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Combining ability and gene action studies in cytoplasmic male sterility-based hybrids in cauliflower

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ABSTRACT

Cauliflower is considered as one of the healthiest foods on earth. It supplies good amount of health promoting photochemicals, high level of anti-inflammatory compounds and has ability to ward-off cancer, heart diseases and even weight gain. A study was conducted in cauliflower comprising five CMS lines and four testers, along with their twenty cross combinations which were evaluated in randomized complete block design in rabi season of 2016-17to know the extent of combining ability and magnitude and nature of gene action for different traits in line x tester mating design. Among parents, line Ogu-HL-3A was found good general combiner for marketable curd weight (73.75) and curd breadth (1.04) and Ogu-119-1A for marketable curd weight (64.58) while among testers, PSBK-1 was good general combiner for marketable curd weight (76.18) and curd breadth (0.75) and Hermia for curd length (0.36), stalk length (0.39) and days to marketable maturity (-1.95). Among crosses, Ogu-HL-3A x 1385 (-6.10) was good specific combiner for days to marketable maturity. For marketable curd weight, Ogu-HL-3A x Hermia (190.05), Ogu-122-1A x PSBK-1 (157.98) and Ogu-HL-1A x Kt-22 (135.63) were found to be best specific combiners. For curd length Ogu-HL-1A x Hermia (1.10), Ogu-122-1A x 1385 (1.01), Ogu-119-2A x Kt-22 (0.97) and Ogu-119-1A x Kt-22 (0.61) were found to be best specific combiners while for curd breadth crosses Ogu-HL-1A x Kt-22 (1.84), Ogu-122-1A x 1385 (1.75) and Ogu-HL-3A x Hermia (1.32) showed significant SCA effects.On the basis of SCA performance, cross combinations Ogu-HL-3A x Hermia, Ogu-119-1A x Kt-22 and Ogu-122-1A x PSBK-1 were found the best for most of the horticultural traits. Estimates of GCA and SCA, additive and dominant components of variances and the ratios of additive to dominant components revealed that preponderance of non-additive gene action was recorded in inheritance of all the characters under study.

Keywords: Cauliflower; line; tester, GCA; SCA; gene action

INTRODUCTION

Cauliflower (*Brassica oleracea* var *botrytis* L) is a cross-pollinated crop having diploid chromosome number 18 and belongs to family Cruciferae. It is one of the most important vegetable crops of cole group grown extensively all over the world. It occupies the pride place among cole crops due to its delicious taste, flavour and nutritive value. Another distinctive name given to cauliflower is 'queen of winter vegetable' (Elahi et al 2015). Cauliflower commonly known as 'Phoolgobhi' was introduced in India from England in 1822 by Dr Jemson (Nath et al 1994). The original introductions were Cornish type which originated in England followed by temperate types originated in Germany and Netherlands in 18th century (Swarup and Chatterjee 1972). Cauliflower is a rich source of vitamin C and minerals such as phosphorus, potassium, calcium, sodium and magnesium. Curd of cauliflower contains 1.9 per cent protein, 5 per cent carbohydrate, 95 per cent water, 48.2 mg vitamin C and 199 mg potassium/100 g of edible portion (Gopalan et al 2011). More intake of cauliflower is related to reduced risk of prostate cancer (Kushwaha et al 2013) as it contains potent anti-cancer compounds such as di-indolylmethane, sulforaphane and selenium. Cauliflower has a good flavour which may be due to the presence of compounds like dimethyl sulfide, dimethyl trisulfide and 3-(methylthio) propyl isothiocyanate (Whitfield and Last 1991). Study of general combining ability and specific combining ability provides information for selecting suitable parents and cross combinations respectively. Combining ability analysis helps in selecting parents and crosses for further exploitation (Munshi and Verma 1999). Combining ability of parents depends upon genetic system present in the parent which predicts the efficiency of selection. In order to exploit different types of gene actions, information regarding relative proportion of genetic variances and combining ability of the parents is essential. Among the different biometrical methods available to determine the genetic information from the performance of hybrids and to identify appropriate cross-combinations, line × tester mating design as proposed by Kempthorne (1957) gives comparable estimate of the genetic make-up of genotypes. The mating design is useful to identify the best general combiners and specific cross combinations amongst a large number of parent lines by attempting relatively lesser number of crosses as compared to other mating designs.

