

SUPPLEMENTARY DATA

Kaur, K., Rinaldo, A., Lovelock, D., Kehoc, M., Kinene, T., Clarke, A., ... Constable, F. (2025). Grapevine red blotch virus (GRBV) in a historical germplasm collection in south-eastern Australia. *OENO One*, 59(3).
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Table S1. The GenBank accession numbers for 143 grapevine red blotch virus (GRBV; *Grablovirus vitis*) genome sequences available on NCBI and their respective country of origin. Victorian GRBV isolates detected in cultivars (names listed) in the CSIRO germplasm collection are in bold.

Accession no.	Country	Accession no.	Country	Accession no.	Country	Accession no.	Country	Accession no.	Country	Accession no.	Country
Courderc noir PV944260	Australia	Perle de Csaba FSAC OR730852	Australia	KX316012	Canada	KF147916	USA	MF795148	USA	MF795174	USA
Chasselas Parsley leafed IC8423 PV944256	Australia	OR730853	Australia	KX316014	Canada	KF751708	USA	MF795149	USA	MF795175	USA
Chasselas Parsley leafed IC8424 PV944257	Australia	OR730854	Australia	KX316015	Canada	KP221559	USA	MF795150	USA	MF795176	USA
Dolcetto PV944259	Australia	OR730855	Australia	KX316016	Canada	KU564247	USA	MF795151	USA	MF795177	USA
Kandahar PV944258	Australia	OR730856	Australia	KX316017	Canada	KU564248	USA	MF795152	USA	MG672441	USA
Muscat Cannon Hall PV944262	Australia	OR730857	Australia	KX316018	Canada	KU564249	USA	MF795153	USA	MH732736	USA
Muscat Gordo Blanco L1V9 PV944264	Australia	OR730858	Australia	KX316019	Canada	KU564250	USA	MF795154	USA	MK928382	USA
Muscat Gordo Blanco L10V5 PV944263	Australia	OR730859	Australia	KX316020	Canada	KU564251	USA	MF795155	USA	MK928384	USA
Opuzensia Rana PV944253	Australia	KX234088	Canada	KX316021	Canada	KU564252	USA	MF795156	USA	MK928385	USA
Parellada PV944265	Australia	KX234093	Canada	KX316022	Canada	KU564253	USA	MF795157	USA	MK928386	USA
Peloursin PV944255	Australia	KX234094	Canada	KX316023	Canada	KU564254	USA	MF795158	USA	MN186403	USA

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Perle de Csaba L6V13 PV944254	Australia	KX234095	Canada	KX316024	Canada	KU564255	USA	MF795159	USA	MN186404	USA
Semillon PV944261	Australia	KX315998	Canada	KX316025	Canada	KU564256	USA	MF795160	USA	MN186405	USA
OR730839	Australia	KX315999	Canada	KY426922	Canada	KY498151	USA	MF795161	USA	MW924113	USA
OR730840	Australia	KX316000	Canada	MH476296	Canada	MF696142	USA	MF795162	USA	OM135586	USA
OR730841	Australia	KX316001	Canada	MH476297	Canada	MF696143	USA	MF795163	USA	OM135587	USA
OR730842	Australia	KX316002	Canada	MH476300	Canada	MF696144	USA	MF795164	USA	OP597754	USA
OR730843	Australia	KX316003	Canada	KX316013	Canada	MF696145	USA	MF795165	USA	OP597755	USA
OR730844	Australia	KX316004	Canada	MH557096	Mexico	MF696146	USA	MF795166	USA	OP597756	USA
OR730845	Australia	KX316005	Canada	KU821056	South Korea	MF795141	USA	MF795167	USA	OP597757	USA
OR730846	Australia	KX316006	Canada	MF276895	Switzerland	MF795142	USA	MF795168	USA	OP597758	USA
OR730847	Australia	KX316007	Canada	JQ901105	USA	MF795143	USA	MF795169	USA	OP597759	USA
OR730848	Australia	KX316008	Canada	KC896623	USA	MF795144	USA	MF795170	USA	OP597760	USA
OR730849	Australia	KX316009	Canada	KC896624	USA	MF795145	USA	MF795171	USA	OP597761	USA
OR730850	Australia	KX316010	Canada	KC896625	USA	MF795146	USA	MF795172	USA	OP597762	USA
OR730851	Australia	KX316011	Canada	KF147915	USA	MF795147	USA	MF795173	USA	NC_022002	USA

