

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 EST sequences; and (c) through genotyping-by-sequencing strategy
- Genotyping of commercially available rootstocks and newly produced genetically diverse interspecific hybrids.

Background:

Improved almond rootstocks possessing field resistance/tolerance to soil borne pests and pathogens is a top priority for the California almond industry. While widely used rootstocks ('Nemaguard', and other peach and peach-almond hybrids) resist root knot nematode infestation, they are susceptible to other soil borne pests and diseases such as *Phytophthora* (crown and root rot), crown gall, *Armillaria* (oak root fungus), ring and lesion nematodes, and replant disorder.

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.

The focus of this project is to identify SNPs, genomic variants associated with resistance to soil borne diseases and pests. Fine scale mapping of SNPs in conjunction with pest/disease screening will facilitate genetic association analyses and enable discovery of genes conferring resistance.

Available SNP primer and genomic DNA sequences from various databases were aligned with the peach draft genome sequence to validate and to search for additional SNPs. There was 100% alignment and uniquely aligned reads ranged from 13.5% to 74% indicating some level of genome duplication. Tissue samples have been collected from a number of commercial rootstocks and rootstocks under various experimental trials for DNA isolation and genotyping-by-sequencing (GBS) while discovering additional SNPs. Of the 446 interspecific hybrids produced in 2012, 373 are in culture and 73% of them are true hybrids. 700 micropropagated plants from 28 hybrids produced in 2011 are ready to enter the disease screening process.

A dozen genotypes representing seven almond, two peach, and two plum species are being sequenced at the Beijing Genome Center. Three root specific cDNA samples from three rootstocks will also be added to the above sequencing project for root specific SNP discovery.

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 11, Exhibit Hall A & B during conference; or on the web (after January 2013) at www.almondboard.com/researchreports
- 2011.2012 Annual Report CD (10.HORT16.Aradhya/Ledbetter); or on the web (after January 2013) at www.almondboard.com/researchreports
- Related projects: 12.HORT4.Duncan, 12.HORT10.Gradziel;12.PATH7.Baumgartner; 12.PATH1.Browne