**California Department of Food and Agriculture PD/GWSS**

**Progress Report**

**July 2013**

**Report title:** Renewal Progress Report for CDFA Agreement Number 03-0282

**Project Title:** Genetic mapping of *Xylella fastidiosa* resistance gene(s) in grape germplasm from the southern United States.

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**Reporting period:** primarily March 2013 to July 2013

**INTRODUCTION**

This project provides the genetic support to molecular breeding efforts (see companion PD breeding project). Identification, understanding and manipulation of novel sources of resistance are the foundation of a successful breeding program. We are exploring multiple genetic backgrounds for Pierce’s disease (PD) resistant grape breeding, developing and testing breeding populations via a greenhouse screen, carrying out genetic mapping of segregating populations to identify genomic regions that carry disease resistance genes, and developing physical sequence maps of resistance regions to identify and characterize grape resistance genes. We have completed mapping of a major PD resistance locus originating from *V. arizonica/candicans* b43-17, which is the basis of our PD breeding efforts. We are pursuing two other resistant *V. arizonica* forms: b42-26 *V. arizonica/girdiana* from Loreto, Baja California; and b40-14 *V. arizonica* from Chihuahua, Sonora. They are morphologically and genetically (both paternally and maternally) different than b43-17, and both posses strong resistance to PD and greatly suppress *X. fastidiosa* levels in stem tissue after greenhouse screening. We made strong progress in identifying one major locus and one minor QTL from b40-14 background. New populations were developed with eight newly identified PD resistant plant material. The breeding part of the program produces and greenhouse screens the seedling populations. While the tightly linked genetic markers generated in these mapping efforts are being used to optimize and greatly accelerate the PD breeding program. These markers are essential to the successful introgression of resistance from multiple sources, and thus for the production of durably resistant grapevines. In response to recommendations from theCDFA-PD board and reviewer recommendations to broaden resistance, we have expanded the search for additional resistance sources by screening wide germplasm collected from different parts of US and Mexico. Initial greenhouse screen results indicate that we have twenty other accessions that possess strong PD resistance. Analysis indicates that the southeastern resistant material is genetically distinct from the species in Mexico and the extension of the Rocky Mountains (Sierra Madre) acted as a physical barrier for the grape species evolution over time period of thousands of years.

**OBJECTIVES**

1. Fine scale mapping of additional QTL for PD resistance in the 04191 ((F2-7 x F8909-17) population.
2. Greenhouse screen and genetically map PD resistance from other forms of *V. arizonica*: b42-26 (*V. arizonica /girdiana*) and b40-14 (*V. arizonica*).
3. Evaluate *Vitis* germplasm collected from across the southwestern US to identify accessions with unique forms of PD resistance for grape breeding. Determine the inheritance of PD resistance from *Muscadinia rotundifolia*, develop new and exploit existing breeding populations to genetically map this resistance.

**4.** Complete the physical mapping of *PdR1a* and *PdR1b* and initiate the sequencing of BAC clones that carry *PdR1a* gene candidates.

**RESULTS**

**Objective 1**. Fine scale mapping of additional QTL for PD resistance in the 04191 ((F2-7 x F8909-17) population (See details in March 2013 report).

In brief, a framework genetic map of the 04191 population (*V. vinifera* F2-7 x F8909-17) was used to identify a quantitative trait locus (QTL) with a minor impact on resistance (contributing 7% of the phenotypic variation to PD resistance) on chromosome 19. This QTL is within a 10 cM interval – a relatively long genetic distance to be effective in marker assisted screening. A total of 1.783 Mbp of sequence of PN40024 was used to develop 7 SSR primers in this region. Three of the seven tested primers gave clean amplifications with polymorphism for the F8909-17 PD resistant parent. These markers were added to the population of 150 seedlings. We are in the process of completing this analysis. Two crosses with 04373-02 and 04373-22 and Pinot blanc were made to study the impact of the this minor QTL from chromosome 19 without impact of major locus from chromosome 14. A total of 100 plants were screened with SSR markers and 43 plants were planted in the field in Spring 2012. These plants are in pipeline to be greenhouse screened during summer 2013.

**Objective 2.** Greenhouse screen and genetically map PD resistance from other forms of *V. arizonica*: b42-26 (*V. arizonica /girdiana*) and b40-14 (*V. arizonica*).

