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An Analysis on the Relationship between Maize Heterosis and Genetic Distance

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Abstract 13 normal maize inbred lines with quite different quantitative traits were used as experimental materials in this paper. The results showed that there was significantly positive correlation between genetic distance and plot yield, mid-parent heterosis, super heterosis, or SCA of yield. In a certain range, the longer the genetic distance between parental inbred lines, the stronger the heterosis. Therefore, in genetic practice, it was necessary to take the molecular genetic distance between inbred lines as an important reference.

Key words Maize, Heterosis, Genetic distance, Yield

1 Introduction

The molecular markers have been applied in the study on genetic diversity of maize inbred lines. Since the use of molecular markers in the study of maize germplasm in the early 1990s, scientists have expected that this technology will be able to change the breeding blindness, and even predict heterosis. Up to now, a large number of molecular markers have been used in germplasm division study, and the results show that the analysis results of molecular level dovetail nicely with genealogical records. RFLP molecular marker technique is used to analyze maize inbred lines, and the division results of heterotic groups by RFLP markers are consistent with lines. Later, SSR, RAPD and AFLP markers are also used to divide the heterotic groups.

2 Test materials and methods

2.1 Test materials 13 normal maize inbred lines with quite different agronomic and quantitative traits and genetic background, provided by Maize Research Institute of Jilin Academy of Agricultural Sciences, were used as experimental materials in this paper, code-named B_1, B_2, B_3, B_4, B_5, B_6, B_7, B_8. B_1, B_2, B_4, B_6, B_7, B_{10}, B_{14} were used as female parents, and B_3, B_5, B_8, B_9, B_{18}, B_{19} male parents.

2.2 Field design In 2010, according to the NC II incomplete diallel experiment design method, 42 cross combinations were prepared, namely $M = p \times q = 42$ test materials, and selfing was conducted to retain parent. In 2011, according to the randomized block design, a total of 55 materials (42 combinations designed in the incomplete diallel cross experiment and 13 corresponding parents) were sown in the experimental field of Maize Research Institute of Jilin Academy of Agricultural Sciences, repeated three times. In the plot, the row length was 5 m, row spacing was 0.65 m, and plant spacing was 0.30 m. The plot management is the same as that of field.

2.3 Determination of agronomic traits The field investigation items included plant height, ear height and stem diameter. The indoor test items included ear length, ear diameter, bald tip length, ear row number, row grain number, 100-grain weight, seed yield and plot yield. 10 representative ears were selected to test the ear characters while other items were tested with plot as unit.

2.4 Analysis of heterosis Super mid-parent heterosis:

$$MHP(\%) = \frac{F_1 - \frac{P_1 + P_2}{2}}{\frac{P_1 + P_2}{2}} \times 100$$

where F_1 is the average trait value of the first generation of hybrid; P_1 and P_2 are trait values of two parents.

Super high parent heterosis: $HPH(\%) = \frac{F_1 - P_h}{P_h} \times 100$

where P_h is the highest trait value in the parent.

2.5 SSR markers The molecular experiment was mainly carried out in the molecular laboratory of Maize Research Institute of Jilin Academy of Agricultural Sciences.

3 Results and analysis

3.1 Analysis of field test results The analysis of variance was conducted on the cross combination and inbred lines yield (Table 1). The results showed that the difference between the combinations reached a very significant level, indicating that there were significant genetic differences in yield trait. Clearly, the field test results were reliable, and could be used for analysis of heterosis and analysis of correlation with SSR results.

Table 1 Analysis of variance of yield

Source of variation	*DF*	*F*	*P*
Block	2	2.4124	0.0959
Combination	41	10.4691	0.0001
Male parent	5	10.5358	0.0001
Female parent	6	2.0351	0.0917

3.2 Genetic distance of 13 inbred lines and cluster analysis According to SSR data, the genetic distance of molecular markers was calculated, and it was found that the genetic distance of the test inbred lines was 0.1272 – 0.9782, and the average distance

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was 0.5136. According to the genetic distance matrix, UPGMA method was used for cluster analysis, to get the SSR clustering diagram of 13 maize inbred lines (Fig. 1). It could be found that with the genetic distance of 0.58 as standard, the test inbred lines could be divided into five groups: Group I including B_1, B_6, B_4, B_{10}, B_{14}, B_{18}; Group II including B_2; Group III including B_5, B_7, B_9; Group IV including B_8, B_{19}; Group V including B_3.

