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

**Final Report**

**July 2012**

**Report title: Final Report for CDFA Agreement Number 03-0293 Amend 4**

**Project Title:** Breeding Pierce’s disease resistant winegrapes.

**Principal Investigator and Cooperating Staff:** M. Andrew Walker and Alan Tenscher, Dept. of Viticulture & Enology, University of California, One Shields Ave., Davis, CA 95616-8749, [awalker@ucdavis.edu](mailto:awalker@ucdavis.edu), 530-752-0902

**Reporting period:** July 2003 to July 2012

**Introduction**

The Walker lab has a long history of breeding for PD resistance having developed rapid screening techniques for *Xylella fastidiosa* (*Xf)* resistance (Buzkan et al. 2003, Buzkan et al. 2005, Krivanek et al. 2005a 2005b, Krivanek and Walker 2005), and possessing unique and highly resistant *V. rupestris* x *V. arizonica* selections, as well as an extensive collection of southern US grape hybrids, to allow the introduction of extremely high levels of *Xf* resistance into commercial grapes. We have genetically mapped PD resistance from *V. arizonica*/*candicans* b43-17 and have identified very tightly linked markers for use in marker-assisted selection (MAS) (Krivanek et al. 2006, Riaz et al. 2006, Riaz et al. 2007, Riaz et al. 2008, Riaz et al. 2009). We have used these markers to rapidly select at each generation of the backcross breeding program as we increase the percentage of *vinifera* in the hybrid progeny (F1 = 50% *vinifera*; backcross (BC) 1 = 75%; BC2 = 87%; BC3 = 94%; BC4 = 97% *vinifera*). Using aggressive training and growing practices we have been able to force a large portion of each generation to flower in the second year, thus reducing the seed-to-seed generation time to two years. In 2009 we produced about 12,000 seeds at the BC4 97% *vinifera* generation; about half of these germinated and about half of the resulting progeny had markers for *PdR1*. About 2,000 plants were planted from this generation and we began selecting them for fruit quality in the Fall of 2011. The goal has been to introgress *PdR1* into the major winegrape variety types to produce new resistant winegrapes that are similar to internationally recognized, high quality winegrapes. We made crosses to produce about the same number of *PdR1* 97% *vinifera* in 2010 and 2011 and these will fruit in 2012 and 2013, respectively.

The best selections are greenhouse screened so that only the selections with the strongest PD resistance are advanced to wine quality testing. We then propagate the best selections to produce 6 to 8 vine replicates that can be used for micro-vinification. This process has been used to produce PD resistant wines at the 94% (BC3) *vinifera* level and these micro-scale wines have scored well in tasting panels; significantly better than those at the 88% *vinifera* level. The best of the 97% *vinifera* selections will then be multiplied for 100 vine commercial scale testing prior to release.

The next phase of the breeding program will be to incorporate resistance from other sources. *PdR1* is a single gene resistance, which increases its chances of breaking down. We are studying other sources of resistance, both single and multiple gene, and have begun the process of crossing these resistance sources into the *PdR1* lines. The breeding program also screens potential parents and genetic mapping populations for a companion project – “Genetic mapping of *Xylella fastidiosa* resistance gene(s) in grape germplasm form the southern United States”. This project is critical to the success of the next phase of the PD breeding program as it will produce genetic markers to these new forms of resistance, which will accelerate breeding progress and to allow the various sources of resistance to be combined into mulit. Without the markers it would be very difficult to determine whether multiple resistances were combined in one background, since the expression of either gene will be very similar – PD resistant plants. In addition to multiple forms of PD resistance we are also making crosses to introduce powdery mildew resistance into our advanced PD resistant lines. Finally, some of the resistant selections host very low levels of *X. fastidiosa* in their xylem. These plants do not express disease, but if the bacteria moved down into the rootstock it might kill the vine. This possibility stimulated the production of rootstocks with *PdR1* and good resistance to a wide range of nematodes. If the PD resistant selections are grafted on these rootstocks they will be resistant from the roots to the shoot tips.

Over the past 10 years, this breeding program has made hundreds of crosses, produced tens of thousands of seeds, planted and trained thousands of seedlings, and greenhouse tested thousands of plants. It is now ready to begin field and wine testing leading to release of new varieties and to strengthen resistance by complexing multiple forms into one line.

**Objectives**

1. Breed PD resistant winegrapes through backcross techniques using high quality *V. vinifera* winegrape cultivars and *Xf* resistant selections and sources characterized from our previous efforts.

2. Continue the characterization of *Xf* resistance and winegrape quality traits (color, tannin, ripening dates, flavor, productivity, etc.) in novel germplasm sources, in our breeding populations, and in our genetic mapping populations.

**Results – Research highlights**

**2003 - 2004** – Many crosses were made and progeny tested to examine resistance in a range of southern *Vitis* species and southeastern US breeder selections. Table 1 displays the range of crosses made. In this phase of the project we were shifting focus from table grapes to wine grapes. We also made the first crosses to produce PD resistant rootstocks.

**2004 - 2005 –** We increased the number of seedlings and high fruit quality selections we test under our greenhouse screen. This screening is very severe, but material that passes the screen is reliably resistant and dramatically restricts *Xylella fastidiosa* (Xf)movement. We are also co-screening for powdery mildew resistance. The heritability of Xf resistance from a range of resistant southeast US (SEUS) cultivar and species parents is not consistent – some parents produce few resistant offspring, while others produce a large percentage – making careful parental screening very important. MAS for *PdR1* is now being applied to seedling populations from *PdR1* resistant parents (Table 2).

**2005 - 2006 –** Marker-assisted selection is reliably being used for *PdR1* resistance. BC2 (88% *vinifera*) have been produced. In this year we attempted to streamline the greenhouse resistance screen so that less space and time would be required to test plants. However, smaller pots and closer spacing did not produce reliable results compared to our wider spacing, 10 cm square pot, 12 to 16 week assay. This year’s crosses produced about 8,500 seeds – many with >75% *V. vinifera* parentage (Table 3). Evaluation of the 75% vinifera progeny found that the plants were much more *vinifera*-like in appearance and that they were losing their wild species characteristics (Table 4).

