

Almond Variety Development: 2012

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Fig. 1. Field crosses using mesh bags to control crossing parents,

The California almond industry is in a historic period of transformation driven by increasing Central Valley acreage along with increasing environmental and market requirements, reductions in resources such as water, agrochemicals, and natural pollinators, as well as the uncertainties of a changing climate. While almond represents a diverse and highly adaptable species, commercial production in California is dependent almost entirely on the variety Nonpareil and a relatively few pollenizers, most of which have Nonpareil and Mission as direct parents. A long-term emphasis of the UCD almond breeding program has been the identification and incorporation of new and diverse germplasm. Genetic solutions to emerging production challenges are now becoming available from this new germplasm, including regionally-adapted selections expressing high levels of self-compatibility, and increased insect, disease and environmental stress resistance. Improved breeding lines also offer opportunities to expand market demand by optimizing phytonutrients in new varieties while minimizing potential health and marketing risks including aflatoxins, salmonella and allergens.

During the current project period, over 4,000 progeny trees from the over 11,000 seedlings generated from 2011 crosses, were transplanted following greenhouse screenings for vigor and disease resistance. Weather conditions for breeding crosses in the spring of 2012 were much more favorable than 2011 and over 30,000 controlled crosses were made with good seed sets achieved. Over 400 of the most promising advanced selections were tested for self-compatibility under controlled (bagged limbs) conditions (Fig. 1) with over 20 individual genotypes showing promising levels of self-compatibility and tree/kernel quality. Over 16,000 bearing trees from diverse genetic sources (summarized in Fig. 2) were evaluated in 2012 for productivity, fruit quality and disease resistance. The most promising of these selections will be further evaluated under controlled conditions for self-compatibility and cropping potential in 2013.

Figure 2. Crossing diagram showing major breeding lineages and their often exotic species origin. Source germplasm ranges from cultivated (peach) and wild related species, European and Asian varieties to heirloom California varieties and breeding lines. (Numbers in brackets denote the total number of progeny trees from different advanced lineages evaluated in 2012 while text color-codes identify species origin. Solid lines denote seed parent while dotted lines denote pollen parent). For each major breeding lineage, sample kernels are displayed representing the general characteristics of both source germplasm as well as advanced breeding selections. Only major lineages with over 200 progeny under evaluation are plotted. Smaller breeding lineages which are typically developed to explore general breeding potential (and occasionally specific breeding objectives such as self-pollination (Fig. 3) or disease resistance (Fig. 4) prior to potentially larger scale hybridizations, encompass approximately 25% of breeding program efforts.

