

**California Cling Peach Advisory Board
2022 Annual Report**

Project Title:	Development of New Cling Peach Varieties
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Summary

The goal of the UCD cling peach variety development program is to breed improved varieties addressing current industry needs while at the same time identifying and incorporating new germplasm that might provide genetic and so more sustainable solutions to emerging and so longer-term industry needs. While previous annual reports have provided a more detailed summary of recently introduced breeding strategies and genetics being developed to solve a broad range of problems resulting from the loss of agrochemicals and affordable labor, this report will attempt more of an overview of the breeding program progress over the last decades from the perspective of a breeder contemplating retirement in the next 5-8 years. This overview includes both the opportunities and challenges for ensuring sustainable productivity over the next decades. A large part of recent breeding success has been the result of the identification and incorporation of new germplasm to provide novel solutions that were previously unavailable within the highly inbred traditional peach germplasm. While the incorporation this new germplasm has allowed the development of new California adapted varieties (including Lilleland, Hesse, Late-Ross, Kader, Vilmos, Shuler and Ogawa) that have reduced the need for fungicides and labor inputs, the further recombination of these different and often independent germplasm sources should offer further improvements in the next generation of breeding varieties. Because this new germplasm is already in a California adapted background, future breeding progress should be accelerated. Because of the novelty of many of these genetic solutions, extensive regional grower testing prior to variety release will still be required. (This report is an expansion of a more condensed breeding summary requested for publication in the upcoming Cling Peach Review).

The current (and next) generation of California processing peach varieties.

Because processing peaches have a lower market value than fresh market peaches, growers require high yields (~ 20 tons/acre) as well as productive orchard lifetimes of 20 years or more to be economically profitable. The only way to confidently recommend varieties having the

required commercial traits (consistent high production over a 20 year orchard lifespan and lacking major defects such as pit-fragmentation under increasingly hot summer temperatures) is to breed varieties with high productivity, quality and environmental resilience and then test these varietal candidates for 15 years or more in the different regions where commercial production occurs. This extensive testing has made processing peach breeding less lucrative

for private breeders, resulting in public programs such as my program at UCD taking on the responsibility. Consequently, most

processing peach varieties released over the last century were developed at UCD or earlier UC/USDA collaborations (Fig. 4). These varieties have also evolved over this time in order to meet changing industry needs. The early 1900s saw the development of peach varieties combining desirable productivity and canning quality with adaptation to Central Valley growing conditions. Emphasis shifted in the latter part the century to ensure production continuity using multiple varieties with overlapping harvest times so that canneries would not have to slow down or even shut down because of a lack of fruit. Despite much progress, supply gaps remained between Carson and Bowen in the Early harvest season, and between Andora and Carolyn in the Late harvest season (Fig. 1). I started breeding processing peach varieties at the

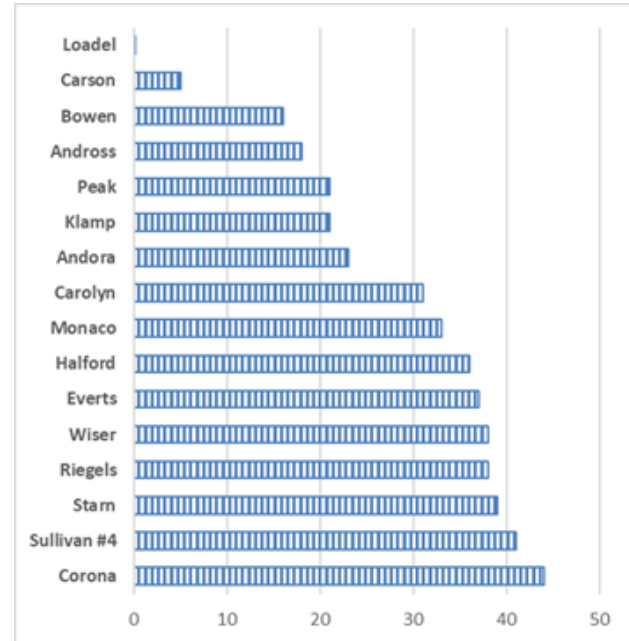


Figure 1. Harvest times for early 1980s processing peach varieties (in days after Loadel) showing harvest gaps between Carson and Bowen and between Andora and Carolyn.

