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Studies on gene action in relation to yield and quality traits in cauliflower (*Brassica oleracea* var. *botrytis* L.)

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Abstract

The present investigation was carried out at Palampur during *rabi* 2012 and 2013 to gather information on the nature of gene action by following line × tester mating design involving five lines and three testers. The analysis of variance revealed significant differences among treatments for days to marketable curd maturity from date of transplanting, gross weight per plant, marketable yield per plant, curd size index, curd depth, curd diameter, per cent marketable curds, stalk length, number of leaves per plant, plant height, harvest index, ascorbic acid content and total soluble solids. The magnitude of dominance variance was higher than additive variance for all the traits except curd depth and total soluble solids which indicated the involvement of non-additive gene action which could be utilized through the development of hybrids in cauliflower. A complete correspondence was noticed between per cent contribution of line × tester interaction (crosses) and non-additive gene action (σ^2D), which reaffirm the importance of hybrids in cauliflower.

Key words: Cauliflower, gene action, GCA variance, SCA variance and line × tester

Cauliflower (*Brassica oleracea* var. *botrytis* L.) (2n=2x=18) belongs to the cole group of vegetables. It was probably originated in the island of Cyprus from where it moved to other areas like Syria, Turkey, Egypt, Italy, Spain and north-western Europe. Syria is considered to be the place of origin for cauliflower. It is one of the important winter vegetables grown throughout India. Today among cole crops, it occupies the pride place in India due to its delicious taste, flavour and being nutritive. It has been rightly described as aristocrat of vegetables. It is grown for its white tender curd commonly used as a vegetable, in curry, soup and for pickling. Cauliflower is a low-calorie food with good dietary fiber, abundant in vitamins (C, B, A, K) and minerals like phosphorus, potassium, calcium, sodium, iron, manganese, magnesium and molybdenum. The leading cauliflower producing countries in the world are China, India, Spain, Italy and France. India is the second major cauliflower producing country after China in the world and contributes 32 per cent in area and 36 per cent in the world production share.

In India, cauliflower is cultivated in an area of 4,04,200 ha with the production of 78,86,700 metric tonnes and its productivity is 19.6 metric tonnes/ ha (Anonymous, 2013), but its potential productivity is 35-40 metric tonnes/ha and maximum productivity of 45.25 metric tonnes/ha has been achieved in New Zealand. In the country, area under hybrids in cauliflower is low as compared to open pollinated and unknown varieties. Thus, for increasing its production and productivity at par with advanced countries, development of hybrids is need of the hour. Hybrids are preferred over the open pollinated varieties on account of their uniform maturity, higher yield and better adaptability under adverse growing conditions. At present, the farmers are purchasing hybrid seeds from the private firms at exorbitant rates. To tide over the situation, there is a need to make concerted efforts to develop quality F_1 hybrids with better productivity and adaptability so as to make available their seeds to the farmers at a reasonable price.

An understanding of the gene action is a pre-requisite for any successful plant breeding programme. In order to exploit different types of gene actions present in the population, information regarding relative magnitude of genetic variances is essential. Investigation was undertaken with the objectives of gaining knowledge on these aspects. Among the different biometrical methods available to determine the genetic information, the "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 less number of crosses as compared to other mating designs.

Materials and methods

In the present investigation, experimental material comprised parents and 15 F_1s produced during *rabi* 2012 by crossing five diverse lines *viz.*, DPCaY-2, DPCaY-3, DPCaY-5, DPCaY-6 and DPCaY-9 with three testers, namely DPCaY-4, DPCaY-8 and Palam Uphar. Variety Palam Uphar (standard check-1) and Hybrid Madhuri (standard check-2) were used as standard checks. The experiment was laid out in randomized block design with 3 replications at Palampur during *rabi* 2013. The spacing between and within rows was 60 and 45 cm, respectively. The observations were recorded on 10 competitive plants in each entrty/replication. The characters studied were days to marketable curd maturity from date of transplanting, gross weight per plant, marketable yield per plant, curd size index, curd depth, curd diameter, per cent marketable curds, stalk length, number of leaves per plant, plant height, harvest index, ascorbic acid content and total soluble solids. The data were subjected to estimation of additive and dominance components of variances and per cent contribution of lines, testers and their interactions as per the formulae suggested by Singh and Chaudhary (1977).

