

Genetic control of the performance of maize hybrids using complex pedigrees and microsatellite markers

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INTRODUCTION

• Recently, some studies have sought to dissect heterosis into quantitative traits in maize. However, conflicting results were obtained, and hypotheses that attempt to describe this phenomenon range from the simple complementation of loci with additive effects, called the dominant hypothesis to more elaborate explanations involving overdominance, genetic collinearity, epistasis, pleiotropy, and the multiplicative action of genes associated with production components (Hochholdinger and Hoecker, 2007).

• One way to study heterosis taking into account the additive, dominance effects with epistatic effects is to consider the traditional diallel as a type of complex pedigree that might involve mating between lines, hybrids, and lines with hybrids, generating an intricate system of crossbreeding (Cockerham 1961, Rawlings and Cockerham 1962a, 1962b).

OBJECTIVE

• This study seeks to quantify the importance of epistatic effects in the heterosis of corn, using complex pedigrees and joining di-, tri-, and tetra-alleles in the single analysis, with and without information from microsatellite markers

MATERIAL AND METHODS

Genotypes and genotyping

- Fifty-one inbred lines from different backgrounds were used in the crossbreeding experiments. Crossbreeding these lineages resulted in the generation of 6 double cross hybrids, 14 three way cross hybrids, and 58 single cross hybrids, for a total of 78 hybrids. The crossbreeding system can be observed in Figure 1.
- Seventy-nine microsatellite markers were used in the genotyping of the 51 lines (Table 1). These markers were distributed throughout the 10 maize linkage groups. The information obtained from these markers was used to construct genetic similarity matrices through the application of the Jacquard coefficient.
- Genetic matrices were built using the following expressions:

$$G_{dd_{kl}} = g_{d_k} g_{d_l}; k=1,2,\dots,n_{dd}; l=1,2,\dots,n_{dd}$$

$$G_{ad_{kl}} = g_{a_k} g_{d_l}; k=1,2,\dots,n_{ad}; l=1,2,\dots,n_{ad}$$

$$G_{aa} = g_{a_k} g_{a_l}; k=1,2,\dots,n_a; l=1,2,\dots,n_a$$

$$G_{ij} = \frac{1}{4} [p(x_i^m = x_j^m) p(x_i^f = x_j^f) + p(x_i^m = x_j^f) p(x_i^f = x_j^m)]$$

Genetic model

$$G = m + \sum_i \rho_i a_i + \sum_{ij} \sigma_{ij} d_{ij} + \left(\sum_i \rho_i a_i \right)^2 + \left(\sum_i \rho_i a_i \right) \left(\sum_{ij} \sigma_{ij} d_{ij} \right) + \left(\sum_{ij} \sigma_{ij} d_{ij} \right)^2$$

$$y = X\beta + Z_1 a + Z_2 d + \Omega aa + \Psi ad + \Phi dd + \varepsilon$$

$$G = m + \sum_i \rho_i a_i + \sum_{ij} \sigma_{ij} d_{ij} + \sum_{ij} \rho_i \rho_j (aa)_{ij} + \sum_{ij} \sum_{jk} \rho_i \rho_j \sigma_{jk} (ad)_{i(jk)} + \sum_{ij} \sum_{kl} \sigma_{ij} \sigma_{kl} (dd)_{ij}$$

RESULTS

Table 3 Model selection based on the Bayesian information criterion (smaller is best) for the additive, dominant, and epistatic effects, considering the model with molecular marker information.