University of California Davis (UCD) in the late 1980s just after UCD released *Ross* and *Dr. Davis*. These varieties, along with the subsequent release of *Late-Ross* and *Lilleland* (having *Ross* as a grandparent) provided production consistency for the crucial Late processing season. *Ross* and *Dr. Davis* were also important in that they brought in new germplasm from South Africa and China. The origins of traditional California processing peach varieties had been traced back to as few as 4-6 founding parents resulting in previous breeding germplasm being highly inbred and so lacking in new genetic options (Fig. 2).

However, breeding varieties to supply fruit during the Early-season Carson-Bowen gap proved more difficult. Often referred to as the Dixon-gap because the original Dixon variety was harvested at this time but was eventually rejected by canners because of its high proportions of split-pits and red-staining of the pit cavities. Fruit ripening during this early-season are particularly susceptible to split-pits and red-pit staining because the process of pit-lignification or hardening occurs at a particularly vulnerable time in early fruit development.

Andross, which has a similar parentage to Dixon, is also susceptible to split-pits/pit-staining, resulting in similar efforts to breed a replacement variety possessing Andross' high productivity but without its pit staining and fragmentation problems. Because time of pit-hardening is a major determinant for the time of fruit development and so harvest, UCD developed breeding progeny originally tended to ripen either around Carson time or, alternatively, later than Bowen, making it difficult to find a good quality breeding selection ripening within this Dixon-gap. Efforts to incorporate new parental germplasm from other processing and fresh market breeding programs to nail this gap were also unsuccessful, and it was soon determined using

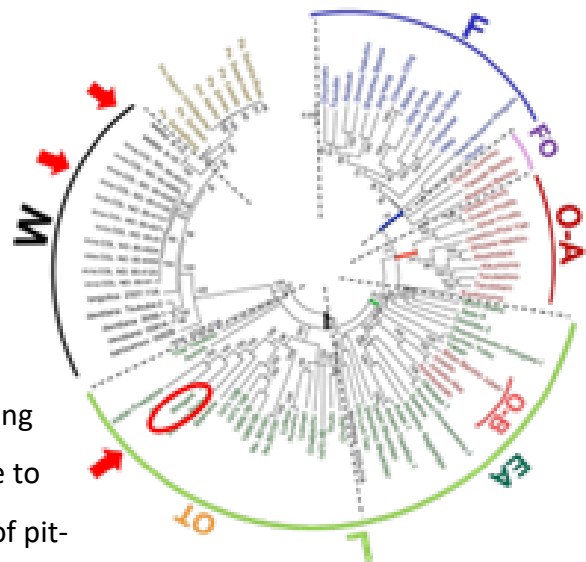


Figure 2. Plot showing germplasm available to peach breeding with the 'F' group representing currently cultivated peach with increasing genetic diversity as the plotted data rotate clockwise away from the 'F' group ending in the very diverse related and wild species (W group).

