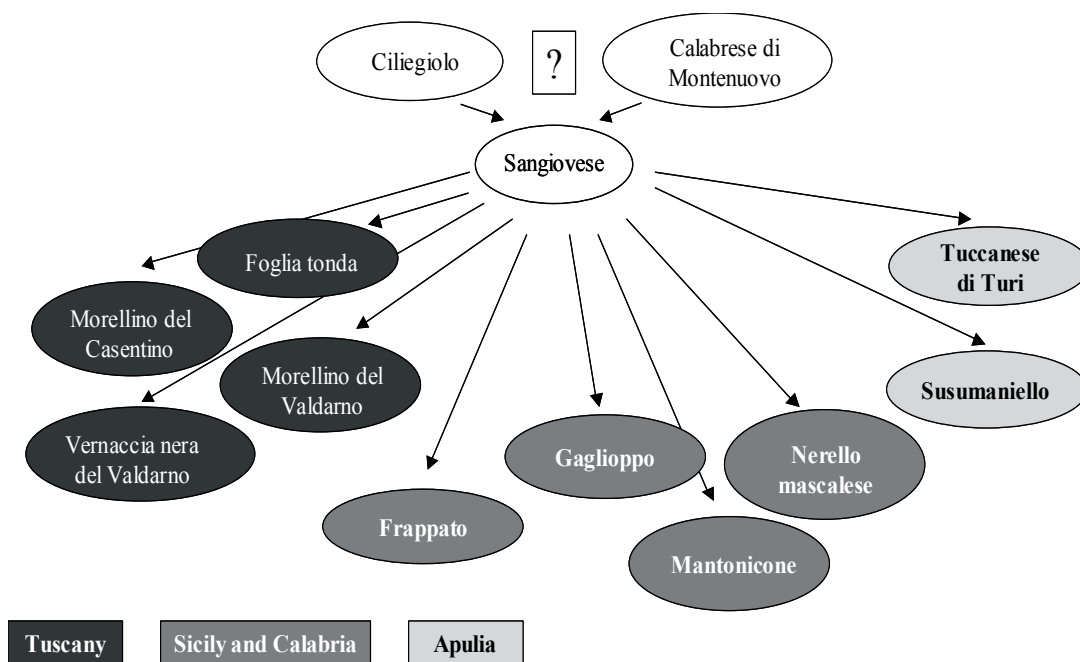


Fig. 2: 'Sangiovese' and first degree related varieties.

Table 2

'Sangiovese' and its progeny molecular data at 36 SSR loci. Allele lengths are in bp

