DNA "FINGERPRINTING" of CRANBERRY VARIETIES USING RAPDs

Richard Novy and Nicholi Vorsa

Blueberry and Cranberry Research Center,
New Jersey Agricultural Experiment Station,
Rutgers University,
Chatsworth, NJ 08019

The majority of cultivated cranberry varieties were selected from native populations in the 1800's and early 1900's from sites primarily in Massachusetts, New Jersey, and Wisconsin. Since their initial selection 100-l50 years ago, varietal identities have become increasingly confused. This is primarily the result of a lack of well defined traits, not influenced by environment, that one can use to distinguish one variety from another.

In biology, there has been rapid progress in the development of various molecular markers that can be used to distinguish two individuals from one another. Molecular markers are also used to assess genetic diversity, relatedness and population genetic structure. There are a number of types of molecular markers that are available. They include biochemical (isozymes) and more recently, DNA markers. We have employed DNA markers based on the polymerase chain reaction, referred to as random amplified polymorphic DNA's or RAPD's. This procedure generates DNA band patterns which can uniquely identify or "fingerprint" a variety.

A 22 Cultivar Study

In an initial study, 22 cranberry cultivars originating from MA, WI, and NJ were analyzed utilizing RAPD's. Of the 22 cultivars, only 17 unique genotypes were identified. Three varietal groups had identical DNA fingerprints--l) 'Early Red', 'Howes' and 'McFarlin', 2) 'Biron' and 'Early Richard', and 3) 'Matthews', 'Habelman 2', and 'Norman LeMunyon'. The identification of varieties with identical DNA fingerprints might lead to the conclusion that several different varieties may be represented by an identical fingerprint. However, based on the distribution of number of band differences between pairs of varieties, we have concluded that in this study varieties with the same fingerprint are essentially genetically equivalent, and that one (or more) of the group has been misclassified.

We have also identified varieties having several DNA fingerprints, leading to the conclusion that a variety may be represented by several different genetic variants. Further RAPD analyses were undertaken with the 'Big Four' cultivars: 'McFarlin', 'Howes', 'Early Black', and 'Searles'.

Early Black

Eight clonal samples of 'Early Black' obtained from NJ, WI, and MA were DNA fingerprinted. Four clones (3 from NJ and 1 from WI) had identical fingerprints and were felt to most likely represent a "True" or "Typical" 'Early Black'. This "concensus" fingerprint differed

from the fingerprints of the four remaining clones. These four clones did not appear to be even closely related to a "Typical" 'Early Black', in fact one had a fingerprint identical to two 'McFarlin' clones from the Northwest. In summary, eight 'Early Black' clones generated five DNA fingerprints.

Howes

Seven 'Howes' sampled from NJ, WI, and MA generated five unique DNA fingerprints. A concensus fingerprint for 'Howes' was identified based upon identical fingerprints for three clones from WI, MA, and NJ, respectively. A "sterile" 'Howes' from MA was closely related to the "Typical" 'Howes", whereas the remaining clones appeared to be unrelated. The 'McFarlin'-'Howes'-'Early Red' fingerprint from the 22 cultivar study was found to be that of 'Howes'. The 'McFarlin' and 'Early Red' clones used in the study were evidently 'Howes' that had been misclassified.

Searles

Two 'Searles' from WI were found to be unrelated based upon their DNA fingerprints. A "Flat" 'Searles' appeared to be most closely related to the "Typical" 'Howes'. An additional three 'Searles', also have given unique fingerprints. Five clones of 'Searles' have generated five unique fingerprints; at this time, no concensus fingerprint has been identified for 'Searles'.

McFarlin

The RAPD analyses of six 'McFarlins' were inconclusive with respect to the identification of a concensus fingerprint for this variety. A larger survey of sixty-eight 'McFarlins' obtained from WA, MA, WI, OR, and NJ 'identified 17 DNA fingerprints for this variety. Twenty-five or 37% of the clones examined were represented by a fingerprint which appears to represent a "Typical" 'McFarlin'. The 'Rezin' and 'Bain' 'McFarlin' have the "Typical" 'McFarlin fingerprint. A group of four clones from a bog in MA and a WA clone appear to be closely related but not identical to the "Typical" group, whereas the remaining 'McFarlins' are clearly unrelated. Nine 'McFarlin' clones, obtained primarily from WA state, appear to be the variety 'Howes', based upon DNA fingerprints.

Conclusions

RAPD technology has shown that a cranberry variety may be represented by several genetic variants. Some variants appear to be the result of varietal misclassification, whereas the remainder are thought to be examples of volunteer seedlings that have become established in a varietal bog. These genetic variants can confound cranberry research studies, and can also seriously impact growers who may unknowingly establish cranberry bogs with less productive variants of a cultivar.