Development of Genomic Tools for Almond Rootstock Improvement

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PROJECT SUMMARY

Objectives:

- Develop a set of molecular markers linked to disease-pest resistance for use in almond rootstock breeding programs.
- Discover single nucleotide polymorphisms (SNPs) using: (a) existing peach and almond sequences; (b) root specific expressed sequence tag (EST) sequences; and (c) through genotyping-by-sequencing strategy.
- Genotyping of commercially available rootstocks and newly produced genetically diverse interspecific hybrids.

Background and Discussion:

Development of improved rootstocks with resistance to soil borne and replant diseases is the key to sustainable production of almond and therefore, it is a top priority for the California Almond industry. 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. Though widely used rootstocks (e.g., Nemaguard, other peach and peach x almond hybrids) resist the attack of root knot nematodes, they are susceptible to other soil borne pests and diseases, such as lesion and ring nematodes, crown gall, *Phytophthora* and *Armillaria*.

In this project an attempt has been made to produce novel interspecific hybrids involving peach, wild almond species and diploid plums that are potential donors of resistance to soil borne diseases and in some cases drought tolerance.

Wild *Prunus* spp. are excellent sources of genes for resistance to soil borne diseases, but the data on disease-pest interactions is lacking rendering selection of species to use for hybridization difficult. For this reason it is critical to evaluate and genetically characterize wild *Prunus* spp., commercially available rootstocks, and newly generated interspecific hybrids.

While hybrids are being screened for disease resistance, genomic tools and methods are being developed to assist in efficient selection of resistant hybrids. Genome sequences of a dozen genotypes of cultivated and wild *Prunus* spp. genotypes that have been used in hybrid generation (*P. dulcis, P. argentea, P. kanuensis, P. davidiana, P. bucharica, P. kuramica, P. arabica, P. persica*, and *P. fenzliana*) are currently being analyzed to identify SNPs compatible across species.

A second approach to discover SNPs and genotype concurrently has also been undertaken using a new method called genotyping-by-sequencing (GBS). A set of all the available rootstocks that are currently being used or under field tests along with our novel hybrids are included in the GBS assay.

During 2013, 13 new interspecific hybrids were tested in replicated trials for crown gall and *Phytophthora* resistance. The results indicated that two genotypes (4-10 and 4-25: Nemared x *P. fenzliana*) are found to posses resistance to both *Phytophthora* and crown gall and (1-2: a open-pollinated *P. cerasifera*) is highly resistant to *Phytophthora*. A second round of disease testing along with more hybrids are planned for 2014.

Project Cooperators and Personnel: John Preece, USDA/ARS, National Clonal Germplasm Repository, Davis, CA; Greg Browne, Dan Kluepfel, USDA/ARS, Crops Pathology and Genetics Research Unit, Davis, CA; Michael McKenry, University of California, Riverside, UC Kearney Ag Center, Parlier, CA

For More Details, Visit

- Poster location 66, Exhibit Hall A and B during conference; or on the web (after January 2014) at www.almondboard.com/researchreports
- 2012.2013 Annual Report CD (12-HORT16-Aradhya/Ledbetter); or on the web (after January 2014) at www.almondboard.com/researchreports
- Related Projects: 13-HORT4-Duncan, 13-HORT10-Gradziel; 12-PATH7-Baumgartner; 13-PATH1-Browne