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Table S2. PCR and tiled amplicon sequencing results of 37 cultivars or clones (total = 111 grapevines) collected from the CSIRO germplasm collection in Irymple and tested seasonally in November 2022 (spring) and February (summer), May (autumn) and July (winter) in 2023 for grapevine red blotch virus (GRBV; *Grablovirus vitis*).

Cultivar	November (spring) 2022	February (summer) 2023	May (autumn) 2023	July (winter) 2023	Tiled amplicon sequencing	Final result ^a
Black Monukka	-	-	-	-	NA ^b	-
Calmeria	-	-	-	-	NA	-
Chasselas Parsley IC8424	-	-	-	+	+	+
Chasselas Parsley IC8423	-	-	-	+	+	+
Early Muscat	-	-	-	-	NA	-
Emperor	-	-	-	+	-	Indeterminate ^c
Kali Sahebi	-	-	+	+	-	Indeterminate
Kandahar	+	+	+	+	+	+
Mantendo	-	-	-	-	NA	-
Montepulciano	-	-	-	-	NA	-
Muscat Cannon Hall	-	-	-	+	-	Indeterminate
Muscat Ottonel	-	-	+	-	-	Indeterminate
Nebbiolo Chiavenas	-	-	-	-	NA	-
Negrette	-	-	-	+	-	Indeterminate
Negro Amaro	-	-	-	-	NA	-
Ohanez	-	-	-	-	NA	-
Opuzensia Rana	+	-	+	-	+	+
Panse Precoce	-	-	-	+	-	Indeterminate
Peloursin	-	-	-	+	+	+

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Perle de Csaba FSAC	+	+	+	+	+	+
Perle de Csaba L6V13	+	+	+	+	+	+
Perlette clone 1	-	-	-	-	NA	-
Perlette clone 2	-	-	-	+	-	Indeterminate
Petit Bouschet	-	-	-	-	NA	-
Pinot noir	-	-	-	+	-	Indeterminate
Pione	-	-	-	+	-	Indeterminate
Poerinha	-	-	-	+	-	Indeterminate
Precose de Malingre	-	-	-	+	-	Indeterminate
Primiera	-	-	-	+	+	+
Rolle	-	-	-	-	NA	-
Roter Zierfandler	-	-	-	+	-	Indeterminate
Ruby Seedless	-	-	-	+	-	Indeterminate
Russian Seedless	-	-	-	-	NA	-
Russian Seedless clone 1	-	-	-	-	NA	-
Russian Seedless clone 2	-	-	-	-	NA	-
Russian Seedless clone 3	-	-	-	-	NA	-
Seedless Emperor	-	-	-	-	NA	-
Total	4/37	3/37	6/37	19/37	8/37	8/37

^a Final result from the combination of PCR, Sanger sequencing and tiled amplicon sequencing results.

^b NA – Not applicable (negative by PCR and Sanger sequencing).

^c Indeterminate (positive by PCR and Sanger sequencing, either low reads or negative by tiled amplicon sequencing due to low or no reads).

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Table S3. The number of reads generated from tiled amplicon sequencing, number of mapped reads and depth calculated using Geneious, assembled contig size of grapevine red blotch virus (GRBV; *Grablovirus vitis*), its percentage similarity to reference genome NC_022002 and GenBank accession number of each GRBV isolate for grapevine cultivars or clones that were tested seasonally and the final GRBV status based on the results of PCR and Sanger sequencing and tiled amplicon sequencing.