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MATERIAL and METHODS

The investigations were carried out at the departmental research farm of Vegetable Science, Dr YS Parmar University of Horticulture and Forestry, Nauni, Solan, Himachal Pradesh during rabi season of 2016-2017 to record the extent of combining ability and magnitude and nature of gene action. The experimental site was located at Nauni, about 14 km away from Solan city at an altitude of 1,270 meters amsl lying between 35.5° North latitude and 77.8° East longitude. The farm area falls in the mid-hill zone of Himachal Pradesh. The experimental material comprised 20 cross combinations obtained by crossing 5 CMS lines viz Ogu-122-1A, Ogu-119-1A, Ogu-119-2A, Ogu-HL-1A and Ogu-HL-3A and 4 testers PSBK-1, Hermia, 1385 and Kt-22 in line × tester mating design. Experimental material was procured from IARI, Regional Station Katrain, Kullu, Himachal Pradesh. During rabi 2016-2017, the F_1 populations of 20 crosses and their parents were transplanted during the month of October 2016. The experiment was carried out in randomized complete block design with three replications. Spacing was kept 60 cm × 45 cm in a plot size of 2.40 m × 2.25 m which accommodated 20 plants per plot. All the cultural practices were followed for raising a healthy crop as recommended in the package of practices for vegetables of Dr YS Parmar University of Horticulture and Forestry, Nauni, Solan, Himachal Pradesh. Observations were recorded on ten plants in each treatment in all three replications on the parameters viz days to maturity, leaves per plant, plant height, gross curd weight, curd weight, leaf length, leaf breadth, curd length, curd breadth, stalk length and ascorbic acid content.

RESULTS and DISCUSSION

Analysis of variance for combining ability depicted remarkable differences among the parents and cross combinations for all the traits under study. Mean sum of squares due to lines and testers were also significant for all the traits when tested against mean sum of squares due to error (Table 1). Similar findings were reported by Pandey and Naik (1989), Gangopadhyay et al (1997), Singh et al (2005) and Varalakshmi (2009). The lines or testers exhibiting significant negative or positive GCA effects were designated as good or poor general combiners respectively for days to marketable maturity. The parental line Ogu-119-1A and testers 1385 and Hermia were good general combiners for days to marketable maturity as these exhibited the significant GCA estimates with negative values of -3.18, -2.48 and -1.95 respectively (Tables 2, 3). Among the crosses, Ogu-HL-3A × 1385 (-6.10), Ogu-122-1A × Hermia (-5.22), Ogu-HL-1A × Kt-22 (-4.80), Ogu-119-1A × Hermia (-4.22), Ogu-119-1A × Kt-22 (-2.22) and Ogu-HL-3A × PSBK-1 (-1.63) exhibited significant negative SCA effects (Table 4). These crosses involved average × good, average × good, average × average, good × good, good × average and average × poor combining parents respectively. Seven crosses were found to be poor specific combiners for this trait. Gangopadhyay et al (1997), Thakur and Singh (1999), Singh et al (2002), Jindal and Thakur (2003), Thakur and Korla (2003), Varalakshmi (2009), Dey et al (2011), Mehra (2012) and Gaur (2014) reported similar results for GCA and SCA effects. For number of leaves per plant, parental line Ogu-HL-3A (-1.07) showed significant negative GCA effects indicating it as good general combiner. Among crosses, six cross combinations showed significant negative SCA effects being maximum in Ogu-HL-1A × 1385 (-3.47) followed by Ogu-122-1A × PSBK-1 (-2.18), Ogu-119-1A × Hermia (-2.07), Ogu-HL-3A × PSBK-1 (-1.93), Ogu-119-1A × Kt-22 (-1.53) and Ogu-119-2A × K-22 (-1.02). Similar results were reported by Thakur and Singh (1999), Garg et al (2003), Jindal and Thakur (2003), Singh et al (2005), Mehra (2012), Gaur (2014), Kumari (2014) and Ram (2014). The lines or testers exhibiting significant positive GCA effects were designated as good general combiners for the characters viz plant height, leaf length, gross curd weight, marketable curd