3.3 Relationship between genetic distance and average or super heterosis of yield

3.3.1 Relationship between genetic distance and average heterosis. The correlation coefficient between genetic distance between inbred lines and average yield heterosis of cross combination was $r = 0.45$ ($n = 41$, $P < 0.01$), indicating that there was a highly significant positive correlation between genetic distance between inbred lines and average yield heterosis of cross combination in this experiment. Through the analysis of field test results (Table 2), it was found that for the eight cross combinations with the highest average yield heterosis, the parents were from different groups (I, III, IV, V), and there was great genetic distance between the parents; for the eight cross combinations with the lowest average yield heterosis, two parents of four combinations were from the same group (I), and two parents of two combinations were from the same group (III). This indicated that the combination constituted by the parents selected from different groups had strong average heterosis, while the combination constituted by the parents selected from the same group had weak average heterosis.

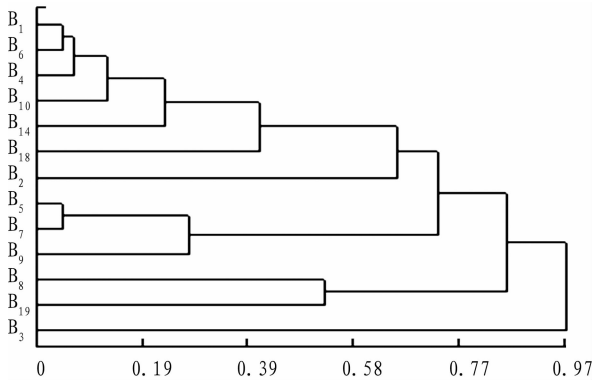

Fig. 1 UPGMA clustering of SSR markers of 13 maize inbred lines

Table 2 Top (last) eight cross combinations in terms of mid-parent value and genetic distance between inbred lines

Top eight				Last eight			
No.	Combination	Genetic distance	Midparent value	No.	Combination	Genetic distance	Midparent value
1	$B_6 \times B_8$	0.760	186.655	1	$B_{10} \times B_{18}$	0.455	−0.138
2	$B_1 \times B_{19}$	0.900	182.509	2	$B_4 \times B_{18}$	0.364	10.074
3	$B_6 \times B_3$	0.951	178.435	3	$B_7 \times B_5$	0.134	15.233
4	$B_4 \times B_9$	0.750	175.037	4	$B_{14} \times B_{18}$	0.333	19.679
5	$B_4 \times B_8$	0.760	174.507	5	$B_6 \times B_{18}$	0.455	20.773
6	$B_{14} \times B_8$	0.833	172.887	6	$B_{10} \times B_9$	0.583	106.114
7	$B_1 \times B_8$	0.760	170.098	7	$B_7 \times B_9$	0.250	111.794
8	$B_{10} \times B_{19}$	0.900	168.771	8	$B_{14} \times B_5$	0.727	132.581

3.3.2 Relationship between genetic distance and super heterosis. The correlation coefficient between super heterosis of cross combination and genetic distance between inbred lines within combination was $r = 0.44$ ($n = 41$, $P < 0.01$), indicating that in this experiment, there was an extremely significant positive correlation between super heterosis of cross combination and genetic distance between parental inbred lines. By analyzing field test results (Table 3), it was found that the parents of eight combinations with the highest super heterosis were from different groups (I, III, IV, V), respectively, and the genetic distance between parents was large; for the eight cross combinations with the lowest super heterosis, the parents of only two combinations ($B_{10} \times B_9$, $B_{10} \times B_9$) were from different groups. This indicated that the combinations of the parents selected from different groups had strong super heterosis, while the combinations of the parents selected from the same group had weak super heterosis.