**2006 - 2007 –** This year’s crosses were focused on broadening the *V. vinifera* winegrape base in our breeding lines. We produced thousands of seed with 87.5% and 75% *vinifera* progeny (Table 5). Many of our current populations have the *PdR1* allele from F8909-08; we made many crosses this year to include the alternate *PdR1* allele from F8909-17. Crosses were also made to produce a new mapping population for a collaborative project with the USDA-Parlier to allow mapping of PD resistance from the resistant Florida selection BD5-117, which will help with comparative evaluations of PD resistance genes. The best sources of PD resistance allow very low levels of Xf to develop in xylem vessels. If these were grafted onto phylloxera resistant rootstocks, the Xf in them might kill the rootstocks. Thus, we made additional crosses to produce a PD and nematode resistant rootstock, and can use MAS for both *PdR1* and the *Xiphinema index* resistance gene, *XiR1*. A number of 88% *vinifera* were evaluated for growth habit, foliar appearance, fruit characters and the first wines were also made (Table 6a through 6d). These had Syrah and Chardonnay as their last backcross parent.

**2007 - 2008 –** The 2008 crosses (Table 7) were made to: 1) Use the *PdR1* allele from 8909-08 to broaden the *vinifera* winegrape lines at the 94% *vinifera* level; 2) Combine *PdR1* with the powdery mildew resistance gene *Run1* at the 90.6% *vinifera* level; 3) Combine *PdR1* with the LG13 powdery mildew resistance gene *REN1* at the 88% *vinifera* level; 4) Use 8909-17 based resistance with diverse *vinifera* winegrapes to produce resistant progeny at the 88% *vinifera* level; 5) Use the F1 progeny of the homozygous PD resistant b40-14 *V. arizonica* to produce a breeding and mapping population that is 75% *vinifera*; 6) use elite winegrapes to broaden and expand the *V. shuttleworthii* breeding lines producing progeny that are 75% and 88% *vinifera* and 7) Produce rootstocks with *PdR1* and broad-based nematode resistance. Inoculations were made to selections with *PdR1* at the 88% and 75% *vinifera* at our Beringer, Napa County trial. Finally, small-scale wine lots were made from five 88% *vinifera* *PdR1* selections from wine grape backgrounds. Fruit evaluation and must analysis were performed on numerous other promising progeny at this level.

**2008 - 2009 –** The 2009 breeding goals were: 1) create 97% *V. vinifera* seedlings with PD resistance using *PdR1* from *V. arizonica* hybrid– F8909-08; 2) create 75% *V. vinifera* seedlings with PD resistance from *V. arizonica* b40-14 (alternate single gene source of PD resistance; and 3) enlarge the *V. arizonica/girdiana* b42-26 (multigenic resistance to PD) mapping population by remaking the *V. vinifera* F2-35 x b42-26 cross. Five hundred and thirty-three seedlings from breeding lines, mapping populations and PD resistant rootstocks were greenhouse screened for Xf resistance. One hundred and seventy-two table and raisin grape selections were also greenhouse screened, with another 175 under testing. Winegrape selections with *PdR1* at the 87.5% and 75% *vinifera* level in our Beringer, Napa County trial were inoculated and a similar trail using selections at the 94% *vinifera* level was planted. Small-scale wine lots were made from three 94% *vinifera* and five 87.5% *vinifera* *PdR1* selections. Fruit evaluation and juice analysis were performed on numerous other promising progeny at the 94% *vinifera PdR1* level. Finally, 32 crosses with 94% *vinifera* *PdR1* selections yielded about 11,500 seeds, which will sprout in 2010 to produce the 97% *vinifera PdR1* generation (Table 8).

**2009 - 2010 –** The 2010 crosses (Table 9) were made to increase the number of 97% vinifera progeny with PdR1. Seedlings from these crosses will begin fruiting in 2012. We also made crosses to bring PdR1 from b43-17 without the *V. rupestris* parentage from F8909-08. This effort is now in the BC3 generation and we will make wines from select progeny to determine whether the *V. rupestris* parentage (associated with very dark juice and strong peppery flavors) has long term detrimental effects to wine quality. We also want to test whether the *V. rupestris* parentage influences the level of PD resistance. Many selections were greenhouse screened for resistance to PD (Table 10) and wines were again from *PdR1* selections at the 88 and 94% *vinifera* level (Table 11).

**2010 - 2011 –** The first of the 97% *vinifera* *PdR1* seedlings began fruiting in 2011 (Table 12). This is the generation we plan to select from for release. We selected 77 as worthy of wine testing on a 6 to 8 vine scale and from these we will select for 100 vine commercial scale testing. Crosses were made to BC5 generation PdR1 progeny, to further backcrossing with non-*V. rupestris* progeny, and to advance resistance from b42-26 an excellent but multi-genic form of PD resistance (Table 13). We planted a new plot in Healdsburg with 94% *vinifera* *PdR1* selections and added new materials to our plot in Yountville, and have distributed cuttings of 87% *vinifera* *PdR1* resistant selections to Texas for a field plot near Fredericksburg. This plot augments trials with the same selections in Auburn, AL, and Galveston, TX. Small-scale wines were made from 94% *vinifera PdR1* selections grown in the UCD vineyards and they were better than Chardonnay and Cabernet Sauvignon, and the PD resistant cultivars Lenoir and Blanc du Bois made with the same quantities of fruit.

**2011 - 2012 –** Table 13 summarizes our PD resistant wine type seedling production, MAS testing and planting from crosses made in 2011. Table 13a details the addition of two new elite *vinifera* backgrounds into our existing 97-98% *vinifera* PD resistant groups in the *PdR1b* line. Since the beginning of our GH screening, we have observed that after greenhouse inoculation *V. arizonica/candicans* b43-17 always has lower Xf titer than any of its descendants. Table 13b shows two small populations developed to evaluate the b43-17 resistance line in the absence of the major *PdR1* resistance locus. In parallel with our continued mapping efforts to identify resistance loci in the b42-26 line, we have been using our greenhouse screen to identify particularly resistant backcross individuals. 07344A-35 is one such genotype having tested highly resistant on three separate occasions; it’s now at the 88% *vinifera* level (Table 13c). Similarly we took the opportunity to cross this same b42-26 resistant individual with one of our most resistant 97% PdR1b resistant genotypes to create a small test population to evaluate the efficacy of combining these two seemingly different resistant lines (Table 13d).