The accession b40-14, a pure form of *V. arizonica*,is homozygous resistant to Pierce’s disease. All seedlings from F1 cross were tested resistant to the disease. Two resistant siblings of this population were used to develop the 07388 (R8918-02 x *V. vinifera*) and 07744 (R8918-05 x *V. vinifera*) populations. In the previous report, we described the preliminary results with 07744 and genetic mapping with 152 markers. From March to July time period, we have tested a total of 606 SSR markers and 224 polymorphic markers were added on the entire set of 122 plants (Table 1). A total of 216 markers were polymorphic for the female resistant parent R8918-05.

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| **Table 1.** List of markers tested and completed for the 07744 population derived from the b40-14 background |
| **Marker series** | **Tested** | **Amplified** | **Polymorphic** | **Completed** |
| VMC, VMCNg | 271 | 161 | 133 | 106 |
| VVI | 93 | 84 | 56 | 50 |
| UDV | 55 | 54 | 35 | 26 |
| VChr | 3 | 3 | 3 | 3 |
| VVMS, VVMD, VrZAG | 35 | 34 | 25 | 22 |
| Other unpublished | 4 | 4 | 2 | 2 |
| EST-SSR (SCU, VVC, CTG) | 145 | 108 | 68 | 15 |
| Total | 606 | 448 | 322 | 224 |

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| **Table 2.** Salient features of framework map of R8918-05, a PD resistant selection used as the maternal parent in the 07744 population. |
| **Chromosome** | **Mapped Markers**  | **Length (cM)** |
| Chr1 | 15 | 72.7 |
| Chr2 | 4 | 59.6 |
| Chr3 | 6 | 37.9 |
| Chr4 | 11 | 98.3 |
| Chr5 | 13 | 60.6 |
| Chr6 | 11 | 40.8 |
| Chr7 | 12 | 88.0 |
| Chr8 | 11 | 54.7 |
| Chr9 | 10 | 87.7 |
| Chr10 | 10 | 74.5 |
| Chr11 | 9 | 79.7 |
| Chr12 | 8 | 52.5 |
| Chr13 | 11 | 71.9 |
| Chr14 | 26 | 97.9 |
| Chr15 | 8 | 35.9 |
| Chr16 | 9 | 67.5 |
| Chr17 | 12 | 56.2 |
| Chr18 | 13 | 136.2 |
| Chr19 | 13 | 55.8 |
| Total  | 212 | 1328.4 |
| Ave marker distance (cM) | 6.3 cM |  |
| Number of gaps > 20 cM | 14 |  |

A framework genetic map of R8918-05 was produced with Joinmap (4.0). A total of 212 markers mapped to 19 grape chromosomes with average distance of 6.3 cM between markers. The updated map did not have fragmented groups and provide adequate genome coverage when comparisons were made to the previously published integrated *Vitis* genetic maps.

QTL analysis was carried out with MapQTL. A major locus for PD resistance was identified on chromosome 14. PD resistance from b40-14 (which we have named *PdR1c*) maps in the same general region as *PdR1a* and *PdR1b* between flanking markers VVCh14-77 and VVIN64 and within 1.5 cM. The LOD threshold for the presence of this QTL was 39 and this major locus explained 80% of the phenotypic variation (Fig. 1).

0

20

40

60

80

100

VVC62

VChr14b

VVIP05

VMC1e12

VMC2h12

VMC9f4

ctg1008359

VChr14a

VMC2b11

VMC6c10

UDV033

VMC5b3

VVMD24

VMCNg2b7.2

VVCh14-77

VVIN64

UDV025

VVIS70

VVIP26

ctg1025882

VVIn94

VVIN70

LOD

% Expl.

VVC62

0.0

VChr14b

6.3

VVIP05

8.4

VMC1e12

23.8

VMC2h12

33.9

VMC9f4

36.9

ctg1008359

37.9

VChr14a

40.8

VMC2b11

41.6

VMC6c10

49.3

UDV033

56.9

VMC5b3

VVIV69

VMC2a5

57.7

VVMD24

62.1

VMCNg2b7.2

68.3

VVCh14-77

71.7

VVIN64

73.4

UDV025

76.9

VVIS70

77.7

VVIP26

78.6

ctg1025882

81.1

VVIn94

90.3

VVIN70

97.9

**14**

**Fig. 1.** Interval mapping of *PdR1* indicating a peak at LDD 39.0 with a 95% confidence interval. The X-axis indicates the position of the markers; LOD values and % variation explained are plotted on the Y-axis.

Using the updated genetic map, we also identified a minor QTL with LOD 2.0 on chromosome 5 that explained 8.3% phenotypic variation for resistance (Fig. 2). We did not find evidence for any other QTL on the remaining 17 chromosomes. Both QTLs explained total of 88% phenotypic variation for resistance within the b40-14 background.

