

GENE EFFECT STUDIES FOR QUALITY CHARACTERS IN CUCUMBER (*Cucumis sativus* L.) USING GYNOECIOUS PARENT

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Six generations (P₁, P₂, F₁, F₂, BC₁P₁ and BC₁P₂) of cucumber were developed from crossing gynoeceious parent (Gy-14) with three commercial varieties (Pusa Uday, Punjab Naveen and Pant Kheera-1) during Feb-May 2017 and September-December 2017 and were evaluated during Feb-May 2018 at Punjab Agricultural University, Ludhiana to find out the genetics of quality characters in cucumber. From the ABCD scaling test and three parameter model of joint scaling test, the absence of non-allelic interactions was detected for total soluble solids, ascorbic acid in Gy-14 × Pusa Uday and Gy-14 × Pant Kheera-1 and mineral matter, improved by selection of desirable segregants followed by pedigree method. Among epistatic interactions, in trait such as ascorbic acid in Gy-14 × Punjab Naveen, dominance × dominance interaction was higher in magnitude, therefore these traits can be improved by heterosis breeding.

Keywords: cucumber, gene interactions, inheritance, quality

INTRODUCTION

Cucumber (*Cucumis sativus* L.) is one of the most important and popular cucurbitaceous vegetable crops grown throughout the tropical and subtropical region of the world. DE CANDOLLE (1886) considered India as the centre of origin of cucumber. Among the cultivated cucurbits, cucumber is one of the most important vegetables grown throughout India for its high nutritive value and medicinal properties. Cucumber is a rich source of vitamins and minerals like vitamin B and C, carbohydrates, calcium (21 mg per 100 g), iron (0.30 mg per 100 g), thiamin (0.03 mg per 100 g), niacin (0.2 mg per 100 g) and riboflavin (0.02 mg per 100 g) (YAWALKAR, 1985; ROE *et al.*, 2013)

Gynoeceium is an important genetic mechanism which is exploited for hybrid development. Gynoeceium based hybrids are becoming popular among cucumber growers because of its high yield, earliness and more number of female flowers. The type and intensity of

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sex expression is important to commercial cucumber production since differences in sex type and flowering can affect harvest date and relative yield. The gynoecious trait is highly influenced by environmental factors; therefore, early phenotypic detection of gynoecy in breeding lines is difficult. The identification of phenotypically pure gynoecious lines is challenging and an important task at early stage of plant growth. Therefore, the knowledge of inheritance of quantitative and qualitative traits including gynoecy is important for using efficient breeding procedure for transfer of desirable genes. The inheritance of gynoecious sex expression in F_1 hybrids of cross of gynoecious \times monoecious is governed by partial dominance (MORE and MUNGER, 1987; PERL-TREVESE and RAJAGOPALAN, 2006), multiple genes (LI *et al.*, 2012), single gene with dominant or incomplete dominance (LOU *et al.*, 2007), single dominant gene (MIBUS and TATLIOGLU, 2004; MIAO *et al.*, 2011; PATI *et al.*, 2015; WIN *et al.*, 2015), oligogene with some background genes modified (SHENGJUM *et al.*, 2013). The prime goal of cucumber breeders have become the introgression of gynoecious gene into commercial inbred lines because gynoecy is dominant over monoecy, therefore, all F_1 plants are highly productive.

Before understanding any breeding programme for specific objective it is necessary for the breeder to have knowledge of basic information regarding the nature of inheritance of various traits in terms of additive and non-additive genetic variance, which could help him in planning the hybridization and selection procedure effectively to get desirable results. Thus routine breeding method as pedigree and pure line selection are ineffective and inadequate to explore the full range of genetic variability and the estimation were mostly biased due to linkage and epistasis for complex characters like yield, quality and yield contributing characters. Knowledge of gene action helps in the selection of parents for use in the hybridization programmes and also in the choice of appropriate breeding procedure for the genetic improvement of various quantitative characters. Hence insight into the nature of gene action involved in the expression of various quantitative characters is essential to a plant breeder for starting a judicious breeding programme. For the breeding of superior hybrids, estimates of gene action assist in appropriate selection of parental lines for hybridization programme and generation mean analysis is also an effective tool to understand the nature of gene effects involved in expression of characters. This information is most important and significant which plays a vital role in pursuing an appropriate breeding procedure applicable to cross-pollinated crops especially cucumber. Genetic information available so far in cucumber crop mainly concerns with heterosis and combining ability studies. But studies on nature and magnitude of gene action for gynoecy, yield and quality traits is limited. A few reports are available on the estimation of additive and dominance effects only, but epistatic effect has been assumed to be negligible and thus ignored. Therefore, present study was conducted to find out the gene effects of quality traits in cucumber using gynoecious parents.

