‘Norton’ grapevine suppresses major grapevine viruses

Wenping Qiu, Susanne Howard,
Sylvia Petersen, Adam Uhls

Missouri State University

- **Major Viral Diseases**
- **Evaluating Norton's resistance**
- **Plant virus-tested grapevines**

Grapevine hosts more than 80 viruses

Major viruses infecting grapevine

Leafroll virus group

- **GLRaV-1: *Grapevine leafroll-associated virus* 1**
- **GLRaV-3: *Grapevine leafroll-associated virus* 3**
- **GLRaV-2, 4, 5, 6, 7, 9**

Nepovirus: Nematode-transmitted Polyhedral virus

- **GFLV: *Grapevine fanleaf virus***
- **ToRSV: *Tomato ringspot virus***
- ***Tobacco ringspot virus and Arabis mosaic virus***

New emerging viruses in the USA

- **Grapevine vein clearing virus**
- **Grapevine red blotch virus**

Vector: mealybugs

Grapevine red blotch virus

AMERICAN JOURNAL of ENOLOGY AND VITICULTURE

Research Article

A Survey of Viruses Found in Grapevine Cultivars Grown in Missouri

James Schoelz, Dean Volenberg, Mustafa Adhab, Zhiwei Fang, Vicki Klassen, Christine Spinka, Maher Al Rwahnih

Am J Enol Vitic. January 2021 72: 73-84; published ahead of print October 09, 2020 ; DOI: 10.5344/ajev.2020.20043

Table 2 Virus prevalence in each grape cultivar.

		Percentage of composite samples in a cultivar that tested positive for each virus										
Cultivar	**No. of samples[a]**	**GRSPaV**	**GLRaV-3**	**GRBV**	**GVE**	**GLRaV-2**	**GVB**	**GVkV**	**GLRaV-2RG**	**GVCV**	**GVA**	**GLRaV-4 str5[b]**
Vignoles	70	100	88.5	4.3	85.7	54.2	65.7	38.5	1.4	1.4	0	0
Vidal blanc	45	100	91.1	24.4	26.7	91.1	0	28.9	0	33.3	0	0
Chardonel	45	46.7	33.3	75.5	8.9	6.7	0	0	0	24.4	0	2.2
Norton	40	0	85.5	77.5	30.0	0	22.5	15.0	72.5	0	2.5	0
Chambourcin	30	100	3.3	26.7	0	26.7	0	3.3	0	0	3.3	0
Valvin Muscat	20	100	10.0	40.0	0	0	0	0	0	20.0	0	0
Vivant	20	15.0	10.0	0	0	0	0	0	0	0	0	0
Traminette	11	36.4	0	0	0	0	0	0	0	0	0	0
Cayuga	10	0	50.0	0	0	0	0	0	0	10.0	0	0
Concord	10	0	100	20.0	100	0	10.0	0	0	0	0	0
Crimson Cabernet	10	0	0	90.0	0	0	0	0	0	0	0	0
Noiret	10	0	0	60.0	0	0	0	0	0	10.0	0	0
Rayon	10	100	50.0	0	0	20.0	10.0	40.0	60.0	0	0	0
Vincent	10	80.0	0	0	0	0	0	0	0	0	0	0
Viognier	10	100	0	20.0	0	0	0	0	0	10.0	0	0
Albania	5	0	100	20.0	100	0	40.0	0	0	0	0	0
Cabernet franc	5	100	0	0	0	0	0	0	0	0	0	0
Catawba	5	0	100	0	80.0	0	80.0	0	0	0	0	0
Cloeta	5	0	100	0	0	0	0	0	0	0	0	0
Hidalgo	5	0	40.0	80.0	40.0	0	0	0	0	0	0	0
Lenoir	5	0	40.0	100	0	100	60.0	0	0	0	0	0
Marechal Foch	5	100	100	100	0	0	0	40.0	0	0	0	0
Muench	5	0	100	0	100	0	20.0	0	0	0	0	0
Wetumka	5	0	100	100	100	0	100	0	0	0	0	0
Saperavi	4	100	0	0	0	0	0	0	0	0	0	0
Survey average[c]	400	58.7	52.7	35.0	31.0	19.0	17.2	13.5	9.2	8.2	0.5	0.2

[a]The number of composite samples (16 petioles, four petioles from four different grapevines) collected for each cultivar.
[b]GLRaV-4 strain 5, abbreviated to GLRaV-4 str5.
[c]The overall percentage of composite samples positive for each virus.

Grapevine vein clearing virus

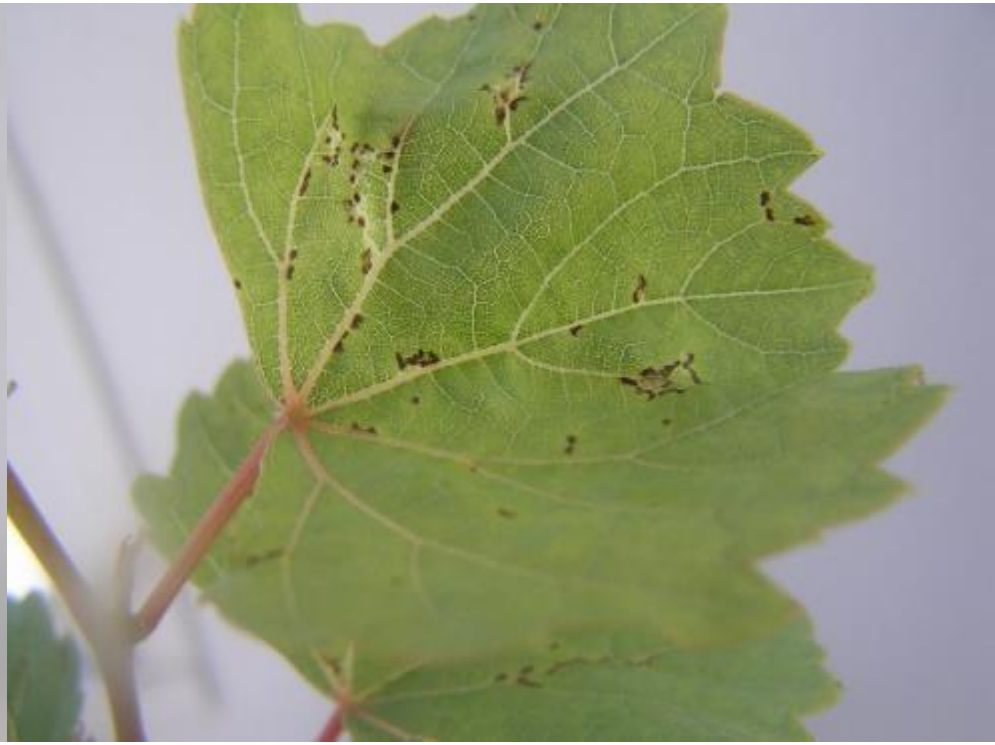
Chardonel

Cabernet Sauvignon


Chardonel

***Vitis rupestris* 'VRU89'**


Vitis rupestris 'VRU1405'



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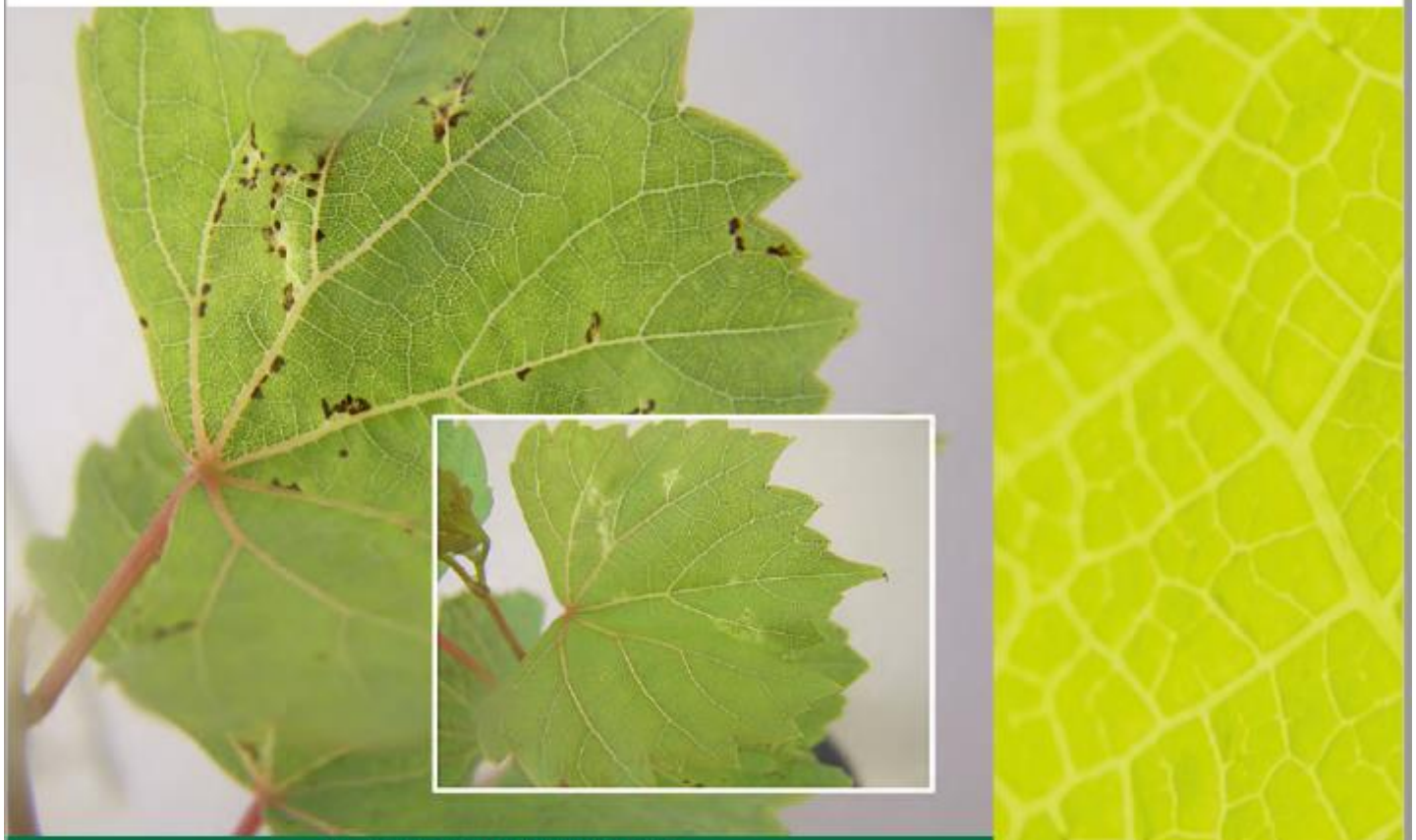
Phytopathology



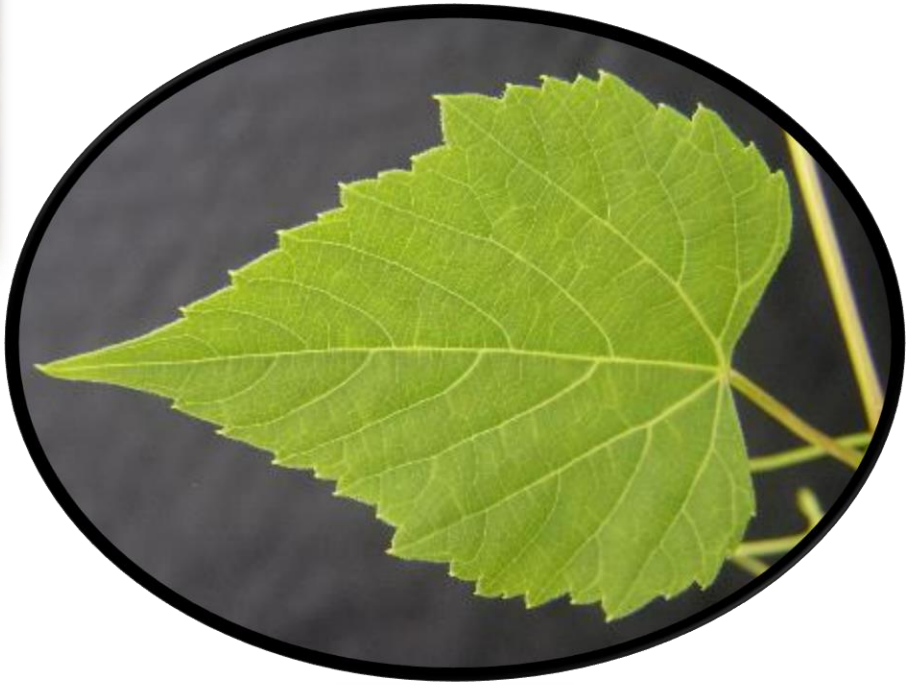
Grapevine vein clearing virus on Wild Grapevine