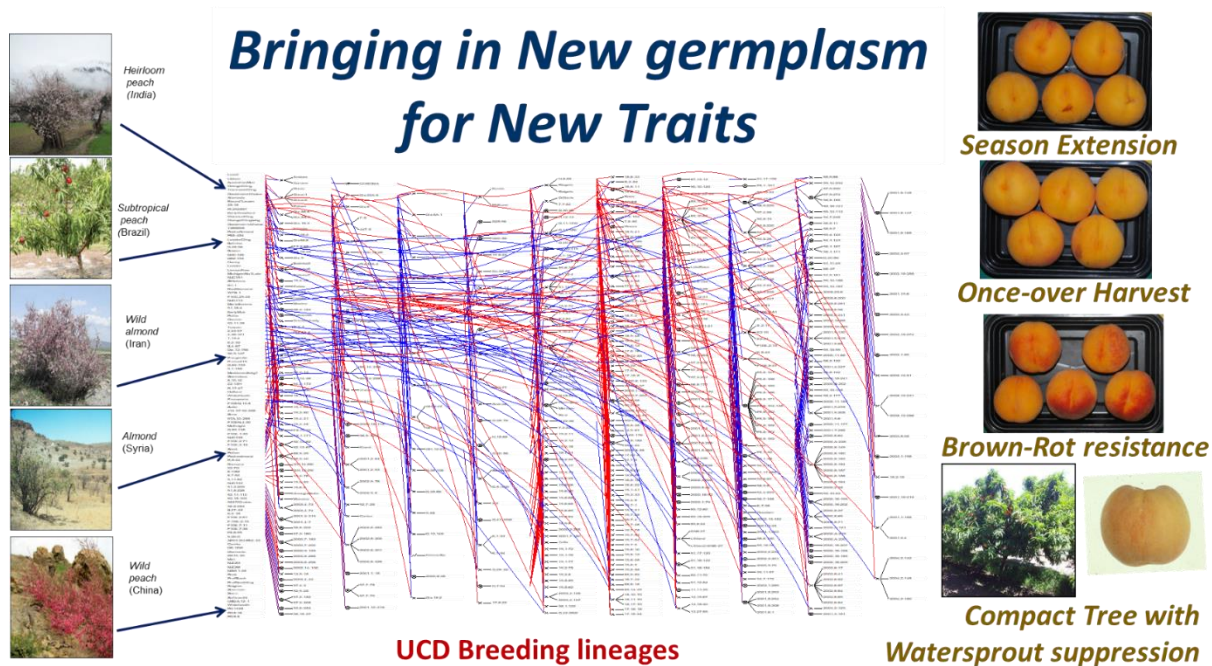


Figure 3. Transferring new genes from related species requires several generations of crosses to processing peach to capture new traits and several additional generations of backcrossing to achieve good productivity and fruit quality.

genomic analysis that even this expanded peach germplasm represented only about 6-8 founding parents with the variety Chinese Cling being a main source of breeding germplasm. This is shown graphically in figure 2, where varieties of processing and fresh market peaches (including the Chinese Cling dominant-parent) are shown in blue under the F-group. The amount of clockwise rotational distance between varieties is an indication of the amount of genetic difference between them. The clustering of both fresh market and processing varieties within the F group documents the high genetic relatedness within this group. As the lines of relatedness rotate clockwise in figure 2, the genetic difference from Chinese Cling increases (as in the O-A group which represents ornamental peaches). At the far end of this expanding circle is the W group which are wild related species and so the most diverse genetics readily accessible to conventional breeding. [The red arrow adjacent to the W group identifies the *Walgant* germplasm from South Africa which is an outlier as it is a commercial processing peach but possesses distinctly different genetics than the standard European/American commercial peach germplasm. Current evidence suggests that the *Walgant* germplasm originated from a unique peach germplasm from India rather than China. While the *Walgant* as well as its parent

