

‘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 ‘Grechanico 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’: ‘Trebbiano 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.

K e y w o r d s : Catarratto, Trebbiano toscano, Grechanico 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 ‘Sangioghezo’; 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 ‘Trebbiano 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

P l a n t m a t e r i a l : 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.

N u c l e a r S S R l o c i a n a l y s i s : 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; VrZAG62 and VrZAG79, SEFC *et al.* 1999; ISV2, ISV3, ISV4 and VMCNG4b9, CRESPLAN 2003). Since two groups of synonymous varieties were found (‘Grechanico 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 CRESPLAN 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). 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: 7.3×10^{-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

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 VOUILAMOZ *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 (CRESPAN *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

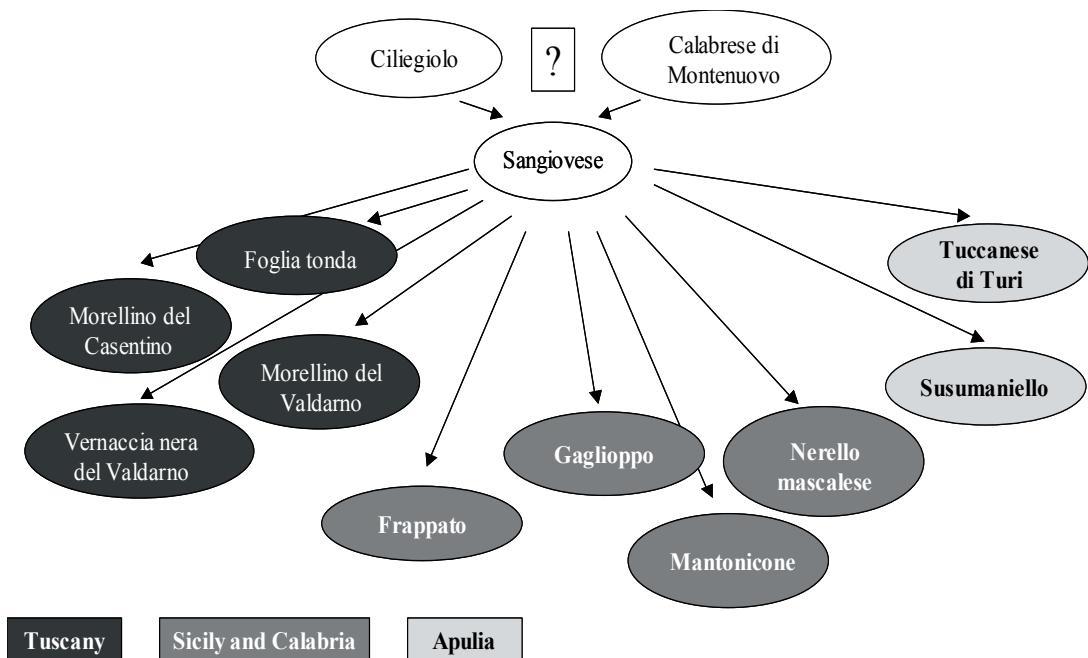


Fig. 2: 'Sangiovese' and first degree related varieties.

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

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

North East Italy, which originated ‘Raboso veronese’ (CRESPLAN *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. ‘Trebbianino 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 significative 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
	Trebbianino 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 3.24×10^{-6} to 8.98×10^{-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-

