*Indian Journal of Agricultural Sciences* **89** (8): 1232–5, August 2019/Article
https://doi.org/10.56093/ijas.v89i8.92832

# Genetics analysis for earliness and yield traits using *Ogura* CMS in snowball cauliflower (*Brassica oleracea* var. *botrytis*)

HANUMAN RAM[1], AMISH K SUREJA[2], S S DEY[3] and B S TOMAR[4]

*ICAR-Indian Agricultural Research Institute, New Delhi 110 012, India*

Received: 17 October 2016; Accepted: 11 February 2019

## ABSTRACT

A study was undertaken to determine the components of genetic variance and gene action effects in snowball cauliflower (*Brassica oleracea* var. *botrytis* L.) lines through line × tester analysis involving 5 Ogura CMS lines and 7 male fertile testers. The mean squares due to lines and testers were significant for most of the characters under study, except for gross plant weight, polar diameter, equatorial diameter, curd weight, curd yield and harvest index and for line × tester, it was significant for leaf length, leaf width, number of leaves per plant, plant height, days to 50% curd initiation and days to 50% curd maturity. Pre-dominance of dominance component of variance was observed for leaf length, number of leaves per plant, plant height, days to 50% curd initiation, marketable curd weight and marketable curd yield. The traits studied had narrow differences among GCV, PCV and broad sense heritability values, suggesting low effect of environment on the expression of phenotype for most of vegetative traits. The variance due to general ($\sigma^2$gca) and specific combining abilities ($\sigma^2$sca) were highly significant indicating the importance of both additive ($\sigma^2$A) as well as non-additive ($\sigma^2$D) type of gene actions. However, the ratios of $\sigma^2$gca/ $\sigma^2$sca (<1) and $\sigma^2$A/$\sigma^2$D (<1) revealed the preponderance of non-additive variance for the inheritance of traits studied except for days to 50% curd initiation and harvest index. The results of the experiment suggest the possibility of improvement of these traits through recurrent selection and hybridisation.

**Key words:** Cauliflower, Cytoplasmic male sterility, Gene action, Line × tester

Cauliflower (*Brassica oleracea* var. *botrytis* L.) is a popular vegetable in the tropical and subtropical regions of the world. In this crop, breeding work has been primarily focussed on early and mid groups, but not on Snowball group due to insufficient genetic variability and specific geographical requirements for seed production.

Snowball cauliflower is the main crop grown during winter season (November–February) in the Indian sub-continent. In cauliflower, $F_1$ hybrids are uniform in maturity, earliness and yields better quality curd with respect to compactness, colour, tolerance/resistance to insect-pests, diseases and unfavorable weather conditions. Self-incompatibility (SI) and male sterility (particularly CMS) are widely used for production of $F_1$ hybrid seeds in cauliflower (Sharma *et al.,* 2004, Dey *et al.* 2013). So far, majority of hybrid cultivars in cole crops have been developed by using SI system. In snowball cauliflower, the SI system is very weak or not present at all (Chatterjee and Mukherjee 1965, Nieuwhof 1963). This also poses a great risk of occurrence of sibs in hybrid seeds besides difficulty in their maintenance and multiplication. In such a situation, CMS system offers a better alternative for production of $F_1$ hybrid seeds in snowball cauliflower. The improvement in the yield and its related traits in most situations is more effectively utilized on the basis of performance of yield components, which are closely associated with curd yield. In order to improve these traits, it is important to get an idea about genetic makeup of the crop and nature of gene action involved in the expression of the characters to various environments.

The line × tester analysis is one of the most appropriate approaches in preliminary screening of the materials for gene action effects and variances since it can evaluate more germplasm at a time and also provides information for selection of suitable parents and breeding methodology being adopted for improving the crop. Therefore, the present investigation has been undertaken to determine the gene action for earliness and yield components using line × tester mating design in snowball cauliflower.

## MATERIALS AND METHODS

The present investigation was carried out during spring summer season of 2013 at IARI Regional Station, Katrain, Himachal Pradesh and winter season of 2013-14 at the research farm of Division of Vegetable Science, Indian

---

[1]Scientist (hramdhanari@gmail. com), ICAR-VPKAS, Almora, Uttarakhand. [2]Principal Scientist (aksureja@gmail. com), [3]Senior Scientist (shyam. iari@gmail. com) , [4] Head (bst_spu_iari@ rediffmail. com), Division of Vegetable Science, ICAR-IARI.