Results and Discussion

Analysis of variance

The analysis of variance indicated significant differences among treatments for all the traits namely, days to marketable curd maturity from date of transplanting, gross weight per plant, marketable yield per plant, curd size index, curd depth, curd diameter, per cent marketable curds, stalk length, number of leaves per plant, plant height, harvest index, ascorbic acid content and total soluble solids when tested against mean squares due to error. It implied that there was sufficient genetic variability among the treatments. The variances due to replications were found non-significant for all traits studied except curd depth (Table 1).

Table 1. Analysis of variance for randomized block design

Trait	Source of variation		
	Replication	Treatment	Error
df	2	23	46
Days to marketable curd maturity from date of transplanting	4.17	357.24*	1.54
Gross weight per plant (g)	842.21	38364.16*	953.59
Marketable yield per plant (g)	1830.46	19072.78*	728.38
Curd size index (cm^2)	15.65	521.58*	5.29
Curd depth (cm)	0.56*	1.12*	0.13
Curd diameter (cm)	0.32	7.24*	0.40
Per cent marketable curds	4.95	43.44*	4.36
Stalk length (cm)	0.00008	1.18*	0.05
Number of leaves per plant	0.03	8.31*	0.99
Plant height (cm)	2.49	40.57*	1.49
Harvest index (%)	14.07	19.15*	4.95
Ascorbic acid content (mg/100g)	1.39	217.67*	1.05
Total soluble solids (^{0} Brix)	0.02	0.65*	0.32

* Significant at $P \leq 0.05$

Estimates of genetic components of variance

An important step in a breeding programme is to choose suitable breeding methodology for purposeful management of generated variability which largely depends on the type of gene action in the population for the trait under genetic improvement (Cockerham, 1961; Sprague, 1966). Among the various designs developed for this purpose, line × tester method (Kempthorne, 1957) not only helps in evaluating parents and crosses for combining ability but also provides information on the nature of gene action controlling the traits under consideration. The nature of gene action has been inferred from estimates of GCA and SCA variances. The estimates of general combining ability variances [σ^2GCA (lines), σ^2GCA (testers) and σ^2GCA (average)], specific combining ability variances (σ^2SCA), additive variances (σ^2A), dominance variances (σ^2D) and proportional contribution of lines, testers and their interactions to the total variances are presented in Table 2. The values of σ^2SCA ranged from -0.04 (TSS) to 2641.09 (gross weight), while σ^2GCA (average) ranged from -1.15 (ascorbic acid content) to 456.23 (gross weight/plant).

The testers showed a higher σ^2GCA than the lines for days to marketable curd maturity from date of transplanting, gross weight per plant, marketable yield per plant, curd size index, curd depth, curd diameter, per cent marketable curds, number of leaves per plant and plant height, whereas σ^2GCA due to lines was higher than the σ^2GCA due to the testers for traits, stalk length, harvest index, ascorbic acid content and total soluble solids. This indicates that both testers and lines have more diversity for the respective traits.

The estimates of σ^2SCA were higher as compared to σ^2GCA (average) for days to marketable curd maturity from date of transplanting, gross weight per plant, marketable yield per plant, curd size index, curd diameter, per cent marketable curds, stalk length, number of leaves per plant, plant height, harvest index and ascorbic acid content indicating the pre-dominant role of non-additive gene action governing these traits. For rest of the traits, σ^2GCA was higher than σ^2SCA. The traits in which σ^2SCA was higher than σ^2GCA (average), σ^2D was also higher than σ^2A. The additive gene action was observed for curd depth and total soluble solids as reflected from their higher additive component of variance than the dominant component of variance. The higher magnitude of σ^2D indicated the involvement of non-additive gene action. Low to moderate heritability in narrow sense was observed, which suggested that heterosis breeding could be useful for obtaining higher gains for the traits studied.

Since, non additive gene action for most of the traits has been found to be predominant, heterosis breeding can prove to be an important tool in cauliflower improvement. However, for the traits *viz.*, curd depth and total soluble solids, where additive variance is high, selection can be followed. These results are in close conformity to the findings of Gangopadhayay *et al*. (1997), Garg *et al*. (2003), Singh *et al*. (2005), Jindal and Thakur (2005), Varalakshmi (2009) and Verma and Kalia (2011).