Table 14a summarizes the estimated number of seeds produced from 10 different crosses that advance the *PdR1a* allele from b43-17 to the 97% *vinifera* level. Previously we identified a PD resistance locus *PdR1c* from *V. arizonica* b40-14 that maps to the same region of LG14 as *PdR1* from b43-17. The geographic separation and different appearance of these plants suggest that this resistance that maps similarly may be different and we are pursuing *PdR1c* as a future breeding resource. Table 14b summarizes the 12 crosses from this background. The 08-331 set bypasses the potential impact of *V. rupestris* on resistance, which is present in the 09-367 set. Both are being retained until we more fully understand the inheritance of PD resistance from b40-14. Table 14c is a remake of the 86% *vinifera* *PdR1b* x b42-26 line pyramiding cross made last year. These seeds will increase the population size should greenhouse screen results from the initial group prove promising. In the BD5-117 resistance line we see definite differences in Xf titer in backcrosses to *vinifera*,but the levels are never as low as our most resistant *PdR1* individuals. We have created a group of selfed and intercrossed individuals with very good wine variety appearance to advance this resistance source. We also are advancing a very promising source of resistance from *V. shuttleworthii*, with 08-365 an unusual individual that is as resistant as our most resistant *PdR1* genotypes (Table 14d). We have selfed one such particularly resistant BC1 individual to find out whether there is any opportunity to exploit this resistance source (Table 14e). The PD resistance in BD5-117 descends in part from *V. shuttleworthii*. Three crosses were also made to combine resistance from *V. shuttleworthii* and BD5-117 (Table 14f).

Table 15 provides a list of PD GH screens initiated and\or completed over the last year. Group A tests genotypes in which *PdR1a* and *PdR1b* alleles are combined; results are due soon. Group B tested BC1 and BC2 progeny and their parents in the Haines City *V. shuttleworthii* line. Results from this screen were used to select the resistant parents for crosses shown in Tables 14e and 14f. Of the 54 accessions tested in the *V. arizonica* Group C, we selected 5 highly PD resistant individuals from 4 diverse geographic locations for new mapping crosses made in 2012. A table of crosses and estimated seeds has been provided there (Table 16). Results from group D, were used to select the three PD resistant rootstocks advanced for possible release (Table 17). Group E lists further efforts with resistance from *M. rotundifolia* and is in conjunction with studies of this group’s powdery mildew resistance. Group F tests the last of our elite 94% *PdR1b* genotypes and the most best looking progeny from parents used in crosses in Tables 14d and 14f and repeated greenhouse screening for the five 94% *vinifera* *PdR1b* genotypes advanced for possible release (Table 17). Our 97% *vinifera* level *PdR1b* resistance line fruited for the first time in 2011. The phenotypically most promising selections were tested in Group G. This was an extremely severe test and the 9 genotypes were highly resistant and will be advanced to larger scale wine testing. Group H is the third greenhouse screen of a subset of the b42-26 (multi-genic PD resistance) mapping population. Genetic markers in this line are essential as we try to pyramid resistance lines as in the crosses made in Table 14c.

Table 17 lists promising PD resistant selections being considered for release. The release process involves passing a severe greenhouse screen multiple times. The number following the “R” in the “# GH Screens” column notes how many times a selection has passed a severe greenhouse screen. These selections also have desirable viticultural traits and have potential for quality wine production. The production of small lot wines from multiple vines field trials in Davis and in PD hot spots in North Coast complete the evaluation process prior to commercial scale wine lots. PD resistant scions need PD resistant rootstocks: 03300-099; 08314-15; and 08314-46. Screening has found that the latter two have very good nematode resistance as well as PD resistance.

We inoculated our Beringer field trial this year on 5/23/2012. If the favorable growing conditions continue we plan to make two small wine lots from this trial in fall 2012.

**Publications**

Doucleff, M., Y. Jin and M.A. Walker. 2003. Mapping *Xiphinema index* resistance in *V. rupestris* x *M. rotundifolia* hybrids. Acta Horticulturae 603:79-81.

Krivanek, A.F. and M.A. Walker. 2003. Progress in understanding the genetics of resistance from the grape *Muscadinia rotundifolia* to the bacterial pathogen *Xylella fastidiosa*. Acta Horticulturae 603:429-432.

Buzkan, N., L. Kocsis, A.F. Krivanek, and M.A. Walker. 2003. Developing rapid evaluations for resistance to *Xylella fastidiosa*, the causal agent of Pierce’s disease. Acta Horticulturae 603:433-440.

Buzkan, N. A.F. Krivanek, A. Eskalen and M.A. Walker. 2003. Improvements in sample preparation and polymerase chain reaction detection techniques for *Xylella fastidiosa* in grapevine tissue. American Journal of Enology and Viticulture 54:307-312.

Doucleff, M, Y. Jin, F. Gao, S. Riaz, A.F. Krivanek and M.A. Walker. 2004. A genetic linkage map of grape utilizing *Vitis rupestris* and *Vitis arizonica*. Theoretical and Applied Genetics 109:1178-1187.

Buzkan, N. L. Kocsis and M.A. Walker. 2005. Detection of *Xylella fastidiosa* from resistant and susceptible grapevine by tissue sectioning and membrane entrapment immunofluorescence. Microbiological Research 160:225-231.

Krivanek, A.F., J.F. Stevenson and M.A. Walker. 2005. Development and comparison of symptom indices for quantifying grapevine resistance to Pierce’s disease. Phytopathology 95:36-43.

Krivanek, A.F. and M.A. Walker. 2005. *Vitis* resistance to Pierce’s disease is characterized by differential *Xylella fastidiosa* populations in stems and leaves. Phytopathology 95:44-52.

Lin, H, E.L. Civerolo, R. Hu, S. Barros, M. Francis and M.A. Walker. 2005. Multi-locus simple sequence repeat (SSR) markers for differentiating strains and evaluating genetic diversity of *Xylella fastidiosa*. Applied Environmental Microbiology 71:4888-4892.

Krivanek, A.F., T.R. Famula, A. Tenscher and M.A. Walker. 2005. Inheritance of resistance to *Xylella* *fastidiosa* within a *Vitis rupestris* x *Vitis arizonica* hybrid population. Theoretical and Applied Genetics 111:110-119.

Krivanek, A.F., S. Riaz and M.A. Walker. 2006. The identification of *PdR1*, a primary resistance gene to Pierce’s disease in *Vitis*. Theoretical and Applied Genetics 112:1125-1131.

Ruel, J.J. and M.A. Walker. 2006. Resistance to Pierce’s Disease in *Muscadinia rotundifolia* and other native grape species. American Journal of Enology and Viticulture 57:158-165.

