Bayesian Mapping of Multiple Traits in Maize: The Importance of Pleiotropic Effects in Studying the Inheritance of Quantitative Traits

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INTRODUCTION

•Understanding the genetic architecture of complex traits remains a great challenge for geneticists. Phenomena such as epistasis, pleiotropy and heterosis make understanding the genetic control of quantitative traits extremely complex, a veritable black box.

• One of these highly complex architectural elements is pleiotropy. Understanding pleiotropy is important for plant breeding because pleiotropy helps link genetic correlations to economically and agriculturally important traits that are also be observed through linkage disequilibrium

• The identification and distribution of pleiotropic QTLs across the genome can be achieved by Bayesian shrinkage multiple interval analysis (Wang et al. 2005; Xu et al. 2009).

•This methodology has some limitations, mainly when the degrees of freedom are restricted to number of parameters adjusted in the full-model, i.e. epistatic effects. One alternative to get around this limitation is to realize model selection or to adjust complex models where the number of parameters is higher than the number of observations.

OBJECTIVE

•In this study, we mapped multiple traits using a Bayesian approach to identify pleiotropic QTLs related to grain yield and its components in maize. In addition, we sought to obtain a better understanding of the inheritance, extent and distribution of the pleiotropic effects related to these traits..

MATERIAL AND METHODS

Genotypes

- To obtain the F_2 population, two inbred lines genetically divergent for several traits were crossed (L-14-04 B and L-08-05F). These lines belong to different heterotic groups: L-14-04 B was derived from the BR-106 population (yellow dent kernels) and L-08-05 F from the IG-1 population (flint and orange kernels). The BR-106 population was developed at EMBRAPA Maize and Sorghum Research Center and the IG-1 population was developed from the ESALQ/USP Department of Genetics by crossing Brazilian and Thai populations
- Two hundred and fifty progenies from the F_2 generation were self-fertilized to yield the $F_{2:3}$ progenies. These progenies were backcrossed to the L-14-04 B parental line to create the RC_1 progenies and also backcrossed to L-08-05 F to create the RC_2 progenies. These crosses were performed in isolated, detasseled blocks and yielded 500 backcross progenies following the Design III procedure.

Genetic Map

- The genetic map and mapping procedure used to obtain it were previously described by Sibov et al. (2003). The molecular analysis was performed at CEBEMEG/Unicamp. Briefly, the F_2 plants that generated the $F_{2:3}$ progenies were genotyped using microsatellite markers.
- A total of 177 markers distributed across the 10 maize chromosomes. The genetic map covered 2,052 cM of the maize genome, with an average distance of 11.6 cM between markers.

QTL Analysis

$$y_{ij} = b_j + \sum_{k=1}^{p} x_{ijk} a_k + \sum_{k=1}^{p} w_{ijk} d_k + e_i$$

$$p(y \mid b, a, d, x, w, \Sigma) = N(\mu, \Sigma)$$

$$\mu = \sum_{k=1}^{p} x_k a_k + \sum_{k=1}^{p} w_{ik} d_k$$

$$p(y \mid \lambda, b, a, d, x, w, \Sigma,) \propto |\Sigma \otimes I|^{-1/2} x \exp\left\{-\frac{1}{2}(y-\mu)`(\Sigma \otimes I)^{-1}(y-\mu)\right\}$$

RESULTS

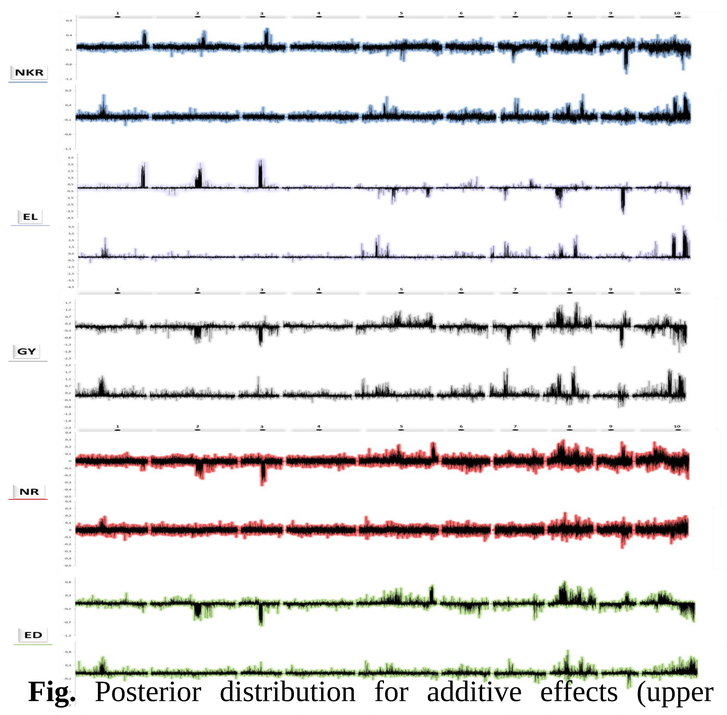


Fig. Posterior distribution for additive effects (upper lines) and dominant effects (lower lines) of the QTLs in the maize genome (chromosomes 1 to 10) responsible for the trait grain yield (GY) and its components defined by number of kernels per row (NKR), number of rows (NR), ear length (EL) and ear diameter (ED).

