

Interspecific Breeding Germplasm for Rootstock Research and Development

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Prunus tangutica from Central Asia

Introduction

Changes in planting practices, including the quantity and quality of land and irrigation water, have led to the need for a new generation of almond rootstocks and a number of public and private efforts have been initiated to develop and test new candidates. Germplasm derived from other species, either directly or through species hybridization, is often pursued to attain the greatest range of vigor, stress and disease tolerance and desirable horticultural traits. However, the acquisition of such exotic germplasm is often difficult and time-consuming. At UC Davis, a diverse germplasm has already been developed combining almond, peach as well as related species including *P. argentea*, *P. bucharica*, *P. davidiana*, *P. fenziiana*, *P. domestica*, *P. mira*, *P. orthosepala*, *P. scoparia*, *P. tangutica* and *P. webbii*. In this project, selected germplasm from the UCD almond and peach breeding programs with value for rootstock improvement have been characterized both phenotypically and at the molecular marker level. Detailed pedigree relationships as well as trait expression data have been transferred to the RosBreed web-site (<http://www.rosbreed.org/>) and published to allow end-user analysis. This germplasm demonstrates extensive diversity both genetically and in the range of traits useful to rootstock improvement programs. Field evaluations have identified unique and potentially useful characteristics in parents and progeny, including modification of tree architecture from *P. scoparia* hybrid rootstocks, drought tolerance in a peach by *P. argentea* hybrid, and a pronounced invigoration of scion growth in advanced interspecies lines.

