

Heterotic Groups in Sunflower

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Abstract

Research was undertaken to determine if heterotic groups could be established amongst a set of parental lines by determining their coancestry using RFLP markers. A dendrogram based on RFLP genetic-similarity analysis of 88 maintainer and 149 restorer inbreds was constructed. The fingerprinting was conducted using a set of 32 RFLP probes representing 34 random markers.

Based on genetic coancestry analysis, parental lines were divided into seven major groups. Of these, three were predominantly maintainer and four were predominantly restorer lines. The groups were separated from each other by an average genetic distance of more than 0.4.

A diallel experiment involving 129 hybrids was conducted in 9 locations to compare the heterosis between and within the identified maintainer and restorer groups.

The results of our experiment, though preliminary, suggest significant differences between tested maintainer-restorer hybrid groups. While the top four yielding hybrid groups were created by crossing CMS-converted maintainers with restorer lines, the mean of hybrids created by intercrossing maintainer lines yielded more than half of the maintainer-restorer hybrid sets. This suggests that the "average" heterosis a breeder typically obtains by crossing maintainers with restorers to create hybrids is not dramatically better than the average one could obtain by combining different maintainer parents. It appears that further evaluation of heterotic potential across these pools and within the maintainer pools is warranted.

Introduction

Cultivated sunflower (*Helianthus annuus* L.) is described as having a narrow genetic base (Vranceanu,1985 ; Korell et al.,1992) and seems to have originated from a small number of ancestral germplasm sources, mostly selections from open-pollinated populations utilized prior to the development of hybrid sunflower (Cheres and Knapp,1998).

Since hybrid sunflower breeding is still a relatively new undertaking and has been dominated by commercial breeding efforts, information on heterotic patterns is lacking in the public domain. The characterization of heterotic groups in sunflower should allow the breeders to work the genetic variability with more efficiency in order to maximize heterosis. The development of various genetic marker systems such as RFLP, AFLP, and SSR's provides the modern breeder with tools to determine genetic relationships between parental lines and hybrids based on DNA similarity.

The goal of our research was to make some preliminary investigations into the possibility of using genetic markers and resulting coancestry determinations to develop potential heterotic groupings.

Materials and Methods

A total of 437 active Pioneer inbreds including 175 maintainer and 262 restorer lines, were fingerprinted using a set of 32 RFLP probes representing 34 random markers. A subset of 88 elite maintainer and 149 restorer lines were chosen for further analysis. Dendrograms and genetic similarity matrices were created using the RFLP fingerprint data.

The subset of 237 inbreds clustered into 7 major groups, three predominantly consisting of maintainer inbreds (A, B, C), and four predominantly consisting of restorer inbreds (D, E, H, J). Hybrids created by intercrossing selected parental lines within these groups were analyzed for yield in a diallel experiment to determine if hybrid performance was related to genetic similarities within and between groups.

Three lines per group were selected to produce hybrids in 1998 as outlined in Table 1.:

- heterosis effect between female and male groups : $(3 \times 3) \times (4 \times 3) = 108$ hybrids
- heterosis effect within female and male groups : $(3 \times 3) + (4 \times 3) = 21$ hybrids

A total of 129 hybrids and 15 checks were tested in the field during 1998 and 1999 using a nested design of 14 groups, 2 replications per location, and 9 locations distributed across four countries as follows:

Argentina	: 2 locations
France	: 4 locations
India	: 1 location
USA	: 2 locations

Grain yield data, adjusted for seed moisture content, was collected at all locations. The India location was discarded for this trait in the final analysis.