Table 3 Top (last) eight cross combinations in terms of super heterosis value and genetic distance between inbred lines

Top eight				Last eight			
No.	Combination	Genetic distance	Super heterosis value	No.	Combination	Genetic distance	Super heterosis value
1	$B_6 \times B_8$	0.760	175.057	1	$B_{10} \times B_{18}$	0.455	−4.260
2	$B_6 \times B_3$	0.951	172.706	2	$B_4 \times B_{18}$	0.364	6.594
3	$B_1 \times B_{19}$	0.900	172.341	3	$B_7 \times B_5$	0.134	10.516
4	$B_4 \times B_9$	0.750	166.767	4	$B_{14} \times B_{18}$	0.333	14.456
5	$B_4 \times B_8$	0.760	162.856	5	$B_6 \times B_{18}$	0.455	14.777
6	$B_{10} \times B_{19}$	0.900	162.359	6	$B_{10} \times B_9$	0.583	84.738
7	$B_1 \times B_8$	0.760	152.842	7	$B_7 \times B_9$	0.250	102.658
8	$B_1 \times B_9$	0.667	150.734	8	$B_{14} \times B_9$	0.652	119.972

3.3.3 Relationship between genetic distance and yield. The correlation coefficient between yield of cross combination and genetic distance between inbred lines within combination was $r = 0.46$ ($n = 41$, $P < 0.01$), indicating that in this experiment, there was

an extremely significant positive correlation between yield of cross combination and genetic distance between parental inbred lines. By analyzing field test results (Table 4), it was found that the parents of eight combinations with the highest yield were from different groups (I, II, IV, V), respectively; for the eight cross combinations with the lowest yield, the male and female parents of most combinations were from the same group, and the parents of only two combinations ($B_{10} \times B_9$, $B_7 \times B_8$) were from different groups. This suggested that it was most likely to select the cross combinations with a strong advantage from different groups, while due to small genetic differences between inbred lines within group, there was a weak advantage, and it was hard to select the combinations with high yield. Therefore, in breeding practice, in order to improve the breeding efficiency, it was necessary to conduct hybridization between groups and avoid hybridization within groups. In a certain range, the greater the genetic distance between inbred lines, the higher the yield of hybrids between inbred lines; on the contrary, the yield of hybrids between inbred lines would be lower. Therefore, the analysis of genetic distance could be used as an important basis for hybrid selection (yield increase). The above analysis results indicated that there was a significantly positive correlation between genetic distance and mid-parent heterosis, super heterosis, yield SCA or plot yield, so it was possible to predict normal maize heterosis.

Table 4 Top (last) eight cross combinations in terms of yield and genetic distance between inbred lines

Top eight				Last eight			
No.	Combination	Genetic distance	Yield (kg)	No.	Combination	Genetic distance	Yield (kg)
1	$B_{10} \times B_{19}$	0.900	8.724	1	$B_10 \times B_{18}$	0.455	3.184
2	$B_1 \times B_{19}$	0.900	8.711	2	$B_4 \times B_{18}$	0.364	3.254
3	$B_2 \times B_{18}$	0.714	8.299	3	$B_7 \times B_5$	0.134	3.414
4	$B_{14} \times B_8$	0.833	8.187	4	$B_6 \times B_{18}$	0.455	3.504
5	$B_2 \times B_{19}$	0.789	8.064	5	$B_{14} \times B_{18}$	0.333	3.753
6	$B_4 \times B_{19}$	0.879	8.007	6	$B_{10} \times B_9$	0.583	6.143
7	$B_2 \times B_3$	0.895	7.980	7	$B_7 \times B_9$	0.250	6.482
8	$B_2 \times B_5$	0.727	7.949	8	$B_7 \times B_8$	0.840	6.739

4 Conclusions

In this experiment, the results showed that in a certain range, the greater the genetic distance between parental inbred lines, the stronger the heterosis, which was consistent with the results of previous studies. Therefore, in the practice of breeding, it was necessary to take the molecular genetic distance between inbred lines as an important reference. From this experiment, it was found that almost all combinations with strong advantages were constituted by hybrids between inbred lines from different groups, but the combinations constituted by hybrids between inbred lines might have no strong advantage, which was in line with the findings about maize inbred lines from Ajmone *et al.*, Wu Minsheng *et al.*, Cao Yongguo *et al.*, and Huang Yiqin *et al.* Experimental results showed that there was a significantly positive correlation between genetic distance and mid-parent heterosis, super heterosis, yield SCA or plot yield, so it was possible to predict normal maize heterosis.

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