No.	Genotype	Origin	% Almond genome	Seed Length (mm)	Seed Width (mm)	Seed Thickness (mm)	Seed Volume (mm ³)	Seed Weight (g)	Seed Density (g/cm ³)	Seed Ratio (g/100g)	Seed Ratio (g/100g)	Seed Ratio (g/100g)	Seed Ratio (g/100g)	Seed Ratio (g/100g)	Seed Ratio (g/100g)	Seed Ratio (g/100g)	Seed Ratio (g/100g)	Seed Ratio (g/100g)	Seed Ratio (g/100g)	
99	A1-23	<i>P. argentea</i> (bitter seed)	100	19.03	13.18	15.25	9.73	12.05	6.04	1.47	0.37	17.28	0.61	0.64	0.61	0.64	0.61	0.64	0.61	0.64
101	F10D-2-14	<i>P. webbii</i> (bitter seed)	100	18.91	12.39	18.20	11.73	11.66	7.26	2.93	0.82	19.09	0.51	0.73	0.58	0.58	0.51	0.73	0.58	0.58
102	F10D-2-14	<i>P. fenziiana</i> (F2)	100	10.55	23.3	16.48	11.38	11.33	8.43	4.54	1.03	19.21	1.66	0.78	1.1	1.1	0.78	1.1	1.1	1.1
103	F10D-2-14	<i>P. fenziiana</i> (F2)	100	10.55	23.3	16.48	11.38	11.33	8.43	4.54	1.03	19.21	1.66	0.78	1.1	1.1	0.78	1.1	1.1	1.1
104	F10D-2-14	<i>P. fenziiana</i> (bitter seed)	100	10.55	23.3	16.48	11.38	11.33	8.43	4.54	1.03	19.21	1.66	0.78	1.1	1.1	0.78	1.1	1.1	1.1
105	F10D-2-14	<i>P. fenziiana</i> (bitter seed)	100	10.55	23.3	16.48	11.38	11.33	8.43	4.54	1.03	19.21	1.66	0.78	1.1	1.1	0.78	1.1	1.1	1.1
106	F10D-2-14	<i>P. fenziiana</i> (bitter seed)	100	10.55	23.3	16.48	11.38	11.33	8.43	4.54	1.03	19.21	1.66	0.78	1.1	1.1	0.78	1.1	1.1	1.1
107	F10D-2-14	<i>P. fenziiana</i> (bitter seed)	100	10.55	23.3	16.48	11.38	11.33	8.43	4.54	1.03	19.21	1.66	0.78	1.1	1.1	0.78	1.1	1.1	1.1
108	F10D-2-14	<i>P. fenziiana</i> (bitter seed)	100	10.55	23.3	16.48	11.38	11.33	8.43	4.54	1.03	19.21	1.66	0.78	1.1	1.1	0.78	1.1	1.1	1.1
109	F10D-2-14	<i>P. fenziiana</i> (bitter seed)	100	10.55	23.3	16.48	11.38	11.33	8.43	4.54	1.03	19.21	1.66	0.78	1.1	1.1	0.78	1.1	1.1	1.1
110	F10D-2-14	<i>P. fenziiana</i> (bitter seed)	100	10.55	23.3	16.48	11.38	11.33	8.43	4.54	1.03	19.21	1.66	0.78	1.1	1.1	0.78	1.1	1.1	1.1
111	F10D-2-14	<i>P. fenziiana</i> (bitter seed)	100	10.55	23.3	16.48	11.38	11.33	8.43	4.54	1.03	19.21	1.66	0.78	1.1	1.1	0.78	1.1	1.1	1.1
112	F10D-2-14	<i>P. fenziiana</i> (bitter seed)	100	10.55	23.3	16.48	11.38	11.33	8.43	4.54	1.03	19.21	1.66	0.78	1.1	1.1	0.78	1.1	1.1	1.1
113	F10D-2-14	<i>P. fenziiana</i> (bitter seed)	100	10.55	23.3	16.48	11.38	11.33	8.43	4.54	1.03	19.21	1.66	0.78	1.1	1.1	0.78	1.1	1.1	1.1
114	F10D-2-14	<i>P. fenziiana</i> (bitter seed)	100	10.55	23.3	16.48	11.38	11.33	8.43	4.54	1.03	19.21	1.66	0.78	1.1	1.1	0.78	1.1	1.1	1.1
115	F10D-2-14	<i>P. fenziiana</i> (bitter seed)	100	10.55	23.3	16.48	11.38	11.33	8.43	4.54	1.03	19.21	1.66	0.78	1.1	1.1	0.78	1.1	1.1	1.1
116	F10D-2-14	<i>P. fenziiana</i> (bitter seed)	100	10.55	23.3	16.48	11.38	11.33	8.43	4.54	1.03	19.21	1.66	0.78	1.1	1.1	0.78	1.1	1.1	1.1
117	F10D-2-14	<i>P. fenziiana</i> (bitter seed)	100	10.55	23.3	16.48	11.38	11.33	8.43	4.54	1.03	19.21	1.66	0.78	1.1	1.1	0.78	1.1	1.1	1.1
118	F10D-2-14	<i>P. fenziiana</i> (bitter seed)	100	10.55	23.3	16.48	11.38	11.33	8.43	4.54	1.03	19.21	1.66	0.78	1.1	1.1	0.78	1.1	1.1	1.1
119	F10D-2-14	<i>P. fenziiana</i> (bitter seed)	100	10.55	23.3	16.48	11.38	11.33	8.43	4.54	1.03	19.21	1.66	0.78	1.1	1.1	0.78	1.1	1.1	1.1
120	F10D-2-14	<i>P. fenziiana</i> (bitter seed)	100	10.55	23.3	16.48	11.38	11.33	8.43	4.54	1.03	19.21	1.66	0.78	1.1	1.1	0.78	1.1	1.1	1.1

Table 1. UCD breeding germplasm parents and introgression lines analyzed for seed characteristics. (A common introgression line would involve the transfer of the desired trait such as self-fruitfulness or nematode resistance from the donor species to the cultivated crop through a series of recurrent backcrosses to the target species). Color shading allows visualization of the relative differences within each trait (column) with red being low to green being high. A large range in phenotypic expression for each trait is available in parent species with much of this diversity successfully transferred through multiple backcrosses to recipient breeding line supporting good heritabilities and so opportunities for future breeding progress.