Agricultural Research Institute, New Delhi. Five genetically diverse Ogura CMS lines of cauliflower, viz. Ogu 13-01, Ogu 101, Ogu 103, Ogu 119 and Ogu 13-85 and seven testers, viz. Kt-18, Kt-22, DB-1305, DB-187, Lalchowk Maghi, Sel-26 and Suprimax Late were crossed in line × tester mating scheme (Kempthorne 1957) to obtain 35 $F_1$ hybrid combinations. The 35 $F_1$ hybrids along with their twelve parental lines were evaluated in a randomized block design with three replications. Seedlings (38 days old) were transplanted providing inter- and intra-row spacing of 45 cm between plants. All recommended package of practices were followed to grow a healthy successful crop. Each treatment comprised 5 rows and 8 plants per row and was replicated thrice. Ten randomly selected plants were labelled in each treatment for recording the observations on 14 quantitative traits, viz. days to 50% curd initiation, days to 50% curd maturity, leaf length (cm), leaf width (cm), number of leaves per plant, plant height (cm), polar diameter (cm), equatorial diameter (cm), gross plant weight (kg), marketable curd weight (kg), marketable curd yield (t/ha), net curd weight (kg), net curd yield (t/ha) and harvest index (%).

Statistical analysis for analysis of variance, components of variance (coefficient of variance, genotypic and phenotypic coefficient of variation), components of genetic variance (additive variance, $\sigma^2$A and dominance variance, $\sigma^2$D) was carried out as reported by Kempthorne (1957) and Singh and Chaudhary (1995).

## RESULTS AND DISCUSSION

*Analysis of variance:* The partitioning of mean squares into replications, lines, testers and line × tester interactions revealed that mean squares due to lines (female parents) were significant for most of the parameters under study except for polar diameter, equatorial diameter, marketable curd weight, marketable curd yield, net curd weight, net curd yield and harvest index. Mean squares of testers (male parents) and lines × testers interactions were significant for traits like leaf length, leaf width, number of leaves/plant, plant height, days to 50% curd initiation and days to 50% curd maturity (Tables 1 and 2). The parents v/s crosses (Heterosis) mean square was highly significant for all the traits (except for plant width) which indicated the expression of heterotic effects in the developed hybrids. Pandey and Naik (1989) also observed similar significant differences in the variance due to line × testers for leaf number, plant height, curd weight and curd size; Singh *et al.* (2005) for leaf number, leaf weight and leaf area; and Verma and Kalia (2011) for days to 50% curd initiation, days to 50% curd maturity and gross plant weight in cauliflower.

*Components of variance:* Mean, range, coefficient of variance (CV%), genotypic ($\sigma^2$g) and phenotypic variance ($\sigma^2$p ), heritability in broad sense (h$^2$bs), genotypic and phenotypic coefficient of variance (GCV and PCV%) and the ratio of GCV/PCV are given in tables 1 and 2. Data obtained in the experiment showed that, the variance widely varied from one trait to another, since the coefficient of variation (CV%) ranged from 3. 90 to 25.28%. The variance for a particular depends upon the genotype × environment interactions for a particular trait. The highest CV (25.28%) was recorded for gross plant weight (kg) followed by marketable curd weight and marketable curd yield, respectively, suggesting that these three characters had the highest variation among the studied genotypes. These traits are obvious to exhibit higher variance due to their highly quantitative nature. On the contrary, the lowest variation (3.90%) was observed for days to 50% curd maturity.