Ampelopsis cordata

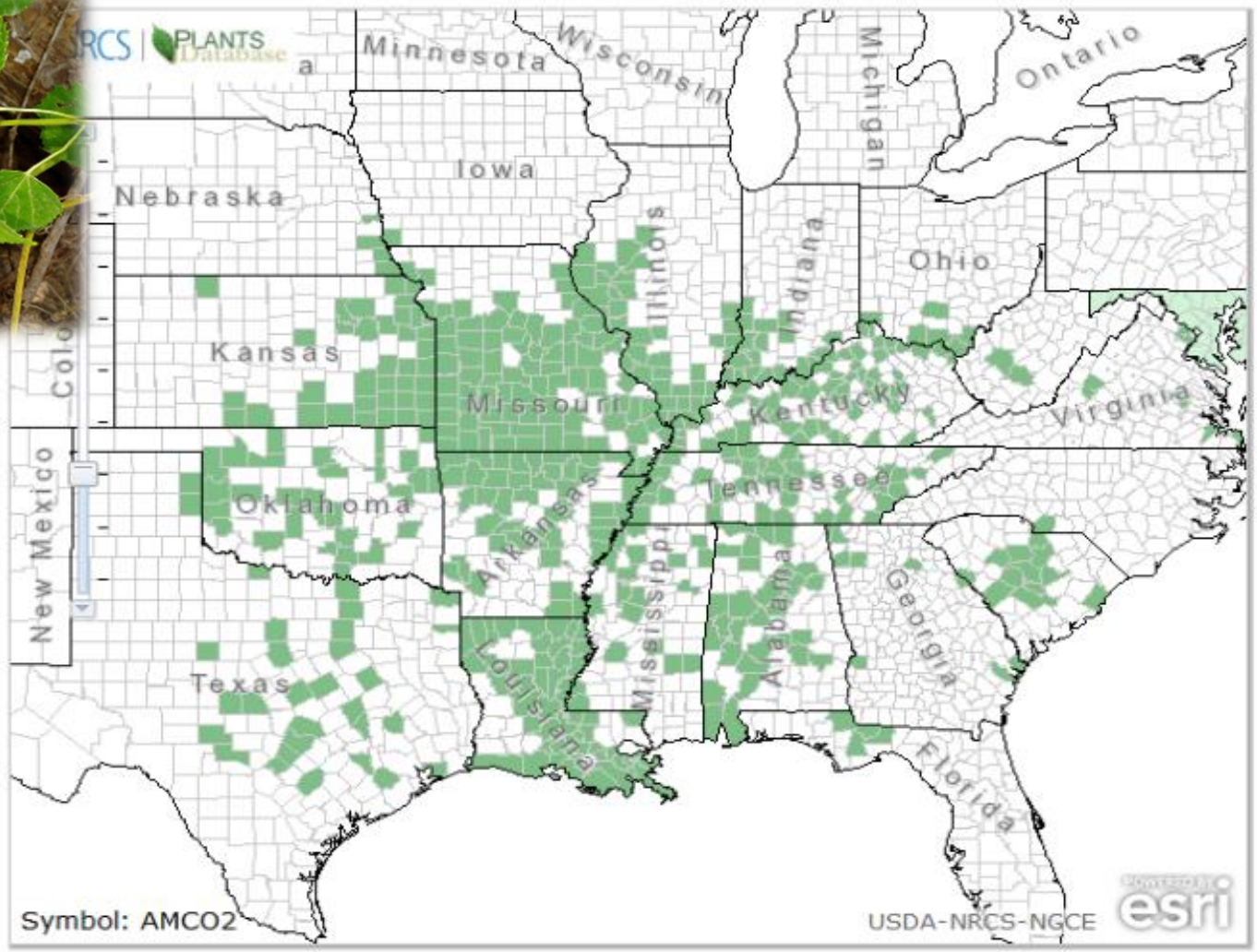
Family: Vitaceae

Genus: *Ampelopsis*

Common name:
Heartleaf peppervine



Range of *Ampelopsis cordata*

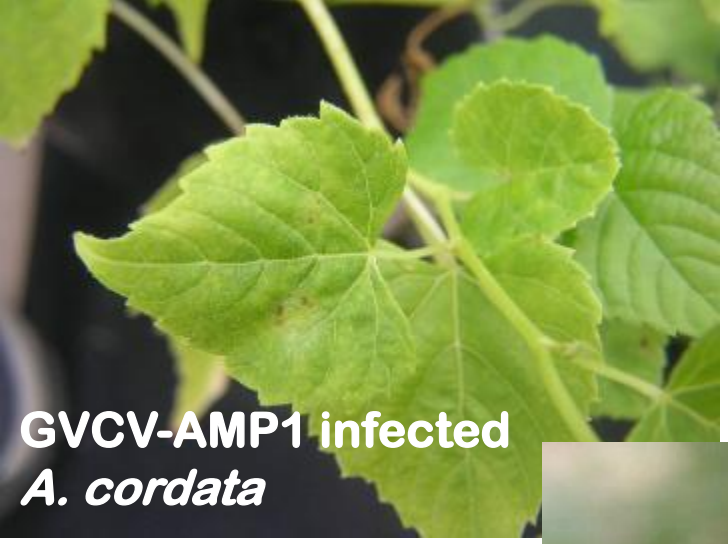


Native
Native, No County Data
Introduced
Introduced, No County Data
Both
Both, No County Data
Absent/Unreported

Native Status:
L48 AK HI PR VI NAV CAN GL SPM NA

Percentage of GVCV in Ampelopsis vines

Location (town, state)	Number of samples	GVCV positive	Percentage
Augusta, MO	102	33	32%
Hermann, MO	14	5	36%
Springfield, MO	89	32	36%
Bolivar, MO	32	9	28%
Kansas City, MO	6	2	33%
Van Buren, MO	11	2	18%
Galena, MO	3	2	66%
Total	257	85	33%



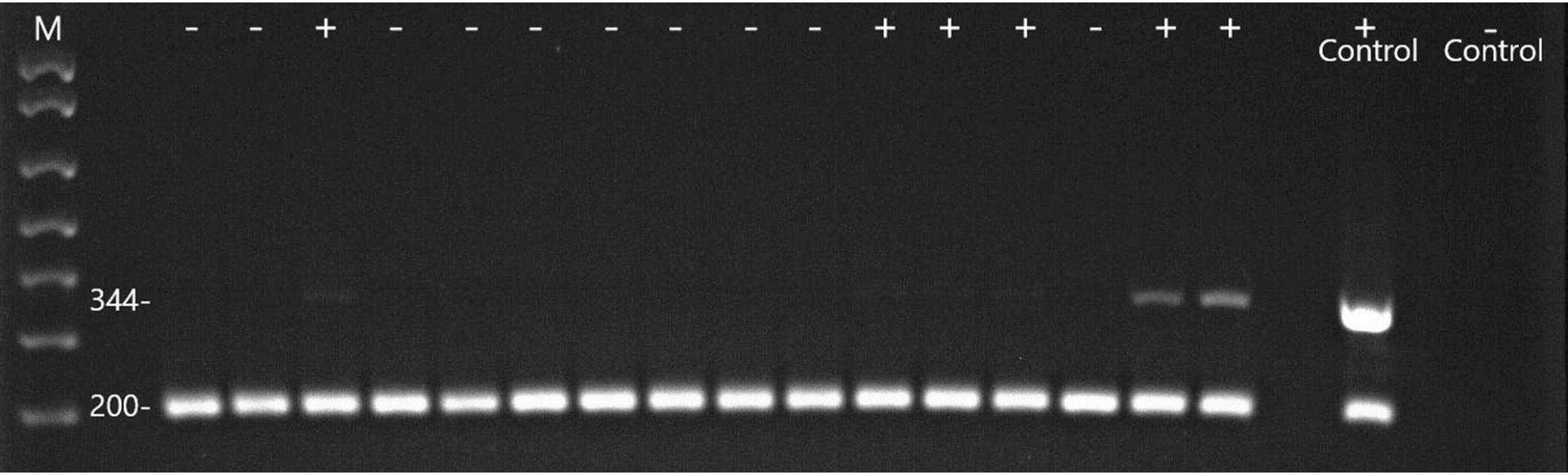
RNA-seq GVCV-AMP1

45 days post transmission of GVCV-AMP1

RNA-seq GVCV-AMP1

GVCV-AMP3

GVCV is detected in single aphids



Epidemiology

Location of samples (Town, MO)	Number of samples	GVCV Positive	Percentage
Springfield	192	80	42%
Battlefield	54	20	37%
Willard	10	3	30%
Saddlebrook	1	1	100%
Mountain Grove	6	3	50%
Plattin	107	39	36%
Hermann[1]	14	7	50%
Augusta	30	10	33%
Coffman	111	49	44%
Total	525	212	40%

Table 4. Genome number of *Grapevine vein clearing virus* (GVCV) in the stylet and body of 20 single aphids measured by quantitative PCR

Sample number[a]	Genome number[b]			
	Stylet		Body	
	Actual	Extrapolated	Actual	Extrapolated
1	7	43	107	609
2	23	131	124	707
3[c]	74	422	89	510
4	29	163	137	783
5	2.46*	14.06*	97	557
6[c]	7	41	383	2,188
7[c]	11	61	234	1,338
8	127	723	23,380	133,600
9	8,993	51,389	299,800	1,713,143
10	45,600	260,571	85,620	489,257
11	13	134	71	705
12	25	245	225	2,245
13	76	762	26	258
14	8	80	37	372
15	47	467	83	825
16	14	141	1.05*	10.5*
17	67	666	113	1,127
18	66	664	23	233
19	7	74	32	323
20	20	197	14	136
Average	2,906	16,683	21,610	123,627

[a] Bold denotes samples in which the head was removed from the body.

[b] The average of three replicated reactions from each sample was used to determine initial template quantity. The initial quantity was transformed to the extrapolated GVCV genome number by accounting for the total amount of DNA extracted and the efficiency of the DNA extraction kit. An asterisk indicates that the GVCV genome number is below the threshold of detection.

[c] Winged aphids.

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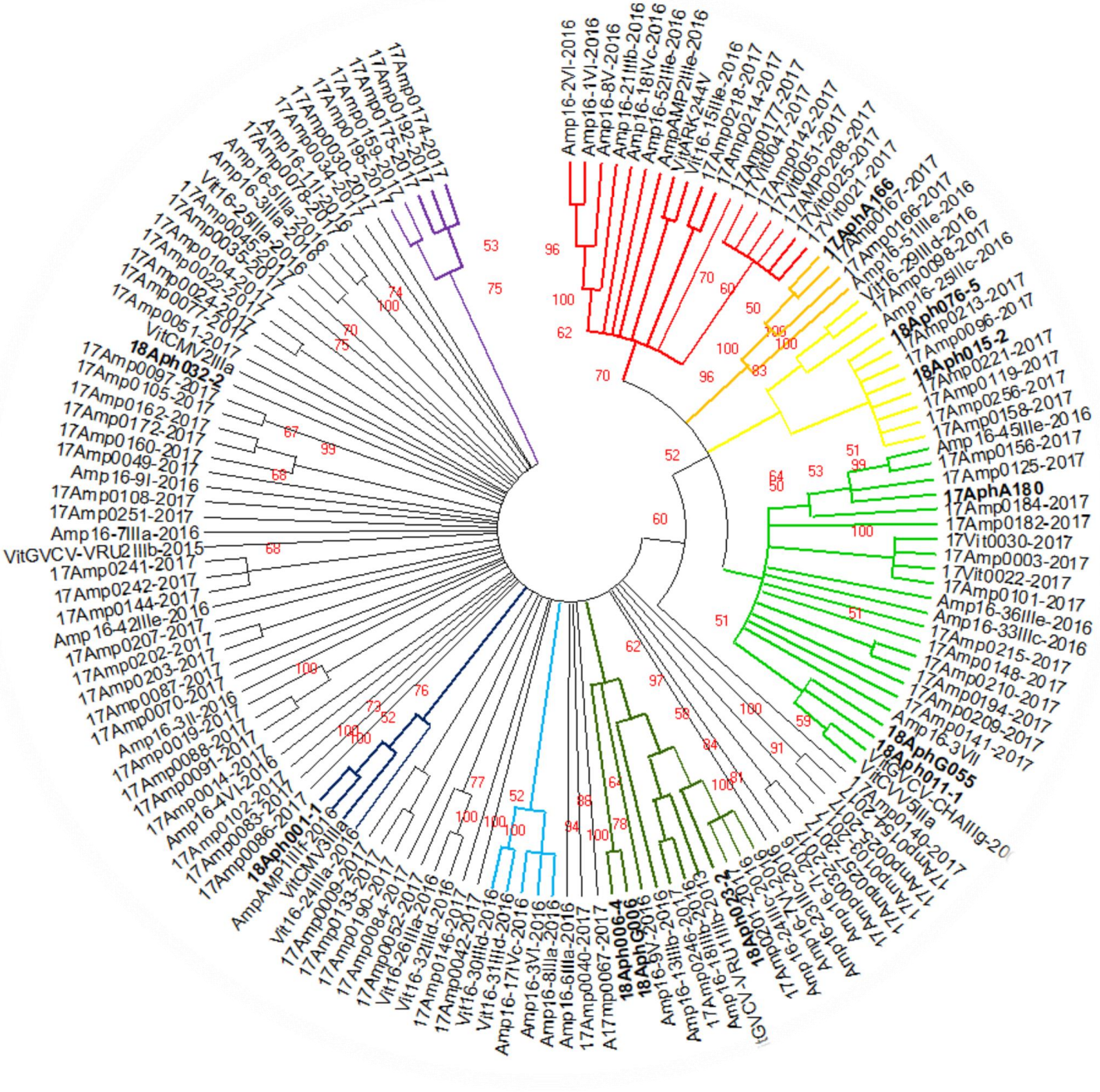
 • DOI: 10.1094/PDIS-10-20-2176-RE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Amp16-1VI-2016
Amp16-8V-2016
Amp16-21IIIb-2016
Amp16-18IVc-2016
Amp16-52IIIe-2016
AmpAMP2IIIe-2016
VitARK244V
Vit16-15IIIe-2016
17Amp0218-2017
17Amp0214-2017
17Amp0177-2017
17Vit0047-2017
17Amp0142-2017
17Vit0051-2017
17AMP0208-2017
17Vit0025-2017
17Vit0021-2017
17AphA166
17Amp0167-2017
17Amp0166-2017
Amp16-5IIIe-2016
Vit16-29IIId-2016
17Amp0098-2017
Amp16-25IIIc-2016
17Amp0213-2017
18Aph076-5
17Amp0096-2017
18Aph015-2
17Amp0221-2017
17Amp0119-2017
17Amp0256-2017
17Amp0158-2017
Amp16-45IIIe-2016
17Amp0156-2017
17Amp0125-2017
17AphA180
17Amp0184-2017
17Amp0182-2017
17Vit0030-2017
17Amp0003-2017
17Vit0022-2017
17Amp0101-2017
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17Amp0148-2017
17Amp0210-2017
17Amp0194-2017
17Amp0209-2017
Amp16-3VII
18AphG055
18Aph011-1
VitGVCV-CHAIIIg-20
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17Amp0154-2017
17Amp0257-2017
17Amp0103-2017
17Amp0232-2017
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Amp16-24IIIc-2017
17Amp0246-2017
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Amp16-8IIIa-2016
Amp16-3VI-2016
Amp16-17IVc-2016
Vit16-31IIId-2016
Vit16-30IIId-2016
17Amp0042-2017
17Amp0146-2017
Vit16-32IIId-2016
Vit16-26IIIa-2016
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17Amp0174-2017

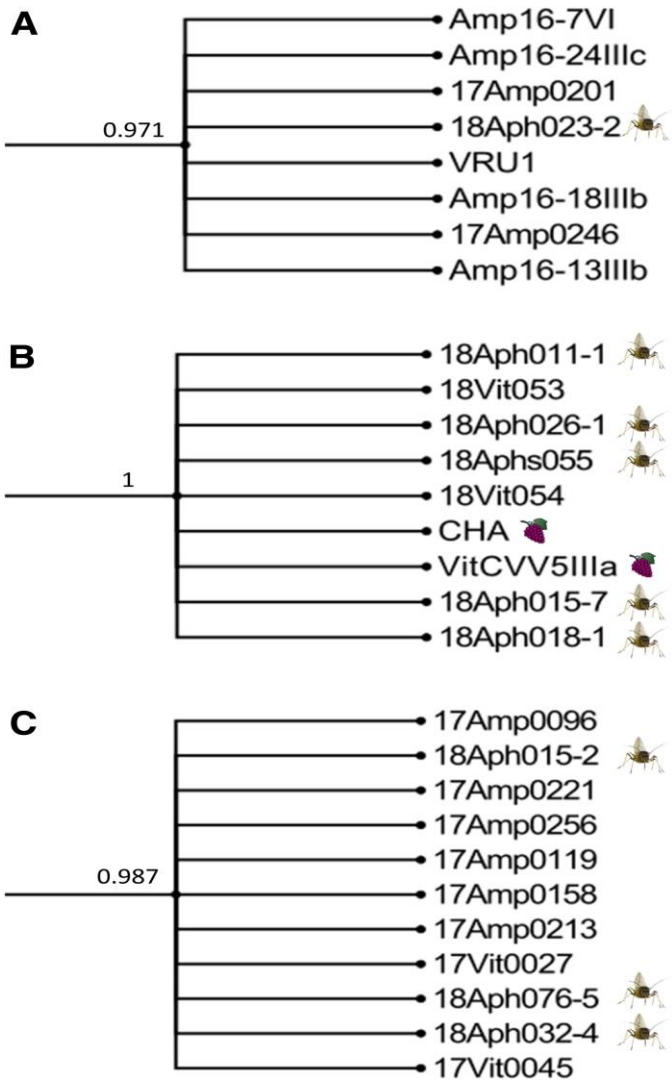

Fig. 2. A, B, and C, Three representative groups from a cladogram of 174 *Grapevine vein clearing virus* (GVCV) isolates showing the close relationship of GVCV isolates from grape aphids as indicated by an aphid illustration, cultivated grapevines in vineyards indicated by a grape cluster, and wild Vitaceae from native habitats. Sample codes that begin with 17, 18, and 19 denote the years 2017, 2018, and 2019, respectively. Numerals after the genus abbreviations indicate the series of sample numbers. Numerals above the branches are bootstrap values. The whole cladogram is provided in Supplementary Figure S2. Amp = host plant *Ampelopsis cordata*, Aph = *Aphis illinoisensis*, VRU = *Vitis rupestris,* Vit = *Vitis* spp., and CHA = 'Chardonel'.

