STUDY OF GENE ACTION FOR RESTORER LINES IN SUNFLOWER

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SUMMARY

Five best sunflower restorer (BR) lines and five elite restorer (ER) lines which were crossed in all possible combinations with half diallel fashion to determine the combining ability, mode of gene action and to quantify the magnitude of heterosis at Oilseeds Research Unit, Dr. PDKV, Akola Maharashtra (India). The ratio of σ^2GCA/σ^2SCA variances was less than unity for plant height, head diameter, filled seeds/head, 100 seed weight, harvest index, oil content and yield/plant indicating non-additive type of gene actions were involved in these traits. The character, days to maturity was governed by preponderance of additive gene action due to variance ratio observed more than unity. The characters days to maturity, head diameter and 100 seed weight showed the predictability ratio nearer to unity indicating greater predictability based on general combining ability alone. Six crosses 270R × Ak-1R, 272R × 273R, 273R × 274R, 586R × 857R, 265R × Ak-1R and 265R × 586R appeared to be worth exploiting. These promising R × R crosses can be used for the development of new R lines in sunflower. It is recommended that in order to get new restorer combinations it is necessary to have at least one elite restorer in combination with best restorer to be incorporated in the breeding programme and vice- versa at least in sunflower.

Key wards: gene action, best and elite restorer lines, combining ability, sunflower

INTRODUCTION

Information on heterosis in sunflower (_Helianthus annuus_ L.) is essential for developing new hybrids. The two important prerequisites exploiting new _cms_ systems in hybrid breeding are availability of stable male sterility and restorer lines. The development of new restorer lines by conventional breeding requires repeated backcrossing of the restorer lines with the recurrent parent, followed by selection of the fertile plants, which is extremely laborious and time consuming due to identification of plants in the backcross progenies that carry genes for restoration. The ideal method to develop new restorer line (R line) is by crossing R × R lines from restorer gene pools, which are already identified for fertility restoration in sun-

flower (Dudhe *et al*., 2009). Combining ability analysis provides information on the nature and magnitude of gene effects on yield and yield attributing characters. This analysis helps in identification of the potential parents and superior cross combinations and also assist in the formulation of a suitable time bound effective breeding program for the genetic enhancement of yield and yield components. The usefulness of a particular cross in exploiting heterosis is judged by the specific combining ability (SCA) effect. Diallel analysis of restorer lines (R lines) can help to identify and develop new R lines which later can be used in sunflower hybrid development programs. Hence, the present investigation was planned to identify best R × R crosses from already identified best restores along with elite restorers from the maintained restorer gene pool by using half diallel method in sunflower.

MATERIALS AND METHODS

The material included five best sunflower restorer (BR) lines *viz*., RHA 272, 274, 857, 859 and Ak-1R from which commercial hybrids were already released in India (Table 1) and five elite restorers (ER) RHA 265, 270, 273, 278 and 586. These restorers were crossed manually during the summer of 2005 by hand emasculation and pollination in all possible combinations in half diallel fashion (excluding reciprocals), so that every BR got crossed with every BR, ER and ER with every ER. In *Kharif* 2006, the 45 hybrids and 10 parents were grown in a randomized block design with three replications with 3 rows, each 2.4 m in length. The data were collected on yield associated traits like days to maturity, plant height, head diameter, filled seeds/head, 100 seed weight, harvest index, oil content and seed yield/plant. The analysis of variance was computed as per Panse and Sukhatme (1954), for all the characters. Combining ability analysis was carried out by using method II model 1 of Griffing (1956), to study the gene action operating in the inheritance of the characters studied and the predictability ratio was calculated as per Baker (1978), to calculate the progeny performance.

Table 1: Hybrids released for cultivation in India with pedigree, year of release, adaptation zone and few yield contributing traits

Hybrid	Pedigree	Year of release	Seed yield kg/ha	Duration days	Oil content %	Adaptation zone
BSH-1	CMS 234A × RHA 274	1980	1000-1400	85-90	40-42	All India
PKVSH-27	CMS 2A × AK-1R	1996	1200-1500	85-90	40-43	Vidharbha region of Maharashtra
DSH-1	DSF-15A × RHA 857	1997	1200-1400	85-88	41-44	Northern Karnataka
TCSH-1	CMS 234A × RHA 272	2000	1200-1500	85-90	40-44	Tamil Nadu
NDSH-1 (NDSH 15)	CMS 234A × 859R	2003	1200-1500	88-90	40-42	Andhra Pradesh

RESULTS AND DISCUSSION

Mean square values showed that significant differences were observed among mean values for all the yield associated traits except for harvest index. The characters which showed significant differences were days to maturity, plant height, head diameter, filled seeds/head, 100 seed weight, oil content and seed yield in sunflower.