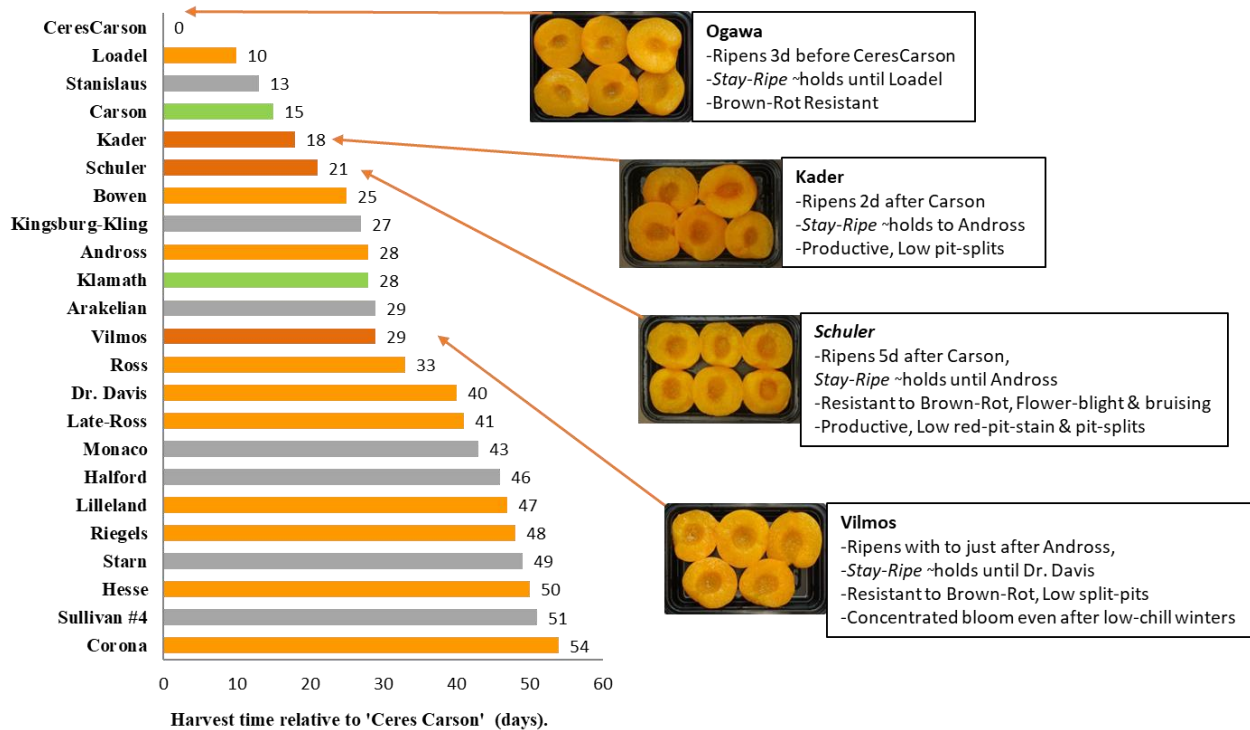


Figure 4. Harvest times for current California processing peach varieties including the four new UCD varieties.

[Orange bars identify UC varieties; green bars identify Zaiger Genetics varieties; gray bars are grower selections (Kingsburg-Kling is an Early maturing budsport of Dr. Davis.)]

variety Kakamas has proven too soft and too highly (orange) colored for California use, the related South African peach Woltemade (brought into the US as PI 234198) has been a very valuable source of fruit quality and productivity including a source for the stay-ripe trait, being the great grandparent to the Shuler variety].

However, most other recent plant introductions proved of poor quality and often too genetically inbred to be of much value to future breeding and UCD breeding program began investigating/incorporating germplasm from related species, including almond and wild peach, but this required several generations of selective breeding to recover good quality peach-type fruit (Fig. 3) adapted to California growing conditions. These efforts have been successful in breeding the peach varieties *Kader* and *Schuler* that combine good productivity and processing quality with a harvest time within the Dixon-gap (Fig. 4).

Both *Kader* and *Schuler* also possess the 'stay-ripe' trait which suppresses the usual fruit softening and degeneration following the tree-ripe stage, allowing fruit to hold on the tree for a

week or more, providing the option for delayed harvest (Fig. 5). Schuler also contains a novel gene which essentially shuts down any red anthocyanin pigment formation within the fruit as an added barrier to red pit-staining and associated pit-splitting even under the hot early summer temperatures conducive to pit-staining. This trait is known as the highlighter trait because the absent of red



anthocyanin pigments in the fruit flesh result in the

Figure 5. Advanced UCD clingstone peach selection possessing the stay-ripe trait which allows fruit to maintain good on-tree processing quality for 2 weeks after initial ripening.

remaining yellow to yellow-gold carotenoid pigments having a brighter appearance. Other independent breeding sources for the highlighter trait include breeding parent 2011,23-83, and breeding lines 14,2- 114 to 163, that were derived from germplasm of Dr. Dick Okie's now terminated peach breeding program in Georgia.

Both Kader and Schuler also possess improved fruit brown-rot resistance, including improved resistance to flower blight, further reducing the need for fungicide applications. The UCD variety *Vilmos* has also been recently released as a possible replacement for Andross. In addition to the stay-ripe trait and improved brown-rot resistance, *Vilmos* possesses new genetics that result in a more concentrated bloom (and so more uniform harvest) even under the increasingly common low-chill winters. Finally, the UCD variety *Ogawa* is being released to extend the Extra-Early harvest season 3 to 4 days before Ceres-Carson. (Zaiger Genetics has also released the American and Calaveras varieties, further filling gaps in this Extra-Early season). *Ogawa's* exceptional fruit size, good post-harvest fruit firmness (common with the stay-ripe trait; see figure 5), along with improved fruit brown-rot resistance and good fruit color, have made it a particularly useful variety for organic peach production because the very early harvest allows canning before processing plant contamination by traditionally grown peaches.