SSR loci	LG	Sangiovese	Foglia tonda	Frappato	Gaglioppo	Mantonicone	Morellino del Casentino	Morellino del Valdarno	Nerello mascalese	Susumaniello	Tuccanese di Turi	Vernaccia nera del Valdarno
VVS1	20	181	181	181	181	181	181	181	181	181	181	181
		181	190	181	181	181	190	181	190	181	181	190
VVS2	11	133	133	133	133	133	133	133	133	133	133	133
		133	143	143	151	151	133	143	143	143	143	143
VVS29	1	171	171	171	171	171	171	171	171	171	171	171
		171	171	171	171	171	171	171	171	171	171	171
VVMD5	16	226	228	226	226	226	228	226	226	226	228	226
		236	236	226	226	240	236	236	236	232	236	240
VVMD7	7	239	239	239	239	249	239	239	239	239	247	239
		263	263	239	263	263	263	247	249	249	263	239
VVMD17	18	212	212	221	220	212	212	212	212	212	221	221
		221	222	222	221	220	221	224	221	221	224	222
VVMD21	6	243	249	243	243	243	249	249	243	243	243	243
		249	256	249	249	249	256	249	249	249	266	243
VVMD24	14	210	208	210	210	210	210	210	210	216	214	210
		216	216	210	210	216	216	216	216	219	216	216
VVMD25	11	245	245	245	245	245	245	245	245	245	245	245
		245	259	259	245	259	245	259	245	259	259	259
VVMD26	1	249	249	249	249	249	249	249	249	249	249	249
		249	249	249	251	249	249	251	251	251	249	249
VVMD27	5	179	185	179	179	179	181	185	179	179	179	179
		185	185	185	185	185	185	189	179	189	185	189
VVMD28	3	237	239	237	231	231	247	247	231	237	237	237
		247	247	261	237	247	261	247	247	239	261	239
VVMD31	7	212	204	212	210	212	212	212	212	210	212	204
		212	212	216	212	216	212	212	216	212	216	212
VVMD32	4	253	257	251	253	253	257	241	253	257	253	257
		257	273	253	257	257	273	257	257	263	253	273
VVMD36	3	264	258	264	264	264	264	264	264	250	264	258
		264	264	276	296	296	270	264	296	264	270	264
VrZAG 21	4	202	204	190	200	190	204	204	190	190	202	204
		204	206	202	204	204	206	206	204	204	214	206
VrZAG 62	7	193	193	193	193	193	187	195	195	195	193	193
		195	193	195	201	201	193	203	201	199	193	195
VrZAG 64	10	137	139	137	139	137	139	137	137	139	137	137
		139	159	139	141	137	159	137	141	159	139	139
VrZAG 79	5	242	238	242	242	242	242	242	250	250	242	244
		258	242	248	250	250	242	244	258	258	258	258
VrZAG 83	8	190	190	190	190	190	190	190	190	188	194	188
		194	200	194	194	190	200	200	190	190	194	190
ISV2	14	143	143	157	165	141	143	143	141	143	143	143
		165	151	165	169	143	169	165	143	143	143	151
ISV3	2	139	139	139	133	133	133	133	133	133	133	139
		139	145	139	139	139	139	139	139	139	139	145
ISV4	11	177	169	177	177	177	177	169	169	177	191	169
		197	177	183	191	191	197	197	177	183	197	177
VMC 1e12	14	254	250	250	250	254	250	246	250	254	260	250
		260	260	254	260	254	254	254	254	260	260	254
VMC NG 4b9	6	158	158	158	150	150	158	168	150	168	166	158
		168	168	164	168	158	168	176	168	172	168	162
VMC 4g6	6	127	127	129	127	127	127	127	127	127	127	125
		143	143	143	129	129	143	133	129	129	137	143
VMC 2h9	6	117	117	117	117	117	117	117	117	117	117	117
		117	139	123	117	117	117	123	123	117	123	139
VMC 3d7	10	163	163	163	161	163	163	161	161	163	163	161
		163	169	177	163	163	169	163	163	177	163	163
VMC 2g2	6	119	119	119	119	119	119	119	119	119	119	119
		119	141	125	119	119	119	125	125	119	125	141
VMC 6e10	5	95	95	95	113	95	95	97	95	119	93	97
		119	119	117	119	111	119	119	113	121	95	119
VMC 4h6	9	158	158	152	158	158	158	158	158	158	152	158
		158	162	158	158	158	162	158	158	164	158	162
VMC 4c6	5	157	163	157	163	157	157	163	157	157	157	163
		163	166	163	163	163	163	163	163	163	163	166
VMC 2h4	12	214	214	198	198	198	208	200	198	214	214	214
		214	234	214	214	214	214	214	214	214	214	234
scu 05	12	156	156	156	160	156	160	156	156	160	156	160
		160	160	171	165	165	169	160	156	163	156	160
UCH11		236	242	246	236	242	236	236	236	236	242	236
		262	262	262	236	262	262	244	262	263	262	242
VMC 5g6.1		125	125	121	139	139	139	142	139	125	142	133
		142	141	142	142	142	142	151	142	151	151	142

Table 3

Molecular data of 'Garganega' and first degree related varieties at 36 SSR loci. Allele lengths are in bp

