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Research Article

Genetic Analysis for Earliness and Yield Components using Gynoecious and Monoecious Lines in Cucumber (*Cucumis sativus* L.)

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Abstract

Twenty one F_1 hybrids were developed from crossing of 7 diverse genotypes including two gynoecious lines of cucumber in a half diallel mating system. These twenty one F_1 hybrids along with their seven parents were evaluated to study the gene action in gynoecious and monoecious lines for various earliness and yield components in cucumber. Analysis of variance revealed the presence of highly significant differences among the genotypes representing that these were diverse for the traits studied. The prevalence of over dominance effect for node number of first female flower, days to first female flower anthesis, days to fruit set from opening of first female flower, days to first fruit harvest, number of fruits per plant and total yield per plant, whereas nearly dominance effect was observed for number of fruits per plant and partial dominance effect was observed for fruit length, fruit diameter and average fruit weight. For average fruit weight, narrow sense heritability was greater than 50% which is an indication of predominance of additive gene action, while for remaining traits narrow sense of heritability was less than 50%, which suggests the preponderance of non-additive gene action. Therefore, in the present study, the predominance of non-additive gene action and low narrow sense heritability was recorded for most of the important earliness and yield contributing characters suggested the significance of heterosis breeding to obtain higher gain in cucumber improvement.

Keywords: Gene action, cucumber, earliness, gynoecious

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Introduction

Cucumber (*Cucumis sativus* L., 2n = 2 x =14) is an important summer vegetable of cucurbitaceae family. In India it is cultivated from higher altitude to plains including river beds. In north Indian plains, two crops are grown in a year *i.e.* spring-summer and *kharif*, while in hills it is cultivated as an autumn summer crop. Cucumber is well known for its economic importance as food plant, mainly grown for its edible tender fruits used as salad, pickles, dessert fruit, rayata preparation and even brined on commercial scale in almost every part of the world. It is an ideal crop for the peoples suffering from jaundice, constipation and other associated diseases. India is being home of cucumber possesses vast genetic variability for vegetative and fruit characters. The one of the most important factors limiting fruit yield in slicing and processing cucumber are low fruiting ability and yield suppression due to its inherent fruiting habits [1]. Development of high yielding gynoecious lines or hybrids mainly depends on genetically superior parents, together with suitable breeding methodology. Gynoecious varieties are becoming popular among cucumber growers because of its high yield, earliness and best suited to protected cultivation [2-3]. The nature and magnitude of gene action involved in expression of quantitative traits is important for successful development of crop varieties. Also, the correct choice of parents for hybridization is crucial for development of cultivars.

Depending on the genetic architecture of the traits, recombinant breeding is the most appropriate approach to combine various desirable traits. Therefore, it is essential to have knowledge of gene effects concerned with inheritance of many traits to formulate any breeding methods. The success of selection mostly depends upon the amount of genetic variability present in the parental lines used. Selection generally carried out from locally existing germplasm results in low magnitude of improvement due to less variability. Therefore, a broad genetic base should be utilized for faster and higher magnitude of success. Use of diverse genotypes in hybridization programme creates such broad genetic base [4]. In spite of wide genetic variability available in this crop little attention has been given for improvement of this crop. Hayman (1954) [5] and Griffings (1956) [6] offered an excellent mean of obtaining information on magnitude and direction of dominance and over-dominance besides the nature and extent of gene action involved in the inheritance of quantitative traits.

Information on types of gene action that governs the inheritance of important quantitative characters can help breeders to select suitable parents and devise an appropriate breeding strategy. A large number of studies have been carried out in cucmber, but less information on genetic architecture of quantitative traits using gynoecious lines is available in this crop. Hence, an attempt was made to investigate the gene action (inheritance pattern) of different quantitative characters in 7×7 half-diallel set for formulation of a sound breeding programme in cucumber.