VChr5c

0.0

VMC3b9

2.6

VVMD27

VrZAG26

3.4

VrZAG79

11.6

UDV041

19.7

VVIt68

23.1

VMC6e10

36.5

VMC16d4

41.8

VVMD14

51.9

VrZAG89

54.5

VMC2e9

56.2

VMC4c6

60.6

**5**

0

2

4

6

8

10

VChr5c

VMC3b9

VVMD27

VrZAG79

UDV041

VVIt68

VMC6e10

VMC16d4

VVMD14

VrZAG89

VMC2e9

VMC4c6

LOD

% Expl.

Fig. 2. A genetic map and interval mapping results for a small effect QTL on chromosome 5 derived from the b40-14 background.

We are designing more primers to reduce the gap between markers on chromosome 5 by utilizing the Pinot noir genome sequence. A total of 275 seedlings from five different crosses were also tested with markers that are in linkage with the major locus on chromosome 14; seven of recombinant lines were saved and planted in the field in Spring of 2013. These recombinant lines are scheduled for greenhouse testing and the addition of other flanking markers. These recombinant lines will help to reduce the gap between the markers on chromosome 14. The updated data will be used for a manuscript describing the genetic map and QTL identification from the b40-14 background.

The F1 population 05347 (F2-35 x b42-26) represents b42-26 background, a third resistant accession that was collected from Loreto, Baja California in 1960. A total of 918 SSR primers were tested, 763 amplified b42-26 DNA successfully, and 180 markers were polymorphic. The level of polymorphic markers is relatively low at 23%. We have not observed such a low level of polymorphism in any other genotype so far, likely to be the result of a very isolated and now inbred population. Because the main focus of the work is to develop a genetic linkage map of the resistant parent, only markers that are polymorphic for b42-26 were used. We have completed 173 of polymorphic markers on the entire population of 239 progeny. Analysis with updated marker data is in process.

Greenhouse screening was completed on 164 accessions, however results were not conclusive due to uneven greenhouse temperatures. For traits that segregate quantitatively, it is extremely important to obtain consistent phenotypic data. We have repeated and completed the greenhouse screen on 199 seedlings that rooted successfully. Thirty-five of the seedlings were tested 3 times, 77 tested twice and 87 were tested once. An ANOVA on the 35 genotypes tested in all three trials indicated that only genotype matters and there we no significant interactions. The same was true for the 77 genotypes tested twice when compared pair wise. The updated results will be used for QTL analysis after completion of genetic mapping and QTL analysis with b40-14 background.

**Objective 3.** Evaluate *Vitis* germplasm collected from across the southwestern US to identify accessions with unique forms of PD resistance for grape breeding.

We have made tremendous progress in assessing diversity and population structure of southwestern US accessions from March to July time period. It is thought that southeastern germplasm co-evolved with *X. fastidiosa* and developed resistance to this disease. Our focus has been on 3 accessions of *Vitis* that Olmo collected in northern Mexico in 1960 (as reported in objective 1 and 2). Two of these accessions are complexes of multiple *Vitis* species and it is not known which particular species is controlling PD resistance. This point is confounded by the complete fertility among the *Vitis* species and the great number of hybrids that occur in the wild. It is extremely important for a breeding program to incorporate multiple unique resistance mechanisms, understand genetic diversity, and the mode of inheritance to facilitate decision making for resistance breeding.

In order to better understand the nature of PD resistance and the genetic diversity and gene flow of grape species in the southern US and Mexico, we examined a diverse collection of species from these areas. One of the objectives was to determine whether PD resistance from the Gulf states and southeastern US is similar to that of eastern coastal (and wet) Mexico. And whether this eastern resistance differs from PD resistance found in the southwestern US and central (and drier) Mexico. We examined a collection of 219 (sixty more from previous report) accessions of these species, which includes Olmo’s Mexico collections (which he sampled across northern and central Mexico from the west to the east). DNA was collected from all those genotypes and six *V. vinifera* accessions were added as outliers. A total of 22 SSR markers were selected for their polymorphism and coverage of all 19 grape chromosomes (Table 3). All amplified products were run on the ABI 3500 genetic analyzer and analyzed with the Gene Mapper program to obtain fingerprint profiles. Hierarchical clustering (Ward method) and Principal Coordinate Analysis were carried out with DARWIN software (version 5.0.158) to determine the number of groups. STRUCTURE V2.3.1 was used to infer the number of pseudo-populations or clusters with 22 markers.