Table 1. Analysis of variance for line x tester analysis in cauliflower

Source	Mean sum of square								
	Replications	Treatments	Parents	P vs C	Crosses	Lines	Testers	Line x tester	Error
df	2	28	8	1	19	4	3	12	56
Character									
Days to marketable maturity	0.05	61.85*	55.25*	10.79*	67.32*	83.43*	35.42*	69.92*	3.08
Number of leaves/plant	3.94*	9.56*	6.25*	0.03	11.46*	8.23*	4.75*	14.21*	1.15
Plant height (cm)	1.12*	52.41*	89.00*	48.99*	37.18*	44.27*	101.27*	18.79*	0.96
Leaf length (cm)	2.58	54.75*	79.61*	145.86	39.48*	55.16*	95.98*	20.13*	2.82
Leaf breadth (cm)	4.16	12.27*	16.41*	12.77*	10.50*	11.53*	18.24*	8.22*	2.22
Gross curd weight (g)	9881.45	173288.64*	48190.86*	2566941.98*	99979.63*	52238.46*	5052.31	157037.16*	8351.34
Marketable curd weight (g)	339.26	88912.37*	40992.51*	1201321.08*	50541.33*	29186.85*	10766.32*	67603.24*	2243.20
Curd length (cm)	0.15	3.47*	3.76*	29.26*	37.75*	3.5831.987*	1.43	1.59*	0.18
Curd breadth (cm)	0.41	10.63*	7.98*	133.18*	5.39*	9.01*	3.40*	4.68*	0.47
Stalk length (cm)	0.21*	2.88*	3.15*	4.51*	2.68*	3.37*	0.15	3.09*	0.06
Ascorbic acid content (mg/100g)	12.23	996.46*	380.34*	2374.36*	1183.36*	330.80*	300.53*	1688.25*	8.48

weight and curd breadth etc. In case of plant height, the parental lines Ogu-HL-3A (2.70) and Ogu-HL-1A (1.39) recorded significant positive GCA thereby indicating that they were good general combiners for this trait. In case of testers, Hermia (2.31) was the best general combiner for plant height. Among crosses, six crosses showed significant positive SCA effects being maximum in Ogu-119-1A × Kt-22 (5.67) followed by Ogu-122-1A × PSBK-1 (3.93), Ogu-119-2A × 1385 (3.83), Ogu-HL-3A × Hermia (2.26), Ogu-HL-1A × PSBK-1 (1.49) and Ogu-HL-1A × Kt-22 (1.29). Similar findings were also reported by Singh et al (2005), Mehra (2012), Gaur (2014), Ram (2014), Verma and Kalia (2015) and Verma and Kalia (2016). Two lines exhibited significant positive GCA effects for leaf length viz Ogu-HL-3A (3.16) and Ogu-HL-1A (1.76) and showed good general combining ability while Ogu-119-1A (-2.68) and Ogu-119-2A (-2.12) were poor general combiners. In case of testers, Hermia (2.10) was the best general combiner whereas Kt-22 (-1.94) was the poor general combiner. Significant positive specific combining ability effects were observed for four crosses viz Ogu-119-1A × Kt-22 (4.86), Ogu-122-1A × PSBK-1 (3.69), Ogu-119-2A × Hermia (2.19) and Ogu-HL-3A × Hermia (2.11). These results are in conformity with those of Mehra (2012), Gaur (2014), Ram (2014) and Verma and Kalia (2016). For leaf breadth, no significant positive and negative GCA effects were exhibited by the lines as well as testers; so all parents were designated as average general combiners for the trait. Out of twenty cross combinations, five crosses viz Ogu-HL-1A × Kt-22 (3.59), Ogu-HL-3A × Hermia (2.51), Ogu-122-1A × PSBK-1 (1.65), Ogu-HL-1A × Hermia (1.52) and Ogu-119-2A × 1385 (1.43) were the best combinations due to their significant positive SCA effects for leaf breadth. These results are in conformity with those of Mehra (2012), Gaur (2014), Ram (2014) and Verma and Kalia (2016). Among the parental lines, Ogu-HL-3A (164.37) was the best general combiner for gross curd weight. In case of testers, no significant positive GCA effects were exhibited by the testers. Among the crosses, Ogu-HL-1A × PSBK-1 (245.86), Ogu-119-2A × 1385 (217.23), Ogu-119-1A × 1385 (169.91), Ogu-HL-1A × Kt-22 (147.60), Ogu-HL-3A × Hermia (122.50) and Ogu-122-1A × Hermia (104.83) were the best specific combiners for gross curd weight. Gangopadhayay et al (1997), Thakur

