Heterosis for yield and oil content of sunflower lines developed from bi-parental populations

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ABSTRACT

Improvement of grain yield and oil content remains the major objective of many sunflower breeding programmes worldwide. Different sets of S_3 CMS lines developed from bi-parental populations were evaluated in hybrid combination at two sites to estimate heterosis for oil content and grain yield. Results showed that standard heterosis of testcross hybrids of S_3 CMS lines ranged from -14.4 to 16.0% and -5.9 to 11.4% for yield and oil content, respectively, indicating their potential for obtaining specific combinations of superior hybrids between the S_3 CMS lines and the testers in comparison to the current checks. High panmictic and positive heteroses were obtained, 49.8 to 114.9% for yield and 6.1 to 28.4% for oil content suggesting that if open-pollinated varieties (OPVs) were to be developed from the bi-parental populations, their performance would be inferior to their corresponding hybrids for the traits evaluated.

Keywords: Bi-parental - cytoplasmic male sterility (CMS) - heterosis - panmictic.

INTRODUCTION

Sunflower production in South Africa is done under rainfed conditions and is mainly concentrated in the Northwest and Free State provinces, which are characterised by low rainfall, shallow and/or sandy soils. The major breeding objectives of the public sector sunflower programme in South Africa have remained unchanged, namely, continued improvement for yield, yield stability and oil content (Chigeza, 2007). Quantitative evaluations of traits such as yield require vigorous testing in two or more environments with a view to either managing or exploiting genotype-environment interaction (Eisemann et al., 1990). In early stages of selection, testing in two or more environments is constrained by the limited amount of seed and large numbers of entries involved. Thus, multi-environment trials are normally carried out with advanced generation materials.

In sunflower, the cytoplasmic male sterility (CMS) system, which involves the use of CMS line (A), maintainer line (B) and fertility restorer line *(Rf),* has allowed breeders to exploit heterosis through the development of three-way and single-cross hybrids (Miller et al., 1980). Heterosis, which is defined as some measure of F_1 performance relative to its parental performance (Shull, 1952), has extensively been exploited in cross-pollinated crops although its genetic basis is still not well understood (Lamkey and Edwards, 1998). Several types of heterosis have been proposed. In studies involving cross-pollinated crops, such as maize and sunflower, estimation of heterosis for yield and other agronomic traits is either based on mid-parent (MP) or better parent (BP) heterosis and is often expressed as a percentage (Duvick, 1999). The major drawback of these approaches is that they lack relevance in applied plant-breeding approaches since inbreds are normally not the final product grown by the farmers. Nonetheless, they can be useful in determining the price ratio of seed and grain in seed production. Estimation of heterosis based on MP or BP requires that both parental lines are also included in the trials or planted adjacent to the testcrosses, which may not be practically possible when large number of testcross hybrids are involved. Another measure of heterosis is the relative standard heterosis, defined as the superiority of experimental F_1 hybrids as compared to the performance of the checks (Patnaik et al., 1990). The use of standard heterosis is based on the argument that in developing new hybrids, the aim is to surpass the performance of existing commercial hybrids in the trait of interest. While the argument is practically valid, the check may not be in any way related to the experimental hybrids being developed, making an interpretation of heterosis based on the genetic background of the parental populations difficult (Lamkey and Edwards, 1998). Panmictic-midparent heterosis, defined as the difference between the mean of the F_1 hybrid and the mean of the two random-mating parental populations (Lamkey and Edwards, 1999), can be used complementary to standard heterosis if the genetic background of the parental population is to be interpreted. In sunflower, instead of using the mean performance of both populations, mid-parent

heterosis, it is more appropriate to use the female parent population because female parents are single-headed, a trait required in sunflower production. On the other hand, the male parents are multi-headed so as to ensure a long period of pollen availability to the female during seed production. Hence, direct improvement for yield for the male parent is not practiced, so that to interpret heterosis using the male line or parental population will not be relevant.

Thus the objectives of this study were to quantify standard and panimictic heterosis of testcrosses formed from lines derived from different bi-parental populations of sunflower.

MATERIALS AND METHODS

A total of 240 genotypes divided into seven unequal sets based on source of the seed or genetic relationships were used for study as indicated in Table 1. The populations (Pop1, Pop 2, Pop3 and Pop4), from which the S_3 CMS lines were derived, were formed by crossing two B lines with different genetic backgrounds. The male testers T1 and T2 were randomly selected from the improved male lines in the ARC sunflower breeding programme.

Table 1. Genetic material used for the study.