Just as the release of Ross and Dr. Davis in the mid-1980s, transformed the next generation of processing peach varieties through the use of new genetics and new breeding strategies, the much greater genetic diversity brought in during the last 3 decades (Figures 2 and 3) provide valuable new genetic options for addressing challenges associated with climate change and the loss of traditional fungicides as detailed and earlier annual reports. The greatest challenge to the next generation of peach production, however, is the rapidly increasing labor costs. In addition to possessing improved disease resistance and tolerance to milder winters/hotter summers, the next generation of California processing peach varieties must facilitate greater efficiencies in orchard management, particularly harvest. A major challenge has been the need to reduce multiple-harvests of the same orchard, ideally allowing single-pass harvest by hand or by machine. Obtaining uniformly ripening fruit is particularly difficult, however, because even fruit on the same tree will vary in their ripening time based on initial flowering time as well as differences in within-tree shading. The *stay-ripe* trait was developed to solve this problem because it allows early-ripening fruit to maintain on-tree processing quality for a week or more until most unripe fruit are also ready for harvest. In addition to allowing single-pass harvest, the extra-ripening time improves overall yield (more fruit harvested) and processing quality (more fruit at full-ripe stage). The genetics controlling this trait are complex and we are still researching developmental and molecular markers to improve future breeding efficiency with some advanced stay-ripe breeding lines cable of maintaining on-tree fruit quality for up to 2 weeks

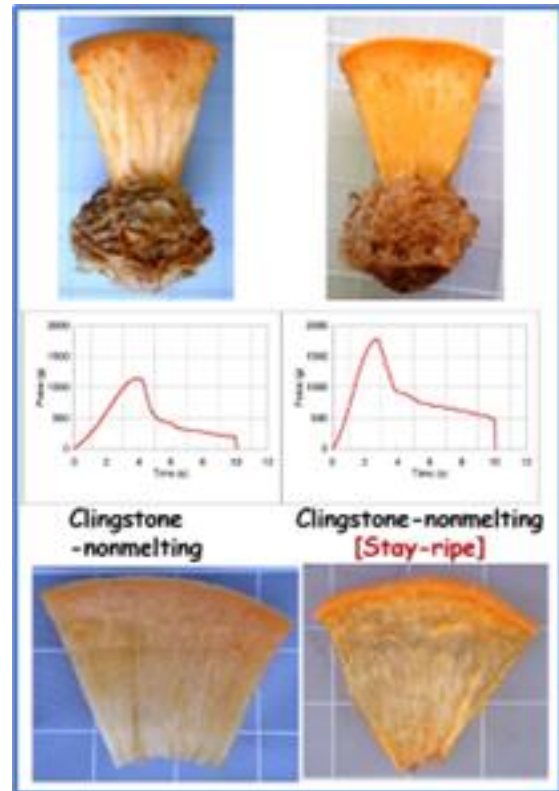


Figure 6. Differences in Stay-ripe fruit flesh structure Including more lateral crosshatching of flesh fibers resulting in firmer fruit texture (graft shows flesh firmness in pounds from the skin (0 on plot x-axis) to the pit cavity at right).

(Fig. 5) though small fruit size remains a challenge. The previously described South Africa/India derived Woltemade germplasm has been the source for the extended stay-ripe trait in Schuler and this continues to be an important breeding source for stay-ripe extension of 2 weeks or more past initial tree full ripe. [This extended duration is being targeted to buffer against higher summer temperatures (and so even faster fruit deterioration) anticipated in future climate-change scenarios.] Other promising sources for the stay-ripe trait include the peach species *Prunus mira* (as represented by UCD breeding line 04,12-139) and almond (peach breeding parents F8-8-156, 05,10-133).

The stay-ripe trait also contributes a general improvement in fruit firmness at initial tree-ripe stage (figure 6) which appears to be associated with a more highly textured fruit flesh. We are utilizing this more diverse germplasm to identify useful developmental/biochemical as well as molecular markers as predictors for this trait to improve future breeding efficiency. The stay-ripe trait differs from the slow-ripening trait used in fresh market peach varieties such as Red-Top and Autumn-Flame in that the stay-ripe suppresses fruit deterioration following the tree-ripe stage while the slow-ripening slows down the ripening process towards full tree-ripe (usually through some sort of ethylene pathway suppression). The slow-ripening trait can sometimes cause a failure of normal ripening of tree fruit as is frequently seen in the Autumn-Flame variety in years of warmer or cooler than normal summer temperatures. We are experimenting with incorporating the slow-ripening with the stay ripe trait with our most advanced breeding material currently represented by almond derived breeding lines 14,1-50 to 99. Incorporating stay-ripe into fresh market freestone varieties is not effective because the separation of the stone from flesh (freestone) at tree ripe severs the vascular connections between the developing flesh and the peach leaves resulting in inevitable fruit degeneration from lack of nutrients, particularly sugars and calcium.