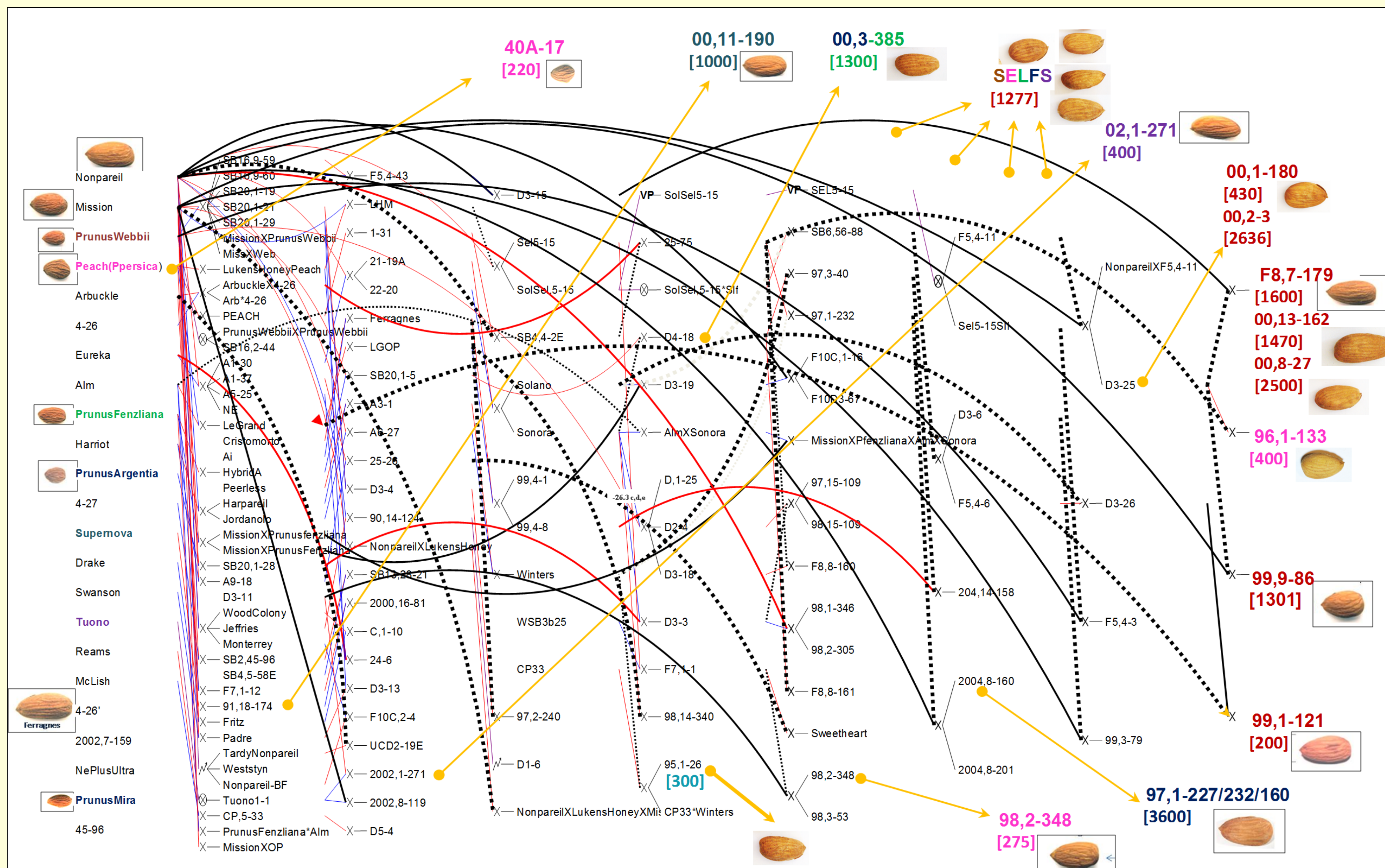
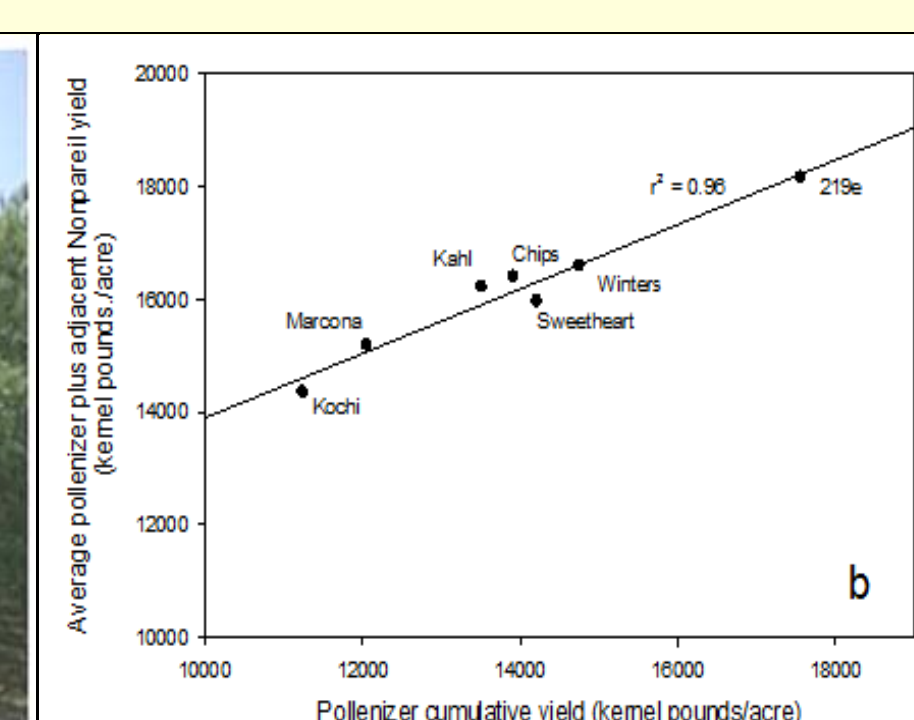
