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Parentage analysis in Hungarian grapevine cultivars of 'Seibel'-'Seyve-Villard' origin

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Summary

Viticulture is worldwide endangered by powdery (*Erysiphe necator*) and downy mildew (*Plasmopara viticola*) fungal diseases. These pathogens derive from North America and got into Europe with infected grape cuttings in the 19th century. Because of the vulnerability of the traditional European grapevine cultivars an interspecific hybrid breeding program was started in France with crossing *Vitis* species originating from North America and *V. vinifera* L. varieties. The results of this activity pioneered by Albert Seibel, Bertille Seyve and Victor Villard were hybrids having good quality and carrying partial resistance against fungal pathogens. 'Seibel' and 'Seyve-Villard' grapes were applied in the resistance breeding programs in Hungary, too. We analyzed 22 out of these hybrids, their putative parents and international reference varieties (altogether 40 genotypes) with microsatellite and ScORA7-760 resistance QTL-linked marker.

Key words: Grape hybrids; SSR, ScORA7-760; powdery and downy mildew.

Introduction

The cultivation and breeding of grapevine (*Vitis vinifera* L.) goes back to ancient times. On the effect of selection, changing of growing conditions thousands of cultivars have arisen or have been brought about. Breeding fungus resistant grape varieties became an inevitable question for the European viticulture in the 19th century, when powdery mildew (PM) and downy mildew (DM) were dragged along with infected grape cuttings from North America to Europe. *V. vinifera* cultivars of European origin were defenceless against these diseases, therefore introgression of resistance genes from wild *Vitis* species was started for protecting grape and wine production against the severe yield loss and quality decrease. This hybrid breeding program was pioneered by Albert Seibel, Bertille Seyve and Victor Villard in France resulting in interspecific hybrids having better quality than 'direct producing' grapes and carrying partial resistance against fungal pathogens (SKELTON 2010, CATRELL 2014). These so called 'Seibel'- and 'Seyve-Villard' grapes were used by Hungarian breeders also to improve local cultivars.

Our aim was to analyze 22 of these Hungarian hybrids and their putative parents with microsatellite markers. Determining the allele combination of these varieties made it possible to confirm or exclude the registered parent-progeny relationships (CSEPREGI and ZILAI 1980; HAJDU and ÉSIK 2001, HAJDU 2010). Since the analyzed Hungarian grape varieties were produced for breeding purposes and found to be at least tolerant to different extent against PM and DM infections (KOZMA 1995) we tested them for resistance QTL-linked marker (ScORA7-760), described by AKKURT *et al.* (2007), as well. The ScORA7-760 SCAR marker was developed from a RAPD fragment in a 'Regent' x 'Lemberger' mapping population, in which the fungus resistant parent, 'Regent' has 'Seyve-Villard' and 'Seibel' ancestors. AKKURT *et al.* (2007) proved correlation between PM resistance and amplification of the 760 bp PCR fragment and recommended it for marker assisted selection.

Material and Methods

Twenty-two Hungarian interspecific hybrids and their 15 putative parents were studied (Table). DNA isolation and microsatellite analyses were carried out according to HALÁSZ *et al.* (2005). Nine nuclear SSR primer pairs VrZag62, VrZag79, VVMD5, VVMD7, VVMD25, VVMD27, VMD28, VVMD32 and VVS2 were chosen according to the GenRes081 and GrapeGen06 EU project (THIS *et al.* 2004; MAUL *et al.* 2012). For parentage analysis Identity 1.0 statistics was applied (WAGNER and SEFC 1999). ScORA7-760 marker was used to check for the presence of QTL related to PM and DM resistance as reported in AKKURT *et al.* (2007). Resistance characteristics of the 22 cultivars were evaluated according the OIV N° 452 and 455 descriptors (KOZMA 1995).

Results and Discussion

Based on the parentage analysis using SSR markers, the 22 Hungarian varieties grouped into 4 classes confirming or contradicting previous pedigree records (Table). In group 1, there were varieties for which the data of 9 SSR loci proved the parentage. In group 2, the maternity cannot be excluded (no paternal samples were available), while in the case of group 3 two or more alleles disproved one of

Table

Confirmation or contradiction of parentage of 22 Hungarian grape varieties of 'Seibel'/'Seyve-Villard' origin and presence or absence of ScORA7-760 fragment in the varieties and powdery and downy mildew symptoms

