



# Factors influencing QTL mapping accuracy under complicated genetic models by computer simulation

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**ABSTRACT.** The accuracy of quantitative trait loci (QTLs) identified using different sample sizes and marker densities was evaluated in different genetic models. Model I assumed one additive QTL; Model II assumed three additive QTLs plus one pair of epistatic QTLs; and Model III assumed two additive QTLs with opposite genetic effects plus two pairs of epistatic QTLs. Recombinant inbred lines (RILs) (50-1500 samples) were simulated according to the Models to study the influence of different sample sizes under different genetic models on QTL mapping accuracy. RILs with 10-100 target chromosome markers were simulated according to Models I and II to evaluate the influence of marker density on QTL mapping accuracy. Different marker densities

did not significantly influence accurate estimation of genetic effects with simple additive models, but influenced QTL mapping accuracy in the additive and epistatic models. The optimum marker density was approximately 20 markers when the recombination fraction between two adjacent markers was 0.056 in the additive and epistatic models. A sample size of 150 was sufficient for detecting simple additive QTLs. Thus, a sample size of approximately 450 is needed to detect QTLs with additive and epistatic models. Sample size must be approximately 750 to detect QTLs with additive, epistatic, and combined effects between QTLs. The sample size should be increased to >750 if the genetic models of the data set become more complicated than Model III. Our results provide a theoretical basis for marker-assisted selection breeding and molecular design breeding.

**Key words:** Quantitative trait loci mapping accuracy; Sample size; Recombinant inbred lines; Marker densities; Computer simulation