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RESEARCH

Grapevine vein clearing virus Is Prevalent and Genetically Variable in Grape Aphid (*Aphis illinoisensis* Shimer) Populations

Adam Uhls, Sylvia Petersen, Cory Keith, Susanne Howard, Xiaokai Bao, and Wenping Qiu

Affiliations

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Abstract

Grapevine vein clearing virus (GVCV) causes severe stunting and death of cultivated grapevines and is prevalent in native *Vitis* spp. and *Ampelopsis cordata* in the Midwest region of the United States. GVCV can be transmitted from wild *A. cordata* to *Vitis* spp. by grape aphid (*Aphis illinoisensis*) under greenhouse conditions, but its prevalence, genetic composition, and genome number in native grape aphids are unknown. In this study, we collected grape aphids from native Vitaceae across the state of Missouri in 2018 and 2019, and conducted diagnostic, genetic, and quantitative analyses. GVCV was detected in 91 of the 105 randomly sampled communities on 71 Vitaceae plants (87%). It was present in 211 of 525 single grape aphids (40%). Diverse GVCV variants from aphids were present on both GVCV-negative and GVCV-positive plants. Identical GVCV variants were found in grape aphids sampled from wild and cultivated Vitaceae, indicating that viruliferous aphids likely migrate and disperse GVCV variants among wild and cultivated Vitaceae. In addition,

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Caption

Symptoms of bacterial leaf spot on *Cucurbita pepo* leaf 5 days after spray inoculation (L. Li et al.). Photo credit: B. J. Li. Symptoms of Fusarium wilt on cyclamen (V. Guarnaccia et al.). Photo credit: M. L. Gullino.

SUMMARY

- GVCV is native to the Midwest.
- GVCV infects 33% of *Ampelopsis* plants.
- GVCV is present in 40% of grape aphids.
- GVCV spreads and evolves in wild plants and cultivated grapevines.

GVCV Chronology

2004 Investigation of the disease in Missouri
2009 Discovery of GVCV in Chardonel
2011 Publication of GVCV-CHA reference genome
2013 Discovery of GVCV in native *Vitis rupestris*
2014 Publication of GVCV-VRU1 genome
2015 Discovery of GVCV-VRU2 in *V. rupestris*
2016 Discovery of GVCV-AMP1, AMP2 and AMP3 in native *Ampelopsis cordata*
2017 Discovery of grape aphid as a vector
2018 Incidence of GVCV in grape aphids
2019 Confirming Norton's resistance to GVCV
2020 Genetic diversity of GVCV in grape aphids
2021 Infectious clone and ORF II function

Prevention

Growing virus-resistant grapevines can prevent viral infection

Tableau 1

Nombre d'origines regroupées pour la recherche de résistance

Number of accessions tested for resistance

Espèce	Nombre d'origines testées	Espèce	Nombre d'origines testées
Vignes Américaines	**49**	**Vignes Asiatiques**	**18**
V. riparia	10	*V. Colgnetiae*	4
V. Longii ou solonis	3	*V. Thunbergii*	2
V. arizonica	2	*V. betulifolia*	1
V. californica	2	*V. Ishikari*	1
V. candicans	2	*V. Pagnucii*	1
V. cordifolia	2	*V. pentagona*	1
V. coriacea	2		
V. doaniana	2		
V. Simpsonii	2	**Vignes Euro-asiatiques**	**576**
V. baileyana	1		
V. bicolor	1	proles Occidentalis	251
V. Champinii	1	proles Pontica	169
V. cinerea	1	proles Orientalis	95
V. girdiana	1	Origine indéterminée	10
V. monticola	1	Autres origines	3
V. palmata	1	Obtentions	48
V. rubra	1		
Hybrides interspécifiques	**86**	**Ampelopsis**	**3**
		Parthenocissus	**2**
TOTAL		**734**	

Wild *V. aestivalia* or its var. Norton was not included

AMERICAN JOURNAL of ENOLOGY AND VITICULTURE

Article

Tolerance and Resistance to Viruses and Their Vectors in *Vitis* sp.: A Virologist's Perspective of the Literature

Jonathan E. Oliver, Marc Fuchs

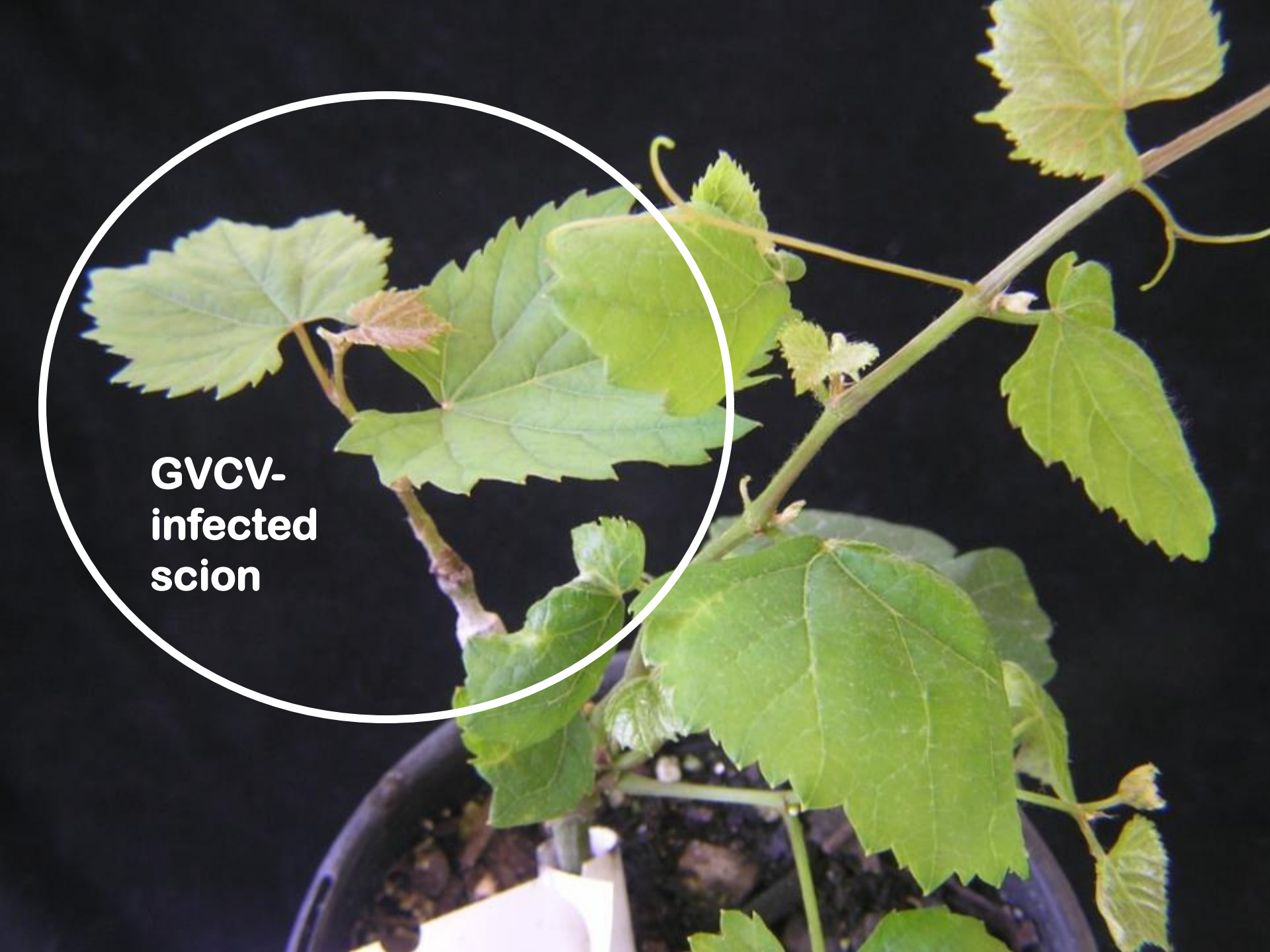
Am J Enol Vitic. December 2011 62: 438-451; published ahead of print August 31, 2011 ; DOI: 10.5344/ajev.2011.11036

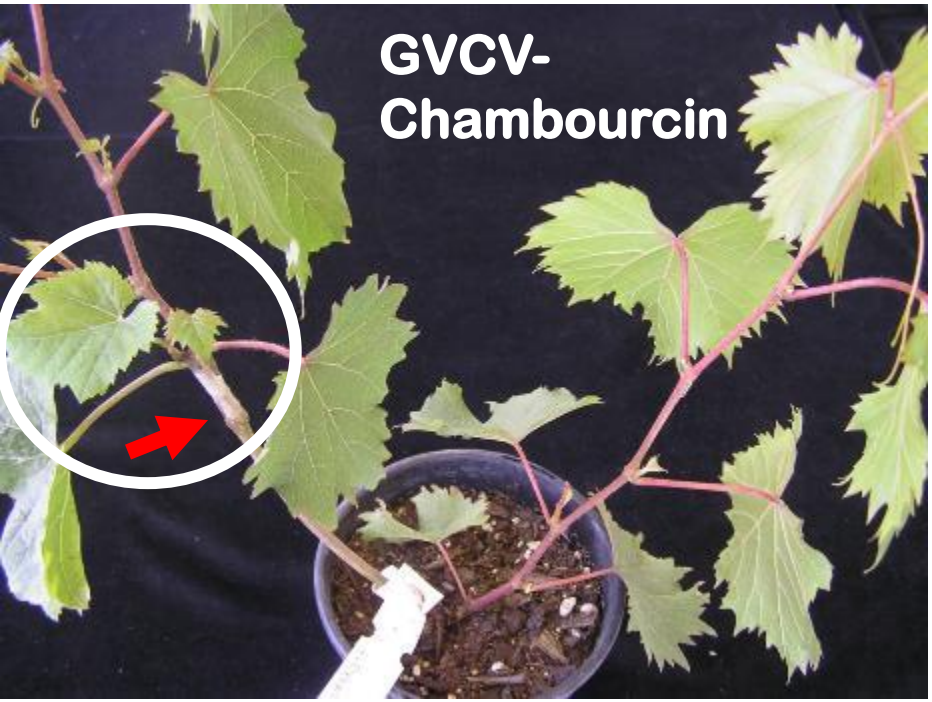
Observations and Conclusions

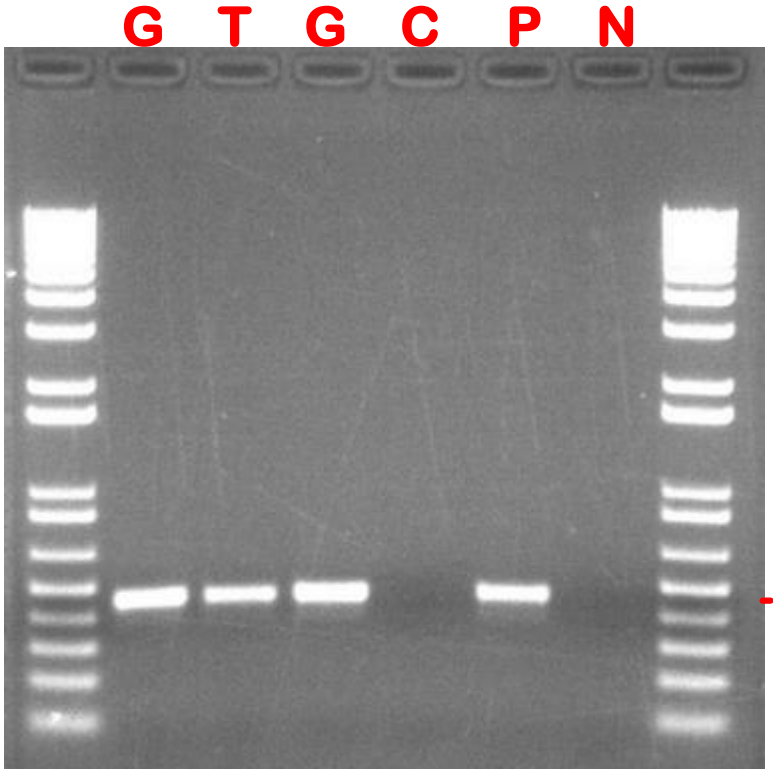
Despite a long history of cultivation, numerous viruses and viral diseases, and extensive efforts to identify useful sources of natural resistance to viruses or their vectors in wild and cultivated *Vitis* and *Muscadinia* germplasm, there remains no proven useful resistance to grapevine viruses.