Traits	Cooperator	Germplasm evaluated	Species
Compatibility, Nematode (ring and root knot) resistance	Burchell Nursery	50 clones	<i>P. argentea</i> , <i>P. bucharica</i> , <i>P. davidiana</i> , <i>P. mira</i> , <i>P. persica</i> , <i>P. plum spp.</i> , <i>P. scoparia</i> , <i>P. tangutica</i> , <i>P. webbii</i> .
Disease & Nematode resistance, Replant	Sierra Gold Nursery	20 clones & ~1000 seed	<i>P. argentea</i> , <i>P. davidiana</i> , <i>P. mira</i> , <i>P. persica</i> , <i>P. scoparia</i> , <i>P. tangutica</i> , <i>P. webbii</i> .
Productivity, Compatibility, Architecture	Fowler Nursery/Paramount	5 clones	<i>P. argentea</i> , <i>P. davidiana</i> , <i>P. mira</i> , <i>P. persica</i> , <i>P. scoparia</i> .
Disease/pest resistance, hybrid vigor	UCD scion breeding	50 clones & ~4000 seedlings	<i>P. argentea</i> , <i>P. bucharica</i> , <i>P. davidiana</i> , <i>P. mira</i> , <i>P. persica</i> , <i>P. plum spp.</i> , <i>P. scoparia</i> , <i>P. tangutica</i> , <i>P. webbii</i> .
Productivity	Mathew Gilbert	15 clones	<i>P. argentea</i> , <i>P. fenziiana</i> , <i>P. mira</i> , <i>P. persica</i> , <i>P. webbii</i> .
Botrytopheria resistance	Jose Chaparro (UF)	40 clones	<i>P. argentea</i> , <i>P. bucharica</i> , <i>P. fenziiana</i> , <i>P. mira</i> , <i>P. pedunculata</i> , <i>P. persica</i> , <i>P. plum spp.</i> , <i>P. tangutica</i> , <i>P. triloba</i> , <i>P. webbii</i> .
Root lesion and root-knot nematode resistance	Andreas Westphal	7 clones	<i>P. argentea</i> , <i>P. davidiana</i> , <i>P. mira</i> , <i>P. persica</i> , <i>P. tangutica</i> , <i>P. webbii</i> .
Phytophthora resistance	Greg Browne	3 clones & ~200 seedlings	Plum interspecies, Almond spp. Seedlings & seed
Crown gall resistance	Dan Kluepfel	200 seedlings & 400 seed	<i>P. persica</i> x <i>P. tangutica</i> (F2, F3)

Table 2. List of current germplasm and cooperators pursuing: a) large-scale field evaluations and trait validations (blue) and b) gene discovery including mechanisms of gene action (gold).

Approach

The genetic characterization of parent species, species-hybrids and subsequent breeding progeny has been completed using over 500 molecular markers showing a fairly uniform distribution over all eight of the *Prunus* chromosomes. While rootstock improvement has benefited from the increased understanding of both the extensive genetic as well as phenotypic (disease/stress resistance, etc.) variability available in almond and its related species, traditionally breeding remains very tedious and time-consuming. The use of molecular markers is increasingly being used to improve breeding efficiency by allowing geneticist to identify genotypes and so traits of interest at much earlier stages in the breeding program. These molecular markers have frequently been shown to be species-specific, which confounds their utility when wide species crosses or divergent species introgression is attempted. To evaluate molecular marker cross-species efficacy, genetically diverse Rootstock Breeding lines were evaluated using available RosBreed markers to determine whether markers were able to detect genetic differences in this highly variable germplasm.