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| Table 3. List of SSR markers used for fingerprint analysis of 165 selections. |
| Marker name | Dye label | Chromosome  | Amplified product size range |
| VVIp60 | HEX | 1 | >300 |
| VrZAG93 | NED | 2 | 180-240 |
| APT3 | 6-FAM | 2 | 266-466 |
| VVIb23 | 6-FAM | 2 | 250-320 |
| VVMD28 | 6-FAM | 3 | 216-270 |
| VVMD32 | NED | 4 | 240-280 |
| VVMD27 | NED | 5 | 170-220 |
| VrZAG79 | 6-FAM | 5 | 230-280 |
| VVMD21 | 6-FAM | 6 | 240-260 |
| VVMD31 |  6-FAM | 7 | 200 |
| VVMD7 | NED | 7 | 220-270 |
| VrZAG62 | HEX | 7 | 175-215 |
| VMC1b11 | HEX | 8 | 150-190 |
| VVIq52 | 6-FAM | 9 | 70-90 |
| VVIv37 | 6-FAM | 10 | 140-180 |
| VVS02 | 6-FAM | 11 | 120-170 |
| VMC4f3.1 | HEX | 12 | 160-290 |
| UDV124 | 6-FAM | 13 | 170-230 |
| VVIP26 | HEX | 14 | 120-180 |
| VVIv67 | HEX | 15 | 350-400 |
| VVMD5 | 6-FAM | 16 | 210-290 |
| VVIn73 | 6-FAM | 17 | 240-270 |
| UDV108 | HEX | 18 | 200-276 |
| VVIp31 | 6-FAM | 19 | 150-220 |

After exclusion of those accessions that did not have enough representation in the study set, analysis was carried out on set of 180 accessions with three methods. All three methods; hierarchical clustering (Ward method), principle coordinate analysis (PCA) and a model-based clustering method implemented in the program STRUCTURE revealed three main groups. Figure 3. presents the results of PCA with three distinct groups and Fig. 4 presents the groupings revealed with the STRUCTURE program displayed on the geographic location map. Most of the accessions from the Mexican species collections appear to be introgressive hybrids among *V. arizonica, V. berlandieri, V. candicans (V. mustangensis), V. cinerea* var. *tomentosa, V. girdiana*, and *V. monticola* (Fig. 5). Strong resistance to PD occurs in *V. arizonica/candicans*, *V. arizonica/girdiana*, *V. arizonica/monticola* forms.

Fig. 3. Principle Coordinate Analysis constructed with genotypic data from 22 SSR markers on 159 accessions using DARWIN software. The axis 1 and 2 presents 9.13 and 5.74 percent of the variation, respectively

-.4

-.35

-.3

-.25

-.2

-.15

-.1

-.05

.05

.1

.15

.2

.25

.3

.35

.35

.3

.25

.2

.15

.1

.05

-.05

-.1

-.15

-.2

-.25

-.3

-.35

**Axis 1**

**9.13 %**

**Axis 2**

**5.74 %**

*V. aestivalis* like

*V. cinerea* like

*V. arizonica* like

Fig. 4. Grouping of accessions revealed by clustering program STRUCTURE. Representation of genetic composition of species for each accession is represented as a bar chart. Yellow color represents *V. arizonica* like accessions, blue is for *V. cinerea* like and red is for *V. aestivalis* like accessions. It is noted that *V. arizonica* is complex mix of different species and further analysis only with that group separates these species into different clades.



Fig. 5. PCA analysis with only *V. arizonica* like group separated *V. girdiana* (dark brown) and glabrous *V. arizonica* (lime green) from the other groups.