Prevention

Evaluating Resistance of Grape Cultivars to GVCV


GVCV-
infected
scion

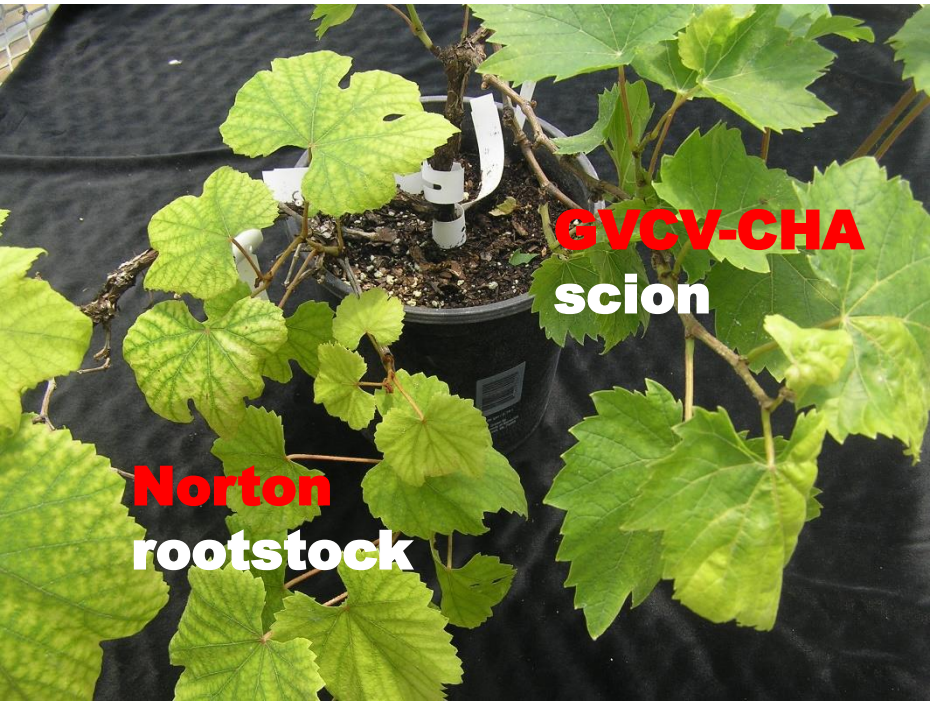


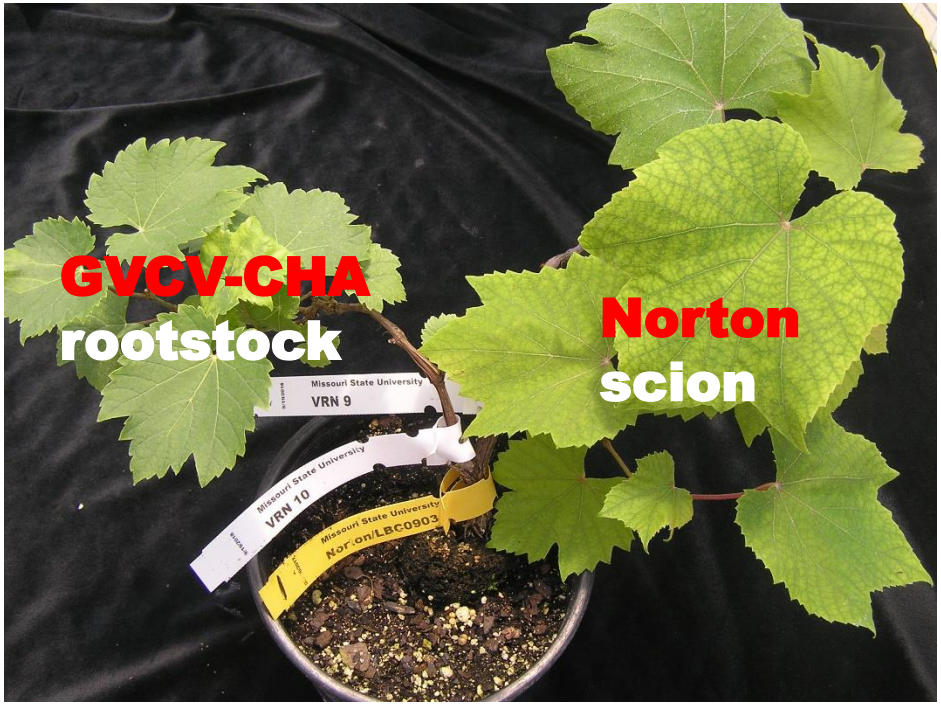


G: GVCV-infected Chardonel
T: GVCV-Traminette
C: GVCV-infected Chambourcin
P: positive control

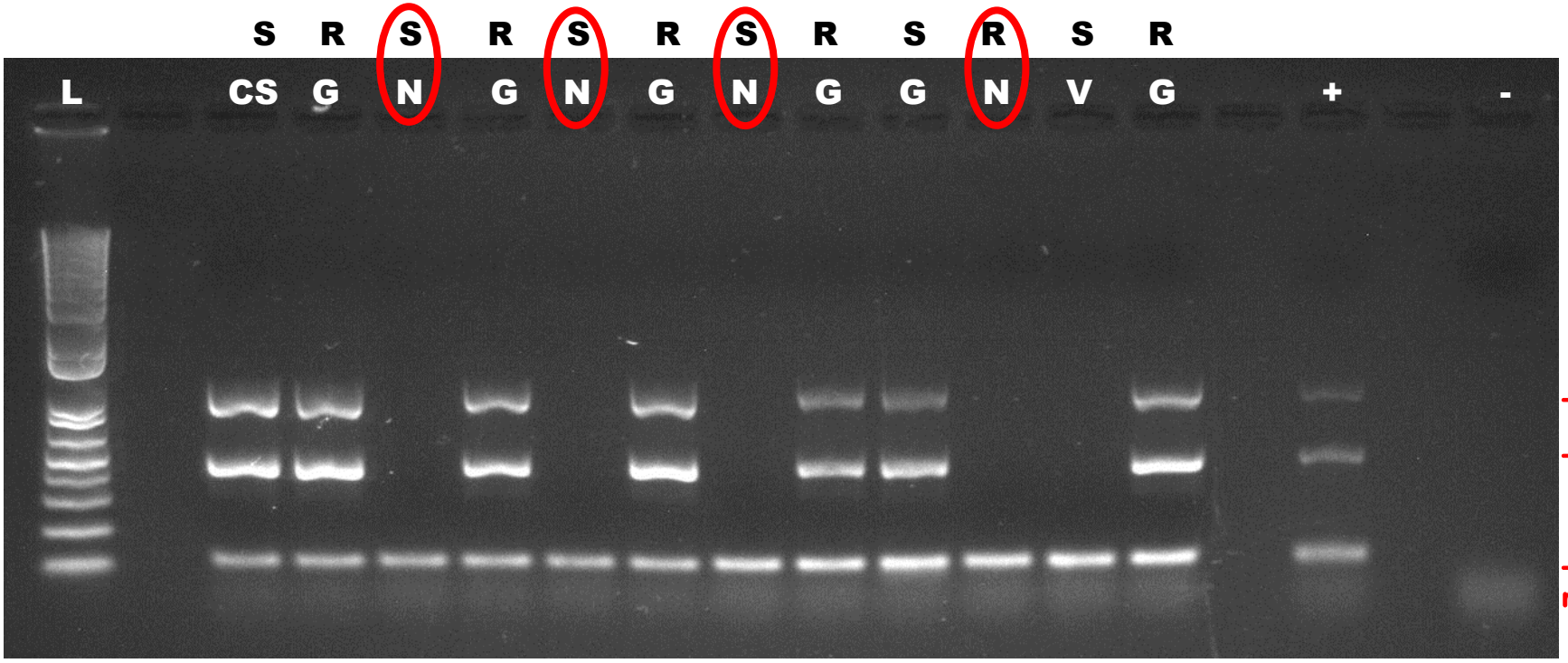
Norton-The Greatest Grape

Evaluating Norton's resistance to GVCV





Norton is resistant to GVCV



L----Ladder
CS----Cabernet Sauvignon
G----GVCV infected Chardonel
N----Norton
V----Vignoles
S----Scion
R----Rootstock

Evaluating Norton's Resistance

Scion/Rootstock (number of grafted vines)	Dates of Grafting	GVCV Detection		vsRNA profiles					
		PCR	RNA-seq	Reads per million	Percentage of genome assembled	21-nt	22-nt	24-nt	>24nt
Norton/	09/03/2013 (three years1)	-	-	4.73	Not Assembled	51	8	2	0
GVCV-Chardonel (1)		+	+	33029.01	100	403,627	93,338	15,303	5,595
Norton/	06/09/2015 (one year)	-							
GVCV-Chardonel (2)		+							
Norton/	07/06/2017 (one year)	-							
GVCV-Chardonel (3)		+							
GVCV-Chardonel/	06/15/2013 (three years)	+	+	3398.77	99.59	37,310	13,414	1,674	1,108
Norton (1)		-	-	0.94	Not Assembled	100	24	5	1
Cabernet Sauvignon/	6/22/2015 (one year)	+							
GVCV-Chardonel (1)		+							
GVCV-Chardonel/	6/14/2013 (three years)	+	+	8237.21	100	79,226	8,259	1,313	2,715
Cabernet Sauvignon (1)		+	+	40713.82	100	319,114	83,238	13,476	12,332
Chardonel/	7/6/2017 (one year)	+							
GVCV-Chardonel (1)		+							

Evaluating Norton's Resistance

Table 1. Assessment of 'Norton' resistance via graft-transmission to grapevine vein clearing virus (GVCV) by polymerase chain reaction (PCR)

Scion	Rootstock	Vines grafted	Vines analyzed	Age of grafted vines in years	Detection of GVCV	
					Scion	Rootstock
Norton	GVCV-Chardonel[a]	6	6	1–3	–	+
GVCV-Chardonel	Norton	3	1	3	+	–
Cabernet Sauvignon	GVCV-Chardonel	3	1	1	+	+
Chardonel	GVCV-Chardonel	3	1	1	+	+
GVCV-Chardonel	Cabernet Sauvignon	3	1	3	+	+

[a] GVCV-infected 'Chardonel' grapevine was used as virus inoculum.

SHORT COMMUNICATION

North American Grape 'Norton' is Resistant to Grapevine Vein Clearing Virus

Wenping Qiu, Sylvia M. Petersen, and Susanne Howard

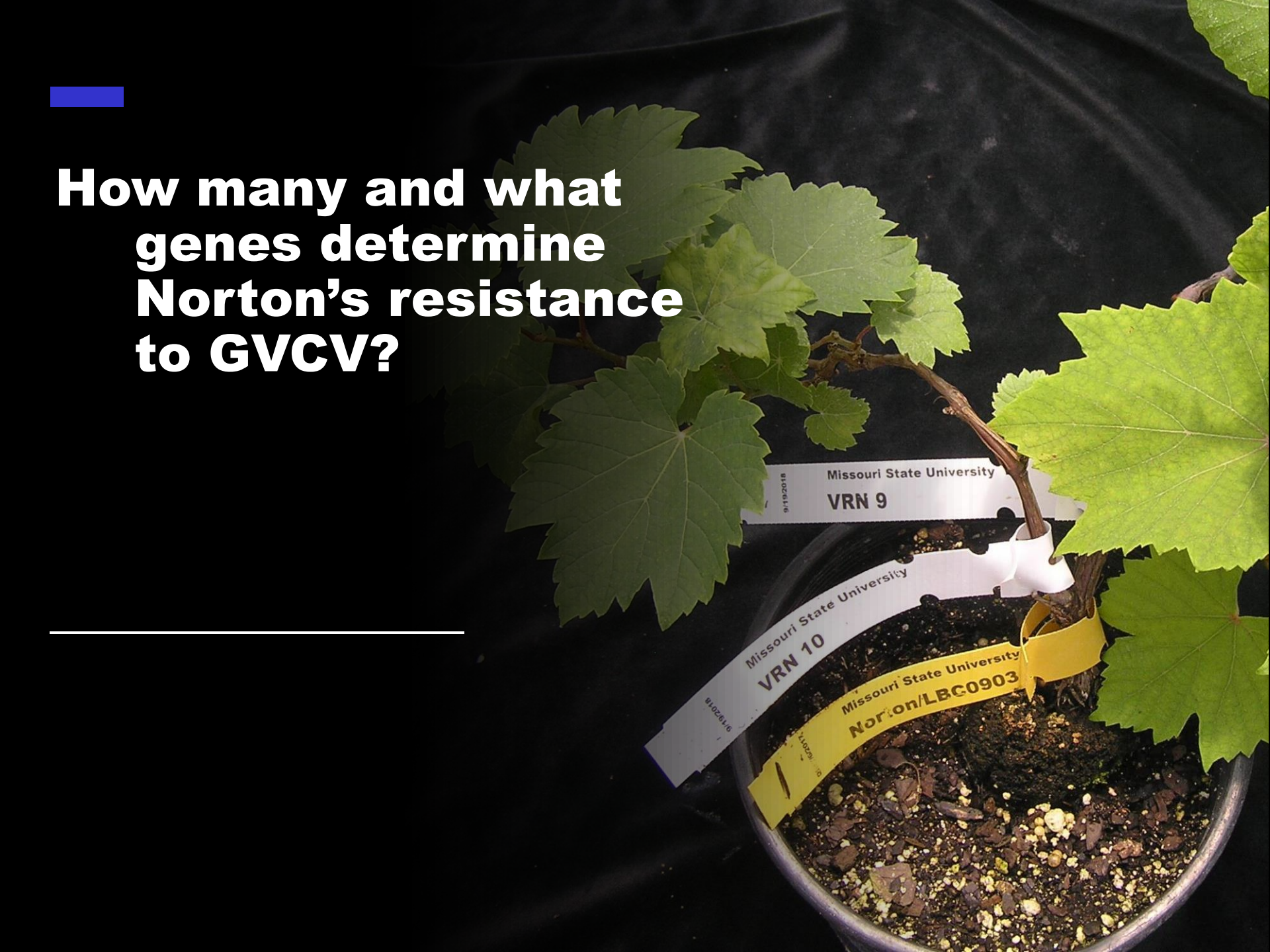
Affiliations

Published Online: 10 Jun 2020 | https://doi.org/10.1094/PDIS-10-19-2161-SC

CONCLUSION

Cultivars	Responding to GVCV
Chambourcin	Resistant
Norton	Resistant
Vignoles	To be verified
Traminette	Tolerant
Cayuga White	Tolerant
Vidal Blanc	Susceptible
Chardonel	Susceptible
Chardonnay	Susceptible
Cabernet Sauvignon	Susceptible
Valvin Muscat	Susceptible
Vignette	Susceptible

How many and what genes determine Norton's resistance to GVCV?