Group	Variety progeny	Parent 1 (P ₁)	Parent 2 (P ₂)	No. of mis-matching alleles P ₁	No. of SSR loci	No. of mis-matching alleles P ₂	ScORA 7-760 bp	Downy mildew (1-9)*	Powdery mildew (1-9)*
1.	Bianca	Seyve-Villard 12375	Bouvier	0	9	0	760	7	7
	Göcseji zamatos	Seyve-Villard 12286	Medoc noir	0	9	0	-	7	4
	Medina	Seyve-Villard 12286	Medoc noir	0	9	0	-	4	7
	Nero	Seyve-Villard 12375	Medoc noir x Csabagyöngye	0	9	0	760	6	5
	Palatina	Seyve-Villard 12375	Szőlőskertek királynője	0	9	0	-	6	5
	Reflex	Pannónia kincse	Seibel 5279	0	9	0	760	7	7
	Reform	Csabagyöngye	Seibel 5279	0	9	0	760	6	5
	Refrén	Glória Hungariae	Seibel 5279	0	9	0	760	7	7
	Suzy	Seyve-Villard 12375	Pannónia kincse	0	9	0	-	7	no data
	Teréz	Seyve-Villard 12375	Olimpia	0	9	0	760	7	7
	Vértes csillaga	Seyve-Villard 12286	Medoc noir	0	9	0	760	7	7
2.	Eszter	Seyve-Villard 12375	Magaracsi csemege I.	0	9	0	760	6	7
	Flóra	Seyve-Villard 12375	Magaracsi csemege II.	0	9	0	760	no data	no data
	Lidi	Seyve-Villard 12375	Magaracsi csemege III.	0	9	0	-	7	5
3.	Dunagyöngye	Seibel 4986	Csabagyöngye	0	9	5	-	4	6
	Fanny	Seyve-Villard 12375	Téli muskotály x Olimpia	0	9	2	760	5	5
	Viktor	Zalagyöngye	Kadarka	0	9	8	760	7	7
	Zalagyöngye	Seyve-Villard 12375	Csabagyöngye	3	9	0	760	5	5
4.	Csillám	Seyve-Villard 12375	Csabagyöngye	5	9	7	-	6	5
	Pölöskei muskotály	Zalagyöngye	Gloria Hungaria x Erzsébet királyné	6	9	7	760	7	7
	Sarolta	Zalagyöngye	Gloriae Hungariae x (Szőlőskertek királynője x Téli muskotály)	3	9	1	760	3	5
	Viktória gyöngye	Seyve-Villard 12375	Csabagyöngye	8	9	4	760	7	7

* Meaning of the numbers (1-9): scale according to OIV N 452 and 455 descriptors.



Figure: Analysis of grape varieties of 'Seibel'-'Seyve-Villard' origin with ScORA7-760 marker. MM: DNA molecular weight marker (fragment sizes in bp: 80, 100, 200, 300, 400, 500, 600, 700, 800, 900, 1031).

the putative parents. In group 4 neither the maternal, nor the paternal origin corresponded to the breeding records.

The 22 varieties were supposed to have at least tolerance against PM and DM, therefore they were tested for the presence of resistance QTL (ScORA7-760 marker) of 'Seibel'-'Seyve-Villard' origin. At the same time their PM and DM symptoms were also observed and evaluated as it can be depicted in the Table, where higher values indi-

cate higher level of PM or DM tolerance (KOZMA 1995). Despite the proven 'Seibel'-'Seyve-Villard' origin of the varieties, the DM and PM infection rate was different (in range 3-7). Offsprings deriving from the same cross displayed variable symptoms (e.g. 'Göcseji zamatos', 'Medina' and 'Vértes csillaga'). The 760 bp long PM QTL allele could be amplified in 15 out of the examined 22 Hungarian cultivars (Figure), among them there are the members of

group 1 and 2, in which parentage or at least the maternal origin has been confirmed by SSR analysis. In these varieties, 'Seyve-Villard 12375', '12286' or 'Seibel 5279' is one of the parents. No ScORA7-760 marker could be detected in 7 out of 22 varieties, among which there are cultivars both with proven ('Göcseji zamatos', 'Medina', 'Lidi', 'Palatina', 'Suzy') and disproven ('Dunagyöngye', 'Csillám') origins. However, their 'Seyve-Villard 12375', '12286' or 'Seibel 4986' components carry the ScORA7-760 marker. 'Csillám' is an exception, since the parentage of 'Seyve-Villard 12375' has not been confirmed by the SSR data. The presence or absence of ScORA7-760 marker did not show unambiguous correlation with the level of fungal infection. Our further objectives are to find the true crossing partners of the varieties with disproven parentage. Determination of right pedigree and identification of PM and DM resistance QTLs can be important in complex breeding programs aiming at production of durable resistance.

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