

Effect of Marker-Tagged QTL on Heritability from a Simulated Data

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With the development of high throughput genotyping, application of DNA markers, particularly SNP markers in tree breeding has become closer to a reality. We simulated a data set to examine the effect of QTLs on heritability estimates. For the study, a population of 6 individuals with 12 linkage groups and 40 loci were created. Trees were mated using the PLABSIM software to produce 15 full-sib crosses each with 10 progeny. We assigned random phenotypic values to 480 loci that are distributed across the genome with an average of 6 cM distance between any two loci. Ten loci out of 480 were randomly chosen to be QTLs, and different weights were given to examine the effects on heritability. Data were analyzed by fitting a linear mixed model to obtain variance components using ASReml. Likelihood ratio tests were carried out to test the significance of SNP markers. SNP-tagged QTLs have a significant effect on genetic variances and thus on heritability. As expected, as the QTL effects increased, the heritability estimates increased. The relationship between QTL effect and heritability was gradual for smaller QTL effects, and the slope increased substantially for higher level of QTL effects. Results for implications in tree breeding will be presented.

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