Table 1 Genetic analysis for vegetative traits in snowball cauliflower

| Source of variation | Leaf length (cm) | Leaf width (cm) | No.of leaves/ plant | Plant height (cm) | Gross plant weight (kg) |
|---|---|---|---|---|---|
| | | | *Mean sum of squares* | | |
| Parents (P) | 181.77** | 23.49** | 19.34** | 164.91** | 0.19 |
| Crosses (C) | 111.13** | 25.53** | 7.55** | 111.23** | 0.07 |
| Parents v/s Crosses | 23.64* | 0.02 | 9.17** | 21.32* | 0.32* |
| Males (T) | 249.23** | 29.79** | 21.36** | 209.68** | 0.07 |
| Female (L) | 21.88** | 6.89** | 21.14** | 20.97* | 0.37* |
| Male v/s Female (L×T) | 416.54** | 52.05** | 0.005 | 472.08** | 0.10 |
| | | | *Components of variance* | | |
| Mean | 45.45 | 18.20 | 16.69 | 53.45 | 1.31 |
| Range | 36.33 | 13.25 | 12.10 | 43.17 | 0.93 |
| | 62.27 | 25.92 | 22.42 | 69.17 | 1.89 |
| CV % | 6.24 | 7.19 | 8.70 | 5.58 | 25.28 |
| σ 2g | 126.12 | 24.49 | 10.41 | 122.11 | 0.10 |
| σ 2P | 134.16 | 26.20 | 12.52 | 131.01 | 0.21 |
| h$^2$BS | 0.94 | 0.93 | 0.83 | 0.93 | 0.49 |
| GCV% | 13.07 | 15.52 | 7.92 | 11.03 | 1.79 |
| PCV% | 14.21 | 17.02 | 11.87 | 12.22 | 19.64 |
| GCV/PCV | 0.92 | 0.91 | 0.67 | 0.90 | 0.09 |
| | | | *Components of genetic variance* | | |
| $\sigma^2$ gca | 6.03 | 3.15 | -0.03 | 5.23 | 0.001 |
| $\sigma^2$ sca | 26.26 | 3.17 | 1.83 | 26.80 | -0.002 |
| $\sigma^2$ gca/ $\sigma^2$ sca | 0.23 | 0.99 | -0.02 | 0.19 | -0.50 |
| $\sigma^2$A | 12.063 | 6.305 | -0.056 | 10.45 | 0.003 |
| $\sigma^2$D | 26.263 | 3.17 | 1.827 | 26.8 | -0.002 |

*, ** Significant at P=0.05 and P=0.01 probability, respectively through F test.

The difference between the genotypic ($\sigma^2$g) and phenotypic ($\sigma^2$p) variances indicated the contribution of environmental variance effects. Low values of differences between $\sigma^2$p and $\sigma^2$g indicated the lesser environmental effect on the character. Selection based on the phenotypic values will be effective only when the phenotypic values and genotypic values are nearly same. In this respect, all the characters studied have closer values of $\sigma^2$g and $\sigma^2$p as well

Table 2 Genetic analysis for earliness and yield attributing traits in snowball cauliflower

| Source of variation | Days to 50% curd initiation | Days to 50% curd maturity | Polar diameter (cm) | Equatorial diameter (cm) | Marketable curd weight (kg) | Marketable curd yield (t/ha) | Net curd weight (kg) | Net curd yield (t/ha) | Harvest index (%) |
|---|---|---|---|---|---|---|---|---|---|
| *Mean sum of squares* | | | | | | | | | |
| Parents (P) | 133.30** | 152.32** | 1.04 | 3.09 | 0.037 | 71.12 | 0.017 | 32.69 | 33.22 |
| Crosses (C) | 77.15** | 71.67** | 0.68 | 1.73 | 0.028 | 54.36 | 0.012 | 22.46 | 66.50 |
| Parents v/s Crosses | 596.00** | 474.33** | 12.68** | 21.52** | 0.418** | 808.26** | 0.164** | 318.41** | 188.43** |
| Males (T) | 22.71 | 76.30** | 0.67 | 1.91 | 0.039 | 75.81 | 0.021 | 40.41 | 43.96 |
| Female (L) | 194.16** | 181.23** | 1.04 | 0.36 | 0.042 | 81.18* | 0.014 | 28.05 | 23.05 |
| Male v/s Female (L×T) | 553.35** | 492.81** | 3.30** | 21.10** | 0.001 | 2.80 | 0.003 | 4.92 | 9.45 |
| *Components of variance* | | | | | | | | | |
| Mean | 75.79 | 90.98 | 7.72 | 12.27 | 0.72 | 31.63 | 0.47 | 20.52 | 36.35 |
| Range | 60.67 | 75.67 | 6.31 | 9.41 | 0.44 | 19.36 | 0.29 | 12.61 | 26.67 |
| | 85.00 | 103.33 | 8.81 | 14.38 | 1.03 | 45.17 | 0.66 | 29.04 | 47.65 |
| CV % | 6.02 | 3.90 | 11.01 | 11.77 | 20.99 | 20.97 | 19.12 | 19.11 | 19.39 |
| $\sigma^2g$ | 101.86 | 99.72 | 1.04 | 2.49 | 0.04 | 74.76 | 0.02 | 31.35 | 61.20 |
| $\sigma^2P$ | 122.66 | 112.33 | 1.76 | 4.57 | 0.06 | 118.84 | 0.02 | 46.72 | 110.88 |
| $h^2BS$ | 0.83 | 0.89 | 0.59 | 0.54 | 0.63 | 0.63 | 0.67 | 0.67 | 0.55 |
| GCV% | 5.87 | 5.04 | 0.4 | 0.25 | 6.08 | 6.08 | 6.27 | 6.32 | 5.97 |
| PCV% | 8.35 | 6.16 | 11.32 | 12.19 | 20.6 | 20.6 | 20.26 | 20.27 | 20.35 |
| GCV/PCV | 0.70 | 0.82 | 0.04 | 0.02 | 0.30 | 0.30 | 0.31 | 0.31 | 0.29 |
| *Components of genetic variance* | | | | | | | | | |
| $\sigma^2$ gca | 4.89 | 10.06 | 0.01 | -0.07 | 0.000 | 0.12 | 0.00 | 0.60 | 3.16 |
| $\sigma^2$ sca | 11.45 | 5.16 | -0.05 | -0.08 | 0.002 | 4.49 | 0.001 | 1.14 | 0.58 |
| $\sigma^2$ gca/ σ2 sca | 0.43 | 1.95 | -0.13 | 0.92 | 0.00 | 0.03 | 0.00 | 0.52 | 5.47 |
| $\sigma^2A$ | 9.788 | 20.128 | 0.013 | -0.14 | 0.00 | 0.246 | 0.001 | 1.195 | 6.319 |
| $\sigma^2D$ | 11.451 | 5.159 | -0.048 | -0.076 | 0.002 | 4.49 | 0.001 | 1.141 | 0.578 |