Materials and Methods

The present investigation was carried out during 2012-13 at research farm of Division of Vegetable Science of Indian Agricultural Research Institute, New Delhi. Seven genetically diverse inbreds of cucumber developed in different parts of the country showing considerable amount of morphological variation *viz*., P_1 (Gynoecious Pickling Cucumber-1), P_2 (Pant Parthenocarpic Cucumber-2), P_3 (DC-1), P_4 (Kalyanpur Green), P_5 (Swarna Poorna), P_6 (Punjab Naveen), and P_7 (Pusa Uday) were crossed in 7 x 7 half dialled (excluding reciprocal) fashion [5] to obtain 21 F_1 hybrid combinations during spring -summer, 2012-2013. Sufficient quantity of F_1 seeds were obtained for evaluation in the *Kharif*, 2013-14. Twenty eight genotypes (21 F_1 and 7 parental lines) were grown under field condition in a randomized block design, and were replicated three times. The crop was sown in rows of 1.5 m apart with spacing of 60 cm between the plants. Each treatment comprised of twenty hills. Two plants were allowed to grow in each hill and finally one plant was retaining for final observations. Standard and uniform agronomic practices recommended under irrigated conditions were followed throughout the growing seasons to raise a healthy and successful crop for better phenotypic and morphological expression. Ten plants were randomly selected for taking observations after discarding the border plants at both the ends. The fruits were harvested at marketable stage. Observations on individual plant basis were recorded on ten quantitative characters (**Table 1**). The components of variances were estimated following diallel method of numerical approach given by Hayman (1954) [5].

Results and Discussion

Analysis of variance showed that there were highly significant differences among experimental genotypes indicating that the parents were diverse for the characters studied. Estimates of component of genetic variation and various statistical parameters for different characters are given in **Table 1**.

The estimates of H^2 and D were highly significant while H_1 and H_2 were significant for node number of first female flower. The value of D was higher than H_1, showed that additive genes were more than dominant genes. The environmental influence (E) on the inheritance of this trait was non-significant. The mean degree of dominance $(H_1/D)^{½}$ was greater than one (1.15) therefore, 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 (0.23), 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 1.07 while the group of genes, which controlled the characters (h^2/H_2) and exhibited dominance was 4.68. Narrow sense heritability being 48.07% showed preponderance of non-additive gene action.

For days to first female flower anthesis the estimates of D, H_1, H_2, F and H^2 were highly significant while E was non-significant. The higher value of H than D indicated preponderance of non-additive gene action. The mean degree of dominance $(H_1/D)^{½}$ was 1.14 showed over-dominance. The proportion of genes with positive and negative effects ($H_2/4H_1$) in the parents was found to be 0.21 denoting asymmetry at loci showed dominance. The proportion of dominant and recessive genes $[(4DH_1)½ + F/ (4DH_1)½ - F]$ was 1.83 and the number of group of genes (h^2/H_2) was 2.39 which controlled the characters and exhibited dominance. Narrow-sense heritability being 47.71% indicated non-additive gene action.

Results pertaining to days to first fruit set from opening of first female flower, the estimates of h^2 were highly significant, H_2 was significant where as D, F, H_1 and E were non-significant. The value of H_1 was higher than D, showed the presence of dominant alleles in parents. The negative values of F showed recessive alleles were more frequent. The mean degree of dominance $(H_1/D)½$ being 2.47 indicating over-dominance. The proportion of genes with positive and negative effects ($H_2/4H_1$) was 0.26, showing dominance. The proportion of dominant and recessive genes $[(4DH_1)½ + F/ (4DH_1)½ - F]$ in the parents was 0.77, while the group of dominant genes (h^2/H_2) was 1.04. Narrow sense heritability being 8.61% exhibited predominance of non-additive gene action

Table 1 Estimates of genetic components of variation and various statistical parameters for ten quantitative traits