**V.arizonica**

-.5

-.45

-.4

-.35

-.3

-.25

-.2

-.15

-.1

-.05

.05

.1

.15

.2

.25

.3

.35

.3

.25

.2

.15

.1

.05

-.05

-.1

-.15

-.2

-.25

-.3

-.35

-.4

-.45

-.5

-.55

**A14**

**A20**

**ANU05**

**ANU09**

**ANU14**

**ANU18**

**ANU21**

**ANU25**

**ANU42**

**ANU46**

**ANU48**

**ANU50**

**ANU51**

**ANU53**

**ANU56**

**ANU57**

**ANU67**

**ANU77**

**ANU78**

**b40-14**

**b40-61**

**b41-13**

**b43-17**

**b43-57**

**b46-48**

**b47-32**

**C23-94**

**GC5**

**GC6**

**NM03-17SO1**

**PSRUPESTRIS**

**SAZ7**

**SC11**

**SC26**

**SC30**

**SC36**

**SC39**

**SC52**

**TO3-15**

**TX9726**

**TXNM081**

**TXNM083**

**A1**

**A28**

**T10**

**V.arizonica**

**V.arizonica**

**b43-14**

**b47-27**

**b47-33**

**b43-12**

**b40-13**

**b40-34**

**b40-50**

**b43-15**

**b43-36**

**b43-56**

**b47-06**

**V23-98**

**TX67-03**

**b40-29**

**b42-26**

**b47-5**

**b46-43**

**b47-28**

All accessions that are part of this study are being greenhouse tested summer/fall 2013, and results will be available in Fall 2013. The goals of this study are to investigate the phylogeographic diversity of plant material collected from Gulf coast states and the southern US and determine relationships between species, PD resistance and the genetic control of that resistance, so that we can better understand the evolution of resistance and the range of resistance mechanisms and their control.

To determine the inheritance and nature of resistance of the best forms, we made crosses in 2012 to develop breeding lines with four of the most resistant accessions. Small breeding populations were planted in Spring 2013. In 2013, we made additional crosses to expand the existing populations as well as used four new PD resistant accessions to develop breeding populations (Table 4). Seedlings that were generated from 2012 crosses were tested with markers and true to cross seedlings were transferred to the field. Currently these small populations are in the pipeline for greenhouse screen test. All crosses that were made in 2013 will be evaluated in 2014.

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| Table 4. Crosses made in 2013 to develop genetic maps in new accessions from southern US and Mexico germplasm. Crosses 08-319-29 and 08326-61 are female flowered selfed progeny of Zinfandel and Cabernet franc, respectively. F2-35 is also female and a cross of Cabernet Sauvignon x Carignane. |
| Resistant Source/ new or existing | Geographic Origin - Appearance Phenotype | Pure *Vinifera* Types used in 2013 crosses | Estimated # of Seed  |
| ANU5 | Littlefield, AZ | Alicante Bouschet | 250 |
| expands existing | *V. girdiana* |  |  |
| b40-29 | Chihuahua, MX | F2-35 | 1250 |
| expands existing | *V. arizonica* | 08319-29 | 2000 |
| b41-13 | Ciudad Mante, MX | F2-35 | 750 |
| new | *V. arizonica-mustangensis-champinii* |  |  |
| b43-57 | Guadalupe, MX | Malaga Rosada | 1000 |
| new | *V. arizonica-mustangensis-champinii* | Rosa Minna | 900 |
| b46-43 | Big Bend, TX | 08326-61 | 850 |
| expands existing | *V. arizonica glabra-monticola* |  |  |
| b47-32 | Big Bend, TX | F2-35 | 1950 |
| expands existing | *V. arizonica glabra-monticola* | 08326-61 | 70 |
| SC36 | San Diego, CA | Palomino | 350 |
| new | *V. girdiana* | Grenache | 600 |
| T 03-16 | Lahitas, TX | Palomino | 175 |
| new | *V. arizonica* | Grenache | 20 |

**Objective 4.** We have used three categories of sequences (shotgun reads, fosmid reads and 454) to work on the BAC clone H69J14 that carries the PD resistance gene(s). From the assembly of this sequence, we identified 6 copies ranging from 2Kb to 3.1Kb in the resistance region. Copies 1 – 4 are 97-99% similar and differ in size (potentially tandem repeats of one gene), they were up to 78% similar to the four copies of genes from the Pinot noir (PN40024) sequence. We utilized CENSOR software to screen query sequences against a reference collection of repeats to generate a report capable of classifying detected repeats. All four PN40024 genes carry DNA transposons as well as LTR retrotransposon indicating that the region is quite complex.

A detailed comprehensive comparison of the H69J14 clone sequence to the PN40024 sequence is not possible due to major re-arrangement of repetitive elements between the two genomes, and the presence of gaps in the contigs of the H69J14 BAC clone. We are in process of using FGS technology, which helps close these gaps. For this purpose, we identified three overlapping BAC sequences (H15B20, H69J14 and H64M16) that span about 450Kb of the physical sequence. Complete assembly of this region will allow a more precise comparison to susceptible PN40024, which will help identify differences in the expressed and non-expressed regions and help us identify the susceptible allele of the *PdR1b* gene. We have received the partial results of the FGS technology, sequence assembly will be carried out when all data is available.

