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Combining ability and gene action analysis in sunflower(*Helianthus annuus* L.)

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Abstract

The present investigation was made to study the combining ability and gene action in sunflower. Five standard CMS lines and nine restorers were included as parental material. Forty five hybrids were developed andevaluated in RBD at Oilseeds Research Station, Latur during *Rabi* season 2018-2019 for 9 characters *viz.,* days to 50 percent flowering, days to maturity, plant height, head diameter, seed yield per plant, seed filling percentage, 100 seed weight, volume weight and oil content.CMS 10A was good general combiner for days to 50% flowering, days to maturity, head diameter, 100 seed weight, seed yield per plant, volume weight and seed filling percentage. Similarly CMS 519A and CMS 62A were found to be good general combiners for seed yield and component traits. Among the testers, TSG-04 was good general combiner for days to 50% flowering, days to maturity, plant height and 100 seed weight. Similarly, TSG-281 and SCG-04 exhibited good general combining ability for oil content and component traits. Out of 45 hybrids, five hybrids *viz*. CMS 62A X SCG-04, CMS 234-1017A X TSG-327, CMS 234-1017A X TSG-111, CMS SUN-35-519A X TSG-289 and CMS 519A X TSG-289 exhibited the significant desirable *sca* effect for seed yield and component traits. The variance component due to specific combining ability was greater in magnitude than that of general combining ability for all the characters except seed yield per plant, volume weight and seed filling which indicated that the non-additive gene action played important role for the inheritance of these traits whereas seed yield per plant, volume weight and seed filling were governed by additive gene action.

Keywords

Sunflower, combining ability, line x tester, gene action.

INTRODUCTION

Sunflower (*Helianthus annuus* L.) is an annual flowering plant which belongs to the family compositae with chromosome number 2n=34. It is the second most important oilseed crop in the world after soybean with an account of its wide range of adaptability and high oil content (40-50 %) and protein (23%). It can be grown successfully in different parts of the world due to its wide adaptability, photo-insensitivity and thermo-insensitive nature.Sunflower took prime position in the oilseeds economy both at national and global level. In India during 2017-18 sunflower was cultivated in an area of 2.86 lakh ha. with a production of 2.11 lakh tones and average yield of 738 kg/ha.In Maharashtra sunflower was cultivated on an area of 22.5 thousand hectare with the production of 11.5 thousand tones and productivity of 510 kg/ha. Karnataka, Maharashtra, Andhra Pradesh and Odisha are the important sunflower growing states.Line x tester analysis has been widely used for genetic analysis in large number of crop plants. It is an efficient technique for evaluating large number of inbreds for their combining ability, besides this technique also provides information on GCA and SCA, which are useful to study gene action controlling various characters to adopt appropriate breeding strategy. The concept of combining ability is meant for reducing the number of crosses to be advanced. It enables to select desirable parents and specific cross combinations. Allard pointed out that selection of parents on the basis of performances is not a viable indication of their superior combining ability. The choice of parents should be based on complete genetic information and knowledge of combining ability of parents and not merely on yield performance.

MATERIALS AND METHODS

The experimental material for the study included five CMS lines as female parents and nine restorers as male parents which were crossed in line x tester method to produce 45 new hybrids in*kharif*2018. The resulting 45 hybrids, 14 parents and 2 checks were studied in randomized block design with two replications during *Rabi*-2018 at Oilseeds Research Station, Latur.The morphological observations on 9 quantitative characters were recorded by selecting randomly 3 competitive plants in each plot and in each replication. The mean values of all treatments for the characters under study were worked out. Standard error and critical difference at 1 and 5 % level of significance were calculated by using the formula (Panse and Sukhatme, 1967). Combining ability analysis and the testing of significance of different genotypes was based on the procedure given by kempthorne (1957). In order to understand the nature of gene action, the ratio was worked out by taking in to account the estimated variance of *gca* and *sca*. It is generally accepted in biometrics that for each of characters studied, where the variance ratio is greater than one, the gene action is additive and wherever the ratio is less than one; the gene action is non-additive.