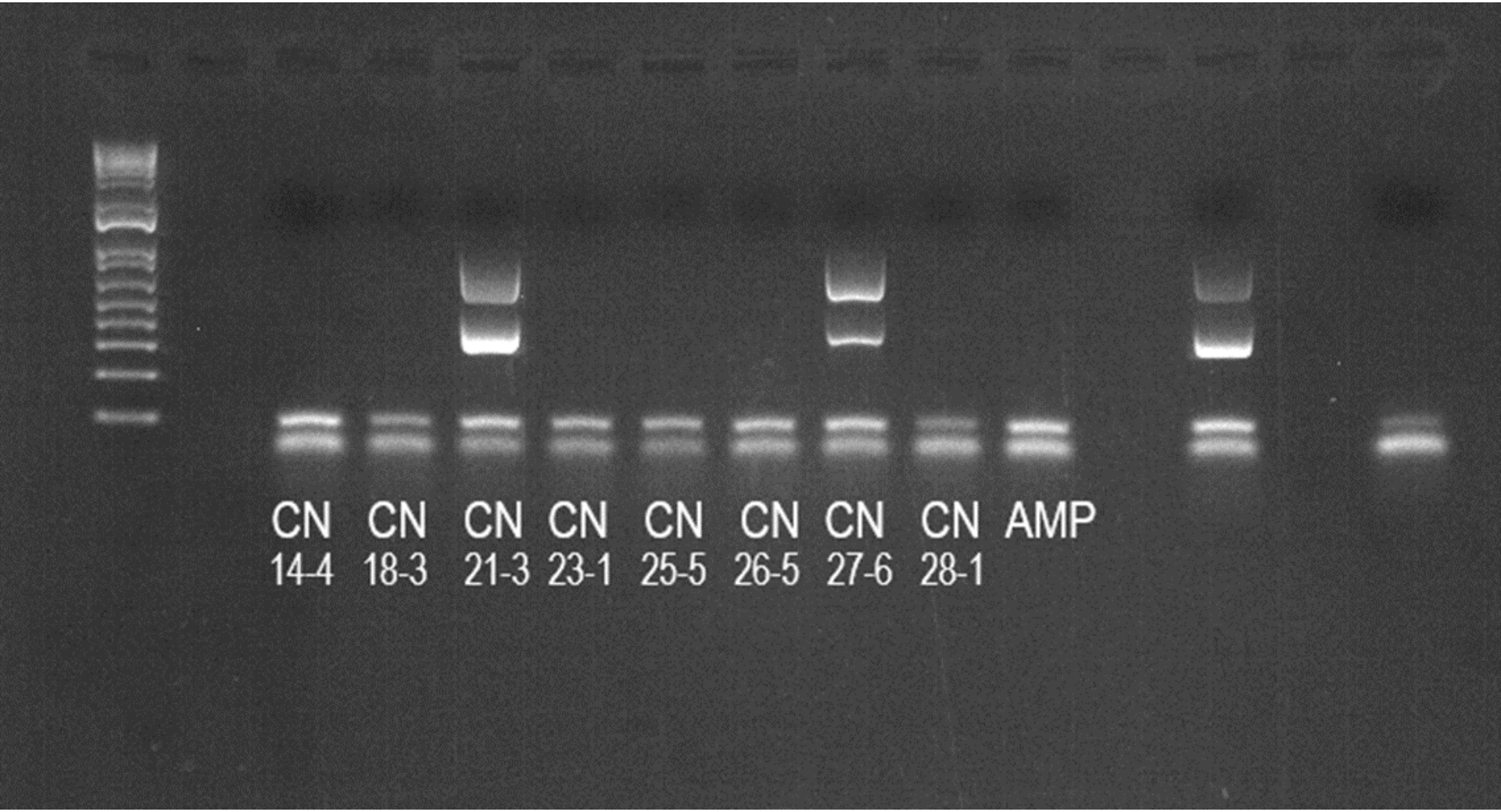


78 Progenies from Norton and Cabernet Sauvignon cross

Resistant to GVCV

Susceptible to GVCV

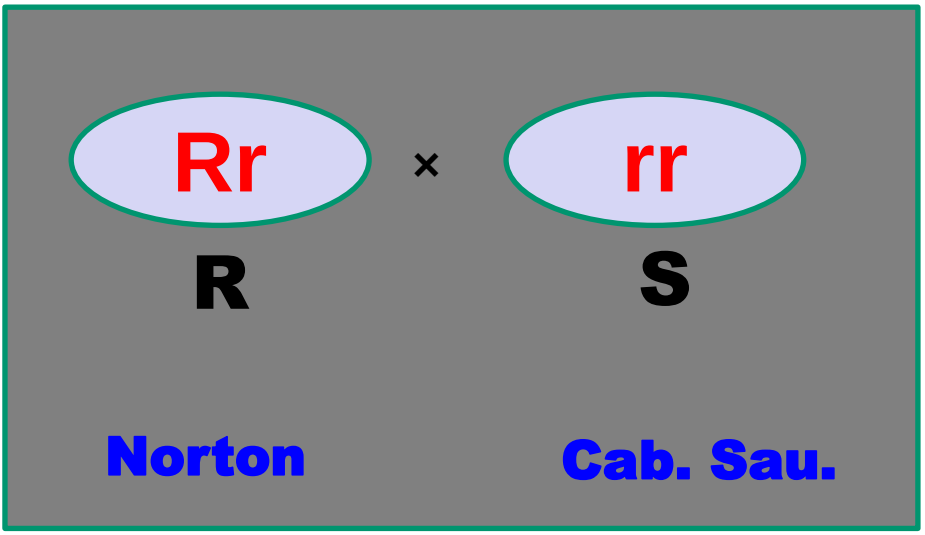
Genetic analysis of 78 progenies from N x CS cross

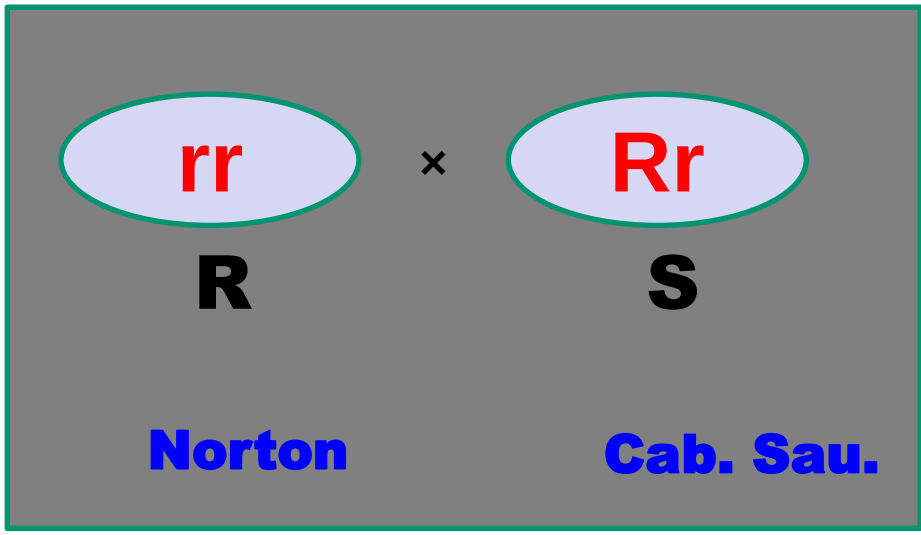


Genetic analysis of 78 progenies from N x CS cross

Susceptible:44; Resistant:34

S:R= 1.3:1 ≈ 1:1





A. Norton Rr x Cabernet Sauvignon rr: resistance is conferred by a dominant R gene in heterozygous background.

B. Norton rr x Cabernet Sauvignon Rr: resistance is conferred by a recessive r gene in a homozygous background.

Two or more genes?

Self-fertilized Norton seedlings (300)

SNG Samples 2021										
Sample ID	Date Sampled	Date Extracted	260/280	Concentration ng/ul	Dilution (DNA)	Dilution (H20)	16s	344 bp	672 bp	159 bp
SNG 2	9/20/2021	9/20/2021	2.15	353.1	0.6	19.4	+	-	-	-
SNG 4	9/20/2021	9/20/2021	2.15	651.8	0.3	19.7	+	+	+	-
SNG 7	9/20/2021	9/20/2021	2.16	729.1	0.3	19.7	+	-	-	-
SNG 9	10/10/2021	10/10/2021	2	47.2	6.4	13.6	+	-	-	-
SNG 11	9/20/2021	9/20/2021	2.17	246.8	0.8	19.2	+	-	-	-
SNG 12	9/20/2021	9/20/2021	1.92	112.6	1.8	18.2	+	-	-	-
SNG 14	9/20/2021	9/20/2021	2.16	888	0.2	19.8	+	+	+	+
SNG 15	9/20/2021	9/20/2021	2.19	584.6	0.3	19.7	+	+	-	+
SNG 16	9/20/2021	9/20/2021	2.15	763	0.3	19.7	+	-	-	-
SNG 17	10/10/2021	10/10/2021	2.02	50.3	6	14	+	-	-	-
SNG 22	10/10/2021	10/10/2021	2.03	134.5	2.2	17.8	+	+	+	+
SNG 23	10/10/2021	10/10/2021	2.05	156.9	1.9	18.1	+	-	-	-

Can Norton resist viruses other than GVCV?

Seven viruses are in ‘Kishmish Vatkana’ grapevine

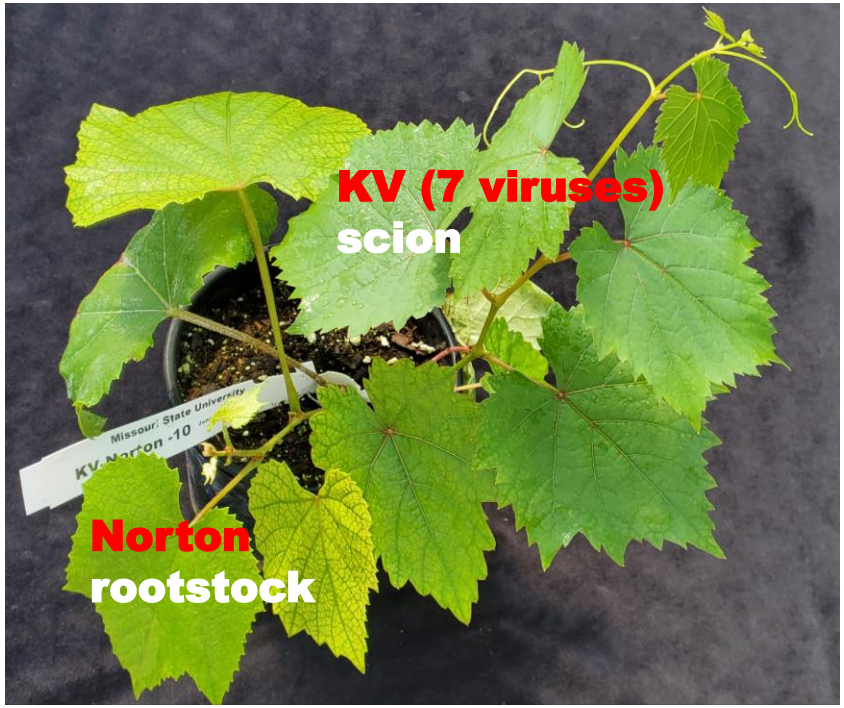
TABLE 1
Classification and genome features of the seven viruses analyzed in this study[z]

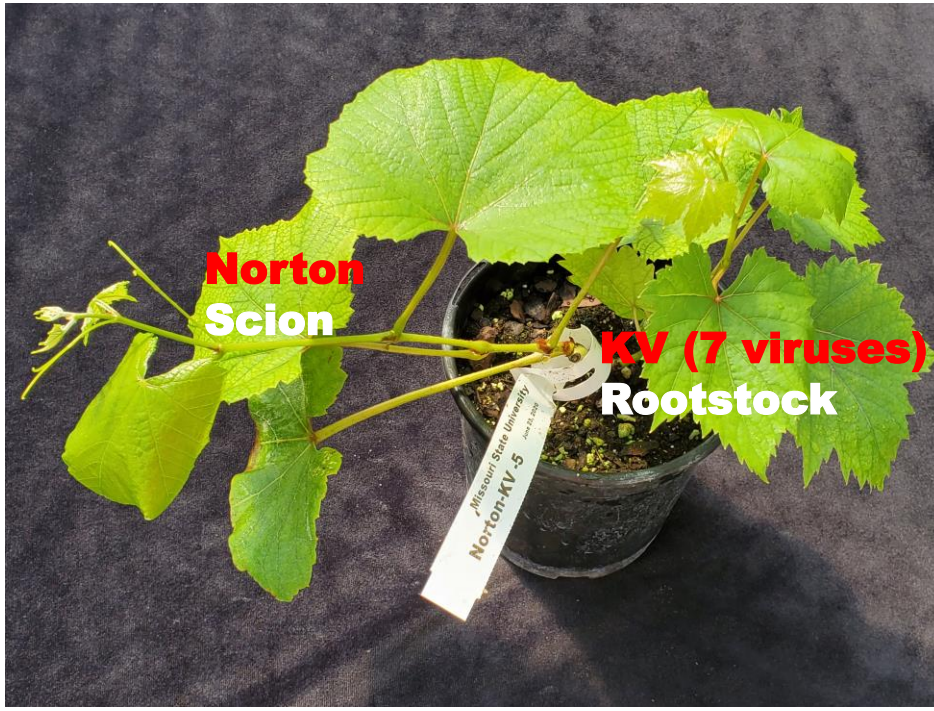
Viruses	Family	Genus	Genome	Genome size (nt)	Number of sgRNAs
Grapevine fleck virus (GFkV)	*Tymoviridae*	*Marculavirus*	ss (+) RNA	Approximately 7,500	2
Grapevine leaf roll-associated virus 1 (GLRaV-1)	*Closteroviridae*	*Ampelovirus*	ss (+) RNA	12,394–18,659	8
Grapevine leaf roll-associated virus 2 (GLRaV-2)	*Closteroviridae*	*Closterovirus*	ss (+) RNA	Approximately 16,500	7
Grapevine leaf roll-associated virus 3 (GLRaV-3)	*Closteroviridae*	*Ampelovirus*	ss (+) RNA	13,400–18,600	9
Grapevine virus A (GVA)	*Betaflexiviridae*	*Vitivirus*	ss (+) RNA	7,400–7,600	3
Grapevine Pinot gris virus (GPGV)	*Betaflexiviridae*	*Tricovirus*	ss (+) RNA	7,259	2
Grapevine rupestris stem pitting-associated virus (GRSPaV)	*Betaflexiviridae*	*Foreavirus*	ss (+) RNA	8,725	3

