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Short Communication

GENE ACTION IN CUCUMBER (*CUCUMIS SATIVUS* L.)

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Cucumber (*Cucumis sativus* L., 2n = 2 x = 14) belongs to family cucurbitaceae is an important summer vegetable of our country. Cucumber has great economic importance as food plant. India is being native place of cucumber possesses vast genetic variability for vegetative and fruit characters. Low fruiting ability and yield suppression due to its inherent fruiting habits are major factors limiting fruit yield in slicing and processing cucumber (Lower *et al.,* 1982). To formulate any breeding method, it is imperative to have knowledge of gene action involved in inheritance of various traits. The success of selection mainly depends upon the extent of genetic variability present it it. Therefore, a higher genetic base should be utilized for faster and higher magnitude of success. Utilization of divergent germplasm in hybridization creates such broad genetic base (Singh, 1998).

In spite of wide genetic variability available in this crop little attention has been given for improvement of this crop. Hence, an attempt was made to investigate the gene action (inheritance pattern) of yield and yield attributing traits.

The present investigation was carried out during 2006-07 at research farm of Division of Vegetable Science of Indian Agricultural Research Institute, New Delhi. Out of the seventeen genotypes of cucumber available for field evaluation, six most promising and diverse genotypes *viz*, Pusa Uday, DC-1, CH-20, CRC-8, CHC-2 and G-338 were crossed in 6 x 6 half dialed (excluding reciprocal) fashion (Hayman, 1954) to obtain 15 F_1 hybrids combinations. Fifteen F_1 hybrids along with 6 parents were grown in randomized block design with three replications. The crops were sown in rows of 1.5m with 50 cm spacing between the plats. All the recommended package of practices was followed to grow a successful crop. Out of 10 plants, 8 were marked for observations. Observations on individual plant basis were recorded on eleven quantitative characters *viz*. days to first female flower opening, node number of first female flower, days to first fruit harvest, fruit weight (g), number of fruits/plant, fruit length (cm), fruit diameter (cm) and yield/plant (g). Gene action was studied by the diallel method of numerical approach given by Hayman (1954).

The estimates of genetic components of variation and various statistical parameters for different characters were represented in Table 1. The genetic component of variation for days to first female flower opening, the estimates of H_1, H_2 and h^2 were highly significant while D was significant. The value of H_1 was more than D, which signify that dominant genes were more than additive genes. The environmental influence (E) on the inheritance of this was non-significant. The mean degree of dominance $(H_1/D)^{½}$ was greater than one (2.42) and indicated role of over dominance for this trait. The proportion of genes with positive and negative effects $(H_2/4H_1)$ in the parents was found to be less than 0.25 (0.22), denoting asymmetry at the loci showing dominance. The proportion of dominant and recessive gene as indicated by $[(4DH_1)^{½} + F/ (4DH_1)^{½} - F]$ was 1.08 while the group of genes, which controlled the characters (h^2/H_2) and exhibited dominance was 2.01. Narrow sense heritability being 14.11% showed preponderance of non-additive gene action.

The estimates for node number of first female flower of D, H_1, H_2 and h^2 were highly significant while F and E were non-significant. The higher value of H than D indicated preponderance of non-additive gene action. Negative values of F indicated that the recessive alleles were more in the parents. The mean degree of dominance $(H_1/D)^{½}$ was 1.50 showing over-dominance. The proportion of genes with positive and negative effects $(H_2/4H_1)$ in the parents was found to be 0.22 denoting asymmetry at loci showing dominance. The proportion of dominant and recessive genes $[(4DH_1)^{½} + F/ (4DH_1)^{½} - F]$ was 1.09 and the number of group of genes (h^2/H_2) was 2.58 which controlled the characters and exhibited dominance. Narrow-sense heritability being 25.56% indicated non-additive gene action.

