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Gene Action and *perse* Performance in Multibranched Restorer Lines of Sunflower (*Helianthus annuus* L.)

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Abstract

A diallel set of 30 F_1s (including reciprocals) involving six restorer parents were studied to assess the nature of gene action and *perse* performance. Higher magnitude of SCA variance than GCA variance was observed for most of the characters studied indicating the predominance of non additive gene. The results indicated that except for volume weight higher magnitude of SCA variance than GCA variance was observed for nine characters viz., days to 50% flowering, head diameter, plant height, leaf size, days to maturity, 100 seed weight, plant yield, oil content and seed yield indicating the predominance of non additive gene action for all these characters. The *per se* performance revealed that parents RHA-274 (1755 kg/ha) and (R-127) (1741 kg/ha) and among the crosses (R-127 × R-5) (2,641 kg/ha), (RHA-275 × R-8297), (2,438 kg/ha) and (R-8297 × RHA-275) (2,427 kg/ha) showed highest seed yield per hectare.

Key words : Gene action, *Per se* performance, Restorer lines, Sunflower.

Sunflower is now quest for new and cheaper sources of edible oil. This has brought into focus many oil seeds that were not being grown. It appears to be specially suited for cultivation in India in view of its wide adaptation and photo period insensitive nature. Large scale cultivation of sunflower in India was started in 1972 with the introduction of Russian high yielding varieties. The estimates of variances due to general combining ability (GCA) and specific combining ability (SCA) revealed that both additive and non additive gene action play an important role in the control of majority of characters. In the present study an attempt was made to asses the gene action governning the quantitative traits in and also to asses the *perse* performance sunflower for multi branched restored lines by employing diallele analysis.

Methods

The material comprised of six restorer lines viz., RHA-274, R-393, R-127, RHA-275, R-8297 and R-5. These parents were crossed in diallel fashion (including reciprocals) to generate 30 hybrids. These crosses along with parents were grown in Randomized Block Design with two replications. The experiment was conducted at regional agricultural research station, Raichur campus located in north eastern dry zone of Karnataka. The crossing and evaluation was

Table 1. ANOVA for ten different characters in 6 × 6 diallel crosses in sunflower restorer lines. *, ** Significant at 5 and 1% probability respectively.

			Mean sums of squares									
	Source	df	Days to 50% flowering	Head diameter (cm)	Plant height (cm)	Leaf size (dm^2)	Days to maturity	Volume weight (g/100 ml)	100 seed weight (g)	Plant yield (g)	Oil content (%)	Seed yield (kg/ha)
1.	Replication	1	0.125	0.244	0.061	0.292	0.888	1.547	0.016	0.036	0.0849	51863.31
2.	Treatment	35	10.496**	5.542**	768.836**	0.606**	8.841**	26.759**	0.991**	91.598**	7.079**	277013.82**
3.	Error	35	0.964	0.061	23.770	0.033	0.517	1.390	0.125	1.990	0.195	15620.87

Table 2. Mean *per se* performance of parents and crosses for ten different characters in restorer lines of sunflower. *, ** Significant at 5 and 1% probability respectively.