Riaz, S., A.F. Krivanek, K. Xu and M.A. Walker. 2006. Refined mapping of the Pierce’s disease resistance locus, *PdR1*, and *Sex* on an extended genetic linkage map of *Vitis rupestris* x *V. arizonica*. Theoretical and Applied Genetics 113:1317-1329.

Doddapaneni, H., J. Yao, H. Lin, M. A. Walker and E.L. Civerolo. 2006. Analysis of the genome-wide variations among multiple strains of the plant pathogenic bacterium *Xylella fastidiosa*. BMC Genomics. Available: http://www.biomedcentral.com/1471-2164/7/225

Lin, H., H. Doddapanneni, Y. Takahashi and A. Walker. 2007. Comparative analysis of ESTs involved in grape responses to *Xylella fastidiosa* infection. BMC Plant Biol. 7:8, doi:10.1186/1471-2229-7-8.

Fritschi, F.B., H. Lin and M.A. Walker. 2007. *Xylella fastidiosa* population dynamics in grapevine genotypes differing in susceptibility to Pierce’s disease. American Journal of Enology and Viticulture 58:326-332.

Riaz, S., S. Vezzulli, E.S. Harbertson, and M.A. Walker. 2007. Use of molecular markers to correct grape breeding errors and determine the identity of novel sources of resistance to *Xiphinema index* and Pierce’s disease. American Journal of Enology and Viticulture 58:494-498.

Fritschi, F.B., H. Lin and M.A. Walker. 2008. Scanning electron microscopy reveals different plant-pathogen interaction pattern in four *Vitis* genotypes infected with *Xylella fastidiosa*. Plant Disease 92:276-286.

Riaz, S., A.C. Tenscher, J. Rubin, R. Graziani, S.S. Pao and M.A, Walker. 2008. Fine-scale genetic mapping of two Pierce’s disease resistance loci and a major segregation distortion region on chromosome 14 of grape. Theoretical and Applied Genetics 117:671-681.

Lowe, K.M., S. Riaz and M.A. Walker. 2008. Variation in recombination rates across *Vitis* species. Tree Genetics and Genomes 5:71-80.

Stover, E., S. Riaz and M.A. Walker. 2008. PCR screening for *Xylella fastidiosa* in grape genebank accessions collected in the southeastern United States. American Journal of Enology and Viticulture 59:437-439.

Riaz, S., A.C. Tenscher, R. Graziani, A.F. Krivanek, D.W. Ramming and M.A. Walker. 2009. Using marker-assisted selection to breed Pierce’s disease resistant grapes. American Journal of Enology and Viticulture 60:199-207

Cheng, D.W., H. Lin, M.A. Walker, D.C. Stenger, and E.L. Civerolo. 2009. Effects of grape xylem sap and cell wall constituents on in vitro growth, biofilm formation, and cellular aggregation of *Xylella fastidiosa*. European Journal of Plant Pathology 125:213-222.

Cheng, D.W., H. Lin, Y. Takahachi, M.A. Walker, E.L. Civerolo and D.C. Stenger. 2010. Transcriptional regulation of the grape cytochrome P450 monooxygenase gene CYP736B expression in response to *Xylella fastidiosa* infection. BMC Plant Biology 10:135.

Yang, L., H. Lin, Takahashi, Y., Chen, F., Walker, M.A. and Civerolo, E. 2011. Proteomic analysis of grapevine stem in response to *Xylella fastidiosa* inoculation. Physiological and Molecular Plant Pathology 75:90-99.

Viana, A.P., S. Riaz and M.A. Walker. 2011. Evaluating genetic diversity and optimizing parental selections in a segregating table grape population. American Journal of Enology and Viticulture 62:285-290.

Riaz, S., R. Hu and M.A. Walker. 2012. A framework genetic map of *Muscadinia rotundifolia*. Theoretical and Applied Genetics 123: DOI 10.1007/s00122-012-1906-7

**Lay Person Summary**

The goal of this breeding program was to utilize single gene resistance from *V. arizonica/candicans* b43-17 to attain a backcross 4 generation (97% *vinifera*) as quickly as possible. We were able to accomplish this goal because of the genetic markers and molecular tools generated by our companion project “Genetic mapping of *Xylella fastidiosa* resistance gene(s) in grape germplasm from the southern United States”. The key advance within that program was the genetic mapping of the single gene resistance in b43-17 (*PdR1*), which has allowed us with aggressive viticultural training to reduce the seed-to-seed cycle to 2 years and rapidly introgress PD resistance into high quality *vinifera* wine grapes. We evaluated fruit from the first 97% *vinifera* progeny last Fall (many more expected to fruit this year) and will make wines from some of these selections this Fall. We will send potential releases to Foundation Plant Services for certification this Winter and next Spring we will expand some to plantings so that they are capable of producing commercial scale wines. While advancing this source of resistance, we have also advanced resistance from several other backgrounds to allow the combination of alternative resistance sources into one background, in an attempt to provide more durable resistance. A related project is producing powdery mildew resistant winegrapes to allow the combination of powdery mildew resistance with PD resistance.

**Relevance**

The ultimate solution to PD is the deployment of resistant varieties. Resistant varieties have been produced in the past, but their quality has not been competitive with *vinifera* winegrapes. The discovery of strong single gene resistance in forms of *V. arizonica* allowed us to attain a much greater percentage of *vinifera* than previous breeding efforts. We have selections that are ready to be used in blends with traditional winegrapes and additional selections that could be used to produce varietal wines. This breeding program has also supplied the resistant germplasm, vineyard maintenance, and greenhouse screening to our companion projects mapping and characterizing PD resistance genes, and for David Ramming’s PD resistant table and raisin grape program at the USDA-Parlier.

