



Mapping QTLs for Grain Yield in Maize: A Bayesian Approach Using Reversible Jump MCMC

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Many traits that are important to agriculture, human health and evolutionary biology, in its majority, can be classified as quantitative, whose phenotypic expression presents continuous variation, attributed to the simultaneous segregation of many genes, in definite regions as QTLs (Quantitative Trait Loci). Efficient and robust identification and mapping onto genomic positions of those genes is a very important goal in quantitative genetics. Mapping QTL is identify its position in the genoma and to estimate its effect. The availability of genome-wide molecular markers provides the means for us to locate and map those QTL in a systematic way. Since the publication of Lander and Botstein (1989), that first proposed interval mapping method for a genome-wide scan of QTL, many statistical methods have been proposed and developed to map QTL , great part of them present Classical boarding. This work will present Bayesian approach. Adopting a Bayesian approach a model is fit to quantitative trait and molecular marker data, instead of fitting to locus. The output of a Bayesian analysis is a posterior distribution on the parameters, fully incorporating prior beliefs and parameter uncertainty. Reversible Jump MCMC (RJMCMC) is used in this work. Bayes Factor is used to estimate the number of QTL. Inference summaries for the locations of the QTL and their effects are derived from the corresponding marginal posterior densities. Through Bayesian interval, significant associations between markers and QTLs were obtained in four chromosomes and five QTLs has been mapped, which explained 11.23% of genetic variation. Most alleles that contributed positively in trait came from parental strain L02-02D. The latter had the highest yield rate. We examine grain yield in maize to illustrate the applied method.

Keywords: Quantitative Trait Loci; Bayesian Approach; Reversible Jump MCMC; Bayes Factor