RESULTS AND DISCUSSION

The mean sum of squares for parents and crosses showed significant differences for all the characters,indicating presence of the sufficient variability in the genetic material. The analysis of variance for combining ability (**table 1**) revealed that the mean sum of squares for variance due to lines were significant and large as compared to testers for characters *viz*., days to 50% flowering, plant height, head diameter seed yield per plant, volume weight, seed filling and oil content. The magnitude of specific combining ability variances was larger than general combining ability variances for the characters, days to 50% flowering, days to maturity, plant height, head diameter, 100 seed weight, and oil content. The magnitude of general combining ability variances was larger than specific combining ability for seed yield per plant, volume weight and seed filling percentage.

Table 1. Analysis of variance for different characters in sunflower.

Sr. No.	Characters	Replication 1 (d.f.)	Treatment 58 (d.f.)	Error 58 (d.f.)
1	Days to 50% flowering	2.1694	26.2326**	2.5143
2	Days to maturity	0.03390	34.4547**	2.4476
3	Plant Height (cm)	14.9491	457.5230**	8.3284
4	Head diameter (cm)	2.5363	6.8887**	0.6722
5	Seed yield/ plant (gm)	8.7867	135.457**	7.4838
6	Seed filling (%)	6.0414	77.1495**	2.0552
7	100-seed weight (gm)	0.3363	0.6031**	0.0601
8	Volume weight (gm/100ml)	5.6848	158.734**	1.3619
9	Oil content (%)	1.6848	17.0437**	0.08535

** and * indicates significant at 1% and 5% respectively.

Perusal of *gca* effects of 14 parents for 9 characters revealed thatthe CMS 10A was found to be good general combiner for days to 50% flowering, days to maturity, head diameter, 100 seed weight, seed yield per plant, volume weight, seed filling and oil content. Similarly CMS SUN-35-519A was found to be good general combiner for seed yield per plant, volume weight and seed filling. CMS-62A was good general combiner for head diameter, seed yield per plant and seed filling.Among the males TSG-04 was found to be good general combiner for days to 50% flowering, days to maturity, plant height and 100 seed weight.TSG-281 exhibited significant *gca* effect for seed yield per plant and oil content. TSG-111 was good general combiner for days to 50% flowering, volume weight and seed filling. SCG-04 was good combiner for 100 seed weight, volume weight and oil content. The present results suggest that these parents possessed the high concentration of favorable genes for the respective traits and may be utilized in crossing programme to develop the varieties/hybrids containing majority of desirable characteristics in sunflower.

For days to 50% flowering negative *sca* effects are considered to be desirable. Out of 45 hybrids, seven hybrids *viz*. CMS SUN-35-519A x TSG-274, CMS 234-1017 x TSG-257, CMS 62A x SCG-04, CMS 234-1017A X TSG-327, CMS 519A X TSG-111, CMS 519A X TSG-269, CMS 62A X TSG-327 recorded the significant negative

Table 2. Analysis of variance for combining ability in sunflower.

Characters	Parents MSS	Lines MSS	Tester MSS	Crosses MSS	Parents v/s Crosses MSS	δ2 gca (ave.)	δ2sca	Error MSS
d.f.	**13**	**4**	**8**	**44**	**1**			**60**
D50%F	23.2087**	11.6000**	23.2222**	33.7285**	381.288**	1.9579**	5.2123**	2.5143
DM	27.2967**	12.6000**	6.5000*	26.0363**	497.915**	-0.6589	13.3887**	2.4476
PH (cm)	156.835**	127.400**	165.555**	540.218**	727.881**	90.1570**	135.603**	8.3284
HD(cm)	2.6813**	4.1625**	2.1805**	5.04350**	142.678**	0.7157**	1.2370**	0.6722
100 SW (g)	5.5742**	1.4660**	3.9344**	24.6662**	4.7430**	0.0088*	0.2293**	3.4886
SPP (g)	48.1037**	5.2475	14.4113	112.71**	2271.73**	28.6290**	16.7174**	7.483
VW(g/100ml)	52.711**	8.4015**	9.4925**	89.888**	4566.24**	21.7135**	16.6726**	1.3619
SF (%)	9.3980**	3.6464	12.992**	63.826**	1544.11**	14.1156**	13.0460**	2.0552
OC (%)	30.1720**	38.72**	29.52**	11.327**	97.895**	0.8361*	4.5649**	0.0853

** and * indicates significant at 1% and 5%, respectively.

Table 3. Estimates of general combining ability (GCA) effect of lines for nine characters in sunflower.