Table 2. Estimates of general combining ability (GCA) effects of lines for different traits in cauliflower

Line	Character										
	Days to marketable maturity	Number of leaves/plant	Plant height (cm)	Leaf length (cm)	Leaf breadth (cm)	Gross curd weight (g)	Marketable curd weight (g)	Curd length (cm)	Curd breadth (cm)	Stalk length (cm)	Ascorbic acid content (mg/100 g)
Ogu-122-1A	-0.18	-0.48	0.02	-0.12	-0.05	-64.39*	-99.92*	-0.33*	-0.12	0.14	-5.06*
Ogu-119-1A	-3.18*	-0.07	-2.52*	-2.68*	-0.35	-43.50	64.58*	0.00	-0.11	0.56*	6.30*
Ogu-119-2A	2.73*	0.35	-1.59*	-2.12*	-0.42	-27.39	-19.92	-0.09	0.28	-0.08	-5.75*
Ogu-HL-1A	-0.27	1.27*	1.39*	1.76*	0.74	-29.08	-18.50	0.29	-1.09*	-0.40*	1.69
Ogu-HL-3A	0.90	-1.07*	2.70*	3.16*	0.08	164.37*	73.75*	0.13	1.04*	-0.22*	2.82*
SE (g_i) lines	0.42	0.28	0.28	0.51	0.37	24.03	7.36	0.11	0.18	0.06	0.78
SE (g_i- g_j) lines	0.59	0.40	0.40	0.71	0.52	33.98	10.41	0.16	0.26	0.09	1.12
$CD_{0.05}$ (g_i- g_j) lines	1.18	0.8	0.8	1.42	1.04	68.07	20.85	0.32	0.52	0.18	2.24

Table 3. Estimates of general combining ability (GCA) effects of testers for different traits in cauliflower

Tester	Character										
	Days to marketable maturity	Number of leaves/plant	Plant height (cm)	Leaf length (cm)	Leaf breadth (cm)	Gross curd weight (g)	Marketable curd weight (g)	Curd length (cm)	Curd breadth (cm)	Stalk length (cm)	Ascorbic acid content (mg/100 g)
PSBK-1	3.72*	-0.15	-0.07	0.64	-0.06	38.43	76.18*	0.06	0.75*	-0.88*	-10.76*
Hermia	-1.95*	0.98*	2.31*	2.10*	0.37	-64.89*	-38.55*	0.36*	-0.48*	0.39*	-9.62*
1385	-2.48*	-0.95*	-0.20	-0.80	0.05	21.67	-47.08*	-0.30*	-0.49*	0.06	4.51*
Kt-22	0.72	0.12	-2.04*	-1.94*	-0.36	4.80	9.45	-0.12	0.22	0.42*	15.87*
SE (g_j) testers	0.36	0.24	0.25	0.44	0.32	20.81	6.37	0.10	0.16	0.05	0.68
SE (g_i- g_j) testers	0.66	0.45	0.45	0.8	0.58	38.00	11.63	0.18	0.29	0.10	1.24
$CD_{0.05}$ (g_i- g_j) testers	1.32	0.90	0.90	1.60	1.16	76.12	23.30	0.36	0.58	0.20	2.48

Table 4. Estimates of specific combining ability (SCA) effects of crosses for different traits in cauliflower