Proportional contribution of lines, testers and their interactions

The proportional contribution of lines ranged from 5.99 (gross weight) to 48.66 per cent (stalk length). The contribution of lines for marketable yield per plant was 13.95 per cent. The proportional contribution of testers ranged from 2.25 (ascorbic acid content) to 86.78 per cent (days to marketable curd maturity from date of transplanting), while contribution of testers for marketable yield per plant was 70.70 per cent. Similarly, the proportional contribution of line × tester interactions ranged from 6.01 (days to marketable curd maturity from date of transplanting) to 69.39 per cent (ascorbic acid content). The contribution of line × tester interactions for marketable curd yield per plant was 13.59 per cent (Table 2).

The contribution of lines was found to be higher than individual contribution of testers and interactions between line × tester for stalk length and total soluble solids. The contribution of testers was found to be higher than individual contribution of lines and line × tester for days to marketable curd maturity from date of transplanting, gross weight per plant, marketable yield per plant, curd size index, curd depth, curd diameter, per cent marketable curds and number of leaves. The contribution of line × tester interactions was found to be higher than individual contribution of lines and testers for plant height, harvest index and ascorbic acid content.

A complete correspondence was noticed between per cent contribution of line × tester interaction (crosses) and non-additive gene action (σ^2D). The results of gene action studies reaffirm the importance of hybrids in cauliflower. The estimates of GCA and SCA variances, additive (σ^2A) and dominant (σ^2D) components of variance and contribution of lines, testers and line × tester interactions revealed that for most of the traits non additive gene action was in preponderance or in appreciable magnitude. Therefore, heterosis breeding will be a better option compared to other approaches . Curd depth and total soluble solids, exhibiting additive gene action suggests the use of selection in segregating populations to develop improved inbred lines.

Table 2. Estimates of genetic components of variance and proportional contribution of lines, testers and their interactions

Trait / Genetic component	Days to marketable curd maturity from date of transplanting	Gross weight per plant (g)	Marketable yield per plant (g)	Curd size index (cm^2)	Curd depth (cm)	Curd diameter (cm)	Marketable curds (%)	Stalk length (cm)	Number of leaves per plant	Plant height (cm)	Harvest index (%)	Ascorbic acid content (mg/100g)	Total soluble solids (^{0}Brix)
σ^2GCA (lines)	3.28	-479.44	248.31	6.08	0.04	0.08	0.44	0.03	0.01	0.11	-0.14	-3.75	0.15
σ^2GCA (testers)	79.77	6597.54	2874.66	147.83	0.23	0.88	12.06	0.02	1.21	1.42	-0.76	-10.74	-0.003
σ^2GCA (average)	6.34	456.23	240.35	11.75	0.02	0.07	0.95	0.005	0.09	0.12	-0.07	-1.15	0.014
σ^2SCA	6.51	2641.09	455.05	19.26	0.003	0.28	1.22	0.02	0.63	4.45	2.73	61.35	-0.04
σ^2A	25.37	1824.91	961.40	47.00	0.08	0.29	3.80	0.02	0.37	0.47	-0.28	-4.62	0.05
σ^2D	26.06	10564.37	1820.20	77.03	0.01	1.10	4.88	0.07	2.52	17.78	10.91	245.43	-0.14
Heritability (narrow sense) %	64.35	23.55	40.47	52.87	46.45	26.19	22.00	19.98	16.01	4.55	-3.26	-3.89	25.52
Genetic advance	5.89	30.19	28.73	7.26	0.29	0.41	6.59	0.09	0.35	0.21	-0.14	-0.62	0.18
Proportional contribution of lines (%)	7.21	5.99	13.95	8.49	19.91	16.50	9.72	48.66	15.49	24.95	30.34	28.36	75.72
Proportional contribution of testers (%)	86.78	70.70	72.46	82.42	68.86	62.12	77.40	25.10	54.41	28.38	2.51	2.25	3.79
Proportional contribution of line × tester interactions (%)	6.01	23.31	13.59	9.09	11.23	21.38	12.88	26.24	30.09	46.67	67.14	69.39	20.48

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