Characters	CMS-519A	CMS-234-1017A	CMS-SUN-35-519A	CMS-62A	CMS-10A
Days to 50% flowering	1.489**	-0.067	1.711**	-0.511	-2.622**
Days to maturity	0.044	-1.400**	1.378**	1.044**	-1.067**
Plant height (cm)	-15.733**	-5.289**	2.544**	2.378**	16.100
Head diameter (cm)	-0.292	-1.481**	-0.392*	0.774**	1.391**
100 seed weight (g)	-0.109	0.019	-0.087	-0.120*	0.297**
Seed yield/plant (g)	-6.438**	-7.427**	2.579**	2.257**	9.029**
Volume weight (g/100ml)	-6.842**	-3.292**	0.952**	-0.009	9.191**
Seed filling (%)	-4.700**	-5.383**	2.817**	1.478**	5.789**
Oil content (%)	0.964**	1.676**	-0.158*	-0.769**	-1.713**

** and * indicates significant at 1% and 5%, respectively.

Table 4. Estimates of general combining ability (GCA) effect of testers for nine characters in sunflower.

Characters	TSG-257	TSG-274	TSG-269	TSG-289	TSG-04	TSG-281	TSG-327	TSG-111	SCG-04
Days to 50% flowering	0.289	2.489**	-0.511	2.289**	-1.911**	-1.711**	-0.511**	-1.111*	0.689
Days to maturity	1.200*	0.400	0.200	-0.600	-1.600**	1.800**	-1.400**	0.400	-0.400
Plant height (cm)	-0.933	1.167	-1.433	-15.13**	-8.633**	9.677**	8.467**	2.467**	4.367**
Head diameter (cm)	-0.107	-0.057	-1.437**	0.653*	-0.377	0.063	0.433	0.433	0.393
100-seed weight (g)	0.136	0.046	-0.224**	0.046	0.326**	-0.594**	-0.054	0.156	0.166*
Seed yield/plant (g)	-0.743	-1.173	-1.953*	-2.303*	-0.403	2.547**	1.057	1.567	1.407
Volume weight(g/100ml)	0.019	-0.941*	0.669	-1.891**	-2.897**	-0.441	0.869*	1.269**	3.339**
Seed filling (%)	-2.031**	-0.491	2.379**	0.589	-0.841	-0.021	0.329	2.179**	-2.091**
Oil content (%)	0.459**	-1.071**	-0.681**	1.739**	-0.491**	0.339**	-0.441**	-0.881**	1.029**