Cross	Character										
	Days to marketable maturity	Number of leaves/plant	Plant height (cm)	Leaf length (cm)	Leaf breadth (cm)	Gross curd weight (g)	Marketable curd weight (g)	Curd length (cm)	Curd breadth (cm)	Stalk length (cm)	Ascorbic acid content (mg/100 g)
Ogu-122-1A x PSBK-1	0.12	-2.18*	3.93*	3.69*	1.65*	74.37	157.98*	0.35	0.58	-1.06*	6.09*
Ogu-122-1A x Hermia	-5.22*	0.68	-0.16	-2.07*	-1.06	104.83*	-40.62*	0.15	-0.53	0.37*	-4.05*
Ogu-122-1A x 1385	0.32	0.62	-0.78	-0.48	0.90	-92.20*	42.92*	1.01*	1.75*	-0.39*	22.86*
Ogu-122-1A x Kt-22	4.78*	0.88	-3.00*	-1.13	-1.49*	-87.00*	-160.28*	-1.50*	-1.80*	1.08*	-24.91*
Ogu-119-1A x PSBK-1	-0.22	2.40*	-3.84*	-3.39*	0.85	-201.65*	-79.85*	0.22	-0.34	0.59*	29.17*
Ogu-119-1A x Hermia	-4.22*	-2.07*	-1.79*	-2.32*	-0.06	12.47	-55.12*	-0.47*	0.03	-0.14	-12.66*
Ogu-119-1A x 1385	6.65*	1.20*	-0.04	0.85	-0.14	169.91*	54.75*	-0.35	0.07	-0.28*	-31.72*
Ogu-119-1A X Kt-22	-2.22*	-1.53*	5.67*	4.86*	-0.66	19.28	80.22*	0.61*	0.25	-0.17	15.21*
Ogu-119-2A x PSBK-1	-0.80	-1.02*	-1.54*	-2.65*	0.48	14.57	-7.02	-0.19	-0.99*	-1.04*	-12.02*
Ogu-119-2A x Hermia	1.53*	-0.15	0.15	2.19*	-2.92*	-219.51*	-127.28*	-1.08*	0.28	-0.54*	14.08*
Ogu-119-2A x 1385	-0.60	1.78*	3.83*	1.42	1.43*	217.23*	117.92*	0.31	0.88*	1.49*	-2.15
Ogu-119-2A x Kt-22	-0.13	-0.62	-2.44*	-0.97	1.01	-12.30	16.38	0.97*	-0.17	0.10	0.09
Ogu-HL-1A x PSBK-1	2.53*	2.73*	1.49*	1.41	-3.28*	245.86*	-55.10*	-0.27	0.54	0.88*	0.11
Ogu-HL-1A x Hermia	2.53*	0.60	-0.46	0.09	1.52*	-20.28	32.97*	1.10*	-1.09*	-0.09	-5.72*
Ogu-HL-1A x 1385	-0.27	-3.47*	-2.32*	-2.52*	-1.83*	-373.18*	-113.50*	-1.38*	-1.29*	-0.69*	7.82*
Ogu-HL-1A x Kt-22	-4.80*	0.13	1.29*	1.03	3.59*	147.60*	135.63*	0.55*	1.84*	-0.11	-2.21
Ogu-HL-3A x PSBK-1	-1.63*	-1.93*	-0.05	0.94	0.31	-133.15*	-16.02	-0.11	0.22	0.63*	-23.35*
Ogu-HL-3A x Hermia	5.37*	0.93	2.26*	2.11*	2.51*	122.50*	190.05*	0.30	1.32*	0.40*	8.35*
Ogu-HL-3A x 1385	-6.10*	-0.13	-0.69	0.74	-0.37	78.24	-102.08*	0.42*	-1.41*	-0.14	3.19*
Ogu-HL-3A x Kt-22	2.37*	1.13	-1.52*	-3.78*	-2.46*	-67.59	-71.95*	-0.62*	-0.12	-0.90*	11.82*
SE (S_{ij})	0.72	0.49	0.49	0.87	0.64	41.62	12.74	0.20	0.32	0.11	1.36
SE (S_{ij}-S_{kj}) common Line	1.48	1.00	1.00	1.78	1.30	84.96	26.01	0.40	0.65	0.22	2.77
SE (S_{ij}-S_{kj}) common tester	1.45	0.97	0.98	1.75	1.28	83.24	25.49	0.40	0.64	0.21	2.71
$CD_{0.05}$ (S_{ij})	1.45	0.98	0.98	1.75	1.28	83.38	25.53	0.40	0.64	0.21	2.71
$CD_{0.05}$ (S_{ij}-S_{kj}) common tester	2.96	1.99	2.00	3.57	2.61	170.20	52.11	0.81	1.30	0.43	5.54
$CD_{0.05}$ (S_{ij}-S_{kj}) common line	2.90	1.95	1.96	3.50	2.56	166.76	51.05	0.79	1.27	0.42	5.43