[z] Abbreviations: nt = nucleotide, sgRNA = subgenomic RNA, and ss (+) RNA = single-stranded, plus-sense RNA.

https://apsjournals.apsnet.org/doi/10.1094/PBIOMES-12-20-0091-R

Evaluating Norton's resistance to seven viruses





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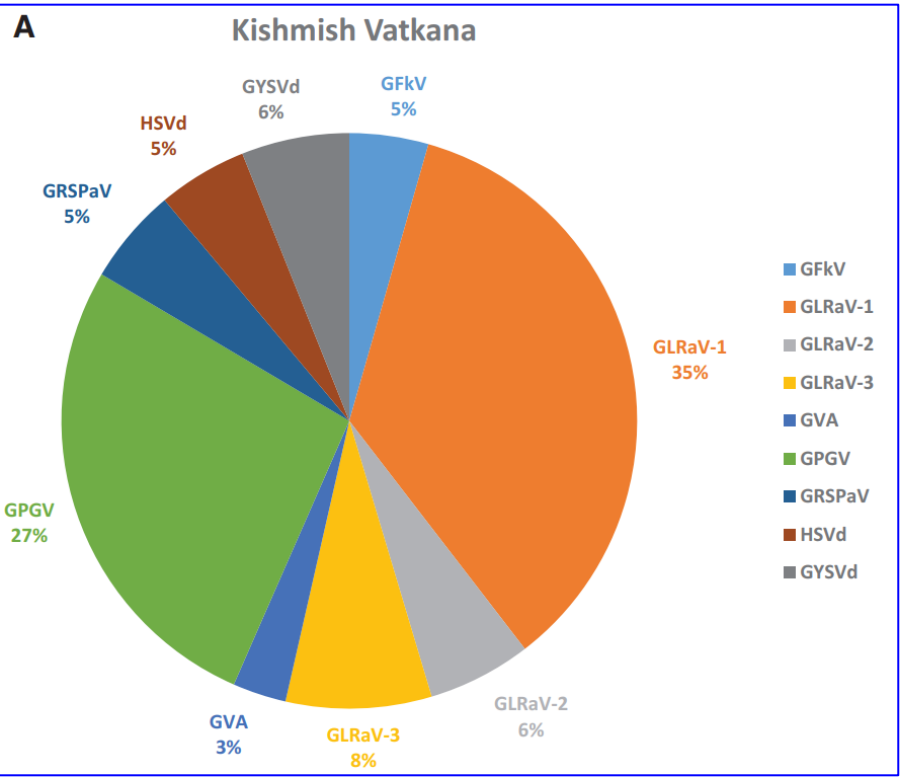
Distribution of viral small RNAs (vsRNAs) of all seven viruses and two viroids between two cultivars



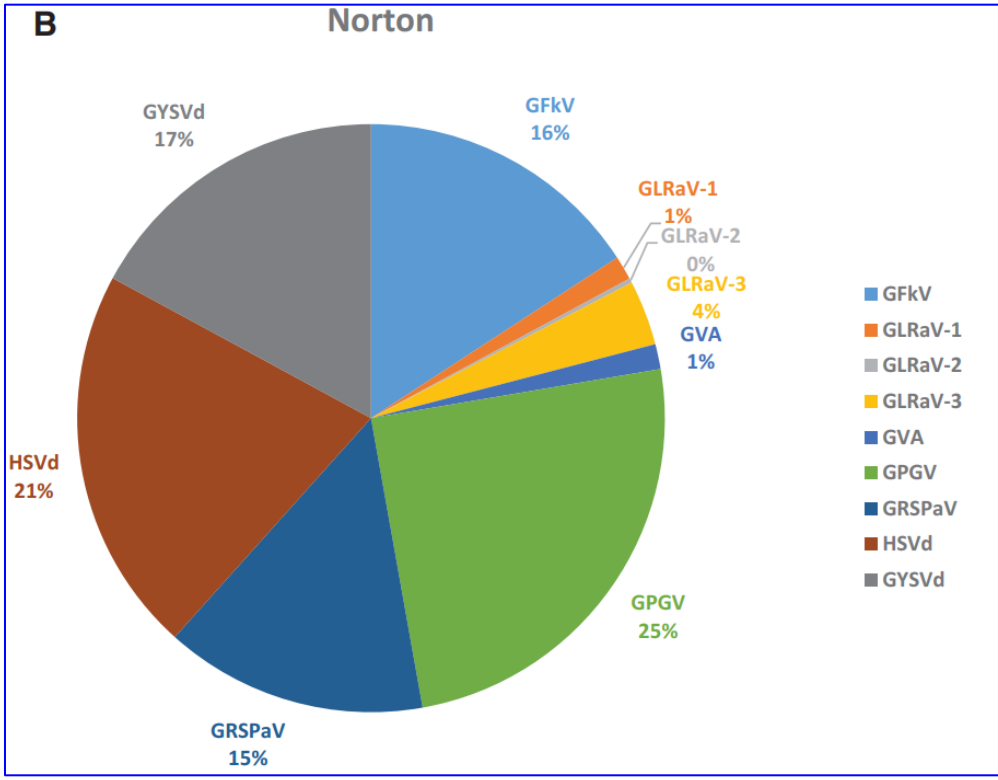


TABLE 2
Statistical analysis of small viral RNA reads per million by cultivar and by graft position[z]

Cultivar, position	GFkV	GLRaV-1	GLRaV-2	GLRaV-3	GVA	GPGV	GRSPaV	Total
Cultivar								
Kishmish Vatkana	561.17 ± 208 b	5,233.5 ± 3,437 a	782 ± 520 a	1,082 ± 636 a	421.5 ± 148 a	3,820 ± 1,919 a	778.33 ± 459 a	12,677 ± 4,408 a
Norton	1,199.2 ± 299 a	89.833 ± 114 b	17 ± 20 b	264.2 ± 141 b	104.5 ± 161 b	1,943 ± 731 b	1,171.3 ± 565 a	4,789 ± 717 b
Position								
Scion	878 ± 285 a	3,521 ± 4,665 a	318 ± 404 a	463.3 ± 312 a	315.2 ± 238 a	3,455 ± 2,093 a	1,104 ± 596 a	10,054 ± 6,064 a
Rootstock	882.33 ± 544 a	1,802.3 ± 2,043 a	481 ± 789 a	882.3 ± 789 a	210.8 ± 212 a	2,308 ± 1,076 a	845.67 ± 478 a	7,413 ± 4,039 a

[z] GFkV = grapevine fleck virus; GLRaV-1, GLRaV-2, and GLRaV-3 = grapevine leaf roll-associated virus 1, -2, and -3, respectively; GVA = grapevine virus A; GPGV = grapevine Pinot gris virus; and GRSPaV = grapevine rupestris stem pitting-associated virus. Different letters indicate significant difference at $\alpha = 0.05$.

Published in: Susanne Howard; Sylvia Petersen; Adam Uhls; Wenping Qiu; *Phytobiomes Journal* 2021, 5, 432-441.
 • DOI: 10.1094/PBIOMES-12-20-0091-R

TABLE 4
Analysis of the copy number of viral fragments per million of β-actin by quantitative real-time PCR by cultivar and by graft position[z]

Cultivar, position	GFkV	GLRaV-1	GLRaV-2	GLRaV-3	GVA	GPGV
Cultivar						
Kishmish Vatkana	50,758 ± 33,817 b	2,449 ± 2,212	1,187,957 ± 507,604 b	13,331 ± 14,292 b	707,195 ± 1,030,855 a	277,965 ± 124,451 a
Norton	96,777 ± 103,797 a	NA	56 ± 56 a	77 ± 82 a	1,790 ± 2,381 a	338,498 ± 219,290 a
Position						
Scion	131,791 ± 119,401 a	NA	537,399 ± 638,539 a	4,334 ± 4,609 a	600,267 ± 1,096,151 a	256,767 ± 17,7405 a
Rootstock	115,744 ± 101,486 a	NA	650,618 ± 856,833 a	9,073 ± 17864 a	108,718 ± 121,269 a	297,554 ± 200,338 a

[z] GFkV = grapevine fleck virus; GLRaV-1, GLRaV-2, and GLRaV-3 = grapevine leaf roll-associated virus 1, -2, and -3, respectively; GVA = grapevine virus A, and GPGV = grapevine Pinot gris virus. Different letters indicate significant difference at $\alpha = 0.05$. NA = not analyzed due to no cycle quantification number for Norton.

Published in: Susanne Howard; Sylvia Petersen; Adam Uhls; Wenping Qiu; *Phytobiomes Journal* 2021, 5, 432-441.
 • DOI: 10.1094/PBIOMES-12-20-0091-R

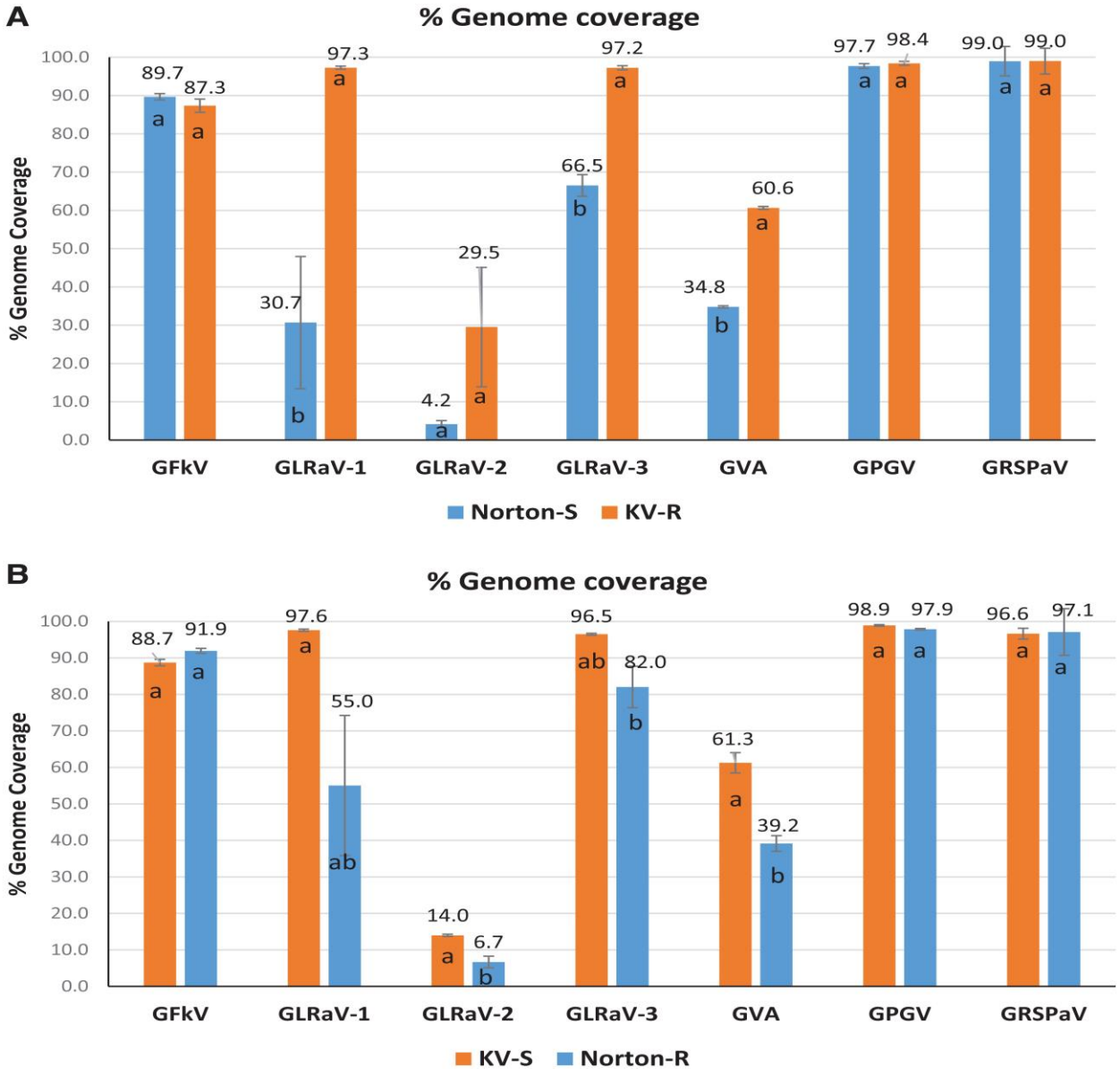


Fig. 2. Comparison of percentages of each viral genome assembled from viral small RNAs (vsRNAs) in scion and rootstock of grape cultivars Kishmish Vatkana and Norton. A, Norton was grafted as scion (Norton-S) onto Kishmish Vatkana rootstock (KV-R) and B, Kishmish Vatkana was grafted as scion (KV-S) onto Norton rootstock (Norton-R).

Published in: Susanne Howard; Sylvia Petersen; Adam Uhls; Wenping Qiu; *Phytobiomes Journal* 2021, 5, 432-441.
 • DOI: 10.1094/PBIOMES-12-20-0091-R

Conclusions

- The total number of vsRNAs of the seven grapevine viruses was significantly less in Norton than in KV.
- Specifically, the total reads of GLRaV-1, GLRaV-2, GLRaV-3, GVA, and GPGV vsRNAs were substantially reduced in Norton.
- The genome coverage by vsRNAs of GLRaV-1, GLRaV-2, GLRaV-3, and GVA was distinct between Norton and KV.

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Conclusions

- GFkV was more abundant in Norton than in KV.
- GLRaV-1 was not detectable in Norton by RT-qPCR.
- GLRaV-2 and GLRaV-3 were much less abundant in Norton than in KV.

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RESEARCH

OPEN

Distinct Responses of *Vitis aestivalis* 'Norton' and *Vitis vinifera* 'Kishmish Vatkana' to Seven Viruses Revealed by Small RNA Sequencing

Susanne Howard, Sylvia Petersen, Adam Uhls, and Wenping Qiu

Affiliations

Published Online: 29 Sep 2021 | https://doi.org/10.1094/PBIOMES-12-20-0091-R

Abstract

Grapevines are frequently infected by multiple viruses. Our previous study showed that Norton grapevine (*Vitis aestivalis*) is resistant to grapevine vein clearing virus (GVCV), a DNA virus in the family *Caulimoviridae*. To study the reaction of Norton to RNA viruses, we transferred seven RNA viruses to Norton from Kishmish Vatkana (KV) (*V. vinifera*) via graft transmission. We profiled viral small RNAs (vsRNAs) of the seven viruses and compared viral titers in Norton and KV. Total vsRNAs

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Caption

Ternary plot representing the relative occurrence of exact sequence variants in seed (top) and soil treatments (bottom).