** and * indicates significant at 1% and 5%, respectively

Table 5. Estimates of specific combining ability (SCA) effects in sunflower

Sr. no.	Characters	Days to 50% flowering	Days to maturity	Plant height (cm)	Head diameter (cm)	100-seed weight (g)	Seed yield per plant (g)	Volume weight (g/100ml)	Seed Filling (%)	Oil content (%)
	Crosses	**1**	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**
1	CMS 519A X TSG-257	0.711	0.356	-5.067*	0.662	0.209	4.888*	0.992	4.970**	2.536**
2	CMS 519A X TSG-274	4.5111**	3.156**	8.833**	1.612**	-0.451*	2.418	0.052	0.430	-3.584**
3	CMS 519A X TSG-269	-2.489*	-2.644*	17.433**	-1.508*	0.269	0.298	4.292**	3.910**	-0.474*
4	CMS 519A X TSG-289	-1.289	0.156	-10.867**	1.902**	0.149	0.298	0.752	5.550**	2.706**
5	CMS 519A X TSG-04	-0.089	0.156	-3.367	-0.068	0.169	-0.602	1.702*	1.880	0.286
6	CMS 519A X TSG-281	-0.289	3.756**	-10.167**	-0.008	-0.211	-0.902	-1.898*	-3.640**	0.906**
7	CMS 519A X TSG-327	3.511**	2.956*	-12.467**	1.622**	0.349	3.288	0.942	-6.390**	-2.264**
8	CMS 519A X TSG-111	-2.889*	-2.844*	1.033	-2.378**	0.039	-2.522	-2.658**	-1.840	0.326
9	CMS 519A X SCG-04	-1.689	-5.044**	14.633**	-1.838**	-0.521**	-7.162**	-4.178**	-4.870**	-0.434*
10	CMS 234-1017A X TSG-257	-3.733**	-2.200	-3.511	-1.549*	0.081	-2.973	-1.958*	-3.047**	-1.876**
11	CMS 234-1017A X TSG-274	0.067	-5.400**	-10.611**	-1.449*	-0.279	-2.093	-3.948**	2.013	1.554**
12	CMS 234-1017A X TSG-269	2.067	-0.200	-17.511**	-1.069	-0.709**	-0.463	-2.508**	-1.307	-0.786**
13	CMS 234-1017A X TSG-289	0.267	-0.400	7.689**	0.341	-0.929**	-4.563*	-4.148**	1.133	-1.206**
14	CMS 234-1017A X TSG-04	-1.533	-0.400	-4.811*	-0.379	-0.309	-1.713	-0.648	-7.637**	1.274**
15	CMS 234-1017A X TSG-281	2.267*	1.200	9.889**	1.431*	0.361*	2.287	1.752*	4.593**	-1.456**
16	CMS 234-1017A X TSG-327	-2.933*	2.400*	14.589**	0.161	0.521**	4.527*	1.292	3.093**	1.574**
17	CMS 234-1017A X TSG-111	1.677	0.600	9.589**	1.411**	0.661**	0.817	4.292**	-0.457	1.564**
18	CMS 234-1017A x SCG-04	1.867	4.400**	-5.311*	1.101	0.601**	4.177*	5.872**	1.613	-0.646**
19	CMS SUN-35-519A x TSG-257	2.489*	2.022	0.156	0.662	0.337	-1.979	6.198**	-2.147*	-0.342
20	CMS SUN-35-519A x TSG-274	-5.711**	-2.178	4.056	-0.488	-0.073	2.601	5.808**	0.963	2.138**
