

Gene-assisted selection: Applications of association genetics for forest tree breeding

Wilcox PL, CE Echt, and RD Burdon. 2007. p 213–249 in Oraguzie NC, EHA Rikkerink, DE Gardiner, and HN De Silva (eds). *Association mapping in plants*. Springer. New York NY USA.

This comprehensive treatment of association genetics and its potential applications in forest tree breeding provides thorough background on the topic for tree breeders and forest geneticists. The authors use this book chapter to clearly define the distinguishing characteristics of forest trees, relative to other crops. Though now slightly dated, the work summarizes the status of genomic information and what we have learned about linkage disequilibrium and nucleotide diversity in tree species. The paper has a nice section on comparisons between MAS using association versus MAS using linkage mapping (within-family selection).

Wilcox et al. favor the use of the term GAS or gene-assisted selection to describe association genetics in forest trees. Though GAS has yet to find widespread use in the literature, it provides an apt description of how association differs from our earlier linkage mapping approaches to characterizing the genetic basis of complex traits. The paper describes a number of generic benefits to GAS and points out that it has applications across all tree improvement strata. A valuable section of the paper details the basic prerequisites for operational implementation of association genetics in tree breeding which includes, among other things, appropriate populations, efficient phenotypic assays, quantitative capabilities, high throughput genotyping, and good marker selection. Authors point out the need for close communication between tree breeders and the genomic scientists, the meshing of organizational and institutional requirements, and the appropriate allocation of resources to various parties.

The chapter concludes with a description of a number of specific types of applications for association genetics in tree breeding, and ultimately the potential limitations and hurdles that must be accommodated or overcome for successful application. This chapter is an important work by accomplished tree breeders and genomics experts and should be read by the tree breeding community.

Reviewed by Nicholas Wheeler