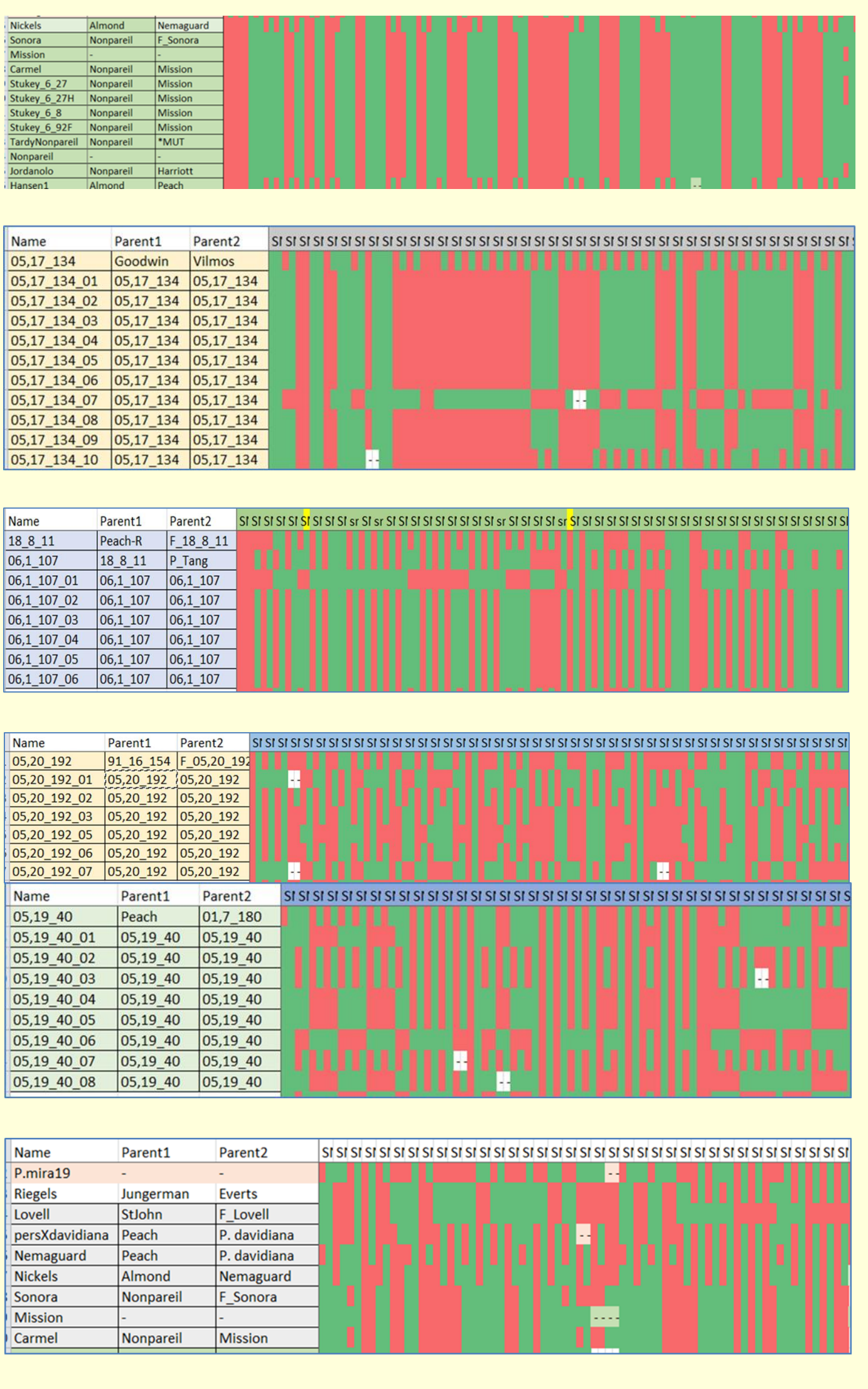


Figure 1. Representative molecular marker plots for different almond cultivars and genotypes as compared to the peach by almond hybrids Nickels and Hansen showing failure of the markers to discriminate among the known heterozygotes in almond. (Note that some markers on the right side of the plot were able to be discriminated, but these were rare).

Figure 2. Results from a almond by peach hybrid introgressed to peach, where parents are highly heterozygous but subsequent introgression progeny show a very distorted inheritance often depending upon individual genotype.

Figure 3. Molecular marker inheritance pattern of peach (top row), a peach by *Prunus tangutica* interspecies hybrid (2nd row) with lower rows showing patterns for 6 F2 progeny (differs of the species hybrid) showing that distortion from expected inheritance patterns differs with different species introgression lines.

Figure 4. Molecular marker inheritance patterns of primal genotypes derived from advanced almond to peach introgression lines (05, 20-192 at top) in *Prunus argentea* to peach introgression lines (05, 19-40 at bottom) as well as patterns for 7 and 8 selfed progeny, respectively, showing largely normal inheritance patterns.

Figure 5. Representative molecular marker patterns from chromosome 1 for different species and species hybrids, showing the value of general trends in identifying possible parentage. The pattern for Nemaguard shows a greater similarity between an established (peach x *P. davidiana*) interspecies hybrid than either almond or *Prunus mira*, supporting the general perception that *Prunus davidiana* was a parent of Nemaguard and the probable donor of Rootknot nematode resistance.

Summary

In much of this diverse germplasm, molecular markers developed for peach showed varying levels of efficacy when applied to species hybrids and their introgression lines. Despite a frequent failure of molecular markers developed in one species to discriminate the genetic alleles of different species, the use of marker-assisted-breeding proved valuable for understanding general inheritance trends as well as identifying possible barriers as well as potential novel opportunities for exotic gene transfer for rootstock improvement.