SSR loci	LG	Garganega <i>alias</i> Greccanico dorato	Albana	Catarratto	Empibotte	Greco bianco del Pollino	Malvasia bianca di Candia a sapore semplice	Marzemina bianca	Trebbiano toscano <i>alias</i> Ugni blanc
VVS1	20	181	181	181	181	181	181	181	181
		181	181	181	181	182	181	190	190
VVS2	11	133	133	143	133	143	133	133	133
		143	143	151	143	145	143	133	143
VVS29	1	171	171	171	171	171	171	171	171
		171	171	171	171	171	171	171	171
VVMD5	16	226	226	226	226	232	226	226	226
		232	232	226	232	232	238	238	232
VVMD7	7	249	247	239	249	239	249	239	249
		253	249	249	253	249	263	253	253
VVMD17	18	222	222	221	221	222	220	212	212
		222	222	222	222	222	222	222	222
VVMD21	6	249	249	243	249	249	249	249	243
		249	256	249	249	249	256	249	249
VVMD24	14	210	210	210	210	210	210	210	210
		210	210	210	216	210	210	210	210
VVMD25	11	245	245	259	243	245	245	245	245
		259	259	259	259	259	259	245	259
VVMD26	1	251	255	249	249	251	249	249	251
		263	263	251	263	251	251	263	263
VVMD27	5	179	179	179	183	179	185	185	179
		194	189	179	194	185	194	194	183
VVMD28	3	239	237	231	239	249	249	239	247
		251	239	239	251	251	251	239	251
VVMD31	7	210	204	210	210	213	210	213	210
		213	210	210	213	213	210	216	212
VVMD32	4	251	251	251	251	251	259	251	251
		259	273	253	273	253	259	253	273
VVMD36	3	254	248	254	266	264	264	244	264
		266	254	296	296	266	266	254	266
VrZAG 21	4	190	202	190	202	202	190	190	202
		202	206	200	206	214	190	202	206
VrZAG 62	7	199	193	199	199	187	199	193	193
		199	199	201	203	199	201	199	199
VrZAG 64	10	137	137	139	137	137	137	139	137
		139	139	141	139	143	139	143	163
VrZAG 79	5	250	250	250	246	250	238	248	244
		250	250	250	250	250	250	250	250
VrZAG 83	8	190	188	194	188	190	190	194	188
		194	194	194	194	194	194	194	194
ISV2	14	141	165	165	141	141	141	141	141
		165	169	169	157	169	169	165	161
ISV3	2	133	133	139	133	139	133	133	133
		139	139	145	139	145	139	139	139
ISV4	11	177	169	177	169	169	177	169	177
		187	187	191	187	177	187	177	187
VMC 1e12	14	240	240	240	240	240	240	240	240
		240	260	254	240	260	260	256	246
VMC NG 4b9	6	176	158	150	158	158	150	166	162
		178	176	176	176	176	176	176	176
VMC 4g6	6	129	133	129	127	133	125	129	125
		133	143	133	133	143	129	133	133
VMC 2h9	6	123	117	117	117	117	117	117	117
		125	125	123	125	123	125	123	123
VMC 3d7	10	163	163	161	163	163	159	163	161
		175	175	175	163	163	175	175	175
VMC 2g2	6	125	119	119	119	119	119	119	119
		127	127	125	127	125	127	125	125
VMC 6e10	5	93	93	93	113	93	93	97	117
		117	121	113	117	93	113	117	117
VMC 4h6	9	152	152	152	158	158	152	152	158
		158	182	162	158	162	162	158	158
VMC 4c6	5	163	163	163	163	163	163	163	157
		163	166	163	163	163	166	163	163
VMC 2h4	12	206	206	206	214	214	206	214	206
		214	214	232	214	214	214	214	214
scu 05	12	165	160	165	156	169	165	160	165
		169	169	165	169	184	165	169	165
UCH11		242	242	236	236	242	242	244	246
		246	260	242	246	242	244	246	246
VMC 5g6.1		139	129	139	151	142	141	141	139
		151	139	151	151	151	151	151	151

North East Italy, which originated ‘Raboso veronese’ (CRESPAN *et al.* 2006); the before described ‘Catarratto’ (0.611) and finally ‘Greco del Pollino’ (0.611), a minor variety present in southern Italy, in particular in Calabria, Basilicata and Apulia, under different synonymous names (COSTACURTA *et al.* 2004) (Fig. 3). Unlike ‘Sangiovese’ related varieties, those found to be close to ‘Garganega’ are spread from North to South Italy and cover a broader area, even if they are less numerous. ‘Trebiano toscano’ is greatly spread also in France (GALET 2000).

