Development of Genomic Tools for Almond Rootstock Improvement

Project Leaders: Malli Aradhya¹ & Craig Ledbetter²

¹USDA/ARS, National Clonal Germplasm Repository, University of California, Davis, One Shields Ave, Davis, CA 95616, (530) 752-9392, mkaradhya@ucdavis.edu

² USDA/ARS, 9611 S. Riverbend Ave, Parlier, CA 93648, (559) 596-2817, craig.ledbetter@ars.usda.gov

PROJECT SUMMARY

Objectives:

- Validate single nucleotide polymorphisms (SNPs) identified through mining of existing *Prunus* sequence databases.
- Sequence a set of diverse cultivated and wild almonds and assemble with existing peach sequences to discover and validate SNPs.
- Use the SNPs to screen wild and cultivated peach and almond germplasm to discover novel sources of resistance to soil borne diseases/pests.

Background:

A number of soil borne pests and diseases affect almond production in California. Currently, soil fumigation is used to combat soil borne diseases. However, human health and air quality regulations, limit the use of soil fumigants.

While currently used peach and peach x almond hybrid rootstocks have some levels of resistance to soil borne diseases, the resistant rootstocks that combine resistance to multiple soil borne pests and diseases with the necessary vigor and compatibility with current almond scions are ideal for successful and sustainable production of almond. Breeding tree crops is time consuming and resource intensive. The use of genetic markers to screen breeding populations, existing and new rootstocks for gene combinations conferring combined durable resistance can accelerate the breeding process enormously.

This project is focused on identifying the genomic markers for resistance to soil borne diseases and pests such as crown gall, crown and root rot, oak root fungus, root knot nematodes, ring nematode, and replant disorder.

Single-nucleotide polymorphisms (SNPs) are the only marker system that would allow highthroughput genotyping for screening to occur in months rather than years. SNPs occur abundantly in plant genomes and are distributed uniformly throughout the genome. Thus, they can be used for fine scale mapping of resistance gene(s) locations. They facilitate genetic association analyses targeting resistance to diseases.

This project is part of a larger project focused on all aspects of rootstock breeding in almond and walnut funded by a USDA Specialty Crop Block Grant.

Project Cooperators and Personnel John Preece, Clay Weeks, 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 27, Exhibit Hall, Session 1; or on the web (after January 2011) at AlmondBoard.com/AICposters
- Related projects: 10-PREC2-Brown and 10-HORT11/11A-Shackel/Sanden