Results pertaining to days to first fruit harvest the estimates of D, H_1, H_2 and h^2 were highly significant where E and F were non-significant. The value of H_1 was greater than D, suggesting the presence of dominant alleles in parents. The negative value of F showed recessive alleles was more frequent. The mean

degree of dominance $(H_1/D)^{½}$ being 2.81 indicating over-dominance. The proportion of genes with positive and negative effects $(H_2/4H_1)$ was 0.2, showing dominance. The proportion of dominant and recessive genes $[(4DH_1)^{½} + F/ (4DH_1)^{½} - F]$ in the parents was 1.44, while the group of dominant genes (h^2/H_2) was 1.71. Narrow sense heritability being 9.78% exhibited predominance of non-additive gene action.

For fruit weight, the estimated value of D, H_2 and h^2 were highly significant and H_1 was significant while other parameters *viz*. E and F were non-significant. The estimated value of D was greater than H_1 which revealed that additive genes were more than dominant genes. Negative value of F indicated predominance of recessive alleles. The mean degree of dominance $(H_1./D)^{½}$ being 0.98 showed partial dominance. The proportion of genes with positive and negative effects $(H_2/4H_1)$ was 0.23, which denotes asymmetry at loci. The proportion of dominance and recessive genes $[(4DH_1)^{½} + F/ (4DH_1)^{½} - F]$ was 0.91 whereas number of group of genes exhibiting dominance and controlling character was 1.68. The narrow sense heritability (68.12%) indicated the additive type of gene action for expression of this character.

The genetic component of variation for number of fruits per plant *viz*. D, H_1, H_2 and h^2 were significant and estimate of E and F were non-significant. The value of H_1 was more than D which showed more prevalence of dominant genes. The positive value of F suggested predominance of dominant alleles in the parents. The degree of dominance $(H_1/D)^{½}$ was 2.21 revealed role of over-dominance. The proportion of genes with positive and negative effects $(H_2/4H_1)$ was 0.21 exhibiting dominance. The proportion of dominant and recessive genes $[(4DH_1)^{½} + F/ (4DH_1)^{½} - F]$ was 1.25 whereas the number of group of genes (h^2/H_2) which showed dominance was 2.38. Narrow sense heritability (17.59%) indicated non-additive gene action.

Results pertaining to fruit length the estimates of D, H_1, H_2 and h^2 were significant. The value of D was more than H_1, exhibiting additive gene action. The positive F value indicated more prevalence of dominant alleles in parents. The mean degree of dominance $(H_1/D)^{½}$ was 0.96 indicating partial dominance. While the proportion of genes with positive and negative effects $(H_2/4H_1)$ in parents was found to be 0.22 denoting asymmetry at loci showing dominance. The proportion of dominant and recessive genes $[(4DH_1)^{½} + F/ (4DH_1)^{½} - F]$ in parents was 1.25 whereas the number of genes (h^2/H_2) which controlled the character and exhibit dominance was 1.18. Narrow sense heritability (68.91%) showed predominance of additive gene action.

The genetical parameters like H_1, H_2 and h^2 were significant while D was highly significant for fruit

Table 1. Estimates of genetic components of variation and various statistical parameters for different characters:

Genetic parameters	Days to1st female flower opening	Node No. of 1st female flower	Days to1st fruit harvest	Fruit weight (g)	Number of fruits/ plant	Fruit length (cm)	Fruit diameter (cm)	Yield/ plant(g)
(D) Additive effect	3.34 ± 1.60*	0.16 ± 0.03**	2.11 ± 1.13**	1187.36 ± 288.52**	0.82 ± 0.41*	12.43 ± 2.57*	0.83 ± 0.16**	65796.44 ± 23402.04**
(H) Dominance effect								
H_1	19.53 ± 4.07**	0.36 ± 0.08**	16.59 ± 2.87**	1068.7 ± 452.5*	3.89 ± 1.05*	11.44 ± 4.31*	0.79 ± 0.32*	331166.02 ± 59408.21**
H_2	16.92 ± 3.64**	0.31 ± 0.08**	14.27 ± 2.56**	1075.20 ± 357.8**	3.33 ± 0.94*	10.52 ± 4.06*	0.67 ± 0.29*	287059.32 ± 53070.84*
h^2	34.15 ± 2.45**	0.80 ± 0.05**	24.42 ± 1.73**	1806.34 ± 2157.4**	7.91 ± 0.63**	0.58 ± 0.24*	0.43 ± 0.21*	466588.84 ± 35720.18**
(F) Gene distribution	-0.22 ± 3.92	-0.10 ± 0.08	-2.15 ± 2.76	-107.43 ± 318.48	0.39 ± 1.01	12.41 ± 4.79	0.85 ± 0.92	-49209.68 ± 57171.21
(E) Environmental effect	0.15 ± 0.61	0.01 ± 0.02	0.18 ± 0.43	48.5 ± 82.7	0.06 ± 0.16	0.25 ± 0.23	0.03 ± 0.02	739.17 ± 8845.14
$(H_1/D)^{½}$	2.42	1.50	2.81	0.98	2.21	0.96	0.98	2.24
$H_2/4H_1$	0.22	0.22	0.22	0.23	0.21	0.22	0.21	0.22
$(4DH_1)^{½} + F/(4DH_1)^{½} - F$	1.08	1.09	1.44	0.91	1.25	1.02	0.72	1.24
h^2/H_2	2.01	2.58	1.71	1.68	2.38	1.18	1.26	1.62
Heritability % (ns)	14.11	25.56	9.78	68.12	17.59	68.91	57.14	14.65

* Significant at 5% level, ** Significant at 1% level

diameter. The value of D was greater than H_1 indicating presence of additive genes. The positive value of F indicated that the dominant allele were more frequent in parents. The mean degree of dominance $(H_1/D)^{½}$ being 0.98 exhibited partial dominance. The proportion of genes with positive and negative effects $(H_2/4H_1)$ was noted 0.21 indicating asymmetry at loci showing dominance. The proportion of dominant and recessive genes $[(4DH_1)^{½} + F/ (4DH_1)^{½} - F]$ in the parents was 0.72 whereas the number of dominant group of genes (h^2/H_2) was 1.26. Narrow sense heritability (57.14%) showed preponderance of additive type of gene action for this trait.

Results pertaining to components of genetic variation for total yield per plant revealed that estimate of D, H_1 and h^2 were highly significant while H_2 was significant. The value of H_1 was greater than D indicating the presence of more dominant genes than additive ones. The negative value of F showed preponderance of recessive alleles for this trait in parents. The value of $(H_1/D)^{½}$ was higher (2.24) indicating over-dominance. The proportion of genes with positive and negative effects $(H_2/4H_1)$ in parents was found to be 0.22 (less than 0.25), which denoted asymmetry at loci showing dominance. The proportion of dominance and recessive genes $[(4DH_1)^{½} + F/ (4DH_1)^{½} - F]$ was 1.24, exhibited distribution of dominant gene. The number of group of genes (h^2/H_2) exhibiting dominance and controlling the character was 1.62. The narrow sense heritability (14.65%) indicated that non-additive type of gene action played an important role in the inheritance of this trait. These results on earliness and fruit characters were in consonance with findings of Balliu *et al.* (2000), Gulamuddin and Ahmad (2002) and Prasad (2002), Bairagi (2003), Sarkar and Sirohi (2005), Kumbhar *et al.* (2005), Munshi *et al.* (2005 and 2006) and Yudhvir and Sharma (2006) in cucumber.

The results of present investigation showed dominance and over-dominance gene actions for all quantitative traits understudy. The diallel analysis on genetic components of variation revealed that over dominance effect for days to first male and female flower opening, node number of first female flower, days to first fruit set, days to first fruit harvest, number of fruits per plant and total yield per plant, whereas nearly dominance effect was observed for vine length and partial dominance effect was observed for fruit weight, fruit length and fruit diameter. Narrow sense heritability was found to be greater than 0.5 for fruit weight, fruit length, fruit diameter and vine length indicating predominance of additive gene action over dominance ones, while for rest of the characters average degree of dominance was found more than 1 and narrow sense of heritability was found less than 0.5 suggested the preponderance of non-additive gene action. Thus, in the present investigation, the predominance of non-additive gene action and low narrow sense heritability was observed for most of the important yield contributing characters which suggested the importance of heterosis breeding to get higher gain in cucumber.

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