DNA Methylation as a Diagnostic Marker for Almond Clonal Ageing and Non-Infectious Bud-Failure (BF)

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PROJECT SUMMARY

Objectives:

Non-infectious bud failure (BF) appears to be a disorder resulting from the failure in function of a normal, required gene rather than the presence of a deleterious gene. Results indicate that BF is associated with DNA methylation which shuts down normal gene expression.

- DNA methylation markers associated with BF expression have been identified.
- Work is continuing to develop methylation-based markers effective in identifying BF-prone varieties and variety clones before actual field expression.

Background and Discussion:

Non-infectious bud failure (BF) is a genetic disorder in almond expressed as a failure of vegetative bud growth leading ultimately to tree decline. Our research indicates that the DNA is identical in both the normal and BF condition and so not distinguishable using standard molecular diagnostics. Recent advances in the understanding of human genomics has shown there is a diversity of epigenetic mechanisms (changes in a gene's ability to function normally rather than changes in the gene identity) that play important roles in development. This study applies epigenetic methods developed primarily in human cancer diagnostics to understand almond BF. BF remains a serious problem for the commercially important cultivars *Nonpareil* and *Carmel*, which together make up approximately 50% of total production. While clonal selection of low BF sources have previously allowed continued plantings of both cultivars, potential for BF in even the best clonal sources of *Carmel* may not be sufficiently low to ensure continued commercial plantings.

Selection of low-BF *Nonpareil* clones in the 1970s and 80s has allowed continued plantings of this dominant variety, though recent BF expression in some sources caution that these may also be progressing towards a new round of BF. BF was also a major contributor to the early abandonment of otherwise very promising cultivars such as *Merced*, and likely will be found in some of the recently released varieties, particularly those which have the BF-susceptible cultivar *Nonpareil* as a parent. This project is thus pursuing methylation-based markers for clones of *Nonpareil* and other important cultivars which differ in the level of BF expression and/or clone age (since BF-potential increases with clone age in susceptible cultivars). We have identified a number of methylation-markers associated with BF expression as well as with clone age. Because of the large number of potential markers and the inherent difficulties in accurately scoring both BF and clone age, we are currently analyzing the data using statistical techniques initially developed in the human genome projects. A strong association might be used as predictor of the ultimate level of BF expression in propagated commercial trees from different clonal sources and, if highly correlated, may help identify the gene(s) controlling this disorder, which in turn might lead to a better understanding of BF development as well as its control.

Project Cooperators and Personnel: J. Fresnedo, M.A. Thorpe, Bruce Lampinen, P. Martinez, UC Davis

For More Details, Visit

- Poster location 48, Exhibit Hall A + B during the Almond Conference; or on the web (after January 2015) at Almonds.com/ResearchDatabase
- 2013-2014 Annual Reports CD (13-HORT7-Gradziel); or on the web (after January 2015) at Almonds.com/ResearchDatabase
- Related project: 14-HORT1-Gradziel