The estimates of general and specific combining ability for parents and specific combining ability effects of crosses are presented in Table 2. The mean squares due to GCA and SCA were significant for all characteristics under study except harvest index indicating substantial genetic variation for the characters. The ratio of σ^2 GCA/σ^2 SCA variances was less than unity for plant height, head diameter, filled seeds/head, 100 seed weight, harvest index, oil content and yield/plant which indicated that non-additive type of gene action was primarily involved in the expressions of these traits. The character, days to maturity were governed by preponderance of additive gene action due to variance ratio observed more than unity. However, gene action assessed from combining ability analysis (Griffing, 1956) is not true indication and may not give proper idea regarding gene actions. Therefore, predictability ratio (GCA *vs*. SCA) was calculated as per Baker (1978), to calculate the progeny performance. The character, days to maturity, head diameter and 100 seed weight showed the predictability ratio nearer to unity indicating greater predictability based on general combining ability alone. Pande (2002) reported non-additive gene action for almost all traits except head diameter. Earlier, Goksoy (2000), reported non-additive gene action for plant height, head diameter and for yield/plant which are in agreement with the present findings.

Table 2: Analysis of variance for combining ability in 10×10 diallel set

Source of variation	DF	Mean squares							
		Days to maturity	Plant height	Head diameter	Filled seeds/ head	100 seed weight	Harvest index	Oil content	Yield/ plant
GCA	9	7.561**	310.221**	20.009**	704.882**	6.313**	2.404	14.459**	19.064**
SCA	45	1.249	123.785**	3.227**	414.260**	0.909**	1.438	10.025**	8.868**
Error	108	0.726	33.902	0.800	108.599	0.239	25.784	2.851	1.967
Estimates of genetic components									
σ^2 g		0.569	23.026	1.600	49.690	0.516	-1.948	0.967	1.424
σ^2 s		0.523	89.883	2.426	35.661	0.669	-24.346	7.174	6.907
Ms GCA / MSCA		6.053	2.506	6.200	1.701	6.944	1.671	1.442	2.149
σ^2 GCA / σ^2 SCA		1.087	0.256	0.659	0.162	0.756	0.080	0.134	0.206
GCA *vs* SCA (Backer,1978)		0.923	0.833	0.925	0.772	0.932	0.769	0.742	0.811

*, Significant at 5 %; **Significant at 1% level of significance

Table 3: Selected R × R crosses showing nature of cross, high *per se* performance of hybrid, better parent heterosis, GCA and SCA effects of the parents for various characters

Sr. No	Nature of cross	Characters/cross	*Per se* performance of hybrid	BP Heterosis	GCA effects of parents		SCA effects of parents
					P1	P2	
			Days to maturity				
1	ER × BR	270R × AK-1R	76.00	-3.80**	-1.29** (H)	-0.82** (H)	-2.67**
2	ER × BR	270R × 272R	77.67	-1.69	-1.29** (H)	-0.90** (H)	-1.09
3	ER × BR	270R × 859R	79.00	0.00	-1.29** (H)	0.93** (H)	-1.51
			Head Diameter				
1	ER × ER	273R × 278R	15.53	43.83**	1.70** (H)	1.27 (H)	1.35
2	ER × ER	272R × 273R	14.80	37.89**	-1.63* (L)	1.78** (H)	3.51**
3	ER × BR	273R × 274R	14.47	34.78**	1.70** (H)	-0.80* (L)	2.35**
4	ER × ER	278R × 578R	14.13	26.57**	1.15** (H)	1.15 (H)	0.50
			Plant height				
1	ER × BR	270R × 272R	77.33	1.75	-6.88** (H)	-7.09** (H)	-7.27
2	EB × ER	272R × 586R	78.67	-7.81	-7.09** (H)	0.29 (L)	-13.10
3	ER × BR	270R × Ak-1R	88.67	6.78	-7.09** (H)	-0.86 (L)	-2.16
			Filled seeds/Head				
1	ER × ER	270R × 278R	88.43	13.62	13.46** (H)	1.88 (L)	14.84
2	ER × BR	586R × Ak-1R	84.64	-60.16**	4.36 (L)	-4.07 (L)	28.45**
3	BR × BR	272R × Ak-1R	84.19	-1.14	-7.30 (L)	-4.07 (L)	31.61**
			100 Seed weight				
1	ER × ER	273R × 278R	6.37	43.61**	1.15 (L)	0.57 (L)	3.10
2	BR × ER	274R × 278R	6.20	93.75**	-0.50 (L)	0.57 (L)	-24.74**
3	ER × ER	265R × 273R	6.10	37.59**	0.78 (L)	1.15 (L)	-0.55
4	ER × ER	265R × 278R	6.03	40.31**	0.78 (L)	0.57 (L)	17.96
			Harvest index				
1	BR × ER	272R × 273R	0.49	206.25**	-4.60 (L)	5.00 (L)	0.25
2	ER × ER	270R × 278R	0.48	317.65**	1.00 (L)	2.00 (L)	0.21
3	ER × BR	265R × Ak-1R	0.48	107.14**	8.00 (H)	-1.00 (L)	0.17
4	ER × BR	265R × 274R	0.46	110.61**	8.50 (H)	-5.00 (L)	0.20
			Oil content				
1	ER × BR	586R × 857R	39.38	27.16**	1.48* (H)	1.10 (L)	5.27**
2	ER × BR	586R × Ak-1R	36.53	3.12	1.48* (H)	0.61 (L)	-1.68
3	BR × ER	274R × 586R	36.41	13.90**	0.80 (L)	1.48** (H)	2.60
4	ER × ER	265R × 278R	36.32	24.48**	0.73 (L)	-1.46* (L)	5.52**
			Yield/plant				
1	ER × BR	586R × 857R	13.29	110.26**	0.67 (L)	-0.54 (L)	6.23**
2	ER × BR	265R × Ak-1R	12.91	152.87**	1.79** (H)	0.67 (L)	3.86**
3	ER × ER	265R × 586R	12.61	147.00**	1.79 ** (H)	0.67 (L)	3.22**
4	ER × ER	270R × 278R	12.08	174.55**	-0.44 (L)	0.81 (L)	4.77**

