Molecular Diagnostics for
Almond Non-Infectious Bud Failure (BF)

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PROJECT SUMMARY

Objectives:

- Evaluate possible inheritance patterns of bud failure (BF) by consolidating both historical and current data from almond x almond and almond x peach breeding populations.
- Develop genetic/epigenetic predictive models.
- Initiate a preliminary assessment of currently available molecular-based diagnostics for the ability to discriminate between high and low BF expression.
- Publish results of BF-heritability studies as a basis for a larger grant from an outside funding agency to develop molecular-based BF prediction methods.

Background and Discussion:

Non-infectious Bud-failure (BF) remains a serious problem for the commercially important cultivars Nonpareil and Carmel, which together make up approximately 50% of total production. Clonal selection of low BF sources has allowed continued plantings of both cultivars after BF first became a problem. However, BF-potential (which is related to the age of the cultivar) in even the best clonal sources of Carmel may not be sufficiently low to ensure continued commercial plantings. Careful selection of low-BF Nonpareil clones in the 1970s, 80s and 90s has allowed continued plantings of this dominant variety, though recent BF expression in some nursery sources caution that these sources may also be progressing towards a new round of BF expression. High BF expression 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 California varieties, particularly those which have the BF-susceptible cultivar Nonpareil as a parent. While clearly inherited in progeny, the genetic control of BF remains elusive.

BF is a genetic disorder in almond which is expressed as a failure of vegetative bud growth leading ultimately to tree decline. Current research indicates that BF does not follow the standard genetic model but rather is due to the failed expression of a gene/gene complex required for normal growth and development. In this case the DNA sequence (gene) is identical in both the normal and BF condition and so greatly diminishes the value of standard molecular markers as predictors of this disorder.

Recent advances in the understanding of whole plant genomics has shown there is a diversity of epigenetic mechanisms—changes in gene expression, rather than the actual genes-- that play important roles in plant development. This has led to a research surge on epigenetic mechanisms, including the development of more accurate molecular-based diagnostics and possible treatments.

BF appears to be an epigenetic disorder. The goal of this project is to identify potentially useful molecular diagnostics for this disorder and leverage our existing data and knowledge to propose almond BF as a model system of epigenetic disorders in plants. This will serve as a basis for attracting more extensive outside research funding to develop molecular-based BF prediction methods and possible treatments.

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For More Details, Visit

- 2011.2012 Annual Report CD (11.HORT7.Gradziel); or on the web (after January 2013) at www.almondboard.com/researchreports

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