**Intellectual Property**: The resistance genes identified in this research will be handled by PIPRA, UC Davis.

Table 1. Seeds from 2004 crosses to produce Xf resistant wine grapes and the number of seedlings planned for 2005 field planting.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Female Parent | Male Parent | Resistance Source | No. Seeds | Seedlings to field |
| BO2SG | Cabernet Sauvignon | *V. smalliana* | 376 | 75 |
| BO2SG | Carignane | *V. smalliana* | 196 | 75 |
| BO2SG | Sauvignon blanc | *V. smalliana* | 404 | 125 |
| BO3SG | Chambourcin | *V. smalliana-simpsonii* | 412 | 50 |
| BO3SG | Petite Sirah | *V. smalliana-simpsonii* | 419 | 50 |
| BO3SG | Cabernet Sauvignon | *V. smalliana-simpsonii* | 371 | 25 |
| BO3SG | Carignane | *V. smalliana-simpsonii* | 350 | 25 |
| BO3SG | Sauvignon blanc | *V. smalliana-simpsonii* | 223 | 125 |
| F2-7 | Midsouth | *V. champinii* | 522 | 50 |
| F2-7 | F8909-08 | *V. arizonica – candicans* | 4,500 | 300 |
| F2-7 | F8909-17 | *V. arizonica – candicans* | 300 | 300 |
| F2-35 | b43-17 | *V. arizonica-candicans* | 323 | 125 |
| F2-35 | b43-36 | *V. arizonica* | 141 | 100 |
| F2-35 | b43-56 | *V. arizonica* | 56 | 25 |
| F2-35 | Midsouth | *V. champinii* | 522 | 75 |
| NC-11J | UCD0124-01 | *M. rotundifolia*-SEUS complex | 175 | 175 |
| UCD0110-050 | UCD01124-01 | SEUS complex x SEUS complex | 750 | 250 |
| Midsouth | Midsouth | *V. champinii* | 500 | 150 |
| NC6-15 | Sauvignon blanc | *M. rotundifolia* | 50 | 25 |
| Total |  |  | 10,590 | 2,125 |







**Table 5.** 2007 crosses and numbers of seed produced.

|  |  |  |  |
| --- | --- | --- | --- |
| Resistant Type | *Vinifera* Parent of Resistant Type | *Vinifera* Types used in 2007 crosses | # Seeds Produced |
| 1a. Monterrey *V. arizonica/candicans* resistance source (F8909-08) to produce progeny with 93.75% *V. vinifera* parentage. | | | |
| U0501 | Syrah | F2-7, F2-35 | 478 |
| U0502 | Chardonnay | F2-7, F2-35 | 2,769 |
| U0503 | Sauvignon blanc | Chardonnay, Palomino, Semillon | 126 |
| U0505 | Cabernet Sauvignon | Chardonnay, F2-7, LCC, Merlot, Palomino, Petite Syrah | 3,229 |
| 1b. Monterrey *V. arizonica/candicans* resistance source (F8909-08) to produce progeny with 87.5% *V. vinifera* parentage | | | |
| 05310 | Alicante Bouschet | Burger, Carignane, LCC | 1,666 |
| 05312 | Cabernet Franc | Zinfandel | 194 |
| 05317 | Tempranillo | Burger, LCC | 371 |
| 05319 | Zinfandel | Cabernet Franc, LCC | 144 |
| A81-17 | A38-7 | Carignane, Grenache noir, LCC | 705 |
| 1c. Monterrey *V. arizonica/candicans* resistance source (F8909-08) and *Run1* powdery mildew resistance. | | | |
| U0501, U0504 | Syrah | e-series, e78 and e88 allele patterns | 499 |
| U0502 | Chardonnay | e-series, e78 and e88 allele patterns | 837 |
| U0505 | Cabernet Sauvignon | e-series, e78 and e88 allele patterns | 642 |
| A81-17 | A38-7 | e-series, e78 allele pattern | 603 |
| 1d. Monterrey *V. arizonica/candicans* resistance source (F8909-08) and *Vitis* PM resistance source. | | | |
| U0505, A81-17 | Cabernet Sauv, A38-7 | Villard blanc | 348 |
| 1e. Monterrey *V. arizonica/candicans* resistance source (F8909-17 allele) to produce progeny with 75% *V. vinifera*. | | | |
| 04373-02 | F2-35 (Cab x Carignane) | Alicante Bouschet, Aligote, Carignane, Chardonnay, Zinfandel | 597 |
| 04373-08 | F2-35 (Cab x Carignane) | Aligote, Cabernet Franc, Carignane | 938 |
| 04373-64 | F2-35 (Cab x Carignane) | Grenache noir | 293 |
| 1f. Other resistance sources. R89 is 50% *vinifera*, 25% resistance source. 05347 is 75% *vinifera* and 25% resistance source | | | |
| R89 (b40-14) | NR | Airen | 238 |
| 05347 (b42-26) | F2-35 | Aligote, Chardonnay, Grenache noir, Zinfandel | 1,877 |
| 1g. Rootstock crosses to combine PD and nematode resistance. | | |  |
| 9621-257 | 9365-85 |  | 653 |
| 9365-43 | 9621-161 |  | 112 |

**Table 6a.** Phenotypic observations of reference varieties and select progeny with the *PdR1* resistance source.

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Genotype | Parentage | Percent *vinifera* | 2007 Bloom Date | Berry Color | Berry Size (g) | Ave Cluster Wt. (g) | Ripening Season | Prod 1=v low 9=vhigh |
| Cab. Sauv. | Cab. Franc x S. blanc | 100% | 5/20/07 | B | 1.0 | 168 | mid-late | 6 |
| Pinot noir | Historic | 100% | 5/7/07 | B | 1.1 | 259 | Early | 6 |
| U0501-12 | A81-138 x Syrah | 87.5% | 5/7/07 | B | 1.0 | 90 | mid-late | 4 |
| U0502-01 | A81-138 x Chardonnay | 87.5% | 5/1/07 | B | 1.6 | 128 | mid-late | 4 |
| U0502-10 | A81-138 x Chardonnay | 87.5% | 5/1/07 | B | 1.4 | 160 | very early | 7 |
| Lenoir | *V. aestivalis* hybrid | <50% | 5/12/07 | B | 0.8 | 201 | Late | 7 |
| Midsouth | DGxGalibert 255-5 | <50% | 5/5/07 | B | 2.2 | 211 | mid-late | 6 |

**Table 6b.** Analytical evaluation of reference varieties and advanced selections with the *PdR1* resistance source. Diglucoside anthocyanins were detected in Midsouth and Lenoir. Juice analysis courtesy of ETS Laboratories, St. Helena, CA.