**LAYPERSON SUMMARY**

A major focus of this project is to broaden the genetic base of PD resistance by searching for and characterizing new forms of PD resistance. Previously, we reported on the screening of 52 accessions of grape species that were collected from across the southern US and northern Mexico. Greenhouse screening of these plants identified 20 new resistant accessions. We expanded this work to over 200 accessions that were acquired from states along the Gulf of Mexico, utilized 22 SSR markers and 14 chloroplast markers to develop fingerprint profiles for them. Analysis with two different programs revealed three major groups. The *V. arizonica* like group was comprised of multiple species with distinct maternal and paternal inheritance. The species within this group are also very distinct from southeastern PD resistant species, once thought to be the only source of PD resistance. Greenhouse screening was completed on subset of genotypes and crosses with 8 new resistant lines were made in 2012 and 2013; the remaining germplasm is in the process of being screened. This germplasm screening provides opportunities to explore and identify resistance loci that may provide different resistance mechanisms allowing us to expand the genetic base of the PD resistance-breeding program. To date, we have utilized 3 different genetic resources to identify PD resistance. Progress was made with b43-17 and b40-14 both of which carry a major locus on chromosome 14, as well as one minor QTL on different chromosomes. For *V. arizonica/candicans* b43-17, minor QTL is identified on chromosome 19 (*PdR2*) and for *V. arizonica* b40-14, minor QTL was identified on chromosome 5. Mapping of a multigenic source of PD resistance from *V. arizonica/girdiana* b42-26 continues – a total of 916 markers were tested, and 170 polymorphic markers (45 more since the previous report) have been added to the entire population of 239 seedlings. We reevaluated the whole population for PD resistance and analysis is in process for the genetic map to get better coverage of all chromosomes, and QTL analysis in b42-26 background.

We plan to combine these multiple resistance sources in our breeding program to ensure broad and durable PD resistance. This project provides the genetic markers critical to the successful classical breeding of PD resistant wine, table and raisin grapes. Identification of markers for *PdR1* has allowed us to reduce the seed-to-seed cycle to 2 years and produce selections that are PD resistant and 97% *vinifera*. These markers have also led to the identification of 6 genetic sequences that may house the PD resistance gene, and which are being tested to verify their function. These efforts will help us better understand how these genes function and could also lead to PD resistance genes from grape that would be available to genetically engineer PD resistance in *V. vinifera* cultivars.

**PUBLICATIONS AND PRESENTATIONS**

**Abstracts**

Bistue C., Agüero C.B., Riaz S., and Walker M.A. 2013. Testing *Vitis arizonica* candidate genes for Pierce’s disease resistance in *Nicotiana tobacum* /SR-1. ASEV 64th National Conference. Monterey, California.

Riaz, S., Tenscher, A., and Walker, M.A. 2013. Phylogeographic analysis of resistance to Pierce’s disease in North American and Mexican species with SSR markers and identification of novel resistance sources. ASEV 64th National Conference. Monterey, California.

**Presentations**

Grape breeding. Napa Valley Vintners. UC Davis, Feb. 27, 2013.

Grape diseases and pests. Wine Executive Program, UC Davis, March 26, 2013

PD resistant wine tasting. Napa County Grape Growers and Winemakers, Oakville, CA April 5, 2013

Sustainable Viticulture. Haas Business School, DNV Top Tech Program, Mondavi Winery, Oakville, CA, April 20, 2013

Pest and disease threats: Decisions and the future of farming. Napa Valley 2030 – Ahead of the Curve, Napa Valley Grape Growers, Napa, May 7, 2013

Marker-assisted selection to optimize grape breeding. Grape Genetics Research Coordination Network. UC Davis, July 11, 2013.

PD resistant wine tasting. Temecula Wine Association, Temecula, CA, July 17, 2013.

PD resistant wine tasting. Healdsburg/Dry Creek Growers and Wineries, Clos du Bois, Healdsburg, CA, July 31, 2013.

**RESEARCH RELEVANCE**

The goal of this research is to explore the genetics of resistance to PD and provide genetic support to our PD resistance breeding of wine, table and raisin grapes. We successfully mapped the resistance genes from a form of *V. arizonica* and used the linked markers to greatly expedite our breeding program. We are now searching for additional forms of PD resistance in other species from a variety of geographic locations across the southern States and Mexico, with the goal of combining resistance from several species together to ensure durable resistance.

**Status of Funds:** These funds are scheduled to be spent by the end of the grant.

**Intellectual Property**: PD resistant varieties will be released through the Office of Technology Transfer (Patent Office) of the University of California, Davis.