Model	BIC	DEV	σ_a^2	σ_d^2	σ_{aa}^2	σ_{ad}^2	σ_{dd}^2
dd	2703.10	2689.11	-	-	-	-	<u>0.30</u>
ad	2708.38	2694.39	-	-	-	0.14	-
aa	2708.70	2694.71	-	-	0.06	-	-
a+dd	2710.87	2689.88	<u>0.10</u>	-	-	-	<u>0.20</u>
d+dd	2711.18	2690.20	-	<u>0.11</u>	-	-	<u>0.19</u>
aa+dd	2711.50	2690.51	-	-	0.03	-	0.13
ad+dd	2711.57	2690.59	-	-	-	0.08	0.12
d	2714.04	2700.05	-	0.33	-	-	-
a+d+dd	2714.50	2693.52	0.07	0.08	-	-	0.15
aa+ad	2715.26	2694.27	-	-	0.03	0.07	-
d+ad	2716.20	2695.21	-	0.07	-	0.11	-
a+ad	2716.20	2695.21	0.07	-	-	0.10	-
a+aa	2716.30	2695.32	0.07	-	0.05	-	-
d+aa	2716.35	2695.36	-	<u>0.08</u>	<u>0.04</u>	-	-
d+aa+dd	2718.91	2690.92	-	<u>0.06</u>	<u>0.02</u>	-	<u>0.11</u>
a+aa+dd	2718.91	2690.92	0.05	-	0.02	-	0.11
d+ad+dd	2718.97	2690.99	-	0.05	-	0.07	0.11
a+ad+dd	2719.03	2691.05	0.05	-	-	0.07	0.10
aa+ad+dd	2719.10	2691.12	-	-	0.02	0.05	0.09
a+d	2720.83	2699.84	<u>0.12</u>	<u>0.18</u>	-	-	-
d+aa+ad	2722.66	2694.68	-	0.04	0.02	0.06	-
a+aa+ad	2722.87	2694.89	0.05	-	0.02	0.06	-
a+d+ad	2723.68	2695.70	0.06	0.05	-	0.08	-
a+d+aa	2724.06	2696.08	0.06	0.07	0.03	-	-
a+d+aa+dd	2726.27	2691.29	0.05	0.05	0.02	-	0.10
a+d+ad+dd	2726.29	2691.31	0.04	0.04	-	0.06	0.09
d+aa+ad+dd	2726.34	2691.36	-	0.04	0.02	0.05	0.08
a+aa+ad+dd	2726.45	2691.47	0.04	-	0.01	0.05	0.08
a+d+aa+ad	2730.18	2695.21	0.04	0.04	0.02	0.06	-
Full	2731.68	2689.70	<u>0.09</u>	<u>0.00</u>	<u>0.00</u>	<u>0.01</u>	<u>0.20</u>
a	2752.26	2738.27	0.36	-	-	-	-

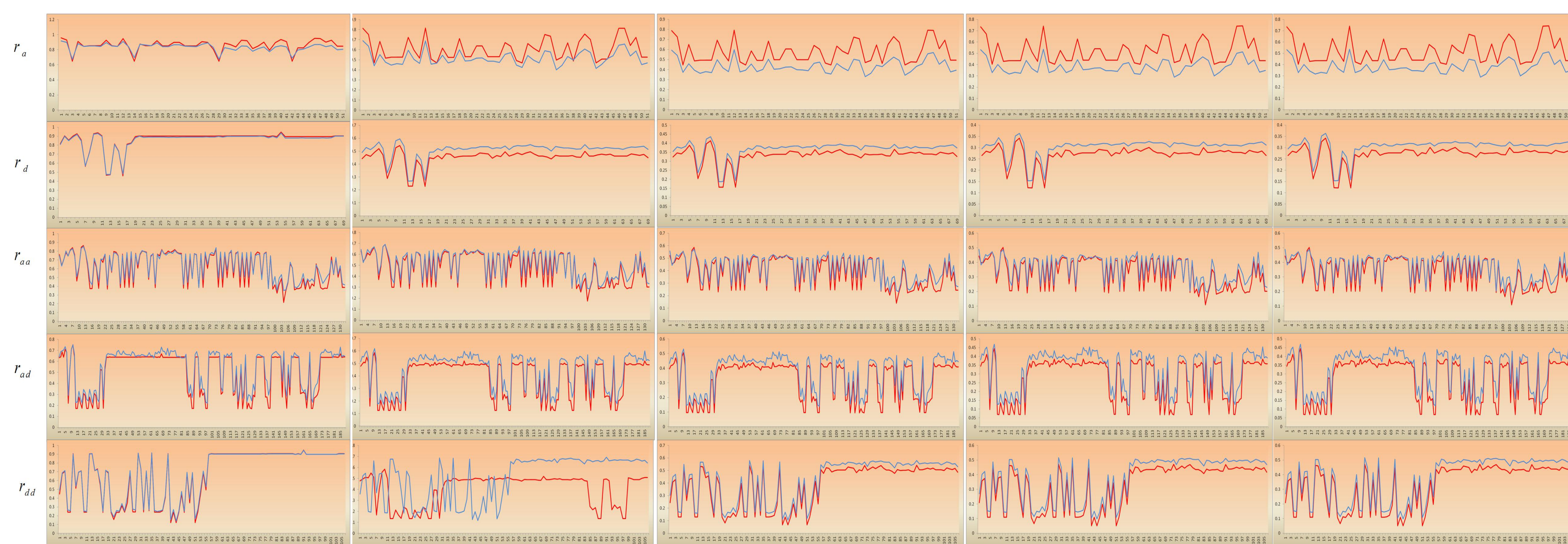


Fig 2. Average predictive accuracy of the additive, dominant, and epistatic genetic effects, considering all the possible combinations of additive and epistatic effects, in which a-e refer to the models containing one, two, three, four, and five parameters, respectively (see Table 1 for genetic models). The red line refers to the model without kinship (NI), and the blue line refers to the model with marker information (MI). The x-axis one refers to hybrid and y-axis to average predictive accuracy