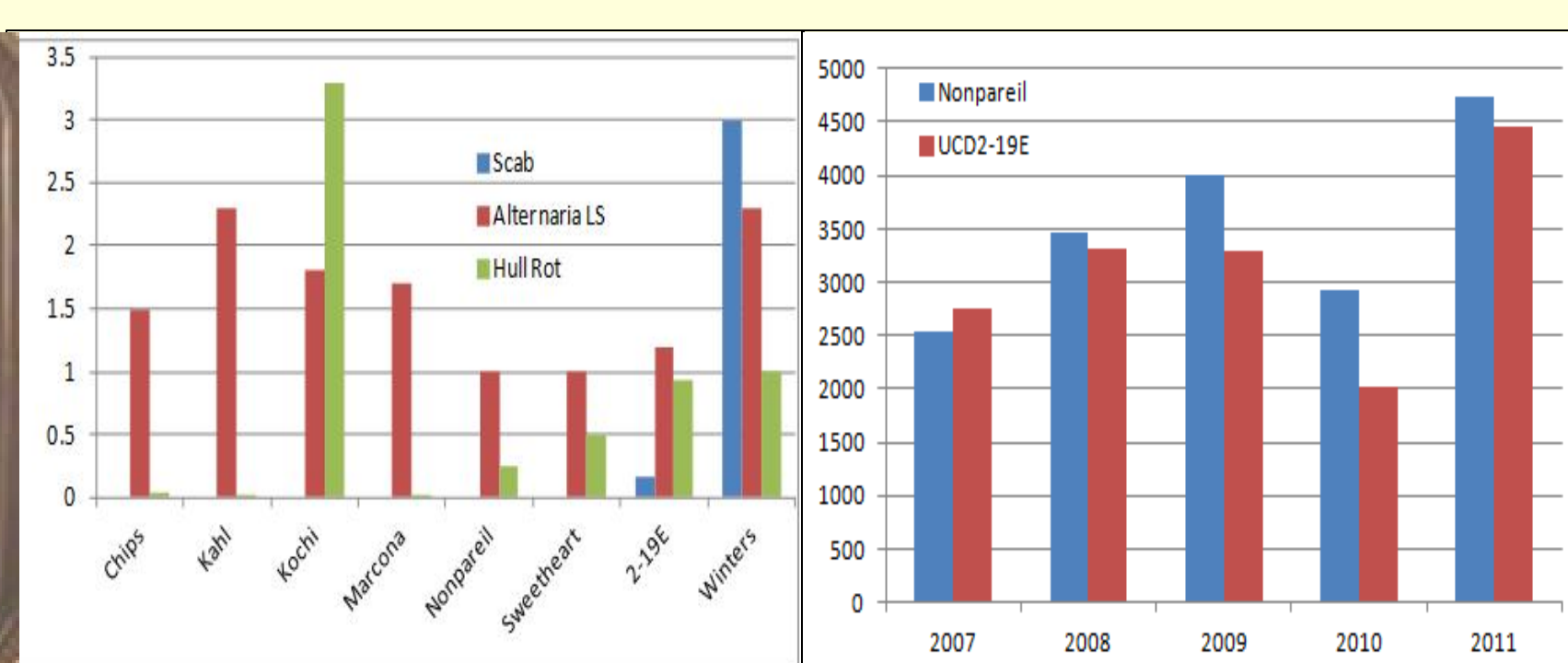