and Singh (1999), Singh et al(2002), Jindal and Thakur (2003), Thakur and Korla (2003), Mehra (2012), Gaur (2014), Kumari (2014), Verma and Kalia (2015) and Verma and Kalia (2016) observed similar results in their study for gross curd weight. The parental lines Ogu-HL-3A (73.75) and Ogu-119-1A (64.58) recorded significant positive GCA for marketable curd weight thereby indicating that these were good general combiners for this trait. In case of testers, PSBK-1 (76.18) was the best general combiner. Among the crosses, eight cross combinations showed significant positive SCA effects for the trait, being maximum in Ogu-HL-3A × Hermia (190.05) followed by Ogu-122-1A × PSBK-1 (157.98), Ogu-HL-1A × Kt-22 (135.63), Ogu-119-2A × 1385 (117.92), Ogu-119-1A × Kt-22 (80.22), Ogu-119-1A × 1385 (54.75), Ogu-122-1A × 1385 (42.92) and Ogu-HL-1A × Hermia (32.97). These crosses involved good × poor, poor × good, average × average, average × poor, good × average, good × poor, poor × poor and average × poor combining parents respectively. Good GCA and SCA effects for marketable curd weight were reported by Gangopadhayay et al (1997), Thakur and Korla (2003), Mehra (2012), Gaur (2014), Kumari (2014), Ram (2014), Verma and Kalia (2015) and Verma and Kalia (2016). In case of curd length, no significant positive GCA effects were exhibited by the lines while in case of testers, Hermia (0.36) was the best general combiner. Six crosses viz Ogu-HL-1A × Hermia (1.10),Ogu-122-1A × 1385 (1.01), Ogu-119-2A × Kt-22 (0.97), Ogu-119-1A × Kt-22 (0.61), Ogu-HL-1A × Kt-22 (0.55) and Ogu-HL-3A × 1385 (0.42) were the best combinations due to their significant positive SCA effects.

These results are in conformity with the findings of Jindal and Thakur (2003), Garg and Lal (2005), Dey et al (2011), Mehra (2012), Gaur (2014), Kumari (2014) and Ram (2014). The parental line Ogu-HL-3A (1.04) recorded significant positive GCA thereby indicating as good general combiner for curd breadth whereas in case of testers, PSBK-1 (0.75) was the best general combiner. Among the cross combinations, Ogu-HL-1A × Kt-22 (1.84), Ogu-122-1A × 1385 (1.75), Ogu-HL-3A × Hermia (1.32) and Ogu-119-2A × 1385 (0.88) showed significant positive SCA effects for the trait. These results are in conformity with the findings of Jindal and Thakur (2003), Garg and Lal (2005), Dey et al (2011), Mehra (2012), Gaur (2014), Kumari (2014) and Ram (2014). In case of stalk length, parental lines Ogu-HL-1A and Ogu-HL-3A were good general combiners as they recorded significant negative GCA values of -0.40 and -0.22 respectively. In case of testers, PSBK-1 (-0.88) was the good general combiner whereas Kt-22 (0.42) and Hermia (0.39) were the poor general combiners.

Among the cross combinations, seven crosses showed significant negative SCA effects being maximum in Ogu-122-1A x PSBk-1 (-1.06) followed by Ogu-119-2A x PSBK-1 (-1.04), Ogu-HL-3A x Kt-22 (-0.90), Ogu-HL-1A x 1385 (-0.69), Ogu-119-2A x Hermia (-0.54), Ogu-122-1A x 1385 (-0.39) and Ogu-119-1A x 1385 (-0.28). These results are in conformity with the findings of Singh et al (2005) and Varalakshmi (2009). For ascorbic acid content, two lines exhibited significant positive GCA effects for ascorbic acid content viz Ogu-119-1A (6.30) and Ogu-HL-3A (2.82) and were good general combiners. Among testers, Kt-22 (15.87) and 1385 (4.51) were the best general combiners. Significant positive specific combining ability effects were observed for nine crosses vizOgu-119-1A × PSBK-1 (29.17), Ogu-122-1A × 1385 (22.86), Ogu-119-1A × Kt-22 (15.21), Ogu-119-2A × Hermia (14.08), Ogu-HL-3A × Kt-22 (11.82), Ogu-HL-3A × Hermia (8.35), Ogu-HL-1A × 1385 (7.82), Ogu-122-1A × PSBK-1 (6.09) and Ogu-HL-3A × 1385 (3.19). The results are in consonance with those of Jindal and Thakur (2003), Dey et al (2014), Kumari (2014) and Ram (2014).