Molecular and biochemical markers are also being developed to identify processing selections with reduced vulnerability to fruit brown rot as well as fruit bruising in new varieties (see Appendix). Currently, our most promising sources for brown rot resistance have been the Bolinha germplasm from Brazil, the D62-193 germplasm from Rutgers University (probably East European derivation) and the almond-derived peach breeding lines F8-8-147 2 to 166. A major

gene for resistance was recently identified in advance breeding lines derived almond resulting in the opportunity for developing a more accurate molecular marker for this trait that could be used for rapid screening of progeny in the greenhouse thus eliminating the need for initial field testing. Intensive selection against fruit bruising has resulted in reduced vulnerability in new varieties including Kester, Vilmos and Schuler. Research with Diane Barrett's group has identified reductions in both phenolic compounds as well as the polyphenol oxidase enzymes as being responsible for this reduced bruising vulnerability indicating the possibility of developing more efficient biochemical and/or molecular genetic markers for more efficient identification/selection in the future. Evidence for a major source of resistance to peach mildew has also been observed in breeding lines derived from the wild almond species *Prunus scoparia*. Given the difficulty of disease screening without the use of molecular markers, we have emphasized pursuit of brown rot resistance as caused by *Monilinia* species but have maintained promising breeding lineages with potential mildew resistance in the breeding lines 10,21-59 & 66; 10,21-60; 11,4-59 to 107; 11,5-7; 11,7-147 to 157; 11, 23-62 (2003,6-169 clone) and 11,23-63 (2003,6-171 clone). An updated listing of national and international efforts to develop molecular markers useful for peach breeding is presented in the Appendix with UCD associated efforts highlighted in yellow. As can be seen, the UCD processing peach breeding program has been a major contributor to molecular marker development. This is mainly a consequence of the very diverse breeding germplasm we have developed since the inbred nature of most other breeding germplasm lacks both the resistance genes as well as the background genetic variability required for effective marker development (as discussed in previous annual reports in the recent publication Gradziel TM. (2022). In: C. Kole, (ed.) Genomic Designing for Biotic Stress Resistant Fruit Crops. Springer DOI : 10.1007/978-3-030-91802).



Figure 7. Narrow-leaf trait being incorporated to improve internal light penetration in otherwise high-density compact trees. [Both red-leaf and green-leaf types are being utilized].

In addition to new fruit traits, the next generation California processing peach orchard will require changes in tree size and structure to facilitate more efficient orchard management. In other orchard crops such as apple and pear, tree size reduction is most commonly achieved by using dwarfing rootstocks and the UC/USDA *Controller-series* of size-reducing rootstocks has recently been released to California growers. (We are also pursuing new rootstocks with

greater resistance to nematodes, phytophthora and oak-root-fungus, see Appendix-A). In addition, the UCD processing peach breeding program has developed a series of *Compact* ($1/2$ to $3/4$ normal size) varieties also exhibiting the stay-



Figure 8. Left: Compact trees trained to a quad-V (note the suppression of watersprout growth). Right: Row of unhedged UCD breeding selections having columnar or pillar tree architecture. (Standard hedged trees on either side).

ripe trait (fig. 6) and these are currently being evaluated under different grower and orchard management practices. The compact tree trait is controlled by a single major gene which also acts to suppress excessive watersprout growth (Figure 6-left), thus reducing annual pruning requirements and making the system more amenable to training trees for optimized mechanical or high throughput hand harvest. The shorter tree size is primarily achieved by reducing the internode length between leaves to approximately $1/2$ to $2/3$ of normal. Consequently, the number of axillary buds available for flower and fruit development remain comparable to a standard tree resulting in an improved harvest index or fruit production per tree size. The shorter internodes also increase leaf density and so shading which sometimes has the undesired consequence of reducing axillary bud and subsequent shoot growth resulting in sections of bare-wood in some breeding selections. To reduce this vulnerability, we are

working to incorporate a major gene which results in a narrow-leaf architecture (figure 7, also obtained from Dr. Okie's USDA breeding program at Georgia) as a possible strategy to improve within-tree light distribution. Current advanced breeding lineages possessing this germplasm include 11,7-264 & 270 and 14,2-50 to 113.