PBIOMES-01-21-0008-R

Photo credit: Itumeleng Moroenyane

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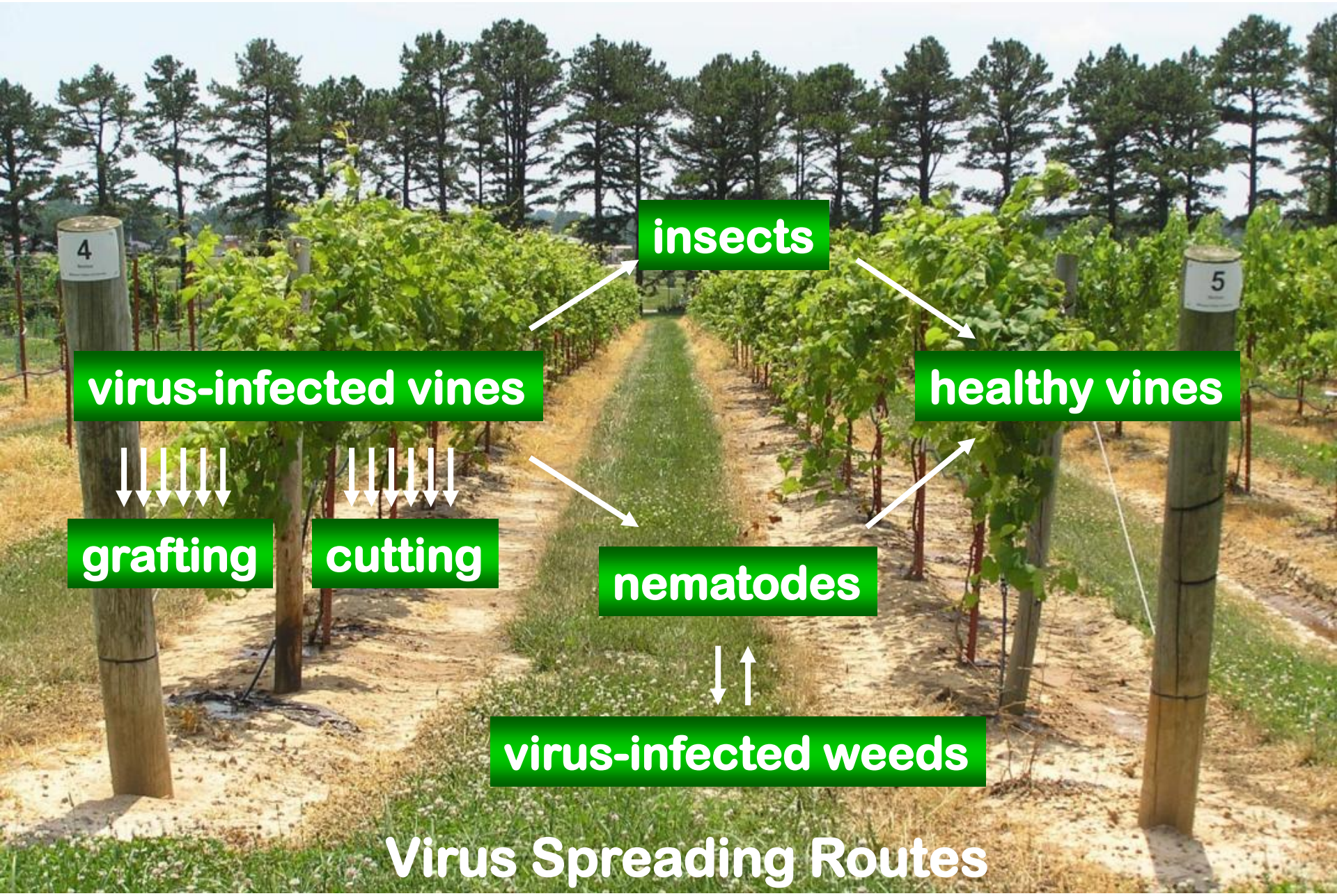
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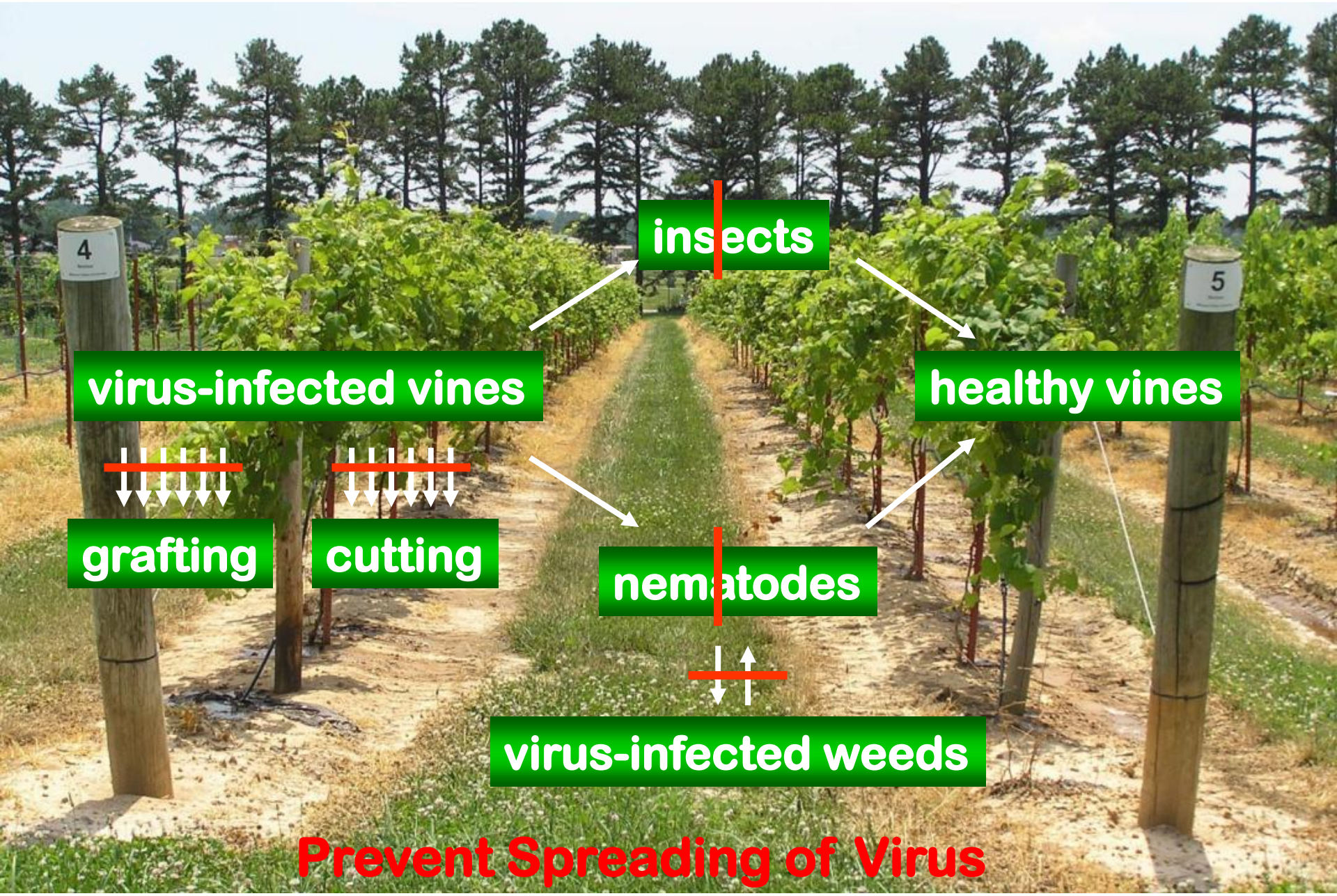
healthy vines
grafting
cutting
nematodes
virus-infected weeds
Virus Spreading Routes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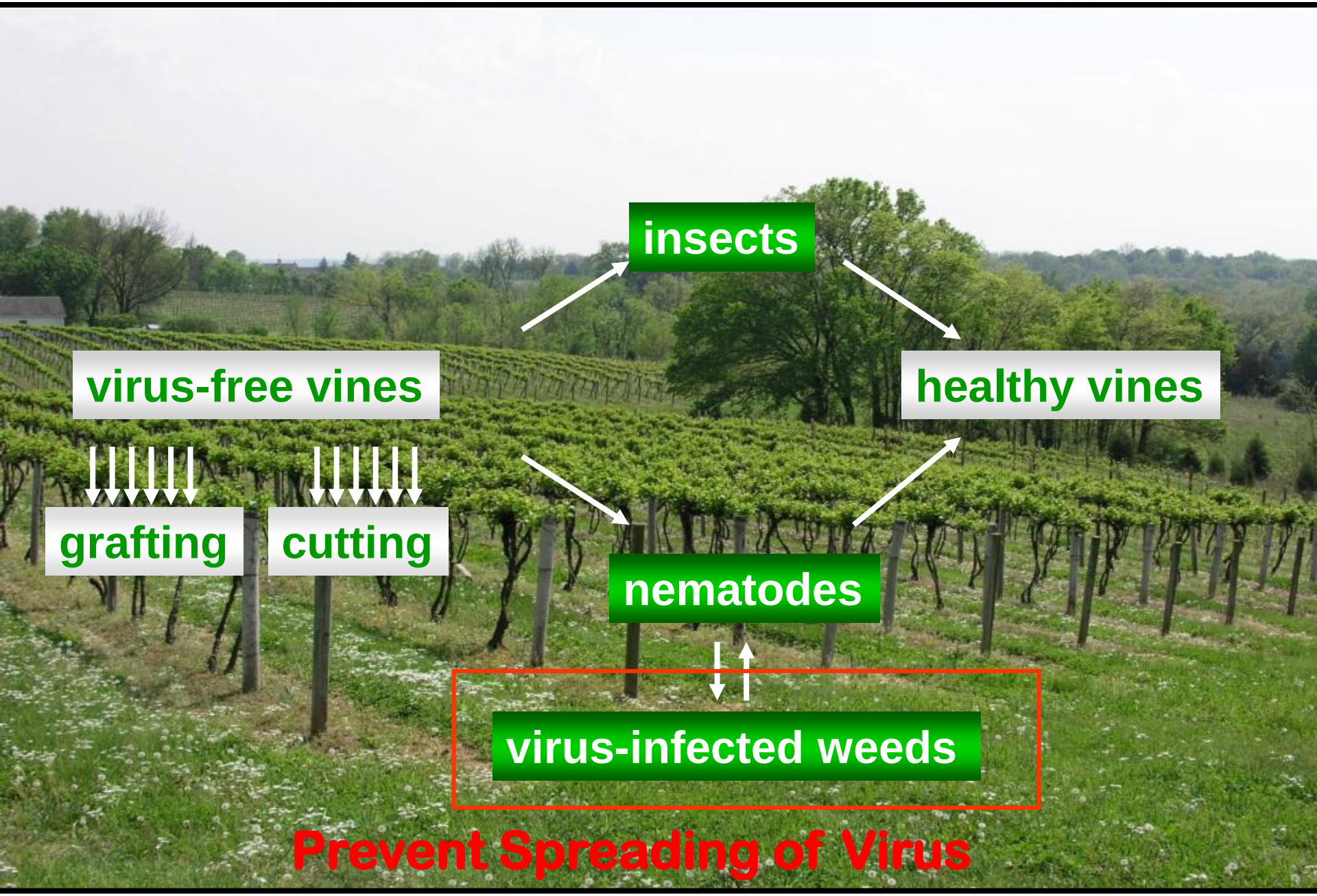
healthy vines
grafting
cutting
nematodes
virus-infected weeds
Prevent Spreading of Virus

Plant certified clean stock

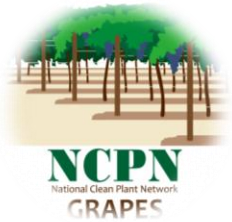

insects
virus-free vines
healthy vines
grafting
cutting
nematodes
virus-infected weeds
Prevent Spreading of Virus

The Midwest Foundation Vineyard

Amount of Clean Cuttings

Varieties	Cuttings
Norton/Cynthiana	4,000
Vignoles	3,500
Chambourcin	4,000
Chardonel	3,500
Vidal blanc	3,000
Traminette	4,000
Cayuga White	4,000
Vivant	2,000
Orion	300
NC-6	300

Virus-tested grape cultivars and amount of hardwood cuttings that are available as a result of NCPN funding



https://ag.missouristate.edu/CleanGrapevine/

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Grapes are susceptible to many viral diseases that may affect berry quality, cause vine decline, and premature vine death. Unlike in fungal and bacterial diseases, chemicals cannot control a viral disease. The most effective strategy to mitigate viral diseases in your vineyard is to start clean by planting clean vines, and utilizing appropriate insect control measures to maintain them, and removing virus-infected vines.