BR/ER=Best/Elite Restorers, H=High, L=Poor

*, Significant at 5%; **Significant at 1% level of significance

Selected R × R crosses showing nature of cross, high *per se* performance of hybrid, better parent heterosis, GCA and SCA effects of the parents for various characteristics are shown in Table 3. As the performance of F_1 hybrids over better parent was significant, the heterosis over better parent has been considered for discussion (Dudhe *et al.*, 2009). The highest positive better parent heterosis was observed for harvest index in the crosses 270R × 278R, which was significantly highest among all the characters studied. For seed yield per plant the same cross recorded highest better parent heterosis and for oil content cross 586R × 857R recorded highest better parent heterosis along with high mean. The high × high crosses with best GCA effects and high mean performance were observed for days to maturity (270R × AK-1R), head diameter (273R × 278R) and plant height (270R × 272R) indicating that additive x additive effects are fixable component and single plant selection would be desirable in segregating generations at least for these characters. One cross for head diameter and for oil content showed low × high GCA effects along with high mean and significant better parent heterosis. Whereas low × low GCA effects along with high mean was recorded in eleven cross combinations for filled seed/head, 100 seed weight, harvest index, oil content and yield/plant. In the present study, low × low GCA combination also produced hybrids with high SCA and this could be attributed to over-dominance or epistatic gene action. All these results revealed that there is no direct relation between GCA effects of the parents and SCA effects of the hybrid combinations. This could be explained from the point of view of gene action since GCA is mostly due to additive gene action whereas SCA is mostly due to over-dominance and epistasis. Cross 586R × 857R is best for yield per plant and oil content is due to low × low for yield/plant and high × low GCA effect for oil content along with high mean which is rare combination. An ideal combination to be exploited is one where high degree of SCA is present in addition to high GCA of both or at least in one parent along with high better parent heterosis. Six crosses 270R × Ak-1R, 272R × 273R, 273R × 274R, 586R × 857R, 265R × Ak-1R and 265R × 586R appear to be worth exploiting. The present results are in the agreement of Pande (2002) and Goksoy *et al.*, (2000) as they also reported crosses having high SCA effects with the parents of either high × high, high × low or low × low GCA effects.

The parent 270 R (elite restorer) were good general combiners for seed yield along with yield-contributing characters like harvest index, filled seeds/head, plant height and for days to maturity. Parent 265R (elite restorer) was good combiner for oil content, harvest index, 100 seed weight and yield per plant. The parent Ak-1R (best restorer) was good general combiner for yield/plant, oil content, harvest index, plant height and days to maturity. Out of twenty nine crosses presented in Table 2 only one BR × BR cross combination (272R × Ak-1R) was observed for character filled seeds per head it indicates that the frequency of getting bet restorer combination by crossing BR × BR is less. Eleven cross combinations were observed for ER × ER and seventeen crosses are either ER × BR or BR × ER combinations which

show better complementation between favourable alleles in elite restorers and elite and better restorers. Hence, it is concluded that in order to get new restorer combinations it is necessary to have at least one elite restorer in combination with best restorer to be incorporated in the breeding programme and vice- versa. Also, these restorer combinations can be seen as new potent restorer lines because the fertility restoration genes are accumulated in these crosses and can be used for the development of new "R" lines in sunflower.

CONCLUSION

Six crosses 270R × Ak-1R, 272R × 273R, 273R × 274R, 586R × 857R, 265R × Ak-1R and 265R × 586R identified with high degree of SCA in addition to high GCA of both or at least in one parent along with high better parent heterosis, these promising R × R crosses can be used for the development of new R lines in sunflower. It is also suggested that simple recurrent selection or bi-parental mating followed by reciprocal recurrent selection among the crosses having desirable yield components may be effective in genetic amelioration of the characters under study. The parent 270 R, 265 R and Ak-1R were good general combiners for yield and yield attributing traits and can be used in synthetic breeding programme. Also from above findings it is recommended that it is better to incorporate more and higher number of ER × ER and ER × BR or BR × ER crosses for the development of new restorer lines, at least in sunflower. The new information generated through this research of specific effects of elite restorers and best restorers on yield traits, which was hitherto lacking, has significant bearing on the development of new restorer lines in sunflower breeding aimed towards the improvement of yield traits. The results will guide the breeders as regards the choice of restorers for developing new restorer lines in sunflower.

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