Location	Cultivar	Mapped reads	Depth	Size of assembled consensus GRBV sequence (nt)	Percent identity of assembled consensus GRBV sequence (nt)	Final GRBV status ^a
Victoria: Seasonal testing	Chasselas Parsley IC8424	1310	71.8	3212	99.1	+
	Chasselas Parsley IC8423	1325	71.1	3209	99.2	+
	Peloursin	2853	78.7	3210	99.2	+
	Kandahar	60434	4,334.6	3210	99.3	+
	Perle de Csaba FSAC	1005	50.2	3201	99.1	+
	Perle de Csaba L6V13	1156	41.5	3208	99.3	+
	Opuzensia Rana	1247	49.6	3205	99.3	+
	Primiera	255	13.5	2577 (80 % coverage of the full genome)	83.0	+
	Emperor	0				Indeterminate ^b
	Muscat Cannon Hall	7				Indeterminate
	Muscat Ottonel	0				Indeterminate
	Kali Sahebi	5				Indeterminate
	Negrette	19				Indeterminate
	Panse Precoce	3				Indeterminate
	Perlette clone 2	2				Indeterminate
	Pinot noir	3				Indeterminate
	Pione	0				Indeterminate
	Poerinha	3				Indeterminate
Precose de Malingre	1				Indeterminate	
Roter Zierfandler	3				Indeterminate	

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	Ruby Seedless	0				Indeterminate
Victoria: CSIRO survey	Couderc noir	3011	52.4	3206	99.2	+
	Dolcetto	2522	45.6	3212	99.2	+
	Semillon	1936	50.7	3211	99.1	+
	Muscat Gordo Blanco L10V5	849	55.2	3208	99.2	+
	Muscat Gordo Blanco. L1V9	498	36.1	3208	99.2	+
	Jacquez	51				Indeterminate
	MI 73-09-90	25				Indeterminate
	Muscat Gordo Blanco. L4V1	9				Indeterminate
	Muscat Gordo Blanco L14V1	8				Indeterminate
	Crouchen clone 1	7				Indeterminate
	Chardonnay Muscat	0				Indeterminate
	South Australia	Muscat cannon hall	11370	808.3	3209	99.2
Parellada IC.74.8244		5396	382.1	3207	99.2	+
Muscat Gordo Blanco AS.70.2266		500	15.1	2058 (64 % coverage of the full genome)	75.4	+
Kishmishi		22	2			Indeterminate
White Vernaccio		13	1			Indeterminate
Montepulciano		11	1			Indeterminate

^a Final result is the combination of PCR, Sanger sequencing and tiled amplicon sequencing results.

^b Indeterminate (positive by PCR and Sanger sequencing, negative by tiled amplicon sequencing due to low or no reads).

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Table S4. PCR, Sanger sequencing and tiled amplicon sequencing results including with mapped reads, depth, size of assembly and percentage identity to the grapevine red blotch virus (GRBV; *Grablovirus vitis*) reference genome (GenBank accession NC_022002) of the GRBV strain detected in pooled cultivars collected from the CSIRO germplasm collection and tested in May 2023 and July 2023 for GRBV.

Cultivar	PCR and Sanger sequencing result of the pool	Tiled amplicon sequencing result of the pool	Mapped reads	Depth	Size of assembled consensus GRBV sequence (nt)	Percent identity of assembled consensus GRBV sequence (nt) to reference genome NC_022002	PCR and Sanger sequencing result of the individual cultivar tested in May 2023	PCR and Sanger sequencing result of the individual cultivar tested in July 2023	Tiled amplicon sequencing result of the individual cultivar	Final result ^a
Crouchen clone 1							-	+	-	Indeterminate ^c
Crinto	+	+	1571	75.64	3207	99.2	-	-	NA ^b	-
Couderc noir							+	+	+	+
Kandahar							+	+	+	+
Kali Sahebi	+	+	109393	7401.85	3206	99.4	+	+	-	Indeterminate
Jacquez							+	-	-	Indeterminate
MI 73-09-90							+	-	-	Indeterminate
Santa Paula	+	+	67120	4397.29	3206	99.4	-	-	NA	-
Semillon							-	+	+	+
Shiraz local							-	-	NA	-
MG 92-56-20							-	-	NA	-
Tyrian MI 73-10-56							-	-	NA	-
MS 15-36	+	+	1554	70.38	3208	99.4	-	-	NA	-
Waltham							-	-	NA	-
Worden							-	-	NA	-
Cienna (MI 73-08-71) clone 1							-	-	NA	-
Cienna (MI 73-08-71) clone 2							-	-	NA	-
MS 71-46-32							-	-	NA	-
Zinfandel	+	+	1619	79.55	3206	99.4	-	-	NA	-
MI 08-91							-	-	NA	-
MS 81-37-02							-	-	NA	-
MU 78-27-38							-	-	NA	-