Entries	Days to 50% flowering	Head diameter (cm)	Plant height (cm)	Leaf size (dm^2)	Days to maturity	Volume weight (g/100ml)	100 seed weight (g)	Plant yield (g)	Oil content (%)	Seed yield (kg/ha)
Parents										
1. RHA-274	59.0**	9.90	139.8	2.57**	88.5**	40.30	4.00	27.80**	37.70	1755*
2. R-393	64.0	10.30	108.5**	2.16	91.0	45.45	5.00**	19.60	39.30**	1377
3. R-127	64.0	9.65	153.5	1.80	91.5	46.30	3.75	18.90	38.25	1741*
4. RHA-275	65.0	10.00	121.5**	1.77	93.5	42.65	3.95	18.25	37.80	1227
5. R-8297	60.0**	12.50**	150.0	2.00	91.0	41.10	4.15	24.00*	37.30	1483
6. R-5	61.0**	8.70	142.7	2.00	91.5	53.55**	3.30	17.85	39.75**	1311
Mean	62.16	10.17	136.0	2.05	91.16	44.89	4.02	21.06	38.35	1482.33
Crosses										
7. RHA-274 × R-393	62.0	13.60**	146.3	3.32**	90.5	44.50	2.95	33.60**	34.65	2100
8. RHA-274 × R-127	62.0	9.80	176.5	2.66	90.5	47.70	4.05	23.45	33.30	1691
9. RHA-274×RHA-275	58.0**	9.50	128.5**	1.70	87.0*	49.55*	3.25	27.95	33.15	2338**
10. RHA-274×R-8297	62.0	11.90	181.4	2.50	89.5	48.20	3.25	34.00**	37.25**	2155
11. RHA-274×R-5	63.0	10.60	139.5*	2.46	90.0	47.15	3.75	23.15	35.55	2084
12. R-393 × R-127	62.0	9.80	109.7**	2.17	89.5	41.20	4.30	16.10	34.15	1266
13. R-393 × RHA-275	61.5	11.80	136.2**	3.29**	89.5	44.80	4.35	29.15**	37.50**	2249*
14. R-393 × R-8297	61.5	10.40	157.5	2.17	89.5	44.05	5.25**	21.10	33.55	1877
15. R-393 × R-5	61.5	9.60	162.3	4.00**	88.5	44.40	5.30**	24.95	39.05**	1944
16. R-127 × RHA-275	58.5**	11.60	156.5	2.43	88.0	49.00	3.30	26.90	36.00	2210
17. R-127 × R-8297	62.5	13.30**	174.0	2.94**	90.5	45.10	4.30	33.95**	34.55	2286*
18. R-127 × R-5	62.0	8.60	150.6	2.16	88.5	48.55	3.70	21.35	36.95*	2065
19. RHA-275 × R-8297	62.0	10.90	156.5	1.75	90.0	47.45	3.40	16.60	39.35**	1416
20. RHA-275 × R-5	62.0	10.75	177.2	2.14	91.0	45.40	2.90	25.40	34.25	2111
21. R-8297 × R-5	62.5	11.30	175.0	2.15	90.5	51.10**	3.75	28.35*	38.20**	2641**
22. R-393 × RHA-274	59.0**	13.35**	121.3**	2.11	86.0**	42.05	3.35	28.10*	34.15	2027
23. R-127 × RHA-274	59.5**	11.70	151.0	2.20	87.0*	47.70	5.25**	22.40	34.65	2255*
24. RHA-275×RHA-274	56.0**	16.00**	164.1	2.87**	85.5**	46.05	5.25**	18.90	37.10**	1694
25. R-8297×RHA-274	61.0	15.20**	160.0	2.99**	88.0	46.05	2.90	44.10**	35.35	2438**
26. R-5 × RHA-274	60.0*	11.95*	130.5**	2.05	90.5	46.55	3.30	24.50	34.75	2099
27. R-127 × R-393	57.0**	11.80	137.0**	1.60	85.0**	39.40	3.65	24.80	36.35	1972
28. RHA-275 × R-393	59.0**	12.50*	146.5	2.00	86.0**	43.10	3.25	29.30**	35.45	1972
29. R-8297 × R-393	64.0	11.50	188.0	2.22	91.0	49.85*	4.10	19.85	37.95**	2011
30. R-5 × R-393	57.0**	11.70	162.5	2.65	86.0**	44.30	3.55	36.40**	34.55	2427**
31. RHA-275 × R-127	59.0**	12.90**	153.5	2.40	88.0	45.00	4.70*	29.15**	34.20	2213
32. R-8297 × R-127	59.0**	10.20	145.0	2.24	87.0*	54.80**	3.90	12.10	38.75**	1144
33. R-5 × R-127	66.0	11.10	119.6**	1.20	93.5	48.30	3.25	22.40	36.20	1766
34. R-8297×RHA-275	60.0*	10.70	143.8	2.42	90.5	50.50**	3.15	24.40	36.20	2305*
35. R-5 × RHA-275	62.0	9.40	146.0	1.70	89.0	53.55**	3.30	18.45	37.05*	1772
36. R-5 × R-8297	60.0*	11.10	161.5	2.86*	89.0	47.15	4.10	12.55	36.75	1111
Mean	60.71	11.45	151.92	2.37	88.83	46.75	3.82	25.11	35.89	1987.96
SE	0.310	0.248	5.173	0.184	0.719	1.179	0.353	1.410	0.442	124.983
CD at 5% level	0.630	0.503	10.500	0.373	1.460	2.394	0.718	2.864	0.898	253.741
CD at 1% level	0.845	0.675	14.093	0.501	1.959	3.212	0.963	3.842	1.205	340.453

done during 2006-2007. Each entry was sown in two rows of 3 m length each with a spacing 60 cm between rows and 30 cm between plants. All the recommended package of practices were followed and observations were recorded on days to 50% flowering, head diameter, plant height, leaf size, days to maturity, volume weight, 100 seed weight, plant yield, oil content and seed yield. The combining ability analysis was carried our following the model proposed by Griffings in 1956.

