

Development of Genomic Tools for Almond Rootstock Improvement

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PROJECT SUMMARY

Objectives:

- Develop molecular markers linked to disease-pest resistance for use in almond rootstock breeding programs.
- Discover single nucleotide polymorphisms (SNPs) using genotyping-by-sequencing strategy.
- Genotype commercial and experimental rootstocks and newly produced genetically diverse interspecific hybrids.

Background and Discussion:

Development of improved rootstocks with durable resistance to soil borne diseases is a priority to the California almond industry. Currently used rootstocks such as 'Nemaguard' and other peach x almond hybrids are susceptible to one or more diseases affecting almond production in California. 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 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. A two step approach was used: (1) produce and evaluate diverse interspecific hybrids for resistance to soil borne diseases; and (2) develop and identify SNP markers linked to resistance to develop effective juvenile selection strategies to rapidly develop improved rootstocks.

During 2014, ~1900 clonal plants from a set of 34 diverse interspecific hybrids involving *P. persica*, *P. argentia*, *P. tangutica*, *P. dulcis*, *P. bucharica*, *P. kuramica*, *P. davidiana*, and *P. kensuensis* have been produced for disease evaluation scheduled for Spring 2015. Meanwhile, 190 diverse hybrids have been sequenced. These include those currently in use, under field testing, and experimental hybrids. This genotyping has yielded ~221 million reads of which 18 million unique reads were aligned to the published peach genome sequence and, after filtering, 164,742 SNPs were assembled. Further SNPs with low LD and low representation across hybrids were filtered out to arrive at 7444 (7k) SNPs for the association analysis.

The association analyses performed following the mixed linear model implemented in TASSEL and PLINK software packages indicated association of several SNPs with crown gall (CG) with R^2 values ranging from 0.09 to 0.11, which is considered significant for complex traits such as disease resistance with low heritability. While these analyses are still preliminary, at this time, we have identified significant association of markers with CG, but the analyses failed to come up with any markers for *Phytophthora*, root knot or lesion nematode infestations. We suspect that lack of consistent and adequate disease testing data has resulted in failure to detect markers associated with disease resistance. We are further filtering the data set using a number of filtering criteria to eliminate leaky data among the SNP loci identified in the GBS analysis for further analyses.

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 50, Exhibit Hall A + B during the Almond Conference; or on the web (after January 2015) at Almonds.com/ResearchDatabase
- 2013-2014 Annual Reports CD (12-HORT16-Aradhya/Ledbetter); or on the web (after January 2015) at Almonds.com/ResearchDatabase
- Related projects: 13-HORT4-Duncan;14-HORT10-Gradziel;14-PATH1-Browne;12-PATH7-Baumgartner