



Effect of Marker-Tagged QTLs on Heritability from Simulated Data

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Introduction

High throughput genotyping is providing an opportunity to use markers in tree breeding and selection programs to increase genetic gains.

Objectives

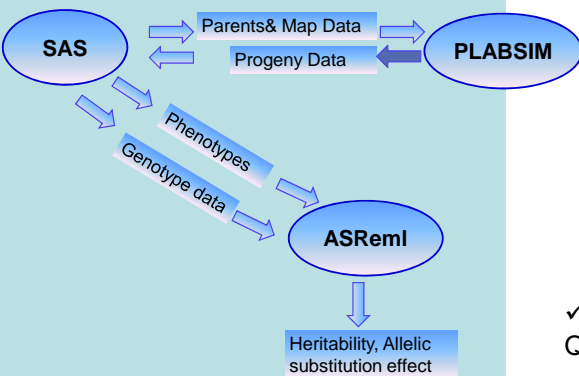
Determine the effect of changing the magnitude of simulated QTL effects on heritability, and calculate the significance of allelic substitution effect.

Simulations and Data Analysis

6-parents diallel data and genetic map data were generated with SAS.

The parents were mated using Plabsim. Phenotypic values and QTL effect were assigned to progeny using SAS.

The final data were analyzed using ASReml to estimate QTL effect, allelic substitution effect and heritability.



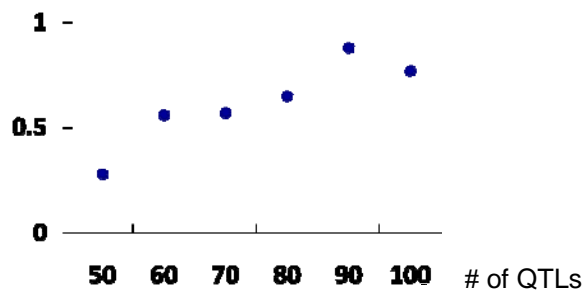
Allelic substitution effect in mixed model

$$y = Xb + e$$

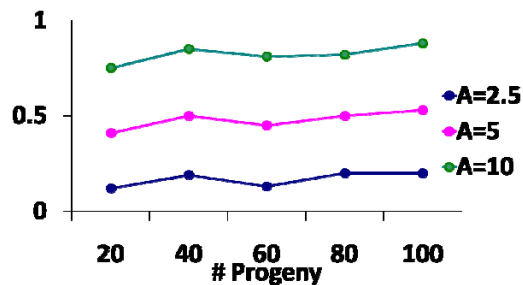
$$y = \mu + \text{SNP}(a) + \text{SNP}(d) + e$$

Where **b** is a vector of solutions for additive allelic effect, **X** is the design matrix. SNP(a) and SNP(b) are additive and dominance marker effects.

Results



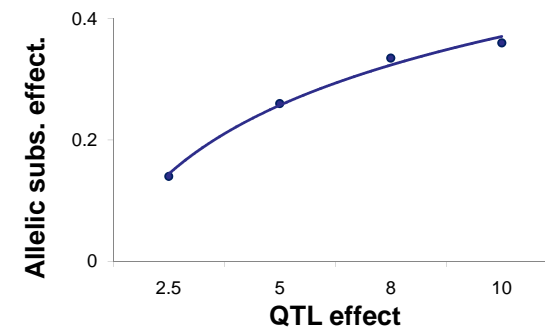
Heritability increased as the number of QTLs increased, at a constant allele effect. The reason for the decrease in heritability with 100 QTLs might be the random noise.



✓ Heritability increased as the # of the progeny and the QTLs effects (A=2.5 to A=10) increased.

✓ All of the 10 loci which were assigned as QTLs were significant (P<0.001) at the genome-wide level.

✓ Allelic substitution effects increased as the QTL effect increased, but not in direct proportion.



Conclusions

➤ For selection based on markers to be successful in a breeding program, the markers should explain a considerable portion of phenotypic variance.

➤ This will largely depend on whether they are in linkage equilibrium with the trait loci or not. The degree of linkage equilibrium is determined by the effective population size and pedigree structure of the breeding population