MATERIALS AND METHODS

The genetics of yield and other characters of cucumber were studied using P_1 , P_2 , F_1 , F_2 , BC_1P_1 and BC_1P_2 populations of cross between gynoecious line (Gy-14) as female parent and three commercial varieties (Pusa Uday, Punjab Naveen and Pant Kheera-1) as male parents, developed at Vegetable Research Farm, Department of Vegetable Science, Punjab Agricultural University, Ludhiana, during years 2017 and 2018. Six generations (P_1 , P_2 , F_1 , F_2 , BC_1P_1 and

BC₁P₂) of three crosses (Gy-14 × Pusa Uday, Gy-14 × Punjab Naveen and Gy-14 × Pant Kheera-1) were developed during summer and rainy season of 2017 and were evaluated during summer season of 2018. The nursery was raised in plug trays using cocopeat: perlite: vermiculite in ratio of 3:1:1. The seedlings were transplanted in the first week of March on both sides of 2.0 meter wide raised bed with plant to plant spacing of 45 cm. The crop was raised as per recommendations given in the Package of Practices of Vegetable crops, Punjab Agricultural University, Ludhiana (ANONYMOUS, 2017). Data were recorded from single plants with 10 plants of each parent (P₁ and P₂) and F₁, 20 plants of each backcross (BC₁P₁ and BC₁P₂) and 40 plants of F₂ each of three crosses. The studied characters were quality traits such as total soluble solids (°brix), ascorbic acid content (mg/100g flesh weight) and mineral matter (%).

The total soluble solids (TSS) content was recorded with the help of hand refractometer. Total of all the fruit observations was averaged to workout average total soluble solids of each plant. Ascorbic Acid (mg/100g flesh weight) or vitamin C content of cucumber fruit was estimated by using 2, 6-dichlorophenol indophenol dye method suggested by AOAC (1990), whereas the Mineral content (%) was estimated using hot furnace.

The observed means of the six generations and their standard errors were used to estimate the scaling test (A, B, C, D) given by MATHER (1949) and HAYMAN and MATHER (1955) used to test the presence of epistasis. Significance of any one of the scaling test depict the presence of epistatic interactions. The adequacy of the simple additive dominance model (mean, additive, and dominance effects) was determined by χ^2 test. Where the simple model proved to be inadequate, joint scaling test was applied and epistatic interactions- additive × additive [i], additive × dominance [j] and dominance × dominance [l] were added to the model, as proposed by MATHER and JINKS (1982). The significance of genetic parameters (m, [d], [h], [i], [j] and [l]) were tested using t-test. In the complete six parameter model, chi-square adequacy test was not possible, because the degrees of freedom was reduced to zero, but whenever estimation of six parameters signified one or two interaction parameters as non-significant they were eliminated and remaining parameters were re-estimated along with testing the adequacy of model using chi-square test.

RESULTS AND DISCUSSION

Generation means of TSS, ascorbic acid and mineral matter

The mean values of F₁ of all the three crosses were intermediate between their respective parental means but these were higher than the corresponding mid-parental means, which suggested partial dominance towards the higher parent i.e. P₂ in all the three traits (Table 1). Whereas the F₂ showed variations, for TSS, in crosses Gy-14 × Pusa Uday and Gy-14 × Punjab Naveen, F₂ means were higher than its corresponding F₁ means but in cross Gy-14 × Pant Kheera-1, F₂ mean was lower than its corresponding F₁ mean indicating some degree of inbreeding depression in the cross. Similarly for mineral matter, the F₂ mean were lower than their respective F₁ means in crosses Gy-14 × Punjab Naveen and Gy-14 × Pant Kheera-1 indicating some degree of inbreeding depression but in cross Gy-14 × Pusa Uday F₂ mean was higher than its corresponding F₁ mean. Alternatively, though the mean value of vitamin C content of F₁ of cross Gy-14 × Pant Kheera-1 lied in between its parental means it skewed too much towards the better parental mean (P₂) and was almost equal to it, indicating complete dominance for the character. The F₂ means of other two crosses were lower than their

corresponding F_1 means indicating some degree of inbreeding depression. B_2 means were higher than the corresponding B_1 means in all the crosses as the recurrent parent involved in B_2 has higher mean value than that of recurrent parent involved in corresponding B_1 's, indicating the behaviour as per expectations.

Table 1. Generation means of six generations in different crosses

Crosses	Generations						
	P ₁	P ₂	F ₁	F ₂	B ₁	B ₂	M.P.
Total soluble solids							
GY-14 × Pusa Uday	2.630 ±0.080	3.140 ±0.095	3.050 ±0.091	3.060 ±0.055	2.895 ±0.060	3.090 ±0.064	2.885
GY-14×Punjab Naveen	2.630 ±0.080	3.270 ±0.093	3.040 ±0.070	3.055 ±0.058	2.955 ±0.055	3.105 ±0.075	2.950
GY-14 × Pant Kheera-1	2.630 ±0.080	3.130 ±0.093	3.040 ±0.087	3.000 ±0.052	2.915 ±0.053	3.120 ±0.051	2.880
Ascorbic acid content							
GY-14 × Pusa Uday	2.244 ±0.044	3.338 ±0.110	3.036 ±0.062	2.855 ±0.066	2.613 ±0.037	3.357 ±0.076	2.791
GY-14 × Punjab Naveen	2.244 ±0.044	3.882 ±0.088	3.206 ±0.133	3.080 ±0.076	3.051 ±0.114	3.530 ±0.080	3.063
GY-14 ×Pant Kheera-1	2.244 ±0.044	3.269 ±0.092	3.250 ±0.091	2.959 ±0.068	2.976 ±0.091	3.324 ±0.090	2.756
Mineral matter							
GY-14 × Pusa Uday	0.929 ±0.032	0.978 ±0.042	0.930 ±0.042	0.932 ±0.031	0.894 ±0.028	0.979 ±0.028	0.953
GY-14 × Punjab Naveen	0.929 ±0.032	1.006 ±0.048	0.954 ±0.027	0.946 ±0.031	0.914 ±0.017	0.981 ±0.022	0.967
GY-14 × Pant Kheera-1	0.929 ±0.032	0.987 ±0.039	0.969 ±0.032	0.935 ±0.029	0.911 ±0.018	0.962 ±0.024	0.958