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Alicante Bouschet								-	-	NA	-
Aledo clone 1	+	+	1233	50.39	3207	99.4		-	-	NA	-
Aledo clone 2								-	-	NA	-
Alden								-	-	NA	-
Agadaj	+	+	1247	49.61	3210	99.2		-	-	NA	-
Arnsburger								-	-	NA	-
Arinto								-	-	NA	-
Arbois	+	+	1339	50.84	3208	99.3		-	-	NA	-
Arbane								-	-	NA	-
Aspiran								-	-	NA	-
Cabernet-Sauvignon clone 1	+	+	2180	78.71	3208	99.3		-	-	NA	-
Cabernet-Sauvignon clone 2								-	-	NA	-
Cabernet franc Sanzey								-	-	NA	-
Burgrave	+	+	1156	41.49	3210	99.3		-	-	NA	-
Bourboulenc clone 1								-	-	NA	-
Best's K ex Great Western R1V98								-	-	NA	-
Corbeau	+	+	1283	50.69	3207	99.3		-	-	NA	-
Chardonnay Muscat								+	-	-	Indeterminate
Caino								-	-	NA	-
Dolcetto	+	+	1350	52.43	3206	99.0		-	+	+	+
Demir Kapija								-	-	NA	-
Delizia di Vaprio								-	-	NA	-
Crouchen	+	+	1471	59.97	3207	99.4		-	-	NA	-
Croattina								-	-	NA	-
Corvinon								-	-	NA	-
Corvina Veronese	+	+	1487	53.64	3207	99.4		-	-	NA	-
Fiano								-	-	NA	-

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Fernao Pires								-	-	NA	-
Fer 10-26A1	+	+	1816	71.86	3210	99.3		-	-	NA	-
Feher Szagos								-	-	NA	-
Ezerfurtu								-	-	NA	-
Etraire de la Dui as Corbeau	+	+	1889	71.06	3210	99.3		-	-	NA	-
Emperatriz								-	-	NA	-
Ehrenfelser								-	-	NA	-
Grand noir de la Calmette	+	+	1358	52.44	3210	99.1		-	-	NA	-
Golden Champion								-	-	NA	-
Godello								-	-	NA	-
GM 647-2	+	+	1292	45.66	3210	99.4		-	-	NA	-
GM 643-16								-	-	NA	-
Bombino Nero								-	-	NA	-
Bonarda	+	+	1185	40.96	3207	99.4		-	-	NA	-
Bourboulenc clone 2								-	-	NA	-
Perle de Csaba FSAC								+	+	+	+
Perle de Csaba L6V13	-	NA	NA	NA	NA	NA		+	+	+	+
Peloursin								-	-	NA	-
Opuzensia Rana								+	-	+	+
Ondenc	-	NA	NA	NA	NA	NA		-	-	NA	-
Ohanez								-	-	NA	-
Naza Valenciana								NA	NA	NA	-
Muscat Oliver IV71.2319	-	NA	NA	NA	NA	NA		NA	NA	NA	-
Muscat Gordo Blanco. L4V1								NA	+	-	Indeterminate
Muscat Gordo Blanco. L1V9								NA	+	+	+
Muscat Gordo Blanco Tetraploid ex Sweeney	-	NA	NA	NA	NA	NA		NA	-	NA	-
Muscat Gordo Blanco L15V5								NA	-	NA	-

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Muscat Gordo Blanco L14V5							NA	-	NA	-
Muscat Gordo Blanco L14V1	-	NA	NA	NA	NA	NA	NA	+	-	Indeterminate
Muscat Gordo Blanco L10V5							NA	+	+	+
Muscat Gordo Blanco Tetraploid ex Jones							NA	+	-	Indeterminate
Muscat Flame IV71.2318	-	NA	NA	NA	NA	NA	NA	-	NA	-
Chasselas ex Tas							NA	-	NA	-
Muscat Ottonel IC69.8102							+	-	NA	-
Muscat Cannon Hall	-	NA	NA	NA	NA	NA	-	+	-	Indeterminate
Muscadelle							NA	-	NA	-

^a Final result for an individual cultivar or clone is the combination of PCR, Sanger sequencing and tiled amplicon sequencing results. The tiled amplicon sequencing results for individual cultivars or clones is presented in Table S3.