Table 3. ANOVA for combining ability in 6 × 6 diallel crosses for various characters in sunflower restorer lines. *, ** Significant at 5 and 1% probability respectively.

Source	df	Mean sums of squares: Days to 50% flowering	Head diameter (cm)	Plant Height (cm)	Leaf size (dm^2)	Days to maturity	Volume weight (g/100 ml)	100 seed weight (g)	Plant yield (g)	Oil content (%)	Seed yield (kg/ha)
1. GCA	5	6.358**	2.800**	1201.956**	0.227**	5.120**	48.348**	0.567**	52.313**	3.461**	28268.027**
2. SCA	15	4.251**	1.826**	272.343**	0.264**	5.190**	4.481**	0.544**	51.156**	4.988**	181709.649**
3. Reciprocals	15	5.875**	3.706**	223.969**	0.366**	3.416**	10.618**	0.423**	38.270**	2.118*	132048.206**
4. Error	35	0.048	0.030	13.385	0.016	0.258	0.695	0.062	0.995	0.097	7810.439

Results and Discussion

The analysis of variance for restorers showed significant differences for all the characters (Table 1). Further crosses were also found to differ significantly from each other for all the characters studied revealing the existence of genetic diversity in parental material and justifying their selection for combining ability analysis. Variability and *per se* performance of parents is of prime importance and is a yard stick for selection of better parents for breeding programme in any crop plants. The results of *per se* performance of parents and crosses revealed that parents RHA-274 (59 days) and R-8297 (60 days) were earliest in flowering, however the parent R-8297 and the crosses RHA-275 × R-127, R-8297 × RHA-274 and R-8297 × RHA-275 were earliest to flowering and days to maturity (Table 2). The parents RHA-274 (27.80 g) and R-8297 (24.00 g) and the crosses RHA-275 × R-8297 (44.10 g) and R-8297 × RHA-275 (36.40 g) exhibited highest plant yield. Among the parents RHA-274 (1,755 kg/ha) and (R-127) (1,741 kg/ha) and among the crosses (R-127 × R-5) (2,641 kg/ha), (RHA-275 × R-8297) (2,438 kg/ha) and (R-8297 × RHA-275) (2,427 kg/ha) showed highest seed yield per hectare.

Table 4. Variance due to GCA, SCA and their proportion for ten different characters in sunflower restorer lines.

Characters	Variance due to GCA	Variance due to SCA	GCA/SCA proportion
1. Days to 50% flowering	0.525	4.203	0.124
2. Head diameter (cm)	0.230	1.795	0.128
3. Plant height (cm)	99.050	258.950	0.382
4. Leaf size (dm^2)	0.017	0.247	0.068
5. Days to maturity	0.405	4.932	0.082
6. Voleme weight (g/100 ml)	3.971	3.786	1.048
7. 100 seed weight (g)	0.042	0.481	0.087
8. Plant yield (g)	4.278	50.161	0.085
9. Oil content (%)	0.280	4.890	0.057
10. Seed yield (kg/ha)	1704.799	173899.210	0.009

From the analysis of variance for combining ability, it is evident that variance due to both GCA, SCA and reciprocals were significant for all characters (Table 3). However the results revealed that except for volume weight higher magnitude of SCA variance than GCA variance was observed nine characters viz., days to 50% flowering, head diameter, plant height, leaf size, days to maturity, 100 seed weight, plant yield, oil content and seed yield indicating the predominance of non-additive gene action for all these characters (Table 4). The results were in agreement with Rudra Naik et al. (1), Reddy and Madhavilatha (2), Pavani et al. (3) and Vishwanath and Shanker Goud (4). The variance ratio was less than one for all these characters due to higher magnitude of SCA variances than GCA variances. For volume weight GCA variance is higher compared to SCA variance which indicates additive gene action. The results were in line with results of Sindagi et al. (5), and Kini (6). The variance component due to specific combining ability (SCA) was greater in magnitude than that of general combining ability (GCA) (Table 3) for all the characters viz., except volume weight indicating the predominance of non-additive gene action the results were in agreement with Rudra Naik et al. (1), Reddy and Madhavilatha (2). Pavani et al. (3) and Vishwanath and Shanker Goud (4).

In conclusion higher magnitude of SCA variance than GCA variance was observed for most of the characters studied indicating the predominance of non additive gene. While *per se* performance revealed that parents RHA-274 (1,755 kg/ha) and (R-127 (1,741 kg/ha) and among the crosses (R-127 × R-5) (2,641 kg/

ha), (RHA-275 × R-8,297) (2438 kg/ha) and (R-8297 × RHA-275) (2,427 kg/ha) showed highest seed yield per hectare.

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