Genetic parameters	Node number of first female flower	Days to first female flower anthesis	Days to fruit set from opening of first female flower	Days to first fruit harvest	Number of fruits per plant	Fruit length (cm)	Fruit diameter (cm)	Average fruit weight (g)	Vine length (cm)	Yield per plant (g)
D (Additive effect)	0.71**	15.22**	0.05	27.19**	12.19**	7.50**	0.49**	1383.79**	321.94**	47702*
	±0.04	±1.53	±0.05	±2.94	±1.78	±0.29	±0.04	±13.71	±11.61	±22813
F	0.03	9.31**	-0.03	16.38*	-3.26	-4.50**	-0.43**	-236.86**	-1911.83**	-51301
	±0.09	±3.68	±0.12	±7.05	±4.28	±0.69	±0.09	±32.89	±27.85	±54730
H_1 (Dominance effect)	0.34*	19.76**	0.27	24.21**	11.99*	1.74	0.18	106.14**	77.01**	187025**
	±0.09	±3.69	±0.12	±7.08	±4.29	±0.69	±0.09	±33.01	±27.95	±54923
H_2	0.31*	16.50**	0.28*	15.40*	9.96*	2.00**	0.11	111.39**	36.85	17433
	±0.08	±3.25	±0.10	±6.23	±3.78	±0.61	±0.08	±29.08	±24.63	±48395
H^2	1.45**	39.45**	0.29**	17.46**	15.34**	15.57**	0.19**	392.60**	1.14	464710**
	±0.05	±2.19	±0.07	±4.18	±2.54	±0.41	±0.05	±19.53	±16.54	±32504
E	0.07	1.65	0.04	2.50*	0.69	1.0*	0.07*	51.54*	14.47**	7145
	±0.04	±0.54	±0.02	±1.04	±0.63	±0.18	±0.03	±4.85	±4.10	±8065
$(H_1/D)^{1/2}$	1.15	1.14	2.47	1.01	0.99	0.48	0.61	0.28	0.49	1.94
$(H_2/4H_1)$	0.23	0.21	0.26	0.16	0.21	0.29	0.15	0.26	0.12	0.23
$[(4DH_1)1/2 + F / (4DH_1)1/2 - F]$	1.07	1.83	0.77	2.33	0.74	1.27	0.04	0.54	-0.8	0.06
(h^2 / H_2)	4.68	2.39	1.04	1.13	1.54	7.79	1.73	3.52	0.03	26.66
Heritability % (narrow sense)	48.07	47.71	8.61	48.36	40.44	41.53	35.34	73.1	49.63	15.16

For days to first fruit harvest, the estimated value of D, H_1 and H^2 were highly significant where as H_2 and F was significant while E was non-significant. The estimated value of D was greater than H_1 which revealed that additive genes were more than dominant genes. The mean degree of dominance (H_1/D)½ being 1.01 showed over dominance. The proportion of genes with positive and negative effects $(H_2/4H_1)$ was 0.16, which denotes asymmetry at loci. The proportion of dominance and recessive genes [(4DH1)½ + F/ (4DH1)½ - F] was 2.33 whereas number of group of genes exhibiting dominance and controlling character was 1.13. The narrow sense heritability (48.36%) indicated the non additive type of gene action for expression of this character. These results for earliness characters were in similar with findings of Bairagi (2003) [7], Balliu *et al*., (2000) [8], Gulamuddin and Ahmed (2002) [9], Kumar (2010) [10], Kumbhar (2005) [11], Munshi (2005) [12] Munshi 2006 [13] Prasad (2002) [14] and Sarkar and Sirohi (2005) [15].

The genetic component of variation for number of fruits per plant viz. D and H^2 were highly significant and estimates of H_1 and H_2 were significant and estimate of E and F were non-significant. The value of D was more than H_1 which showed additive genes were more than dominant genes. Negative value of F indicated predominance of recessive alleles. The degree of dominance (H_1/D)½ was 0.99 revealed role of partial 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 [(4DH1)½ + F/ (4DH1)½ - F] was 0.74 whereas the number of group of genes (h^2/H_2) which showed dominance was 1.54. Narrow sense heritability (40.44%) indicated non-additive gene action.

Results pertaining to fruit length the estimates of D, F, H_2 and H^2 were highly significant and H_1 was non-significant while, the value of D was more than H_1, exhibiting additive gene action. Negative value of F indicated predominance of recessive alleles. The mean degree of dominance (H_1/D)½ was 0.48 indicated partial dominance. While the proportion of genes with positive and negative effects $(H_2/4H_1)$ in parents was found to be 0.29 denoting asymmetry at loci showed dominance. The proportion of dominant and recessive genes [(4DH1)½ + F/ (4DH1)½ - F] in parents was 0.29 whereas the number of genes (h^2/H_2) which controlled the character and exhibit dominance was 7.79. Narrow sense heritability (41.53%) showed predominance of non-additive gene action.

