

A BAYESIAN APPROACH TO MAP QTL AND TO DETECT EPISTATIC EFFECTS IN A MAIZE POPULATION

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- **ABSTRACT:** *The use of molecular markers has been the main tool to study the inheritance of quantitative traits, since it allows to estimate the position on the chromosomes and the effects of the QTL that control these traits. The great difficulty of mapping QTL relates to the fact that the number of QTL is unknown and hence the dimension of the parametric space is also unknown. Bayesian approaches used with Markov Chain Monte Carlo method (MCMC) have been applied to infer QTL number, their positions in the genome and their genetic effects. The challenge is to obtain the sample from the joint posterior distribution of these parameters, since the number of QTL may be considered unknown and hence the dimension of the parametric space changes according to the number of QTL in the model. In this study, a Bayesian approach was applied, using a code implemented in the statistical program R, in order to map QTL for traits in a tropical maize population: plant height, ear height and grain yield. So, multiples QTL and epistatic effects were considered in the model and the number of QTL was considered as known. The MCMC methods were used to create a sample from the joint posterior distribution of the parameters. Models were adjusted with the crescent number of QTL and Bayes factor was used to select the most suitable model and, consequently, to estimate the number of QTL that control the traits assessed. The results from this study were compared to the results obtained using the frequentist approach for mapping QTL.*
- **KEYWORDS:** *Bayes Factor; Bayesian inference; MCMC QTL mapping.*

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