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Genotype | L-malic acid (g/L) | °Brix | potassium (mg/L ) | pH | TA (g/100mL) | YAN (mg/L (as N) | catechin (mg/L) | tannin (mg/L) | Total antho-cyanins (mg/L) |
| Cab. Sauvignon | 2.19 | 24.9 | 2460 | 3.65 | 0.62 | 227 | 59 | 250 | 404 |
| Pinot noir | 2.43 | 26.5 | 2190 | 3.83 | 0.49 | 279 | 321 | 842 | 568 |
| U0501-12 | 4.20 | 29.4 | 2900 | 3.87 | 0.68 | 420 | 88 | 802 | 979 |
| U0502-01 | 2.90 | 25.9 | 2530 | 3.77 | 0.61 | 301 | 91 | 564 | 380 |
| U0502-10 | 4.92 | 23.7 | 2220 | 3.48 | 0.85 | 301 | 87 | 588 | 845 |
| Lenoir | 4.32 | 26.9 | 2920 | 3.67 | 0.75 | 164 | 195 | 341 | 1801 |
| Midsouth | 4.60 | 18.2 | 2220 | 3.49 | 0.81 | 278 | 32 | 230 | 971 |

**Table 6c.** Sensory evaluation of reference varieties and advanced selections with the *PdR1* resistance source.

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Genotype | Juice Hue | Juice Intensity | Juice Flavor | Skin Flavor | Skin Tannin (1=low, 4= high) | Seed Color (1=gr, 4= br) | Seed Flavor | Seed Tannin (1=high, 4= low) |
| Cab. Sauv. | pink-brown | light-med | fruity-CS | fruit jam | 2 | 3 | nutty-full | 4 |
| Pinot noir | pink-brown | medium | hay, honey | mildly fruity | 1 | 4 | spicy | 4 |
| U0501-12 | red | med-dark | fruity | fruit jam | 2 | 4 | neutral | 2 |
| U0502-01 | pink-brown | medium | fruity-PN | sweet fruit | 1 | 3 | spicy | 1 |
| U0502-10 | pk-red-orng | med-dark | slight vegetal | mildly fruity | 1 | 4 | nutty,spicy | 1 |
| Lenoir | red | dark | mildly fruity | fruity | 1 | 4 | nutty | 1 |
| Midsouth | red-orange | med-dark | veg-fruity | neutral | 1 | 4 | neutral | 4 |

**Table 6d.** 11/1/07 tasting results of 2007 vintage wine rated on a 1= poor to 5 = very good scale. There were 9 tasters from the faculty and staff at UCD.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Variety/  Selection | Group Total | Low Score | High Score | Descriptors: color; aroma; flavor and texture |
| U0501-12 | 33.5 | 2 | 4.5 | dark purple; grapy, smoky, blueberry; warm, chocolate, rich, balanced, structured |
| U0502-07 | 32 | 2.5 | 4 | dark purple; grapy, earthy-smoky; rich, good structure & balance |
| Cabernet Sauvignon | 27 | 2 | 5 | red with hint of brown; herbal, weedy, bell pepper; warm, flat, with good tannin structure |
| U0502-10 | 27 | 1 | 5 | dark purple; bright red fruit, odd herbal-plastic note; non-vinifera flavor, okay structure |
| Lenoir | 26 | 2 | 4.5 | dark purple-black; blackberry, dried fig, slightly weedy, odd non-vinifera herbal character; lacks structure |
| U0502-01 | 24 | 1.5 | 4 | light-medium red with hint of brown; candy, red fruit; moderate body, slightly earthy, oxidized |
| Pinot noir | 20 | 1 | 3.5 | light pink-red; simple red fruits; odd vegetal, cherry, light |
| Midsouth | 18.5 | 1 | 3 | red with slight brown edge; vegetal, oxidized, simple |





Table 9. Crosses made in 2010.

|  |  |  |  |
| --- | --- | --- | --- |
| Resistant Type | *Vinifera* Parent\grandparent of Resistant Type | *Vinifera* Types used in 2010 crosses | Estimated # of Seed |
| 9a. Monterrey *V. arizonica/candicans* resistance source (F8909-08) to produce progeny with 96.875% *V. vinifera* parentage. F2-35 is 100% *vinifera* cross of Cabernet Sauvignon x Carignane. | | | |
| 07355-020 | Petite Sirah\Cabernet Sauvignon | Barbera | 85 |
| 07370-028 | F2-35\Chardonnay | Chardonnay, Riesling | 750 |
| 07371-020 | F2-35\Chardonnay | Barbera | 350 |
| 07355-075 | Petite Sirah\Cabernet Sauvignon | Muscat blanc (Maternal Parent) | 500 |
| 07329-037 | Chardonnay | Muscat blanc (Maternal Parent) | 75 |
| 07370-084 | F2-35\Chardonnay | Viognier (Maternal Parent) | 150 |
| 07713-051 | F2-35\Chardonnay | Viognier (Maternal Parent) | 150 |
| 07355-075 | Petite Sirah\Cabernet Sauvignon | Alicante Bouschet (Maternal Parent) | 75 |
| 9b. b43-17 *V. arizonica/candicans PdR1a*resistance source avoiding *V. rupestris* from F8909-08 to produce progeny with 93.75% *V. vinifera* parentage. | | | |
| 08329-035 | Tannat, Chenin blanc | Cabernet Sauvignon | 85 |
| 08329-074 | Tannat, Chenin blanc | Cabernet Sauvignon, Carignane | 900 |
| 08329-095 | Tannat, Chenin blanc | Cabernet Sauvignon | 240 |
| 9c. Crosses to the b42-26 *V. arizonica/girdiana* resistance source to produce progeny that are 75% *vinifera* and 25% resistant. | | | |
| 07344A-09 | Grenache | Carignane | 225 |
| 07344A-11 | Grenache | Carignane, Cabernet Sauvignon, Chardonnay | 315 |
| 07344A-12 | Grenache | Carignane | 180 |
| 07344A-15 | Grenache | Carignane | 360 |
| 07344A-25 | Grenache | Carignane | 360 |
| 07344A-32 | Grenache | Carignane | 180 |
| 07344A-33 | Grenache | Carignane, Cabernet Sauvignon | 180 |
| 07344A-51 | Grenache | Carignane | 225 |
| 07344A-54 | Grenache | Carignane, Cabernet Sauvignon | 270 |
| 07344A-56 | Grenache | Carignane, Cabernet Sauvignon | 270 |
| 07344A-61 | Grenache | Carignane, Cabernet Sauvignon | 360 |
| 9d. Cross to increase the 07344 b42-26 75% *vinifera* for a possible mapping population. | | | |
| 05347-02 | F2-35 | Grenache | 760 |

