

BREEDING BLACK WALNUTS IN THE AGE OF GENOMICS

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ABSTRACT

Molecular markers have been used in several walnut species to help reconstruct breeding program pedigrees (Pollegioni et al. 2009), to characterize genetic structure in natural *Juglans* populations (Hoban et al. 2010, Karimi et al. 2010, Robichaud et al. 2010, Victory et al. 2006), to determine the impact of different timber harvest scenarios on residual levels of genetic diversity (Robichaud et al. 2010), and to quantify the effects of interspecific hybridization on subsequent reproduction success (Hoban et al. 2009). Pijut et al. (2007) reviewed technological applications of molecular markers used on several temperate hardwood tree species. Modern genomics-based tools are currently being used in several black walnut (*J. nigra*) studies.

A number of informative microsatellite markers, also called single sequence repeat (or SSR) markers, have been developed for black walnut (Robichaud et al. 2006). These markers have been used to help identify all trees currently in the University of Missouri (MU) germplasm collection through the development of “genetic fingerprints” for each tree, which can then be compared with standardized phenological descriptors to confirm identity (Coggeshall and Woeste 2010). These same markers have also been used to confirm the parentage (or pedigree) of black walnut trees derived from hand pollinations, as well as to identify new, full sib seedling families derived from large open-pollinated seedling populations through paternity exclusion techniques. Further, both temporal and spatial patterns of pollen flow in seed orchards and natural stands can be quantified using these markers (see Robichaud et al. 2010).

Work is underway to develop the first genetic linkage map for black walnut, based on a suite of genetic markers derived from nuclear DNA and RNA sources. In contrast to morphological markers (such as flower color), these genetic markers are *not* actual genes; instead they *represent* those genes that influence a trait (such as flowering date) in an individual. Such markers are located *near* genes that actually control a trait of interest. Defining the location and arrangement of markers on a genetic map will facilitate the identification of regions of each chromosome that may be associated with commercially important traits. It is anticipated that such knowledge will facilitate future breeding efforts to develop improved black walnuts for both timber and nut production by means of marker assisted selection techniques.

LITERATURE CITED

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