

Integrated Conventional and Genomic Approaches to Almond Rootstock Development

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PROJECT SUMMARY

Objectives:

- Produce interspecific hybrids involving *Prunus* spp. that are potential donors of disease resistance to enlarge diversity among hybrids to improve selection response and genetic gains.
- Intensify genotyping-by-sequencing (GBS) based high density genotyping of rootstocks and perform association analysis to develop efficient marker assisted selection strategies.
- Disease testing of commercial and experimental rootstocks to produce high quality disease phenotype data.

Background and Discussion:

Improved rootstocks with resistance to soil borne pests and diseases and drought/salinity are critical to realize the full genetic potential of scion cultivars and for sustainable production of almond. The current focus of this project is soil borne pests and diseases with view towards also addressing drought/salinity tolerance. With restrictions on use of fumigants and to minimize environmental impact, the industry reliance on rootstocks with field resistance to soil borne pests and diseases is increasing. Host plant resistance is the most durable and sustainable form of protection against soil borne pests and pathogens. In this ongoing long-term rootstock breeding project we will enlarge the taxonomic and genetic diversity of *Prunus* hybrids by involving potential donor species and genotypes. We will continue to develop molecular and genomic tools to improve selection efficiency and rapid development of rootstocks. We will intensify disease evaluation for soil borne diseases such as phytophthora root rot, crown gall, and nematodes and molecular characterization to

decipher the genetic basis of disease resistance for development of effective marker/genomic assisted selection strategies.

During spring, 2015, we produced a number of diverse hybrids: myrobalan plum (*P. cerasifera*) x wild peach (*P. mira*), almond (*P. dulcis*) x Japanese plum (*P. salicina*), peach (*P. persica*) x Japanese plum (*P. salicina*), and peach (*P. persica*) x Nanking cherry (*P. tomentosa*). These hybrids were embryo rescued and are in shoot multiplication stage in Sierra Gold Nursery. We are planning to evaluate them for resistance to soil borne diseases during late spring 2016. We will be building on the ongoing efforts of single nucleotide polymorphism (SNP) discovery by following genotyping by sequencing approach. Genotyping-by-sequencing is cost-effective for both SNP discovery and genotyping simultaneously. GBS permits high density genotyping and flexibility for genetic and association mapping. The SNP genotype data in combination with disease screening data will permit us to analyze for the association of markers with disease resistance loci. Association analysis will be performed with a mixed-model integrating the marker-inferred population structure at an estimated number of subpopulations (Q-matrix) and the pair-wise co-ancestry.

We will collaborate with Georgia Drakakaki, plant sciences, UC Davis to decipher cellular processes governing salt and drought tolerance in almond rootstocks.

Project Cooperators and Personnel: John Preece, USDA/ARS, NCGR, Davis, CA; Greg Browne, Dan Kluepfel, USDA/ARS, Crops Pathology and Genetics Research Unit, Davis, CA; Andreas Westphal, University of California, Riverside, UC Kearney Ag Center, Parlier, CA; Georgia Drakakaki and Tom Gradziel, UC Davis.

For More Details, Visit

- Poster location 48, Exhibit Hall A + B during the Almond Conference; or on the web (after January 2016) at Almonds.com/ResearchDatabase
- 2014 - 2015 Annual Reports CD (12-HORT16-Aradhya/Ledbetter); or on the web (after January 2016) at Almonds.com/ResearchDatabase
- Related projects: 15-HORT10-Gradziel; 15-PATH1-Browne; 15-PATH7-Duncan/Baumgartner; 15-HORT23-Drakakaki