The following wine grape varieties have been tested free of major grapevine viruses by the most sensitive method and are available at the Missouri State Fruit Experiment Station:

Red grapes

Chambourcin

Norton

Introduce NCPN to Senator Blunt on October 14, 2021

Acknowledgements

Missouri Grape and Wine Board
Missouri Wine Marketing & Research Council

MISSOURI WINES®

Missouri State Fruit Experiment Station

NCPN
National Clean Plant Network
GRAPES

USDA-National Clean Plant Network

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19/2010	Missou
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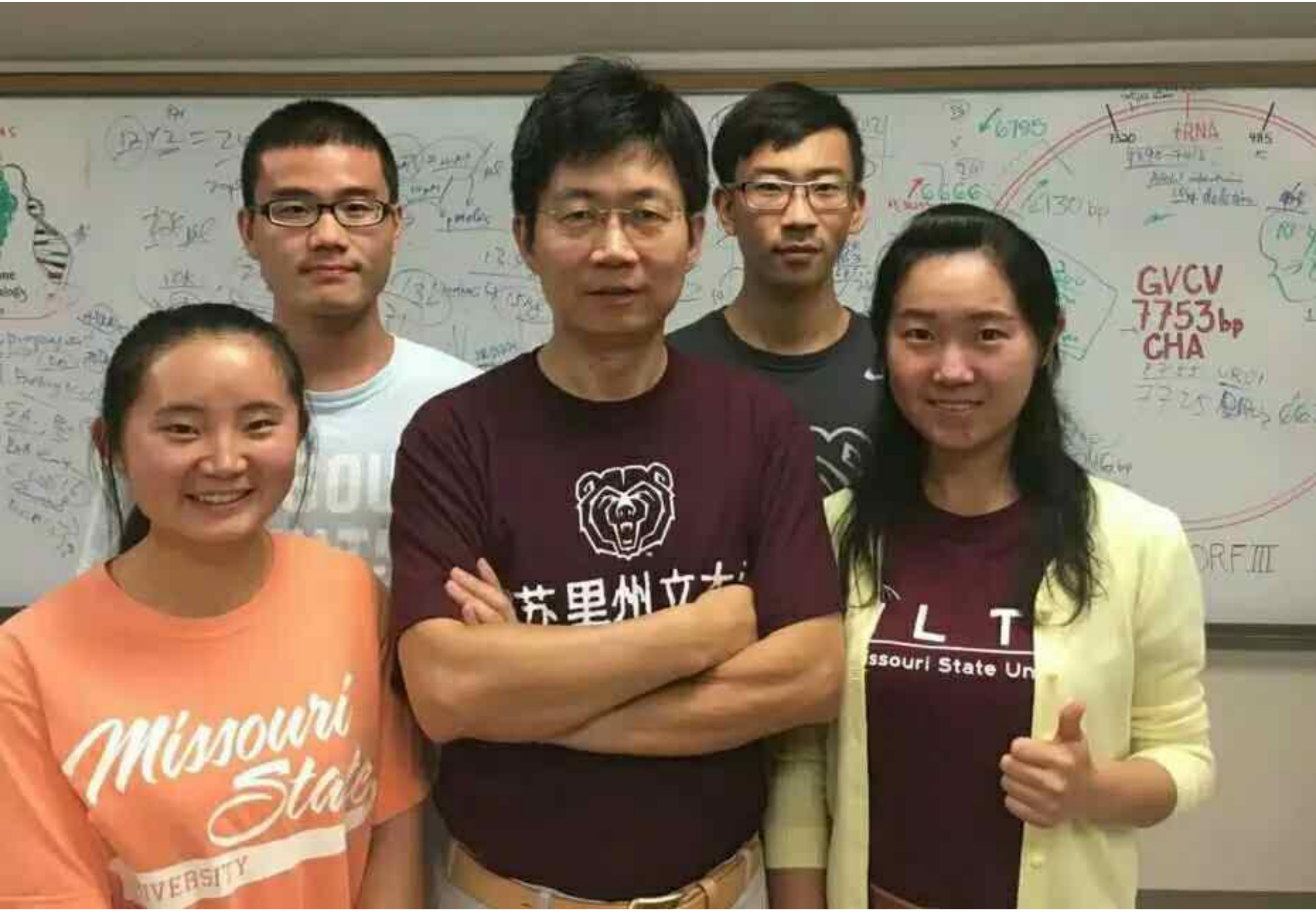
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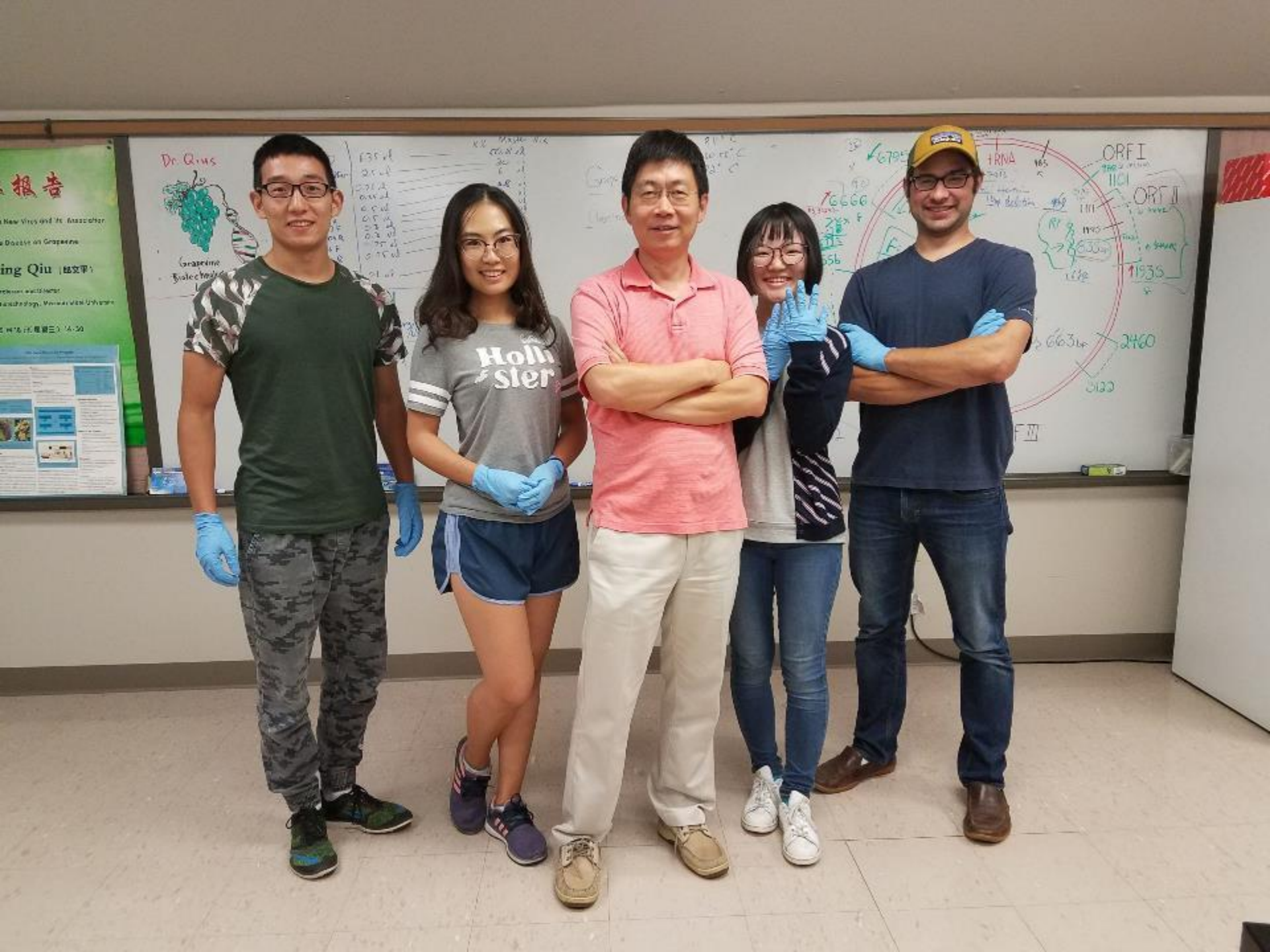
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BEAR
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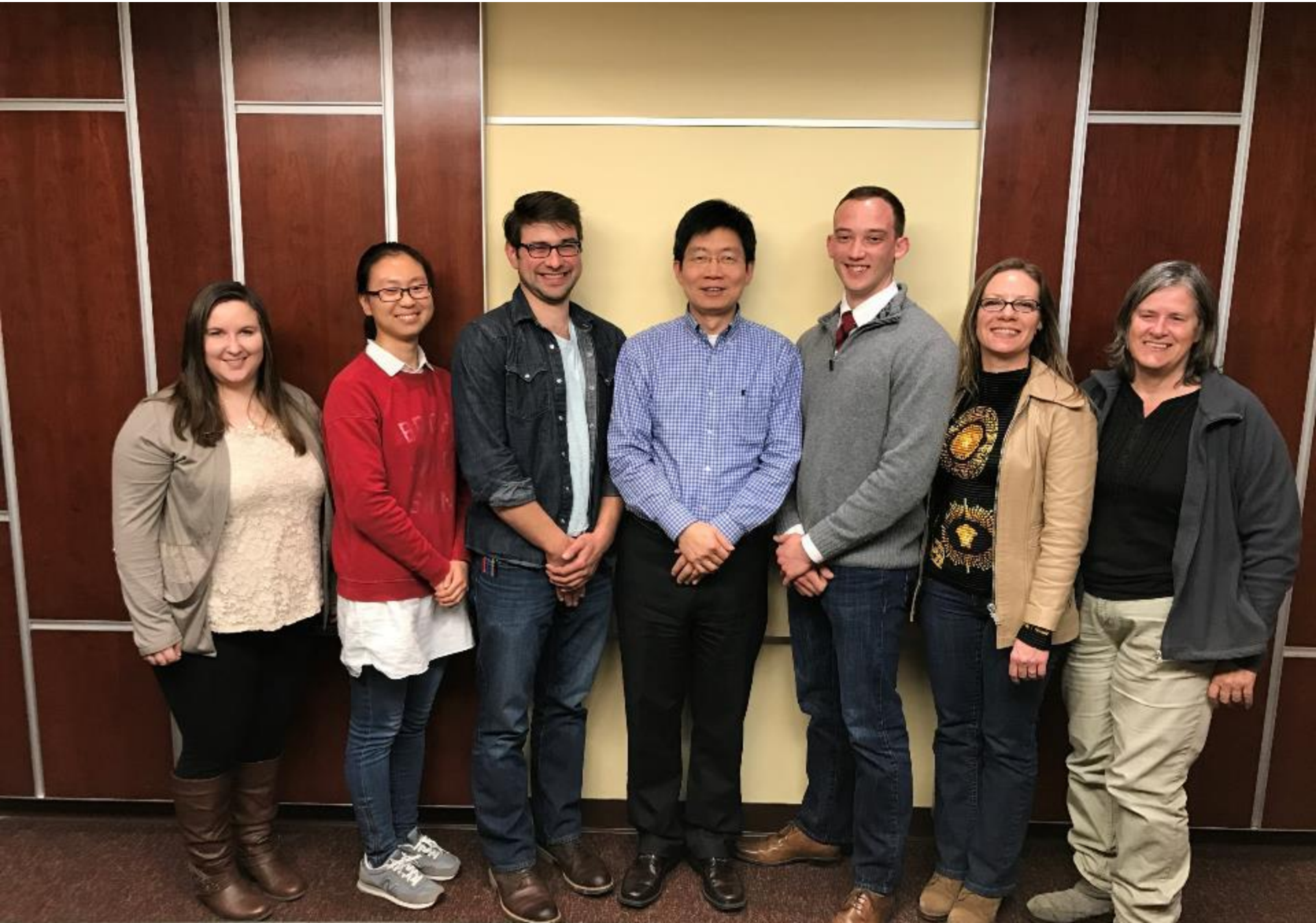

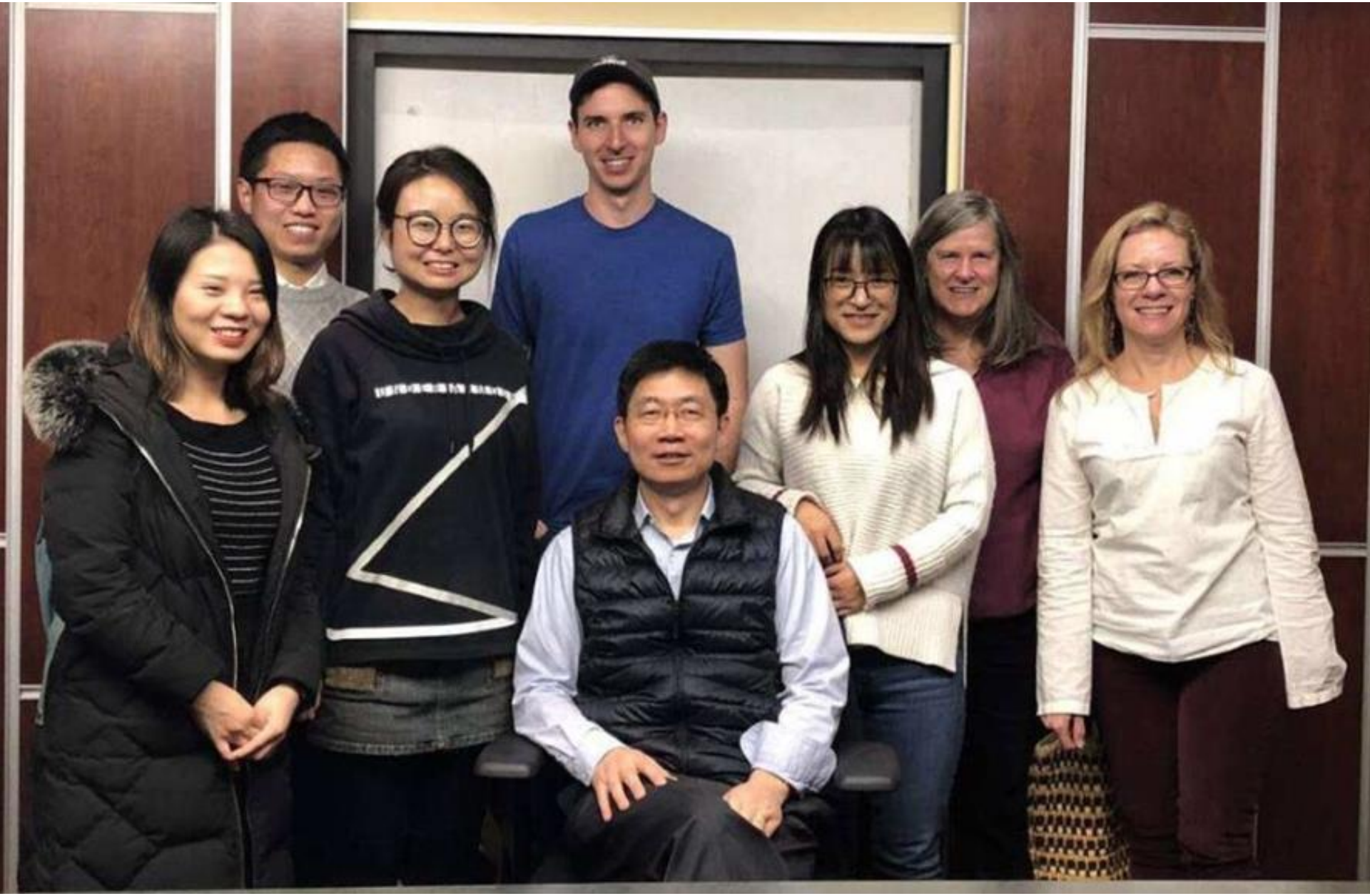


ERCUT
olf Course

ALL SINNED
Romans 5:12

Therefore, just as sin entered the world through one man, and death through sin, and in this way death came to all men, because all sinned

‘Preacher’: Wenping Qiu

10:45-11:45am

Sunday, February 7, 2010

8:30-9:15am

Saturday, February 9, 2013

ALL INFECTED

Repent for what you have done

Accept clean vines for planting

‘Preacher’: Wenping Qiu
10:45-11:45am
Sunday, February 7, 2010
8:30-9:15am
Saturday, February 9, 2013

https://ag.missouristate.edu/CleanGrapevine/

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