CONCLUSIONS

- ✓ Dominant by dominant epistasis was the most important effect related to genetic control of the heterosis in maize.
- ✓ It was also possible to show that the use of molecular markers improves the accuracy of the epistatic genetic and dominance effects.
- ✓ The concept of crossbreeding can be expanded to frontiers well beyond traditional general and specific combining ability

REFERENCES

- Cockerham CC (1961) Implications of genetic variances in a hybrid breeding program. *Crop Science*. v.1. p.47-52
- Hochholdinger F, Hoecker N (2007) Towards the molecular basis of Heterosis. *TRENDS in Plant Science*, 12: 427-432
- Rawlings J, Cockerham CC (1962a) Analysis of double cross hybrid populations. *Biometrics* 18:229. 244.
- Rawlings J, Cockerham CC (1962b) Trialallel analysis. *Crop Science*, 2:228-231.

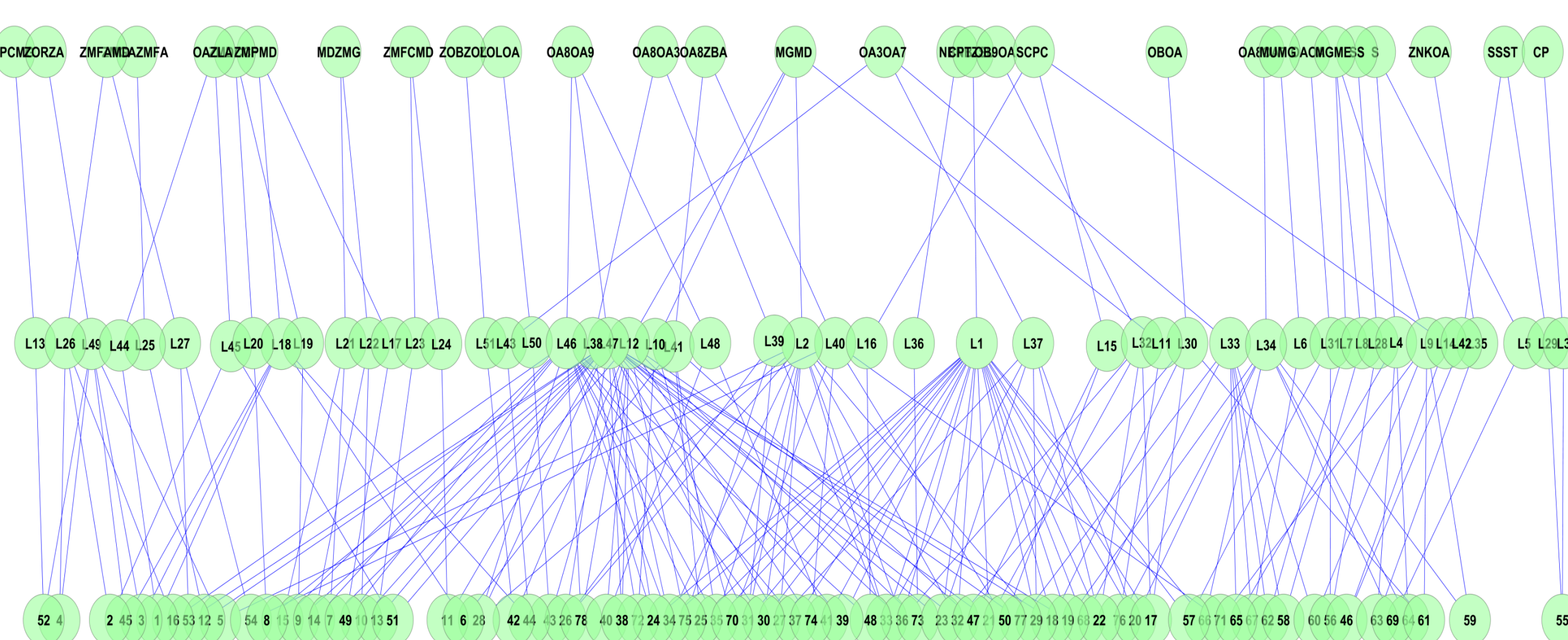


Fig 1 The crossbreeding system in 51 maize inbred lines. The upper circles refer to the backgrounds of each line