Table 1. Diallel study

INBREDS	A_A1	A_A2	A_A3	A_B1	A_B2	A_B3	A_C1	A_C2	A_C3	A_D1	A_H1	A_J1	
R_A1	1			1				1					Between Within
R_B1	1			1				1					
R_C1	1			1				1					
R_D1	1	1	1	1	1	1	1	1	1	1	1	1	
R_D2	1	1	1	1	1	1	1	1	1				
R_D3	1	1	1	1	1	1	1	1	1				
R_E1	1	1	1	1	1	1	1	1	1				
R_E2	1	1	1	1	1	1	1	1	1				
R_E3	1	1	1	1	1	1	1	1	1	1	1	1	
R_H1	1	1	1	1	1	1	1	1	1				
R_H2	1	1	1	1	1	1	1	1	1	1	1	1	
R_H3	1	1	1	1	1	1	1	1	1				
R_J1	1	1	1	1	1	1	1	1	1				
R_J2	1	1	1	1	1	1	1	1	1	1	1	1	
R_J3	1	1	1	1	1	1	1	1	1				
TOT HYB	15	12	12	15	12	12	12	15	12	4	4	4	129

R_D1 Restorer inbred number 1 , in Group D
A_B2 Maintainer inbred number 2 , in Group B

Results and Discussion

Consistent with results presented in other studies by Gentsbittel et al. (1994), our RFLP analysis clearly separated parental inbreds into groups that could be predominantly characterized as either maintainer or restorer pools. This is consistent with the breeding history of sunflower, whereby the maintainer and restorer pools have somewhat different origins (though they also share some ancestry) and have been largely bred independently to maintain heterosis between the pools. Within the two major groups, three maintainer and four restorer subgroups were identified. Inbred lines within these groups generally possessed somewhat common ancestry, being related to historically important public breeding lines.

The average similarity index calculated for 2500 possible pairwise comparisons among 72 Pioneer inbreds was approximately 0.50. This is higher than values reported by Gentsbittel et al. (1994) who found an average of 0.21 but similar to those found by Zhang et al. (1995) who found 0.6 among 26 cultivated sunflower inbreds.

The following statistical model was used to analyze the field data:

$$y_{ijkl} = \mu + a_i + \beta_j + \delta_{k(j)} + c_{l(i)} + (a\beta)_{ij} + (a\delta)_{ik(j)} + e_{ijkl}$$

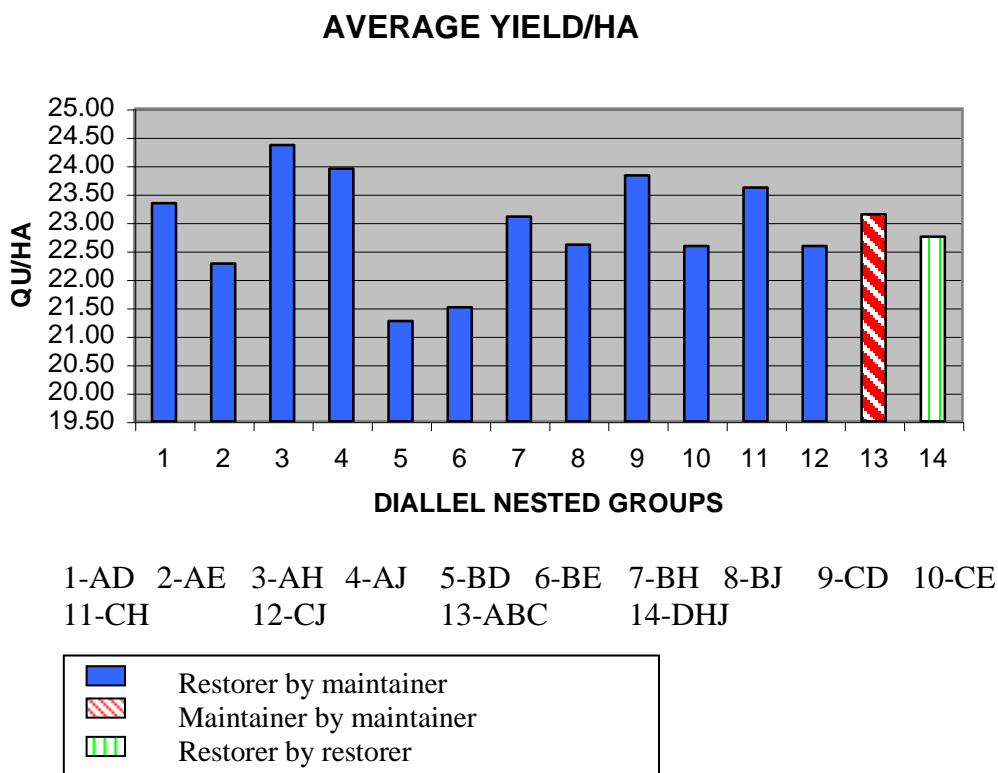
- where:
- . μ : overall mean
 - . a_i : effect of the i^{th} location (random effect)
 - . β_j : effect of the j^{th} group (fixed effect)
 - . $\delta_{k(j)}$: effect of the k^{th} hybrids (nested in group i ; fixed effect)
 - . $c_{l(i)}$: effect of the l^{th} block (nested in location i ; random effect)
 - . $(a\beta)_{ij}$: interaction effect between locations and groups
 - . $(a\delta)_{ik(j)}$: interaction effect between locations and hybrids
 - . e_{ijkl} : residual term