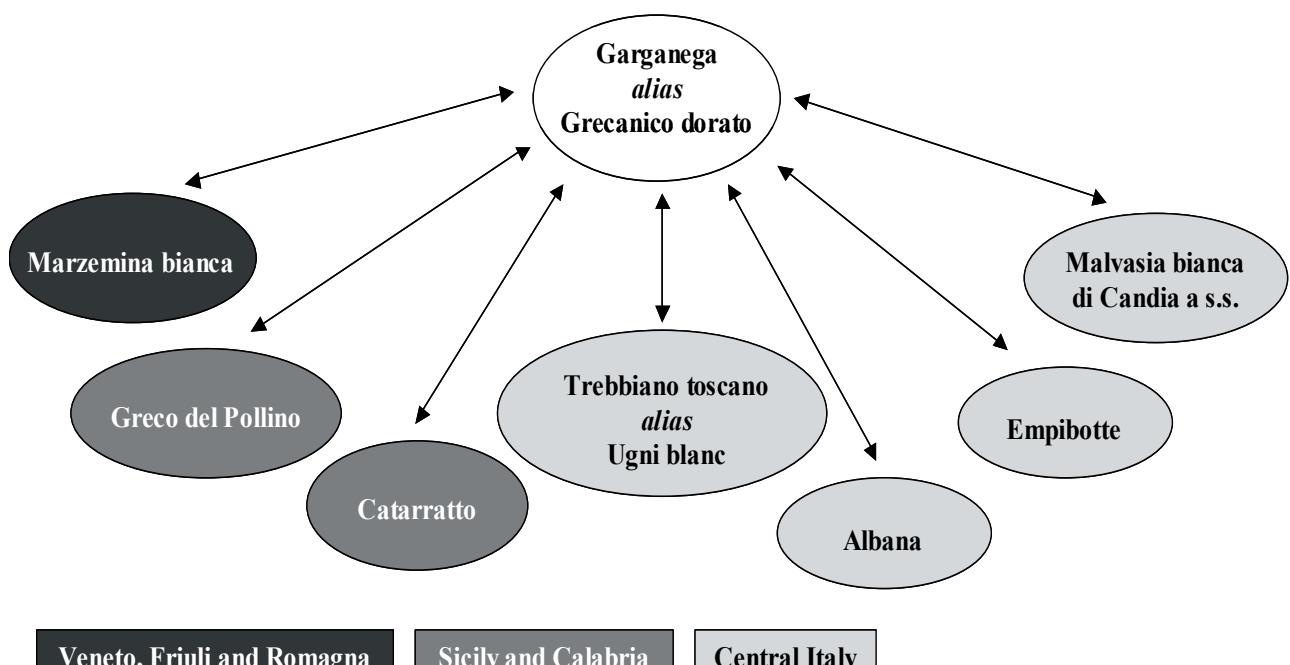


Fig. 3: 'Garganega' and first degree related varieties.

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

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'/'Greco 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 rencontrés en Sicile": this would fill the strange gap on the apparent absence of this variety in central Italy.

Acknowledgements

The authors thank R. Di LORENZO for providing one Greco dorato accession, C. LORENZONI and M. GARDIMAN for advice in molecular data statistical processing. This research was supported by Trattato Internazionale FAO, Progetto Risorse Genetiche Vegetali, funded by the Italian Ministero delle Politiche Agricole, Alimentari e Forestali.

