Methods of identification of almond by pollen ultra structure, isozymes and RAPD markers

A. Vezvaei

Dept. of Horticulture, College of Agriculture, University of Tehran, Karaj.

Pollen grains of ten almond cultivars [*Prunus dulcis* (Mill) *D.A. Webb*, syn. *p. amygdalus Bastch.*] were examined using scanning electron microscopy (SEM). The following parameters were examined: pollen length, within and L/W ratio, distance between germinal furrows (values), the number of pits, the number of ridges and strias, and thier respective widths, all within a standard area of the equatorial region of the exine. These parameters were found to be useful in distinguishing cultivars tested and indicated significant differences between cultivar at the $p<0.01$ level. Six of these cutivars can be identified with one or two characters, while for the remaining cultivars a combination of parameters is necessary for identification.

Isozyme have been used as genetic markers to evaluate gene diversity in several cultivars, genotype and seven wild species. Six isozyme systems namely, AAT, GPI, LAP, MDH, PGM, and SKDH were used. Isozyme analysis of embryos showed that there is a high level of gene diversity between genotypes and between individuals collected from different parts of Iran. These six isozyme systems showed some new alleles which are reported for the first time in the almond. Gene diversity in cultivated genotype collected from the northern parts of Iran was greater than that in cultivated genotypes from southern provinces. Gene diversity in cultivated almond was greater than in the wild species, among wild species *P.lycioides* and *P. scoparia* had the highest polymorphism possibly due to the wide distribution of these species.

RAPD analysis was applied to 12 cultivated and wild species, by using seven primers. All cultivars and species were distinguished by comparisons of different in DNA banding patterns. The dendrogram showed that among the three wild species, *P. lycioides* is more closely related to *P. scoparia* than to *P.reticulata*. In cultivated almonds, with one exception, Australian non-Iranian cultivars were cleary separated from Iranian genotypes.

Comparison of PCR and isozyme banding patterns between cultivated almonds and wild species shows that the variability of bands was lower for wild than cultivated almonds.