Set	Number of genotypes	Description of the material
1	88	Testcross hybrids formed by crossing two male testers T1 and T2 to 44 S_3 CMS lines developed from Pop 1, S_3 CMS inbreds coded Pop1-1 CMS, …Pop1-44 CMS.
2	24	Testcross hybrids formed by crossing two male testers T1 and T2 to 12 S_3 CMS lines developed from Pop 2, S_3 CMS inbreds coded Pop2-1 CMS, …Pop2-12 CMS.
3	52	Testcross hybrids formed by crossing two male testers T1 and T2 to 26 S_3 CMS lines developed from Pop 3, S_3 CMS inbreds coded Pop3-1 CMS, …Pop3-26 CMS.
4	54	Testcross hybrids formed by crossing two male testers T1 and T2 to 27 S_3 CMS lines developed from Pop 4, S_3 CMS inbreds coded Pop4-1 CMS, …Pop4-27 CMS.
5	12	Testcross hybrids formed by crossing two male testers T1 and T2 to 6 parental inbreds, H55, H52, HA89, KB61, KB16 and KB189 mated in pairs to produce the bi-parental populations Pop1, Pop2, Pop3 and Pop4.
6	4	Bi-parental populations Pop1, Pop2, Pop3 and Pop4
7	6	Six commercial checks AGSUN8251, AGSUN5551, PAN7033, PAN7355, Mydelo and DKF 68-22
Total	240	

The 240 entries were then planted in an alpha (0,1) design with two replications at two locations, Potchefstroom, 26.745°S, 27.083°E situated in the Northwest Province and Bothaville, 27.235°S, 26.67°E located in the Free State Province, South Africa. Both trials were machine planted in January 2007 and then thinned at three weeks after emergence. The plant population at Potchefstroom was 36,000 plants/hectare, while that of Bothaville was 28,000 plants/hectare. Recommended agronomic practices were followed at both sites, include basal application of 150 kg/ha fertilizer (3N:2P:1K) incorporated into the seedbed before planting. A further 28 kg/ha N was applied at four weeks after emergence. Grain oil concentration was determined on 12-g, air-dried achenes samples by nuclear magnetic resonance with a Newport Analyzer (Newport-Oxford Instruments Ltd, New-port Pagnell, Buckinghamshire, England).

Data were analysed using GENSTAT version 9, adopting the restriction maximum likehood (REML) methodology (Paterson and Thompson, 1971). The analysis was done using the mixed model procedure based on the reasoning given by Piepho and Möhring (2006), where genotypes within sets were regarded as random. Using the notation of de la Vega and Chapman (2006) the phenotypic observation y_{ijkmp} is the performance of genotype i nested within set j, in incomplete block n, of replicate m of environment k., was given by the following mixed model:

$$y_{ijkmn} = \mu + e_k + (r/e)_{km} + (b/r/e)_{kmn} + s_j + (es)_{jk} + (g/s)_{ij} + (eg)_{ik}\,(s_j) + \varepsilon_{ijkmn}$$

where μ is the grand mean; e_k the fixed effect of the environment k; $(r/e)_{km}$ the random effect of the replicate m nested within the environment k; $(b/r/e)_{kmn}$ the random effect of the incomplete block n nested within the replicate m of the environment k; s_j the fixed effect of the set j; $(es)_{jk}$ is the fixed effect of the interaction of environment k and set j; $(g/s)_{ij}$ the random effect of genotype i nested within set j; $(eg)_{ik}\,(s_j)$ the random effect of the interaction of the environment k with genotype i nested within set j and ε_{ijkmn} is the random error term.

Relative standard heterosis was estimated as the percentage increase or decrease in the performance of genotypes in comparisons to the mean of checks while panmictic heterosis was estimated as the

percentage increase or decrease in the performance of the testcross hybrids compared to the corresponding bi-parental population mean.

RESULTS AND DISCUSSION

Variance components

The combined analysis across the two environments showed significant variation among the genotypes nested within the sets for oil content and yield. The environment main effect was significant for oil content (P<0.01) but not significant for yield (data not shown). The genotypes nested within the sets and their interaction with the environment were the largest source of variation for both percent oil content and yield as indicated by the relative magnitude of the variance components, Table 2.

Table 2. Estimated variance components (±SE) estimates for yield and percent oil content of the sunflower genotypes across the two environments**.**

Parameter	Variance components estimates	
	Yield	Oil Content
$\sigma^2_{r/e}$	1712 ± 2883*	1.082 ± 1.086**
$\sigma^2_{b/r/e}$	2849 ± 4104ns	0.006 ± 0.020ns
$\sigma^2_{g/s}$	29624 ± 12459**	0.352 ± 0.207**
$\sigma^2_{(eg)s}$	39769 ± 16505**	2.367 ± 0.26**
σ^2_{ε}	235132 ± 15533	0.846 ± 0.058

* P<0.05; **P<0.01; for corresponding mean square; ns-not significant.