For all the traits analyzed, the location x group and location x hybrid interaction effects were always highly significant. The F tests for the main fixed effects were performed using the corresponding interaction mean squares as a denominator. The group main effect is also significant (Table 2).

Table 2 . Anova table for grain yield

	Df	Sum of Sq	Mean Sq	F Value	Pr(F)
LOC	7	69233,08	9890,44		
GROUP	13	1366,17	105,09	1,85	0,046512
HYBRID (in GROUP)	94	4110,28	43,73	3,05	0,000000
BLOCK (in LOC)	8	3740,57	467,57		
LOC x GROUP	91	5161,94	56,73	4,60	0,000000
LOC x HYBRID	655	9383,90	14,33	1,16	0,020477
Residuals	821	10114,315	12,32		

Fig.1 .Average YIELD/HA for each group



Yield data (Fig.1) confirmed that some hybrid groups derived from crossing CMS females with restorer lines give statistically better hybrids for grain than those created from crosses between inbreds within maintainer or restorer groups. The best combinations for yield are between CMS females from the group A maintainers and restorer line from groups H and J. Despite this, it is interesting to note that the mean of hybrids created by intercrossing maintainer lines, while not the highest, was higher than 50% of the maintainer-restorer hybrid sets. This suggests that the “average” heterosis obtained by crossing maintainers by restorers is not significantly better than what one could obtain by combining different maintainer parents. This leaves open the possibility of exploiting variability within the maintainer pools for development of future heterotic groups.

Clearly our experiment, with a limited number of hybrids representing each potential heterotic pool combination, can only give us a preliminary view of specific combining ability potential. Follow-up experiments will be required to further elucidate valuable heterotic patterns within our existing germplasm.

Conclusion

Our study indicates that improvement of heterosis may be possible by exploiting sub-groups of within the traditional maintainer and restorer sunflower germplasm pools. It further indicates the potential for exploiting variation within the current maintainer pools to develop long term heterotic groups.

The division between subgroups within these pools are not as clear cut in sunflower as in maize because of a greater degree of common ancestry between sunflower groups (Cheres et al., 1998). Our data suggests that the mean distances between heterotic groups in sunflower tends to be shorter in sunflower than in corn.

The narrow genetic diversity of cultivated sunflower is likely due to the relatively short breeding history of this crop, the narrow base of ancestral germplasm that contributed to today’s elite breeding pools, and the hesitation of commercial breeders to risk exploration of new genetic sources in the face intense commercial competition. It seems critical that over time new germplasm sources be evaluated for their potential contribution to heterosis in sunflower and the genetic diversity of commercial sunflower hybrids.

References

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