21	CMS SUN-35-519A x TSG-269	-0.711	2.022	-0.844	1.092	-0.103	5.531**	3.898**	0.743	4.248**
22	CMS SUN-35-519A x TSG-289	2.489*	-5.178**	6.356**	-0.098	1.077**	6.931**	3.758**	-1.517	-1.122**
23	CMS SUN-35-519A x TSG-04	0.689	-4.178**	21.856**	0.282	-0.653**	7.781**	1.458	5.963**	-2.393**
24	CMS SUN-35-519A x TSG-281	-1.511	0.422	-9.444**	-0.658	-0.033	-6.119**	-6.842**	-4.707**	2.678**
25	CMS SUN-35-519A X TSG-327	2.289*	2.622*	-3.244	-1.278*	-0.423*	-5.579**	-5.702**	0.793	-2.092**
26	CMS SUN-35-519A X TSG-111	-2.111	1.822	-15.244**	-0.278	0.017	-4.339*	-4.102**	2.943**	-2.852**
27	CMS SUN-35-519A X SCG-04	2.089	2.622*	-3.644	0.762	-0.143	-4.829*	-4.472**	-3.037**	-0.262
28	CMS 62A X TSG-257	1.711	3.356**	7.322**	-0.504	-0.280	-1.607	-4.141**	0.292	-1.781**
29	CMS 62A X TSG-274	2.511**	2.156	-3.3778	-0.604	0.210	-3.027	-4.081**	-1.248	0.649**
30	CMS 62A X TSG-269	1.511	3.356**	-10.678**	1.676**	0.730**	-2.047	-3.691**	2.282*	-2.591**
31	CMS 62A X TSG-289	-1.289	6.156**	-10.978**	-1.414*	-0.190	-3.947*	-2.881**	-4.728**	-0.111
32	CMS 62A X TSG-04	0.911	4.156**	-14.978**	0.666	0.430*	-3.747	-2.831**	-0.898	-0.781**
33	CMS 62A X TSG-281	0.711	-8.244**	0.222	0.926	-0.200	0.403	7.419**	1.432	0.339
34	CMS 62A X TSG-327	-2.489*	-6.044**	7.422**	-0.944	-0.690**	3.493	1.709*	-0.068	-0.331
35	CMS 62A X TSG-111	0.111	-3.844**	12.922**	0.306	-0.500**	2.333	4.209**	-0.718	1.509**
36	CMS 62A X SCG-04	-3.689**	-1.044	12.522**	-0.104	0.490**	8.143**	4.289**	3.652**	3.099**
37	CMS 10A X TSG-257	-1.178	-3.533**	1.100	0.729	-0.347	1.671	-1.091	-0.069	1.463**
38	CMS 10A X TSG-274	-1.378	2.267*	1.500	0.929	0.593**	0.101	2.169*	-2.159*	-0.757**
39	CMS 10A X TSG-269	-0.378	-2.533*	11.600**	-0.191	-0.187	-3.319	-1.991*	-5.629**	-0.397
40	CMS 10A X TSG-289	-0.178	-0.733	7.800**	-0.732	-0.107	1.281	2.519**	-0.439	-0.267
41	CMS 10A X TSG-04	0.022	0.267	1.300	-0.501	0.363*	-1.719	0.319	0.691	1.613**
42	CMS 10A X TSG-281	-1.178	2.867*	9.500**	-1.691**	0.083	4.331*	-0.431	2.321*	-2.467**
43	CMS 10A X TSG-327	-0.378	-1.933	-6.300**	0.439	0.243	-5.729**	1.759*	2.571*	3.113**
44	CMS 10A X TSG-111	3.222**	4.267**	-8.300**	0.939	-0.217	3.711	-1.741*	0.071	-0.547*
45	CMS 10A X SCG-04	1.422	-0.933	-18.200**	0.079	-0.427*	-0.329	-1.511	2.641*	-1.757**