Finally, in the last 8 years we have begun work to develop processing peach trees having a columnar or pillar-type architecture (Figure 8) similar to the "fruiting walls" found in apple and pear orchards. The opportunity to efficiently develop such fruiting-walls in processing peach came about fairly recently in our identification of a major gene for the pillar-type growth habit in breeding lineages derived from the wild peach *Prunus mira*. This germplasm has the desirable characteristics of strongly upright primary scaffold growth with a large number of lateral and fruitful hangers. Breeding progeny with good tree architecture have been recovered though further improvements and fruit quality are required. (Fruit in our most advanced breeding lines currently in production tend to be too small and with insufficient flesh color. More advanced breeding lines will come into bearing in 2024). A high-density evaluation/demonstration planting was established at UC Davis pomology fields in 2022. (This plot will be used primarily for harvest strategy/mechanization studies since while fruit size/quality is improved it is still not at commercially required levels).

Appendix 1. Summary of related species sources of traits potentially useful for cultivar and rootstock development (Updated from Gradziel 2022).

Trait/resistance	Organism	Pathogen	Inoculation	Resistance/tolerance	Inheritance	Gene name	LG	Reference
<i>P. cerasifera</i>								
Root-knot nematode	Nematode	<i>Meloidogyne</i> spp.	Controlled	Resistance	Single dominant gene	<i>Ma</i>	7	Claverie et al. (2004a)
Oak root fungus	Fungi	<i>Armillaria mellea</i>	Controlled	Resistance	Quantitative	Not-mapped		Adelberg et al. (2021).
<i>P. davidiana</i>								
Powdery mildew	Fungi	<i>P. pannosa</i> var. <i>persicae</i>	Natural	Tolerance	Quantitative	QTLs	1, 2, 4, 6, 8	Foulgnie et al. (2003)
Sharka	Virus	Plum pox virus	Controlled	Tolerance	Quantitative	QTLs	1, 2, 4, 5, 6, 7	Rubio et al. (2013)
Green peach aphid	Insect	<i>Myzus persicae</i>	Natural	Tolerance	Quantitative	QTLs	1, 2, 3, 4, 5, 6, 8	Sauge et al. (2012)
Root-knot nematode	Nematode	<i>Meloidogyne</i> spp.	Natural	Tolerance	Major gene	Not-mapped		Reighard and Loreti. (2011)
Hull rot	Fungi	<i>Monilinia</i> spp.	Controlled	Tolerance	Quantitative	Not-mapped		Pascal et al. (1998)
Root-knot nematode	Nematode	<i>Meloidogyne</i> spp.	Natural	Tolerance	Major gene	Being-mapped		Gradziel (unpublished)
<i>P. dulcis</i>								
Brown rot	Fungi	<i>Monilinia</i> spp.	Controlled	Tolerance	Quantitative	QTLs	1, 4	Martinez-Garcia et al. (2013a)
Powdery mildew	Fungi	<i>P. pannosa</i> var. <i>persicae</i>	Natural	Resistance	Single dominant gene	<i>Vr3</i>	2	Donoso et al. (2016)
Band canker	Fungi	<i>Botryosphaeria dothidea</i>	Natural	Resistance	Single dominant gene	<i>Botd8</i>	6 or 8	Manero-Castillo et al. (2018)
Root-knot nematode	Nematode	<i>Meloidogyne</i> spp.	Controlled	Resistance	Single dominant gene	<i>RmJa</i>	7	Van Ghelder et al. (2010)
Root-knot nematode	Nematode	<i>Meloidogyne</i> spp.	Controlled	Resistance	Single dominant gene	<i>RmIa</i>	2	Saucet et al. (2016)
Sharka	Virus	Plum pox virus	Controlled	Tolerance	Quantitative	Not-mapped		Martinez-Gomez et al. (2004)
Sharka	Virus	Plum pox virus	Controlled	Tolerance	Quantitative	Not-mapped		Crilli et al. (2016)