Fig. 3. Flower structure encouraging outcrossing at left (showing style and stigma extending well beyond the pollen bearing anther-sacs and so not readily self-pollinated without honeybee visits) versus flower structures encouraging self-pollination (right) showing a flower type where the stigma-style grow (bend) back into the anther area.



Fig. 4. Segregating resistance (left) and susceptibility (right) for flower/leaf blight in a breeding line derived from UCD99,9-86 (see Fig. 2).



Advanced UCD breeding selection 2-19E, which has been developed as a late Nonpareil-bloom pollenizer in which kernel and shell characteristics are comparable to (and so mixable with) Nonpareil (top-left image). Low susceptibility to the important almond diseases hull rot, Alternaria leafspot, and scab have been documented in 2012 Fresno and Kern County grower trials (top-left chart) as have high productivities over the past five years (center plot, in pounds per acre). High yields have been consistently achieved despite a smaller tree size than adjacent Nonpareil trees (top-right image) which contributes to greater yields for the economically important Nonpareil rows. Lampinen et al. have recently shown that orchard productivity of UCD2-19E is comparable to Nonpareil when size and row effects are taken into consideration (top-right chart). UCD2-19E is currently being prepared for patenting and release to California growers.

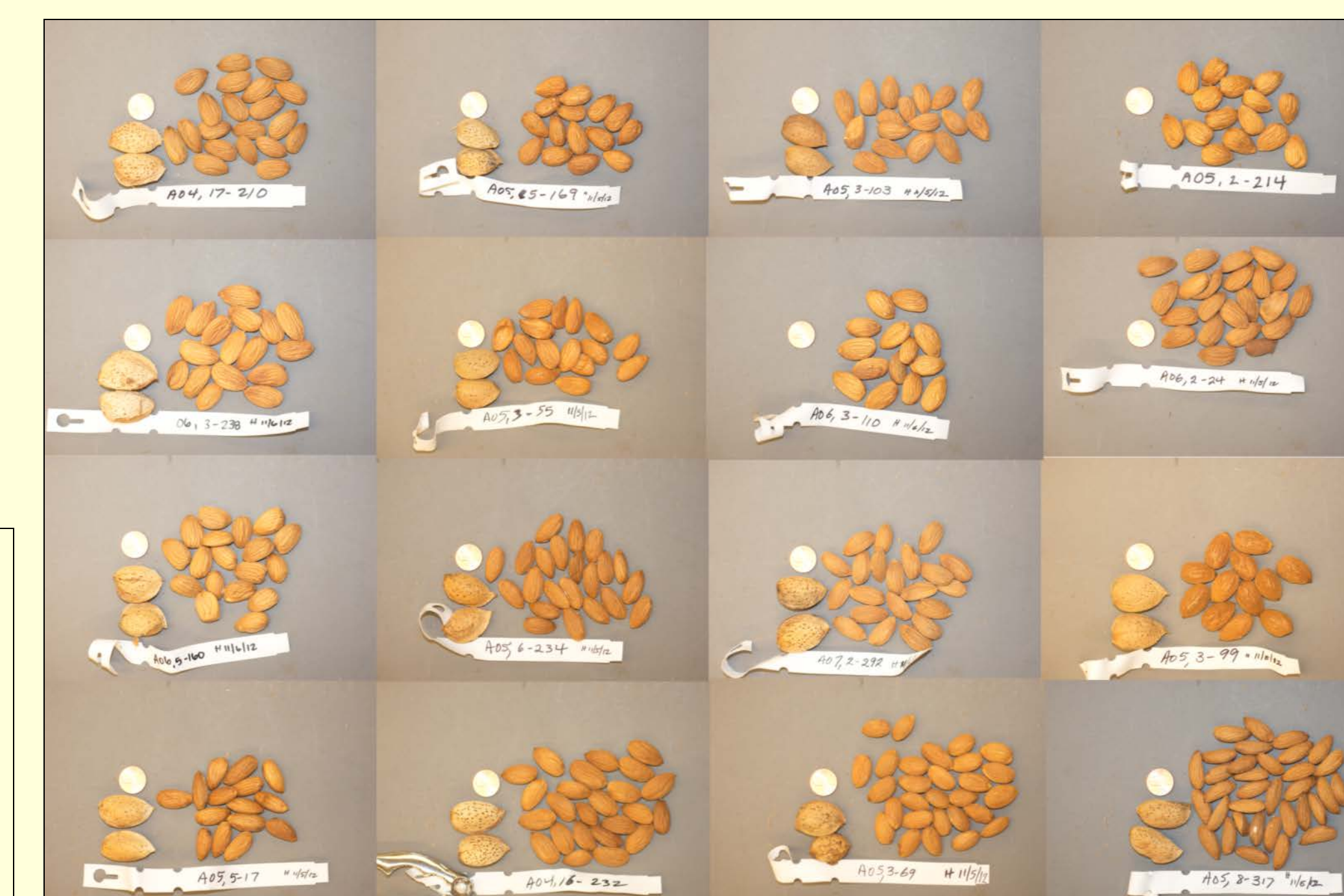
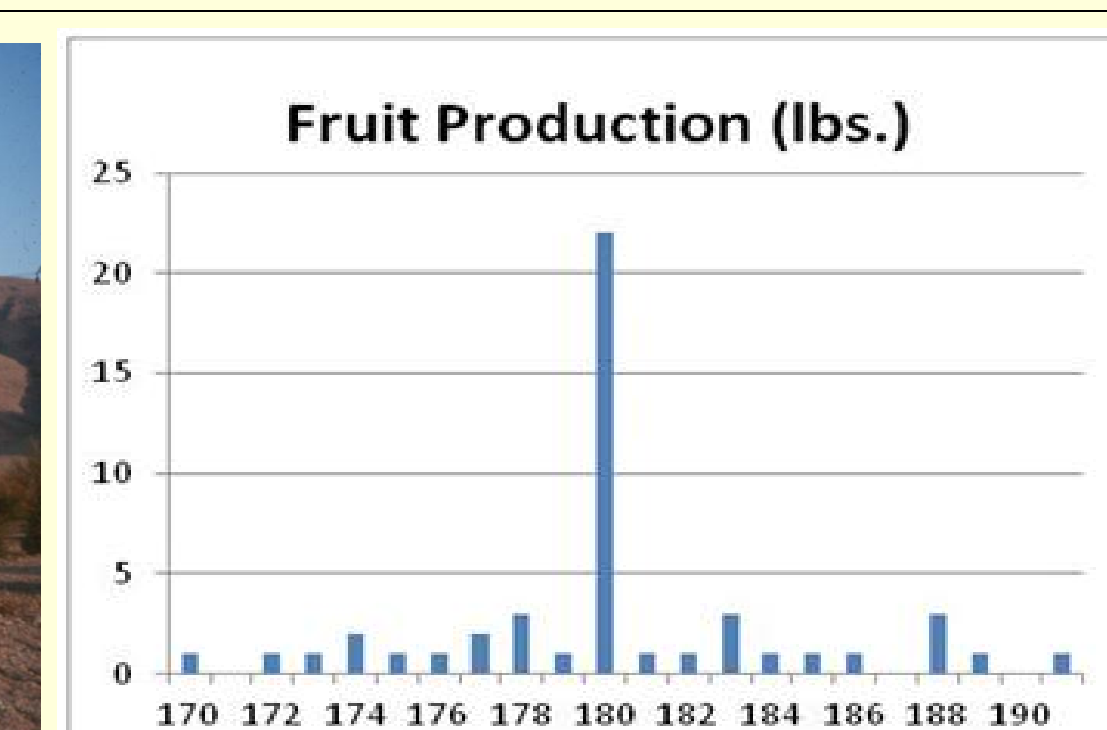
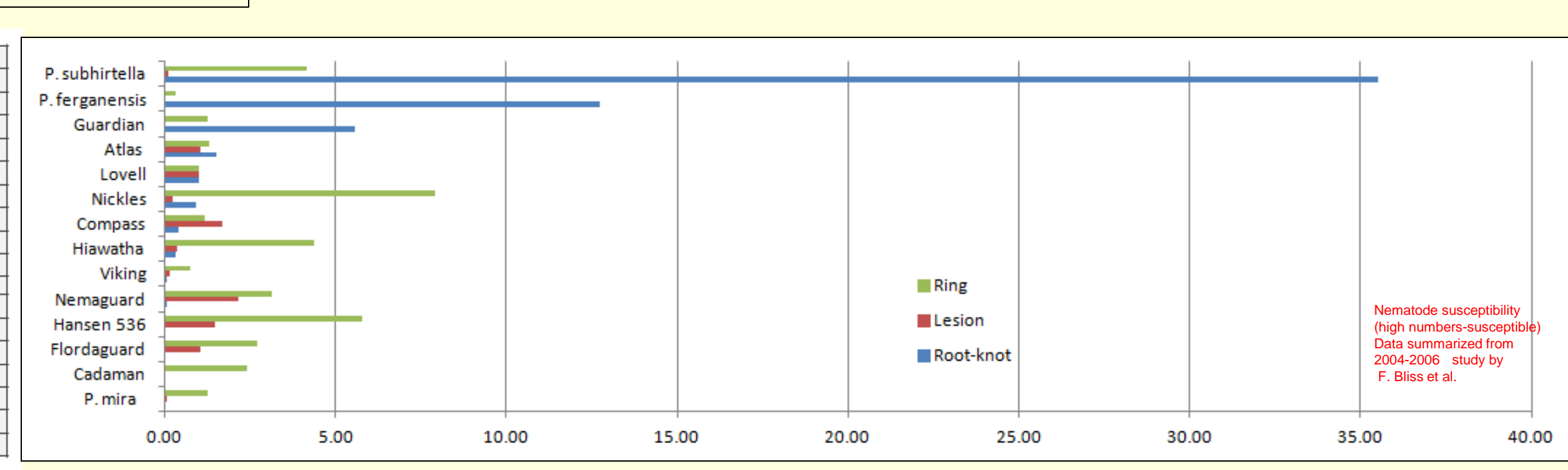


