

## OVERESTIMATION OF MARKER EFFECTS IN ASSOCIATION GENETICS: A CASE STUDY IN *EUCALYPTUS GLOBULUS*

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Genome-wide association studies (GWAS) have become a common approach to discover genes and accelerate plant breeding. Statistical analyses of GWAS have treated marker effects as fixed, one at a time. In doing this, the estimated magnitudes of effect of significant markers are larger than their true values and the proportion of variance explained by them is overestimated. We evaluated this phenomenon, commonly called “Beavis effect”, in a GWAS for growth and wood traits in a *Eucalyptus* population ( $n = 303$ ), genotyped with 7,680 DArT markers. Mixed linear models accounting for population structure were used to estimate marker effects as fixed, using TASSEL, and random by a Bayesian LASSO. The absolute effects of significant markers under a fixed model were 23 to 101 times larger than those estimated under a random model. The proportion of genetic variance explained by each marker varied from 0.9 to 48.4% when fixed and 0.0 to 0.3% when random. These results illustrate how upward biased marker-trait associations can be when fitted as fixed, a matter largely unappreciated by plant geneticists. Consequences include overrated importance of candidate genes, overoptimistic prospects of marker assisted selection and misjudged QTL cloning. Genome-wide approaches treating all markers simultaneously as random provide a solution.