Fruit firmness					Quantitative	Not-mapped		Peace et al. (2005)
Fruit/nut size					Quantitative	Not-mapped		Fresnedo et al. (2020)
Shell hardness					Quantitative	Not-mapped		Sideli et al. (2022)
<i>P. insititia</i>								
Crown gall	Bacteria	Agrobacterium spp.	Controlled	Resistance	Not analyzed			Bliss et al. (1999)
silver leaf	Fungi	<i>Stereum purpureum</i>	Controlled	Resistance	Not analyzed			Bliss et al. (1999)
<i>P. kansuensis</i>								
Root-knot nematode	Nematode	<i>Meloidogyne</i> spp.	Controlled	Tolerance	Major gene	<i>PKMi</i>	2	Cao et al. (2011)
Root-knot nematode	Nematode	<i>Meloidogyne</i> spp.	Controlled	Resistance	Single gene	<i>Mf</i>	2	Mequillan et al. (2018b)
Root-knot nematode	Nematode	<i>Meloidogyne</i> spp.	Controlled	Resistance	Single gene	Not-mapped		Maquillan et al. (2018a)
<i>P. mira</i>								
Root-knot nematode	Nematode	<i>Meloidogyne</i> spp.	Natural	Resistance	Single gene	Not-mapped		Cao et al. (2011)
Powdery mildew	Fungi	<i>P. pannosa</i> var. <i>persicae</i>	Natural	Resistance	Single dominant gene	Not-mapped		Layne and Bassi (2008)
Peach mosaic	Virus	peach mosaic virus	Natural	Tolerance	Major gene	Being-mapped		Pine (1976)
Pillar tree type	Nematode	<i>Meloidogyne</i> spp.	Natural	Tolerance	Major gene	Being-mapped		Gradziel (unpublished)
<i>P. persica</i>								
Hull rot	Fungi	<i>Monilinia</i> spp.	Controlled	Tolerance	Quantitative	QTLs	2, 3, 4	Pacheco et al. (2014)
Powdery mildew	Fungi	<i>P. pannosa</i> var. <i>persicae</i>	Natural	Resistance	Single dominant gene	<i>Vr2</i>	8	Pascal et al. (2017)
Powdery mildew	Fungi	<i>P. pannosa</i> var. <i>persicae</i>	Natural	Resistance	Single dominant gene	Not-mapped		Gradziel (unpubl. 2022)
Bacterial spot	Bacteria	<i>X. arboricola</i> pv. <i>Pruni</i>	Controlled	Tolerance	Single dominant gene	QTLs	1, 4, 5, 6	Yang et al. (2013)
Bacterial spot	Bacteria	<i>X. arboricola</i> pv. <i>Pruni</i>	Controlled	Resistance	Quantitative	QTLs		Kasic (unpubl. 2022)
Sharka	Virus	Plum pox virus	Controlled	Tolerance	Quantitative	QTLs	2, 3	Crilli et al. (2017)
Green peach aphid	Insect	<i>Myzus persicae</i>	Natural	Resistance	Single dominant gene	<i>Rm2</i>	1	Lambert and Pascal (2011)
Green peach aphid	Insect	<i>Myzus persicae</i>	Natural	Resistance	Single dominant gene	<i>Rm1</i>	1	Pascal et al. (2017)
Root-knot nematode	Nematode	<i>Meloidogyne</i> spp.	Controlled	Resistance	Single dominant gene	<i>RmIa/Nem</i>	2	Claverie et al. (2004b)
Ring nematode	Nematode	Mesocriconea xenoplax.	Natural	Tolerance	Quantitative	not-mapped		Gradziel (unpublished)
Lesion nematode	Nematode	Pratylenchus spp.	Controlled	Resistance	Major gene	Being-mapped		Gradziel & Sideli (unpublished)
<i>P. peltanikowii</i>								
Crown gall	Bacteria	Agrobacterium spp.	Natural	Resistance	Not analyzed			Evreinov (1952)
<i>P. salicina</i>								
Root-knot nematode	Nematode	<i>Meloidogyne</i> spp.	Controlled	Resistance	Single dominant gene	Rjap	7	Claverie et al. (2004a)
<i>P. tanquillia</i>								
Crown gall	Bacteria	Agrobacterium spp.	Natural	Resistance	Not analyzed			Kluepfel (unpublished)
<i>P. webbii</i>								
Root-knot nematode	Nematode	<i>Meloidogyne</i> spp.	Controlled	Resistance	Major gene			Gradziel & Sideli (unpublished)
Ring nematode	Nematode	Mesocriconea xenoplax.	Natural	Resistance	Not analyzed			Gradziel (unpublished)