The nature of gene action has been inferred from the estimates of general and specific combining ability variances. The estimates of general combining ability variance, specific combining ability variances, additive variance (σ^2 A), dominance variance (σ^2 D) are presented in Table 5. A perusal of data indicate that the estimates of σ^2 SCA were higher in magnitude as compared to σ^2 GCA (average) for all traits under study thereby indicating the pre-dominant role of non-additive gene action in these traits. The results pertaining to analysis of variance for combining ability are also confirmed from the study of additive (σ^2 A) and dominant components (σ^2 D) of variance. In all the traits studied, where SCA variance was higher than GCA values and dominant components (σ^2 D) of variance were also higher than the additive components (σ^2 A), the role of non-additive gene action has been found. Further variance ratio in F_1 was found less than one for all the traits viz days to marketable maturity (0.12), number of leaves per plant (-0.06), plant height (0.18), leaf length (0.34), leaf breadth (-0.22), gross curd weight (-0.10), marketable curd weight per plant (0.03), curd length

Table 5. Estimates of genetic components of variance for different horticultural traits in cauliflower

Character	σ^2 GCA (lines)	σ^2 GCA (testers)	σ^2 GCA (average)	σ^2 SCA	σ^2 A	σ^2 D	Variance ratio
Days to marketable Maturity	-0.18	4.25	2.28	18.36	9.14	73.44	0.12
Number of leaves/plant	-0.28	-0.21	-0.24	3.82	-0.96	15.29	-0.06
Plant height (cm)	2.11	1.26	1.64	9.22	6.56	36.87	0.18
Leaf length (cm)	4.01	1.32	2.51	7.47	10.06	29.89	0.34
Leaf breadth (cm)	-14.56	-12.06	-1.00	4.46	-3.99	17.85	-0.22
Gross curd weight (g)	-999.27	-5669.83	-3594.03	35756.90	-14376.10	143027.59	-0.10
Marketable curd weight (g)	1108.40	18.96	503.16	15628.10	2012.63	62512.41	0.03
Curd length (cm)	-0.17	-0.10	-0.13	0.81	-0.51	3.26	-0.16
Curd breadth (cm)	0.19	0.04	0.11	1.44	0.43	5.74	0.07
Stalk length (cm)	-0.06	0.21	0.09	0.76	0.37	3.03	0.12
Ascorbic acid content (mg/100 g)	-69.76	82.54	14.85	384.97	59.42	1539.88	0.04

(-0.16), curd breadth (0.07), stalk length (0.12) and ascorbic acid content (0.04). It confirmed the role of non-additive gene action controlling all the traits under study. Since non-additive gene action for most of the traits was found to be predominant, therefore heterosis can prove to be an important tool in cauliflower improvement. Similar findings were observed by Jamwal et al (1991), Gangopadhayay et al (1997), Jindal and Thakur (2003), Singh et al (2005), Varalakshmi (2009), Verma and Kalia (2015), Singh et al (2015) and Verma and Kalia (2016).

From this study, it was found that among parents, line Ogu-HL-3A was good general combiner for marketable curd weight and curd breadth and Ogu-119-1A for marketable curd weight. Among testers, PSBK-1 was good general combiner for marketable curd weight and curd breadth, Hermia for curd length, stalk length and days to marketable maturity and Kt-22 for stalk length and ascorbic acid content. On the basis of SCA performance, cross combinations Ogu-HL-3A x Hermia, Ogu-119-1A x Kt-22 and Ogu-122-1A x PSBK-1 were found best for most of the horticultural traits.

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