References

- ADAM-BLONDON, A. F.; ROUX, C.; CLAUX, D.; BUTTERLIN, G.; MERDINGLU, D.; THIS, P.; 2004: Mapping 245 SSR markers on the *Vitis vinifera* genome: A tool for grape genetics. *Theor. Appl. Genet.* **109**, 1017-1027.
- BOURSIQUOT, J. M.; LACOMBE, T.; BOWERS, J.; MEREDITH, C.; 2004: Le Gouais, un cépage clé du patrimoine viticole européen. *Bull. O I V* (Off. Int. Vigne Vin) **77**, 5-19.
- BOWERS, J. E.; BOURSIQUOT, J. M.; THIS, P.; CHU, K.; JOHANSSON, H.; MEREDITH, C.; 1999 a: Historical genetics: The parentage of Chardonnay, Gamay, and other wine grapes of Northeastern France. *Science* **285**, 1562-1565.
- BOWERS, J. E.; DANGL, G. S.; MEREDITH, C. P.; 1999 b: Development and characterisation of additional microsatellite DNA markers for grape. *Am. J. Enol. Vitic.* **50**, 243-246.
- BOWERS, J. E.; DANGL, G. S.; VIGNANI, R.; MEREDITH, C. P.; 1996: Isolation and characterisation of the new polymorphic simple sequence repeat loci in grape (*Vitis vinifera* L.). *Genome* **39**, 628-633.
- CALÒ, A.; COSTACURTA, A.; 2004: Dei Vitigni Italici. Matteo Editore srl.
- COSMO, I.; POLSINELLI, M.; 1960: Garganega. In: *Principali Vitigni da Vino Coltivati in Italia*. Vol. I, Ed. MAF, Roma.
- COSTACURTA, A.; CALÒ, A.; ANTONACCI, D.; CATALANO, V.; CRESPLAN, M.; CARRARO, R.; GIUST, M.; AGGIO, L.; OSTAN, M.; DI STEFANO, R.; BORSA, D.; 2004: La caratterizzazione di Greci e Grechetti a bacca bianca coltivati in Italia. *Riv. Vitic. Enol.* **3**, 3-20.
- COSTACURTA, A.; CALÒ, A.; CARRARO, R.; GIUST, M.; CRESPLAN, M.; 2005: The Malvasias cultivated in Italy: SSR, ampelographic, chemical profiles and pedigree relationships. *Riv. Vitic. Enol.* **2-3-4**, 55-65.
- CRESPLAN, M.; 2003: The parentage of Muscat of Hamburg. *Vitis* **42**, 193-197.
- CRESPLAN, M.; CANCELLIER, S.; CHIES, R.; GIANNETTO, S.; MENEGHETTI, S.; 2006: The parents of Raboso veronese were discovered: A new hypothesis on its origin. *Riv. Vitic. Enol.* **1**, 3-12.
- CRESPLAN, M.; GIANNETTO, S.; CHIES, R.; STORCHI, P.; 2004: A molecular investigation to define pedigree relationships among Sangiovese and other black varieties cultivated in Central Italy, 109-113. Proc. 2nd Int. Symp. "Il Sangiovese Identità e Peculiarità: Vine Variety Tipico ed Internazionale".
- CRESPLAN, M.; MILANI, N.; 2001: The Muscats: A molecular analysis of synonyms, homonyms and genetic relationships within a large family of grapevine cultivars. *Vitis* **40**, 23-30.
- DI VECCHI STARAZ, M.; BANDINELLI, R.; BOSELLI, M.; THIS, P.; BOURSIQUOT, J. M.; LAUCOU, V.; LACOMBE, T.; VARÈS, D.; 2007: Genetic structuring and parentage analysis for evolutionary studies in grapevine: kin group and origin of the cultivar Sangiovese revealed. *J. Am. Soc. Hort. Sci.* **132**, 514-524.
- GALET, P.; 2000: *Dictionnaire Encyclopédique des Cépages*. Ed. Hachette.
- KONOVALOV, D. A.; MANNING, C.; HENSHAW, M. T.; 2004: Kingroup: A program for pedigree relationship reconstruction and kin group assignments using genetic markers. *Mol. Ecol. Notes* **4**, 779-782.
- LACOMBE, T.; BOURSIQUOT, J. M.; LAUCOU, V.; DECHESNE, F.; VARÈS, D.; THIS, P.; 2007: Relationships and genetic diversity within the accessions related to Malvasia held in the Domaine de Vassal grape germplasm repository. *Am. J. Enol. Vitic.* **58**, 124-131.
- LEFORT, F.; KYVELOS, C. J.; ZERVOU, M.; EDWARDS, K. J.; ROUBELAKIS-ANGELAKIS, K. A.; 2002: Characterization of new microsatellite loci from *Vitis vinifera* and their conservation in some *Vitis* species and hybrids. *Mol. Ecol. Notes* **2**, 20-21.
- MERDINGLU, D.; BUTTERLIN G.; BEVILACQUA L.; CHIQUET V.; ADAM-BLONDON A. F.; DECROOCQ S.; 2005: Development and characterization of a large set of microsatellite markers in grapevine (*Vitis vinifera* L.) suitable for multiplex PCR. *Mol. Breed.* **15**, 349-366.
- PASTENA, B.; 1969: Disamina della piattaforma ampelografica del seicento descritta nell'opera botanica di F. Cupani (1692-1697). In: "Atti Accademia Italiana della Vite e del Vino" vol. XXI.
- PASTENA, B.; 1971: I Catarratti Bianchi. *Atti Accademia Vite Vino*, XX-III.
- SCOTT, K. D.; EGGLER, P.; SEATON, G.; ROSSETTO, M.; ABLETT, E. M.; LEE, L. S.; HENRY, R. J.; 2000: Analysis of SSRs derived from grape ESTs. *Theor. Appl. Genet.* **100**, 723-726.
- SEFC, K. M.; REGNER, F.; TURETSCHEK, E.; GLÖSSL, J.; STEINKELLNER, H.; 1999: Identification of microsatellite sequences in *Vitis riparia* and their applicability for genotyping of different *Vitis* species. *Genome* **42**, 367-373.
- SEFC, K. M.; LOPES, M. S.; LEFORT, F.; BOTTA, R.; ROUBELAKIS-ANGELAKIS, K. A.; IBÁÑEZ, J.; PEJIĆ, I.; WAGNER, H. W.; GLÖSSL, J.; STEINKELLNER, H.; 2000: Microsatellite variability in grapevine cultivars from different European regions and evaluation of assignment testing to

- assess the geographic origin of cultivars. *Theor. Appl. Genet.* **100**, 498-505.
- SEFC, K. M.; LEFORT, F.; GRANDO, M. S.; SCOTT, K. D.; STEINKELLNER, H.; THOMAS M. R. 2001: Microsatellite markers for grapevine: A state of the art. In: K. A. ROUBELAKIS-ANGELAKIS (Ed.): *Molecular biology & biotechnology of the grapevine*. Kluwer Academic Publishers, The Netherlands.
- SODERINI, G.V.; 1590: *Delle Condizioni della Vite e del Frutto che se ne può Ricavare*. Giunti, Firenze.
- THOMAS, M. R.; SCOTT, N. S.; 1993: Microsatellite repeats in grapevine reveal DNA polymorphisms when analysed as sequence-tagged sites (STSS). *Theor. Appl. Genet.* **86**, 985-990.
- VANTINI, F.; TACCONI, G.; GASTALDELLI, M.; GOVONI, C.; TOSI, E.; MALACRINÒ, P.; BASSI, R.; CATTIVELLI, L.; 2003: Biodiversity of grapevines (*Vitis vinifera* L.) grown in the province of Verona. *Vitis* **42**, 35-38.
- VOUILLAMOZ, J. F.; MONACO, A.; COSTANTINI, L.; STEFANINI, M.; SCIENZA, A.; GRANDO, M. S.; 2007. The parentage of 'Sangiovese', the most important Italian wine grape. *Vitis* **46**, 19-22.

Received May 21, 2007