
Identification of Almond Varieties and Lineages Using Molecular Markers

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Objectives:

1. Develop a specific set of molecular markers effective in unequivocally distinguishing among both old and new California almond cultivars and accessions.
2. Utilize these markers to identify/characterize old heritage varieties (including clones still in public and private collections whose identity is uncertain), current varieties and potential future varieties.
3. Use the genetic marker composition of these evaluated almonds to establish their probable lineage including relationships to major commercial varieties.
4. Evaluate potential positive (yield advantage, disease resistance, etc.) and negative (graft incompatibility, bud-failure and disease susceptibility, etc.) association with different lineages as an aid to predicting future opportunities/problems, and to assist breeding efforts.

Interpretive Summary:

The analysis of genetic markers "DNA fingerprinting", widely use in other clonal crops, will be used to identify individual almond varieties and selections. The technology also allows increasingly accurate information regarding the parentage or lineage of the variety or selection. Such information can provide details on the genetic predisposition of that selection, including susceptibility to various afflictions such as Noninfectious Bud-failure, graft-incompatibility, and susceptibility/resistance to important diseases such as blossom blight and hull rot. Precise knowledge of the lineage is also required to identify and develop other molecular markers directly associated with specific traits of horticultural importance such as disease resistance and tree productivity.

Because most California almond varieties appeared to have been derived from only a few founder varieties, particularly *Nonpareil* and *Mission*, the genetic variability in the progeny is limited, which has frustrated genetic fingerprinting attempts in the past. The

presumption that *Nonpareil* and *Mission* are founders of most subsequent almond varieties is based on limited molecular characterization as well as a documented history of their extensive interplanting in the past. However, the contribution of other early almond varieties such as Harriet, Drake, Peerless, or IXL as parents to current varieties can not be ruled out. Knowledge of the true relationship of these early California varieties to present varieties will contribute not only an improved understanding of the current limitations of this germplasm (for example, graft incompatibility on plum), but will also allow a more accurate evaluation of the potential contribution of these older varieties to modern variety development.

We have screened simple sequence repeat (SSR) DNA markers and selected a preliminary set that uniquely characterizes all important almond cultivars grown in California; we will develop more SSR markers as required. Other molecular markers (such as S-alleles) will also be included in our analysis. These markers will be used to DNA fingerprint old heritage varieties and diverse selections. Leaf samples have been collected and DNA extracted from over 150 trees provided by Joe Connell (UC Farm Advisor, Butte County), Tom Gradziel (breeder, UC Davis), nurseries and growers. Anyone with an almond cultivar identification issue should contact one of the collaborators for possible inclusion in the study. Laboratory protocols to generate the DNA fingerprints have been established and work on the current samples is in progress. We also have software and methods in place to analyze the resulting DNA fingerprints, including the discovery or confirmation of probable parents and/or lineages.