*, ** Significant at P=0.05 and P=0.01 probability, respectively through F test.

as GCV% and PCV%, which is confirmed by the estimated GCV/PCV. ratios ranging from 0.67 to 0.92, and broad sense heritability ($h^2$BS) ranging from 0.83 to 0.94 for leaf length, leaf width, No. of leaves/plant, plant height, days to 50% curd initiation, days to 50% curd maturity, suggesting less effect of environment on these traits. Therefore phenotypic selection could be an effective strategy for improvement of these traits in snowball cauliflower. The rest traits have higher environmental influence and hence cannot be improved reliably through phenotypic selection alone. The results are in conformity with the findings of Singh *et al.* (1976), Dhiman *et al.* (1983) in cauliflower.

*Components of genetic variance (gene action):* Using line × tester mating design, the genetic variance could be divided into components of genetic variance, i.e. additive and non-additive genetic variances. Both the lines variance ($\sigma^2$L) and testers variance ($\sigma^2$T) determine the $\sigma^2$gca which is an indicator of additive and additive × additive element of the genetic variance. While, the line × tester variance ($\sigma^2$L × T) determines the $\sigma^2$sca and it indicates the non-additive genetic elements including dominance. According to Kallo (1988), the additive ($\sigma^2$A) and dominance ($\sigma^2$D) were the most important elements.

The estimates of variance components for earliness and yield attributing traits are presented in Tables 1 and 2. The values of $\sigma^2$gca were lower than the $\sigma^2$sca for all the traits except gross plant weight, days to 50% curd maturity, polar diameter, equatorial diameter and harvest index. For number of leaves per plant and equatorial diameter, the $\sigma^2$gca was in negative direction. The proportions of $\sigma^2$ gca/ $\sigma^2$sca were less than unity in all traits except for days to 50% curd maturity and harvest index. Similarly, $\sigma^2$D was greater than $\sigma^2$A for all the traits except leaf width, gross plant weight, days to 50% curd maturity, polar diameter, equatorial diameter, net curd yield and harvest index. The traits like leaf length, plant height, days to 50% curd initiation and marketable curd yield exhibited the ratio of dominance to additive variance higher than unity and hence indicating towards the existence of overdominance for these traits.