The genetical parameters like D, F and H^2 were highly significant while H_1 and H_2 were non-significant for fruit diameter. The value of D was greater than H_1 indicating presence of additive genes. Negative value of F indicated predominance of recessive alleles. The mean degree of dominance (H_1/D)½ being 0.61 exhibited partial dominance. The proportion of genes with positive and negative effects $(H_2/4H_1)$ was noted 0.15 indicated asymmetry at loci showing dominance. The proportion of dominant and recessive genes [(4DH1)½ + F/ (4DH1)½ - F] in the parents was 0.04 whereas the number of dominant group of genes (h^2/H_2) was 1.73. Narrow sense heritability (35.34%) showed preponderance of non-additive type of gene action for this trait.

Results pertaining to components of genetic variation for average fruit weight revealed that estimate of D, H_1, H_2, F and h^2 were highly significant. The value of D was greater than H_1 indicated presence of additive genes. The negative value of F showed preponderance of recessive alleles for this trait in parents. The value of $(H_1/D)½$ being 0.28 exhibited partial dominance. The proportion of genes with positive and negative effects $(H_2/4H_1)$ in parents was found to be 0.26, which denoted symmetry at loci showed dominance. The proportion of dominance and recessive genes [(4DH1)½ + F/ (4DH1)½ - F] was 0.54, exhibited distribution of dominant gene. The number of group of genes (h^2/ H_2) exhibiting dominance and controlling the character was 3.52. The narrow sense heritability (73.10%) indicated that additive type of gene action played an important role in the inheritance of this trait. These results for fruit characters were also similar with the findings of Bairagi (2003) [7], Balliu *et al*., (2000) [8], Gulamuddin and Ahmed (2002) [9], Kumar (2010) [10], Kumbhar (2005) [11], Munshi (2005) [12] Munshi 2006 [13] Prasad (2002) [14] and Sarkar and Sirohi (2005) [15] in cucumber.

Results pertaining to components of genetic variation for vine length revealed that estimate of D, F, H_1, were highly significant while H_2 and h^2 were non-significant. The value of D was greater than H_1 indicating presence of additive genes. The negative value of F showed preponderance of recessive alleles for this trait in parents. The value of $(H_1/D)½$ being 0.49 exhibited partial dominance. The proportion of genes with positive and negative effects $(H_2/4H_1)$ was noted 0.12 indicated asymmetry at loci showing dominance. The proportion of dominance and recessive genes [(4DH1)½ + F/ (4DH1)½ - F] was -0.80, exhibited distribution of dominant gene. The number of group of genes (h^2/ H_2) exhibiting dominance and controlling the character was 0.03. The narrow sense heritability (49.63%) indicated that non-additive type of gene action played an important role in the inheritance of this trait.

The estimates of H_1 and H^2 were highly significant while D was significant for yield per plant. The value of H_1 was greater than D, suggesting the presence of dominant alleles in parents. 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 (1.94) 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 0.23, 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 0.06 while the group of genes, which controlled the characters (h^2/H_2) and exhibited dominance was 26.66. Narrow sense heritability being 15.16% showed preponderance of non-additive gene action.

Conclusion

The knowledge of gene action is very useful to cucumber breeder for the selection of parents for hybridization, the estimation of some other genetic parameters and choice of breeding procedures for the genetic improvement of various quantitative characters. In the results of present experiment the dominance and over-dominance gene actions was showed for most of the quantitative traits. The prevalence of over dominance effect for node number of first female flower, days to first female flower anthesis, days to fruit set from opening of first female flower, days to first fruit harvest, number of fruits per plant and total yield per plant, whereas nearly dominance effect was observed for number of fruits per plant and partial dominance effect was observed for fruit length, fruit diameter and average fruit weight. For average fruit weight, narrow sense heritability was greater than 50% which is an indication of predominance of additive gene action, while for remaining traits average degree of dominance was greater than 1 and narrow sense of heritability was less than 50%, which suggested the preponderance of non-additive gene action. Therefore, in the present study, the predominance of non-additive gene action and low narrow sense heritability was recorded for most of the important earliness and yield contributing characters suggested the significance of heterosis breeding to obtain higher gain in cucumber improvement.

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