Table 10. Groups of plants greenhouse screened for *X. fastidiosa* resistance.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Group | Genotypes | # Genotypes | Inoculation Date | ELISA Date | Resistance Source(s) |
| A | 07744 Mapping population | 39 | 12/16/09 | 4/2/09 | b40-14 |
| B | AW spacing trial | 10 | 1/15/09 | 5/21/09 | F8909-08 |
| C | 07386 Mapping population | 40 | 2/3/09 | 5/21/09 | b40-14 |
| D | 07744 mapping population | 64 | 2/12/09 | 5/21/09 | b40-14 |
| E | 2007 cross families #1 | 67 | 4/21/09 | 8/13/09 | F8909-08 |
| F | 9621 recomb, retest and untested | 72 | 4/21/09 | 8/13/09 | b34-17, b42-26 |
| G | 04191 mapping population #2 | 123 | 10/13/09 | 1/21/10 | F8909-17 |
| H | 04191 mapping population #1 | 51 | 11/24/09 | 2/25/10 | F8909-17 |
| I | PD Rootstocks | 23 | 11/24/09 | 2/25/10 | b43-17 |
| J | 2009 PDR & Vinifera | 50 | 11/24/09 | 2/25/10 | F8909-08 |
| K | 2007 Cross Families #2 | 68 | 12/8/09 | 3/9/10 | F8909-08 |
| L | Xf Strain Trial | 6 | 3/30/10 | 7/6/10 | F8909-08 |
| M | 2007 Cross Families #3 | 145 | 4/13/10 | 7/22/10 | F8909-08 |
| N | PD Rootstocks Retest | 35 | 6/8/10 | 9/7/10 | F8909-08 |
| O | 08 PD Stocks & Recombinants | 22 | 7/15/10 | 10/14/10 | F8909-08 |

Table 11. Results of a blind tasting of 2008 & 2009 vintage wines Note that the 94% *vinifera* PD resistant hybrids faired better this year that the classic vinifera varieties.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Wine Name | % *vinifera* | Total | Max | Min | 12/09/08 Consensus Descriptors: color; aroma; flavor-texture |
| 2009 Vintage White Wines | | | | | |
| 07713-51 | 94% | 20.5 | 4.5 | 2 | straw yellow; honey dew, blossom, Viognier; warm, full, round, touch phenolic |
| Blanc du Bois | ~66% | 18.0 | 4 | 2 | straw yellow; aromatic, floral; simple, tart, green |
| U0502-20 | 88% | 16.5 | 4.5 | 2 | pale yellow; gooseberry, grassy; tart, slightly thin |
| Wine Name | % *vinifera* | Total | Max | Min | 12/09/08 Consensus Descriptors: color; aroma; flavor-texture |
| Chardonnay | 100% | 11.0 | 3 | 1 | med yellow; vinous; buttery, spice, course, lacks balance |
| 2009 Vintage Red Wines | | | | | |
| U0502-10 | 88% | 21.5 | 5 | 2 | dark red-purple; blackberry, current, licorice; cola, low tannin |
| 07355-75 | 94% | 20.3 | 4 | 2.75 | dark inky; stewed dark fruit, chocolate; tannic but lacks body |
| U0505-35 | 88% | 18.8 | 4 | 2 | dark inky; blackberry, black fruit; grapy, tannic |
| U0502-26 | 88% | 18.0 | 4 | 2 | dark purple; grapy, ripe fruit, black olive; black fruit, current; structured, good weight |
| 07355-12 | 94% | 18.0 | 4 | 2 | dark almost black; dark fruit, current, ripe; black pepper, slightly hard tannins |
| U0501-12 | 88% | 15.8 | 5 | 1 | medium purple; fruit leather, strawberry; red fruit, slightly thin |
| Cabernet Sauvignon | 100% | 13.0 | 3.5 | 1 | med red-purple; veggie, cooked; cooked veggie, thin |
| Lenoir | unknown | 12.0 | 3 | 1 | med-dark w\ brown edge; porty, jam, pepper; simple, lacks tannin |
| Barbara | 100% | 11.5 | 3.5 | 1 | light-med; strawberry jam, candied; overripe, lacks weight, slightly bitter |



|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Table 13. 2011 winegrape crosses, numbers of seedlings produced, marker tested, and planted to the field. | | | | | |
| Resistant Type | *Vinifera* Parent\grandparent of Resistant Type | *Vinifera* Types used in 2011 crosses | No. Sdlgs Produced | No. Sdlgs to MAS Test | No. Sdlgs to Field |
| 13a. Monterrey *V. arizonica/candicans* resistance source (F8909-08) to produce progeny between 96.9% and 98.4% *V. vinifera* parentage. F2-35 is 100% vinifera cross of Cabernet Sauvignon x Carignane. | | | | | |
| 07355-020 | Petite Sirah\Cabernet Sauvignon | Nero d'Avola | 277 | 210 | 104 |
| 07370-039 | F2-35\Chardonnay | Nero d'Avola | 303 | 150 | 62 |
| 09-331 | Zinfandel\Petite Sirah | Nero d'Avola, Pinot blanc | 223 | 140 | 63 |
| 13b. Monterrey *V. arizonica/candicans* resistance source (b43-17) to produce progeny with 75% *V. vinifera* parentage for minor PDR gene discovery. | | | | | |
| 04373-02 | F2-35 | Pinot blanc | 122 | 50 | 25 |
| 04373-22 | F2-35 | Pinot blanc | 132 | 50 | 18 |
| 13c. Crosses to the b42-26 *V. arizonica* resistance source to produce progeny that are 87.5% vinifera and 12.5% the resistance source. | | | | | |
| 07344A-35 | Grenache | F2-35 | 53 | - | 25 |
| 13d. Cross made to pyramid *PdR1b* Monterrey *V. arizonica/candicans* and b42-26 *V. arizonica* resistance lines to produce progeny and 86% *vinifera*. | | | | | |
| 09-331 | Zinfandel\Petite Syrah | Grenache\F2-35 | 171 | - | 105 |

|  |  |  |  |
| --- | --- | --- | --- |
| Table 14. PD crosses made in 2012. | |  |  |
| Resistant Type | *Vinifera* Parent\grandparent of Resistant Type | *Vinifera* Types used in 2012 crosses | Estimated # of Seed |
| 14a. Monterrey *V. arizonica/candicans* resistance source *PdR1a* (F8909-17) to produce progeny with 97% *vinifera* parentage. 08-319 and 08-326 are selfs of Zinfandel and Cabernet Franc. | | | |
| 08-312, 08-318 | Cabernet Sauvignon, Carignane | 08-319, 08-326, Cabernet Sauvignon, Riesling, Zinfandel | 1565 |
| 14b. Chihuahua *V. arizonica* resistance source *PdR1c* b40-14 to produce progeny with 88% *vinifera* parentage. The 08331 line has free of *V. rupestris* in its heritage | | | |
| 08-331 | Tannat | 08319, 08326, Grenache, Zinfandel | 430 |
| 09-367 | Cabernet Sauvignon | Carignane, Grenache, Palomino, Zinfandel | 525 |
| 14c. Cross made to pyramid *PdR1b* (F8909-08) Monterrey *V. arizonica/candicans* and b42-26 *V. arizonica* resistance lines to produce progeny 85.9% *vinifera*. | | | |
| 09-331 | Zinfanel\Petite Syrah | Grenache\F2-35 | 530 |