The mean square values for lines, testers and line × tester interactions are highly significant for most of the vegetative traits anddays to 50% curd initiation and maturity. The ratio of σ $^2$gca / $\sigma^2$sca were found less than unity (<1) for all the studied traits except days to 50% curd maturity and harvest index, which indicated the preponderance of non-additive variance in the inheritance of these traits, suggesting that heterosis breeding is effective for the improvement of these traits. The results of present findings are in agreement with the earlier work of Garg *et al.* (2003), Thakur *et al.* (2004), Pal *et al.* (1966) in cauliflower and Prakash *et al.* (2003) in cabbage. The results are also in conformity with the findings of Verma and Kalia (2015) and Saha *et al.* (2015). The results indicated the importance of heterosis breeding and recurrent selection schemes for effective utilization of non-additive genetic variance for improvement of yield and yield attributing traits.

## ACKNOWLEDGMENTS

The first author is thankful to the Indian Council ofAgricultural Research (ICAR) and ICAR-IARI, New Delhi, India for the grant of Junior Research Fellowship and facilities during M Sc programme.

## REFERENCES

Chatterjee S S and Mukherjee S K. 1965. Selection and maintenance of cauliflower (*Brassica oleracea* var. *botrytis* L. ). *Indian Journal of Horticulture* **22**: 60–8.

Dey S S, Bhatia R, Sharma S R and Sureja A K. 2013. Effects of chloroplast substituted Ogura male sterile cytoplasm on the performance of cauliflower (*Brassica oleracea* var. *botrytis* L. ) $F_1$ hybrids. *Scientia Horticulturae* **157**: 45–51.

Dhiman S C, Sharma P P and Arya P S. 1983. Genetic studies in cauliflower (*Brassica oleracea* var. *botrytis* L. ). *South Indian Horticulture* **31**: 77–81.

Garg N, Lal T and Vashisht V K. 2003. Studies on combining ability and gene action in Indian cauliflower (*Brassica oleracea* I. var. *botrytis* L. ). *Crop Improvement* **30**(2): 169–76.

Kallo. 1988. *Vegetable Breeding,* vol. 1, p 61. CRC Press, Inc., N. W., Boca Raton, Florida.

Kempthorne O. 1957. *An Introduction to Genetic Statistics*, pp 468–73. John Wiley & Sons, Inc., New York.

Nieuwhof M. 1963. Pollination and contamination of *Brassica oleracea* L. *Euphytica* **12**: 17–26.

Pal A B and Swarup V. 1966. Gene effects and heterosis in cauliflower. *Indian Journal of Genetics* **26**: 282–94.

Pandey S C and Naik G. 1989. Combining ability studies of quantitative characters in cauliflower (*Brassica oleracea* var. *botrytis* L. ). *Indian Journal of Horticulture* **46**(4): 502–8.

Prakash C, Verma T S and Kumar P R. 2003. Genetic analysis of cabbage using self-incompatible lines. *Indian Journal of Agricultural Sciences* **73**(3): 412–3.

Saha P, Kalia P, Joshi S and Vinod. 2015. Genetic analysis of yield components and curd color of midseason heat tolerant Indian cauliflower (*Brassica oleracea* var. Botrytis L. ). *SABRAO. Journal of Breeding and Genetics* **47**(2): 124–32.

Sharma S R, Singh P K, Chable V and Tripathi S K. 2004. A review in hybrid cauliflower development, *Hybrid Vegetable Development,* p 217–21. Singh P K, Dasgupta S K and Tripathi S K. (Eds. ). The Haworth Press, New York.

Singh D P, Swarup V and Chatterjee S S. 1976. Genetical studies in Indian cauliflower II. Heterosis and combining ability in maturity group II. *Vegetable Science* **3**: 41–6.

Singh D, Varalakshmi B and Reddy M A N. 2005. Combining ability studies in early cauliflower (*Brassica oleracea* var. *botrytis* L. ). *Indian Journal of Horticulture* **62**(1): 27–32.

Singh R K and Chaudhary B D. 1995. Biometrical Methods in Quantitative Genetic Analysis. Kalyani Publishers, New Delhi, India.

Thakur J C, Singh N and Jindal S K. 2004. Genetic analysis of some economic traits in main season cauliflower. *Journal of Research* **41**(1): 68–73.

Verma V K and Kalia P. 2011. Combining ability studies in early and mid-maturity CMS based cauliflower lines. *Indian Journal of Horticulture* **68**(4): 503–6.

Verma V K and Kalia P. 2015. Combining ability analysis and its relationship with gene action and heterosis in early maturity Cauliflower. *Proceedings of National Academy of Sciences, India Section B: Biological Sciences* **87**(3): 1–8.