No couple of these cultivars could originate ‘Garganega’ and even selfing of one of them must be excluded, since no combination can provide the alleles matched in its SSR profile. Therefore, being the parents of ‘Garganega’ still undiscovered, it was difficult to make any hypotheses on its exact relationship with these varieties; the identification of the “missing” parents will allow to clarify the correct pedigree direction.

The presence of ‘Malvasia bianca di Candia a sapore semplice’ in this kinship is interesting, since Malvasias form a complex group of highly heterogeneous varieties (COSTACURTA *et al.* 2005, LACOMBE *et al.* 2007), the majority of which are growing in Italy and whose geographical origin is often unknown.

**Statistical analyses:** The results obtained elaborating SSR data with KinGroup vs2 program are reported in Tab. 4. The probability ratios between the hypothesis that the listed varieties could be really linked to ‘Sangiovese’ or ‘Garganega’ by a first degree relationship, in respect to the probability that they were not, gave positive values, highly significant in respect to the whole population mean, which had a strongly negative value, -3.39 E + 38.

The haplotype probabilities of each one ‘Sangiovese’ and ‘Garganega’ first degree related cultivar are shown in Tab. 5. The computed values, in spite of the great restric-

Table 4

Kingroup likelihood ratios of parent-offspring relationships vs. unrelated, computed with 668 only cvs and over 35 SSR loci

Sangiovese	Morellino del Casentino	25.57
	Tuccanese di Turi	24.66
	Mantonicone	22.77
	Morellino del Valdarno	22.71
	Nerello mascalese	21.68
	Gaglioppo	20.74
	Susumaniello	19.80
	Foglia tonda	19.22
	Frappato	16.69
	Vernaccia nera del Valdarno	16.01
Garganega	Empibotte	29.43
	Malvasia di Candia a s.s.	26.82
	Trebiano toscano	25.28
	Albana	24.53
	Marzemina bianca	24.17
	Greco bianco del Pollino	21.74
	Catarratto	17.55
Whole population mean ratio		-3.39E+38

tions imposed in the calculation, go from  $3.24 \times 10^{-6}$  to  $8.98 \times 10^{-9}$  and indicate clearly that these particular combinations can not be due to instance, but are well explainable with parent-offspring relationships. In summary, both computational approaches contributed to corroborate the hypotheses issued from simple molecular data scrolling.

**Conclusions**

Our findings indicate that ‘Sangiovese’ and ‘Garganega’ were crucial in the evolution of the Italian ampelo-