Table 14. Continued

|  |  |  |  |
| --- | --- | --- | --- |
| 14d. Cross made to self the BD5-117 SEUS resistance lines to produce progeny approximately 75% *V. vinifera*. F2-7 is a cross of Cabernet Sauvignon x Carignane and 100% *V. vinifera.* | | | |
| 03-182 | F2-7 | Selfed & Intercrossed | 1190 |
| 14e. Cross made to self the Haines City *V. shuttleworthii* resistance lines to produce progeny 75 % *V. vinifera*. | | | |
| 08-364 | Tannat | Selfed | 125 |
| 14f. Crosses made to the BD5-117 SEUS and Haines City *V. shuttleworthii* resistance lines to produce progeny approximately 75% *vinifera*. | | | |
| 03-182 | F2-7 | 08364 (Tannat), 08352 (Cabernet Sauvignon) | 180 |

Table 15. Populations and selections that have been or will be greenhouse screened in 2012.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Group | Genotypes | # Genotypes | Inoculation Date | ELISA Sample Date | Resistance Source(s) |
| A | PdR1a & PdR1b together | 122 | 1/13/2011 | 4/14/2011 | b43-17 |
| B | Haines City BC1 & BC2 Progeny | 173 | 3/31/2011 | 7/12/2011 | *V. shuttleworthii* |
| C | New *V. arizonica* Sources | 54 | 5/12/2011 | 8/11/2011 | *V. arizonica* |
| D | PD Rootstocks | 15 | 6/14/2011 | 9/15/2011 | F8909-08 |
| E | Rotundifolia and VR Hybrids | 94 | 11/3/2011 | 2/2/2012 | *M. rotundifolia* |
| F | 94% PdR1b & BD5-117 Source Saves | 109 | 12/15/2012 | 3/16/2012 | F8909-08, BD5-117 |
| G | 97% *PdR1b* Elite Selections | 77 | 3/10/2012 | 6/9/2012 | F8909-08 |
| H | 05347 b42-26 F1 Mapping Population | 84 | 7/3/2012 | 10/4/2012 | b42-26 |

Table 16. Crosses made in 2012 to develop genetic maps of PD resistance from in new accessions from southern US and Mexico germplasm. Crosses 08-319 and 08-326 are selfs of Zinfandel and Cabernet Franc respectively and 100% *vinifera*.

|  |  |  |  |
| --- | --- | --- | --- |
| Resistant Parent | Geographic Origin of Resistance | Pure Vinifera Types used in 2012 Crosses | Estimated # of Seed |
| ANU5 | Littlefield, AZ | Alicante Bouschet | 140 |
|  |  | Grenache | 100 |
| b40-29 | Chihuahua, MX | 08319-07 | 280 |
|  |  | 08319-29 | 45 |
| b31-13 | Ciudad Mante, MX | 08319-07 | 250 |
|  |  | 08319-29 | 95 |
| b46-43 | Big Bend, TX | 08319-07 | 320 |
|  |  | 08319-12 | 150 |
|  |  | 08326-61 | 200 |
| b47-32 | Big Bend, TX | 08319-07 | 190 |
|  |  | 08319-12 | 90 |
|  |  | 08326-61 | 140 |

Table 17. Selections being considered for transfer to FPS prior to larger scale wine testing and release.

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| # GH Screens | Genotype | Parentage | % vin | Color | # Years small lot wine made | Multiple vine trials Davis | Multiple vine trials Napa |
| R3 | 07713-51 | F2-35 x U0502-48 | 94% | W | 3 | Yes | Yes |
| R2 | 07329-01 | U0505-01 x Chardonnay | 94% | B | 0 | Yes | Yes |
| R2 | 07329-31 | U0505-01 x Chardonnay | 94% | B | 1 | Yes |  |
| R2 | 07338-37 | U0505-01 x LCC | 94% | B | 0 | Yes | Yes |
| R2 | 07355-75 | U0505-01 x Petite Syrah | 94% | B | 3 | Yes | Yes |
| R1 | 09330-07 | 07370-039 x Zinfandel | 97% | B | 0 |  |  |
| R1 | 09331-047 | 07355-020 x Zinfandel | 97% | B | 0 | Yes |  |
| R1 | 09331-133 | 07355-020 x Zinfandel | 97% | B | 0 |  |  |
| R1 | 09333-117 | 07355-020 x Chardonnay | 97% | B | 0 |  |  |
| R1 | 09333-178 | 07355-020 x Chardonnay | 97% | B | 1 | Yes |  |
| R1 | 09333-253 | 07355-020 x Chardonnay | 97% | B | 0 |  |  |
| R1 | 09333-370 | 07355-020 x Chardonnay | 97% | B | 0 |  |  |
| R1 | 09340-093 | 07355-020 x Cabernet Sauvignon | 97% | B | 0 | Yes |  |
| R1 | 06325-42 | A81-138 x Alicante Bouchet | 88% | B | 0 |  | Yes |
| R1 | 06325-43 | A81-138 x Alicante Bouchet | 88% | B | 0 |  | Yes |
| R1 | U0502-20 | A81-138 x Chardonnay | 88% | W | 4 | Yes |  |
| R3 | 03300-099 | 101-14 Mgt x F8909-08 | 0% | stock | NR |  |  |
| R2 | 08314-15 | 03300-048 x 06301-93 | 0% | stock | NR |  |  |
| R2 | 08314-46 | 03300-048 x 06301-93 | 0% | stock | NR |  |  |