^b NA – Not applicable (negative by PCR and Sanger sequencing).

^c Indeterminate (positive by PCR and Sanger sequencing, negative by tiled amplicon sequencing due to low or no reads).

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Table S5. The grapevine red blotch virus (GRBV; *Graplovirus vitis*) status cultivars that were present in the CSIRO germplasm collection and which were known to be linked directly or indirectly or had potential linkages to cultivars or clones that were also tested in South Australia.

Cultivar/clone	CSIRO Final result ^a	South Australia (SA) Final result	Linkage between CSIRO and SA	Year imported or selected onshore by CSIRO
Dolcetto	+	– (3 clones)	Source of Dolcetto in Australia is derived from the original 1860's source.	Imported in the 1860's from Europe to Great Western in Victoria.
Kishmishi	–	Indeterminate ^c	Probably supplied to CSIRO and SA from same source.	Imported from University of California Davis (UCD), USA into another collection (now removed) in Victoria in the 1960's.
Muscat Cannon Hall	Indeterminate	+	Possibly supplied to SA from CSIRO.	Local selection ex WA.
Montepulciano FSAC	–	Indeterminate	Three CSIRO clones tested and were negative. SA and CSIRO are the same clone, treated by FSAC.	Imported into into another collection (now removed) in New South Wales, Australia, in the 1970's – origin unknown.
Opuzensia Rana	+	Indeterminate	Link between CSIRO and SA unknown but supply to SA assumed.	Imported by CSIRO from the former Yugoslavia in the 1980's.
Parellada	NA ^b	+	Was grown at CSIRO Merbein, is not present in CSIRO Irymple.	Imported into CSIRO from UCD in the 1970's.
Chasselas Parsley leafed IC85.8424	+	–	Only one clone tested in SA , link to CSIRO uncertain.	Imported into CSIRO in the 1980's – origin unknown.
Chasselas Parsley leafed IC85.8423	+	–		
Perle de Csaba L6V13	+	+	Distributed from CSIRO to SA and Western Australia.	Imported into CSIRO from the UCD in the 1960's.
Semillon SA82	+	–	Same original source.	Local selection from SA, planted at CSIRO in the 1980's.
White Vernaccio	–	Indeterminate	Possibly supplied to SA from CSIRO.	Imported into CSIRO in the 1960's from UCD USA.

^a Final result is the combination of PCR, Sanger sequencing and tiled amplicon sequencing results.

^b NA – Absent in CSIRO germplasm collection.

^c Indeterminate (positive by PCR and Sanger sequencing, negative by tiled amplicon sequencing due to low or no reads).

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Table S6. The grapevine red blotch virus (GRBV; *Grablovirus vitis*) status cultivars tested a part of South Australia survey, which were known to be linked directly or indirectly or had potential linkages to cultivars or clones that were also tested in Victoria and Western Australia.

Cultivar	PCR and Sanger sequencing result	Tiled amplicon sequencing result	Final result ^a
Kishmishi	+	-	Indeterminate ^c
Montepulciano	+	-	Indeterminate
Muscat cannon hall	+	+	+
Muscat Gordo Blanco AS.70.2266	+	+	+
Opuzensia Rana	+	NA ^b	+
Parellada	+	+	+
Perle de Csaba L6V13	+	NA	+
White Vernaccio	+	-	Indeterminate

^a Final result is the combination of PCR, Sanger sequencing and tiled amplicon sequencing results.

^b Cultivars assumed to be positive based on the Victorian and Western Australian positive results.

^c Indeterminate (positive by PCR and Sanger sequencing, negative by tiled amplicon sequencing due to low or no reads).