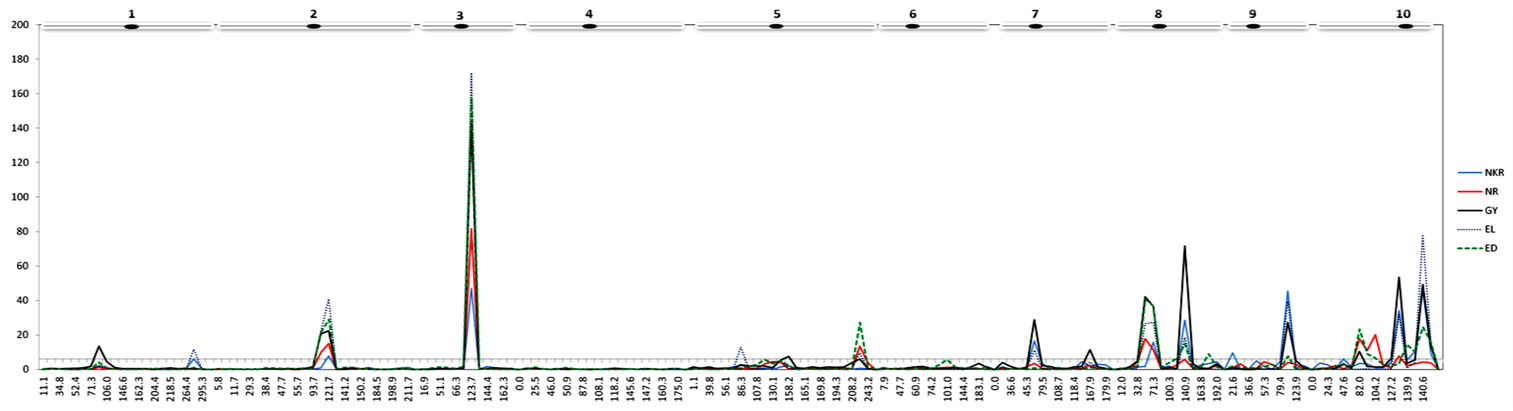


Fig. 1 Profile of the location of QTLs in the maize genome (chromosomes 1 to 10) responsible for grain yield (GY) and its components, defined by the number of kernels per row (NKR), the number of rows (NR), the ear length (EL) and the ear diameter (ED). The horizontal dotted line represents the critical value for the univariate Wald test

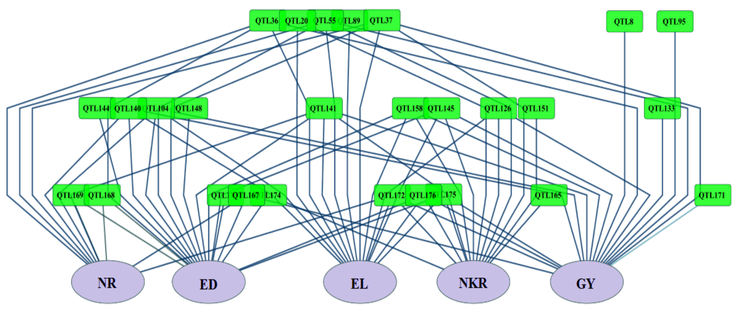


Fig 3 Hierarchical pleiotropic network (A)

CONCLUSIONS

✓ The results of this study suggest that mapping isolated traits limits our understanding of the genetic architecture of quantitative traits. This architecture can be better understood by using pleiotropic networks that facilitate the visualization of the complexity of quantitative inheritance, and this characterization will help to develop new selection strategies.

✓It was also possible to confront the idea that it is feasible to identify QTLs for complex traits such as grain yield, as pleiotropy acts prominently on its subtraits and as this “trait” can be broken down and predicted almost completely by the QTLs of its components.

✓ Additionally, pleiotropic QTLs do not necessarily signify pleiotropy of allelic interactions, and this indicates that the pervasive pleiotropy does not limit the genetic adaptability of plants.

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