Fig. 5. Kernel and shell samples of some of the 2012 self-compatible almond selections currently being evaluated for kernel quality and tree productivity.

Interspecific breeding germplasm for rootstock research & development



Variety	OP (Avg.)
Marianne	21.7%
Lanzell	24.2%
Winters	24.8%
Seneca	25.4%
Palma	25.8%
Carnal	26.3%
Nonpareil	26.3%
Time	26.6%
NR Plus Ultra	26.6%
Fritz	26.6%
Mission	26.3%
Beta	26.3%
Hansen 536	26.9%
Nonpareil	27.4%
Peach	27.8%
(UCD 2000,3-205)	
Probability	0.02



Inter species crosses, an important source for self-compatibility and disease resistance in UCD almond variety development (see Fig. 2), can also contribute to rootstock improvement since many important high vigor and/or disease resistant rootstocks have interspecies origins (chart, above-right). The UCD diversity is demonstrated by the wild almond, *P. scoparia* which thrives in the severe deserts of central Iran (above left). Interspecies hybrids can show continued productivity under high drought stress ('180' in chart at top left) and can modify tree architecture when used as rootstocks (top, middle image). The goal of this project is to collect, preserve, and distribute the diverse germplasm developed at UCD for use by public and private researchers and breeders in order to advance the development of improved rootstocks as well as an improved understanding important disease and drought resistant characteristics (table, above). Associated genomic studies promoting a greater understanding of the genetic basis of rootstock resistance are also being pursued with collaborators at UCD, UCR, USDA/ARS and private nurseries and breeders. (A comparison of 500 molecular markers between peach and complex (peach x almond x *P. scoparia*) tri-hybrid rootstock 2000,3-205 (top) is shown below where color bars represents different markers along the 8 chromosomes.)