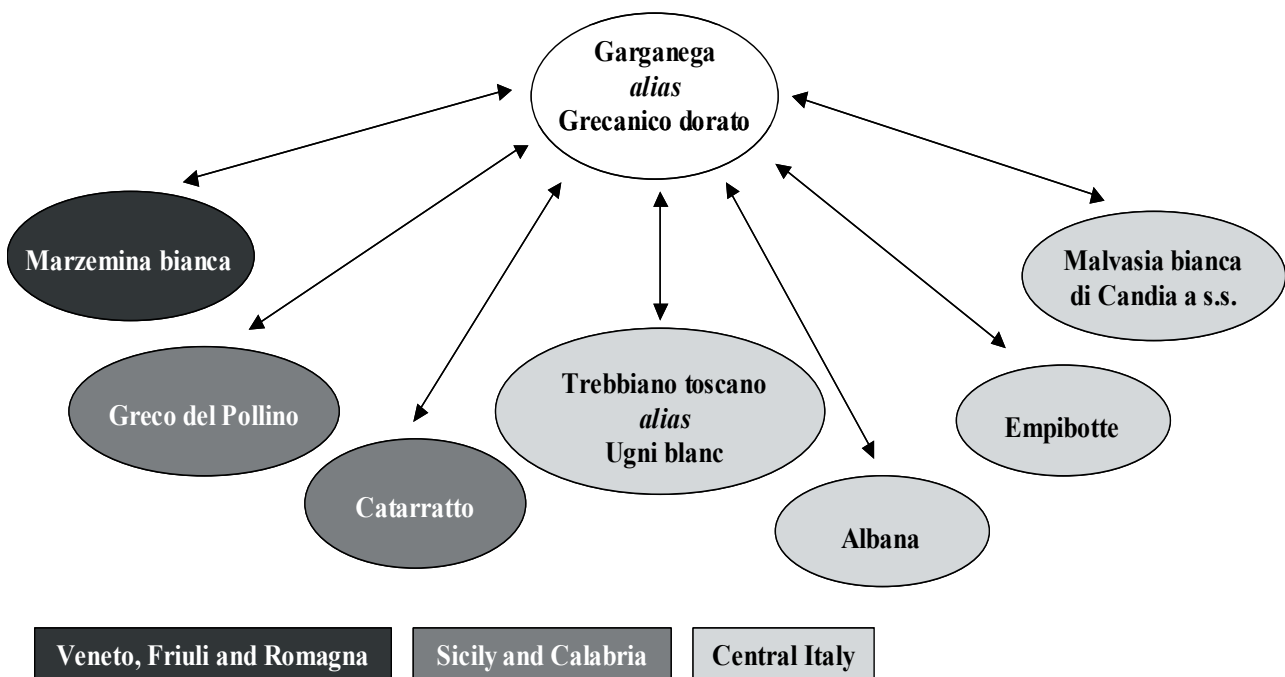


Fig. 3: ‘Garganega’ and first degree related varieties.

Table 5

Haplotype probability (HP) of Sangiovese’s presumed progeny and first degree related varieties linked to Garganega, computed on 15 linkage groups

Sangiovese	Foglia tonda	2.25 x 10 <sup>-7</sup>	
	Frappato	3.24 x 10 <sup>-6</sup>	
	Gaglioppo	6.31 x 10 <sup>-7</sup>	
	Mantonicone	3.12 x 10 <sup>-7</sup>	
	Morellino del Casentino	4.29 x 10 <sup>-7</sup>	
	Morellino del Valdarno	4.71 x 10 <sup>-8</sup>	
	Nerello mascalese	1.58 x 10 <sup>-7</sup>	
	Susumaniello	8.03 x 10 <sup>-8</sup>	
	Tuccanese di Turi	7.73 x 10 <sup>-8</sup>	
	Vernaccia nera del Valdarno	1.15 x 10 <sup>-6</sup>	
	Garganega	Albana	1.89 x 10 <sup>-8</sup>
		Catarratto	4.02 x 10 <sup>-8</sup>
		Empibotte	6.13 x 10 <sup>-9</sup>
Greco bianco del Pollino		8.98 x 10 <sup>-9</sup>	
Malvasia bianca di Candia a sapore semplice		3.79 x 10 <sup>-9</sup>	
Marzemina bianca		7.37 x 10 <sup>-9</sup>	
Trebbiano toscano	2.42 x 10 <sup>-8</sup>		

graphic assortment and demonstrate that ‘Sangiovese’ has clear and dated relationships with Southern Italian varieties. Our data confirm and corroborate, on one side, some of the indications given by DI VECCHI STARAZ *et al.* 2007 about the role played by these two cultivars, also using a mostly different set of SSR markers; on the other side, our work adds new members to the respective families of ‘Sangiovese’ and ‘Garganega’. The detection of missing parents in the two family trees will contribute to clarify the respective temporal appearance of close related varieties. It is interesting to notice an additional synonym of ‘Garganega’/‘Grecanico dorato’ reported by GALET (2000), who stated: “Selon Carpentieri ce plant serait identique au greco d’Arcetri (*i.e.* south of Florence), ou decanico, synonymes non recontrés en Sicile”: this would fill the strange gap on the apparent absence of this variety in central Italy.

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