** and * indicates significant at 1% and 5%, respectively

Table 6.Estimation of gene action for nine characters in sunflower

Sr. no.	Character	Variance gca	Variance sca	Ratio var.gca /var.sca	Gene action
1	Days to 50% flowering	1.9579**	5.2123**	0.3756	Non-Additive
2	Days to maturity	-0.6589	13.3887**	-0.0492	Non-additive
3	Plant height (cm)	90.1570**	135.603**	0.6649	Non-additive
4	Head diameter (cm)	0.7157**	1.2370**	0.5786	Non-additive
5	100-seed weight (g)	0.0088**	0.2293**	0.0383	Non-additive
6	Seed yield/plant (g)	28.6290**	16.7174**	1.7125	Additive
7	Vol. weight (g/100ml)	21.7135**	16.6726**	1.3023	Additive
8	Seed filling (%)	14.1156**	13.0460**	1.0820	Additive
9	Oil content (%)	0.8361**	4.5649**	0.1832	Non-additive

** and * indicates significant at 1% and 5%, respectively

sca effect for days to 50% flowering similar findings were reported by Deengra *et al*., (2012).The negative SCA effects are considered to be desirable for days to maturity. The hybrids, CMS 62A X TSG-281 exhibited the highest significant negative SCA effect followed by CMS 62A X TSG-327, CMS 234-1017A X TSG-274, CMS SUN-35-519A X TSG-289, CMS 519A X SCG-04 indicating these hybrids could be identified as early. Similar finding in sunflower was reported by Deengra*et al*., (2012). For plant height hybrids *viz*., CMS 10A X SCG-04, CMS 234-1017A X TSG-269, CMS SUN-35-519A X TSG-111, CMS 62A X TSG-04 and CMS 519A X TSG-327 exhibited the highest negative significant *sca* effect. The hybrids, CMS 519A X TSG-289, CMS 62A X TSG-269 and CMS 519A x TSG-327 recorded the high positive significant *sca* effects for head diameter which helps in increasing the number of seeds per head, ultimately increases yield. Similar finding in sunflower was reported by Patil*et al.* (2012). For seed yield per plant eight hybrids *viz*., CMS 62A X SCG-04, CMS SUN-35-519A X TSG-04, CMS SUN-35-519A X TSG-289, CMS SUN-35-519A X TSG-269, CMS 519A X TSG-257, CMS 234-1017 X TSG-327, CMS 10A X TSG-281, CMS 234-1017A X SCG-04 exhibited the significant positive *sca* effect. These results were in conformity with the earlier reports of Chandra *et.al*.,(2011) and Qamar*et al*.,(2015).The hybrid CMS SUN-35-519A X TSG-289 recorded the highest significant positive *sca* effect followed by CMS 519A x TSG-289, CMS 234-1017A x TSG-281, CMS 519A x TSG-269 for seed filling percentage, Similar finding was reported by Patil*et al*., (2012).Out of 45 hybrids, ten hybrids showed the significant *sca* effect in desirable direction. For 100 seed weight hybrid CMS SUN-35-519A X TSG-289 exhibited a significant positive *sca* effect followed by CMS 62A X TSG-269, CMS 234-1017A X TSG 111, CMS 62A X TSG 04. Similar finding in sunflower was reported by Patil *et al*., (2012). For volume weight (g/100ml) hybrids *viz*., CMS 62A X TSG-281, CMS SUN-35-519A X TSG-257, CMS 234-1017A X SCG-04 and CMS SUN-35-519A X TSG-274 exhibited the significant highest positive *sca* effect. Similar finding in sunflower were reported by Patil*et al.,* (2012).16 hybrids exhibited the significant *sca* effect for oil content. The hybrids CMS SUN-35-519A X TSG-269, CMS 10A x TSG-327, CMS 62A x SCG-04, CMS 519A x TSG-289, CMS SUN-35-519A x TSG-281 recorded a significant positive *sca* effect.

The information on nature of gene action for yield and yield component traits in different populations is imperative for planning effective breeding programme. In the present study the variance due to SCA was greater than variance due to GCA for all characters, except seed yield per plant, volume weight and seed filling (%). Whereas the presence of additive type of gene action for characters viz., seed yield per plant, volume weight and seed filling (%) was confirmed by the ratio of ($δ^2$gca/ δ2sca) was more than unity for characters indicating additive gene action. Similarly the ratio of GCA/ SCA was less than 1 for days to 50% flowering, days to maturity, plant height, head diameter, 100-seed weight (g) and Oil content (%) which indicated that there is presence of non-additive gene action. In such situations development of hybrids and synthetics can be effectively done, similar results were reported by Radhika *et al.,*(2001), Phad *et al.* (2002).

The variance component due to specific combining ability was greater in magnitude than that of general combining ability (*gca*) for all the characters except seed yield per plant, volume weight and seed filling percentage which indicated that non-additive gene action played importance role for the inheritance of these traits. CMS 10A was good general combiner for days to 50% flowering, days to maturity, head diameter, 100 seed weight, seed yield per plant, volume weight and seed filling. Similarly CMS 519A and CMS 62A found to be good general combiner for seed yield and component traits. TSG-281 and SCG-04 exhibited good combining ability for oil content and component traits. Out of 45 hybrids five hybrids *viz*., CMS 62A X SCG-04, CMS 234-1017A X TSG-327, CMS 234-1017A X TSG-111, CMS SUN-35-519A X TSG-289 and

CMS 519A X TSG-289 exhibited the significant desirable sca effect for seed yield and component traits.

The ratio of *gca/sca* variance for different characters revealed that days to 50% flowering, days to maturity, plant height, head diameter, 100 seed weight and oil content were governed by non-additive gene action and seed yield per plant, volume weight and seed filling percentage were governed by additive gene action.

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