Genotype-environment interaction is normally caused by the magnitude of the variance of genotype performance across environments and changes in genotypic ranks between environments (Allard and Bradshaw, 1964). In this study genotype-environment interaction was a result of the magnitude of variance for yield but for oil content, the genotype-environment interaction was a result of both magnitude and change in rank order of the genotypes in the different two environments as the environment main effect was also significant (data not shown). The ratio of $\sigma^2_{(eg)s}$ to $\sigma^2_{g/s}$ was 1.34 for yield and 6.7 for oil content indicating also that genotype-environment interaction is more pronounced for percent oil content than yield.

Mean grain yield and heterosis

The mean grain yield ranged from 1040 kg/ha (Pop1, Set 6) to 2357 kg/ha (Pop1-1 CMS x T1, Set 1), Table 3. The commercial checks had a mean yield range of 1565 to 2124 kg/ha.

Table 3. Mean performances, range for yield, relative standard heterosis and panmictic heterosis of the genotypes nested within sets across the two locations

	Sets						
	1	2	3	4	5	6	7
Yield performance (kg/ha)							
Mean	1932	1947	1908	1811	1252	1058	1864
Range	1609–2357	1635–2235	1626–2223	1596–2164	1076–1556	1038–1076	1524–2160
SE[1]	168.6	171.4	169.3	169.3	175.1	189.2	183.2
Relative standard heterosis (%)							
Mean	3.6	4.5	2.4	-2.8	-32.8	-43.2	
Range	-13.7–26.4	-12.3–12.8	-12.8–19.3	-14.4–16.0	-42.3– -16.5	-42.4– -44.2	
Panmictic heterosis (%)							
Mean	79.9	87.2	78.2	69.7			
Range	49.8–119.5	57.2–114.9	51.8–107.6	82.5–109.5			

[1]SE based on the means of genotypes within sets

The relative standard heterosis ranged from -44.2% to 26.4%. The mean standard heterosis was negative for sets 4, 5 and 6 indicating better performance of commercial checks in comparisons to genotypes in the stated sets. The panmictic heterosis for yield ranged from 49.8% to 119.5% indicating low yields of the bi-parental populations compared to the testcross hybrids.

Mean percent oil content and heterosis

The mean percent oil content ranged from 33.1% (Pop3, Set 6) to 43.3% (testcross hybrid, Pop3-8 CMS x T1, Set 3), Table 4. Within the sets the range for oil content was small indicating some level of similarity of the genotypes and the past efforts on selection for high oil content.

Table 4. Mean performances, range for oil content, relative standard heterosis and panmictic heterosis of the genotypes nested within sets across the two locations

	Sets						
	1	2	3	4	5	6	7
Oil content performance (%)							
Mean	39.8	39.7	40.2	39.7	39.2	34.0	38.9
Range	36.6–41.7	37.6–41.0	37.2 43.3	37.3–41.4	36.5–40.3	33.1–34.5	38.0–40.0
SE[1]	0.43	0.43	0.43	0.43	0.43	0.43	0.43
Relative standard heterosis							
Mean	2.3	2.0	3.3	2.0	0.8	-12.5	-
Range	-5.9–7.4	-3.3–5.5	-4.4–11.4	-4.1–6.5	-6.1–3.5	-11.3– -13.2	-
Panmictic heterosis							
Mean	15.4	17.4	19.1	16.4			
Range	6.1–21.1	11.2–21.3	10.1–28.4	9.3–21.4			

[1]SE based on the means of genotypes within sets.

The commercial checks had a mean range of 38.0 to 40.0% with a set mean of 38.9%. The relative standard heterosis ranged from –13.2 to 11.4. The mean standard heterosis was negative for set 6 but positive for other sets including the set with inbreds that were used for developing the bi-parental populations. The panmictic heterosis for percent oil ranged from 6.1 to 28.4% indicating that testcross hybrids had a significant advantage over their populations for yield.

In conclusion, the study revealed a high and moderate significant variance for environment-genotype nested within sets interaction for percent oil content and yield, respectively. The relative standard heterosis estimates showed that 3 out of 4 sets from which the S_3 CMS lines were derived had positive mean heterosis indicating the potential of developing new hybrids from specific line x tester combination that would do better for yield and percent oil content as compared to the current commercial hybrids. The panmictic heterosis was highly positive for all the four S_3 CMS line sets when crossed to the two testers. In cross-pollinated crops the panmictic heterosis is useful in whether to develop hybrids or open-pollinated varieties (OPVs). A low and negative panmictic heterosis for yield will favour development of OPVs, while it will be logical to develop hybrids if the panmictic heterosis is high and positive.

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