Gene effects for Total soluble solids

Scaling test analysis of various generations from all the three cross Gy-14 × Pusa Uday, Gy-14 × Punjab Naveen and Gy-14 × Pant Kheera-1 revealed the adequacy of simple additive dominance model and absence of epistatic interactions as none of the components (A, B, C and D) of scaling test were significant (Table 2) which was also confirmed by non-significant chi square value of three parameter model of joint scaling test.

Table 2. Scaling test for different characters

Character	Cross	Scales			
		A	B	C	D
Total soluble solids	GY-14 × Pusa Uday	0.110 ±0.171	-0.010 ±0.183	0.370 ±0.311	0.135 ±0.141
	GY-14×Punjab Naveen	0.240 ±0.153	-0.100 ±0.189	0.240 ±0.297	0.050 ±0.148
	GY-14 × Pant Kheera-1	0.160 ±0.159	0.070 ±0.163	0.160 ±0.299	-0.035 ±0.128
Ascorbic acid	GY-14 × Pusa Uday	-0.054 ±0.105	0.340 ±0.198	-0.233 ±0.316	-0.260 ±0.157
	GY-14×Punjab Naveen	0.652 ±0.267*	-0.029 ±0.226	-0.219 ±0.414	-0.421 ±0.205*
	GY-14 × Pant Kheera-1	0.459 ±0.208*	0.130 ±0.221	-0.176 ±0.344	-0.382 ±0.187*
Mineral matter	GY-14 × Pusa Uday	-0.071 ±0.078	0.049 ±0.081	-0.041 ±0.158	-0.009 ±0.073
	GY-14×Punjab Naveen	-0.055 ±0.054	0.001 ±0.071	-0.060 ±0.148	-0.003 ±0.068
	GY-14 × Pant Kheera-1	-0.076 ±0.057	-0.032 ± 0.069	-0.112 ±0.141	-0.002 ±0.065

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

Therefore, three parameter model of joint scaling test was adequate to explain the variation present in the generations. In the best fit model of joint scaling test, only additive effect was significant indicating the importance of additive effects in the inheritance of this trait (Table 3). For further improving this trait, selection of desirable segregants followed by pedigree method can be employed as additive effects were found important in the inheritance of this trait which may be due to associated gene pairs. Among epistatic interactions, none were significant in any cross, so more generations need to be evaluated.

Table 3. Estimates of gene effects based on joint scaling test and genetic components in best fit model for different characters

Crosses	Gene effects						$\chi^2_{(3)}$	Type of Epistasis
	Main effects			Interaction effects				
	m	[d]	[h]	[i]	[j]	[l]		
Total Soluble Solids								
GY-14 × Pusa Uday	2.906±0.054**	-0.238±0.051**	0.197±0.104	-	-	-	5.443	-
GY-14 × Punjab Naveen	2.975±0.052**	-0.268±0.051**	0.108±0.093	-	-	-	4.747	-
GY-14 × Pant Kheera-1	2.904±0.053**	-0.234±0.047**	0.190±0.102	-	-	-	4.507	-
Ascorbic acid content								
GY-14 × Pusa Uday	2.826±0.049**	-0.600±0.047**	0.202±0.079*	-	-	-	5.060	-
GY-14 × Punjab Naveen	2.221±0.414**	-0.819±0.049**	2.450±1.050*	0.842±0.411*	0.681±0.295*	-1.465±0.694*	11.583**	D
GY-14 × Pant Kheera-1	2.759±0.046**	-0.500±0.046**	0.546±0.095**	-	-	-	6.445	-
Mineral matter								
GY-14 × Pusa Uday	0.955±0.024**	-0.043±0.022*	-0.034±0.046	-	-	-	5.630	-
GY-14 × Punjab Naveen	0.960±0.022**	-0.052±0.020**	-0.019±0.039	-	-	-	1.366	-
GY-14 × Pant Kheera-1	0.944±0.021**	-0.039±0.019*	-0.001±0.039	-	-	-	1.868	-

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

Gene effects for ascorbic acid

In the cross, Gy-14 × Pusa Uday, scaling test analysis of generation means depicts that none of the components were significant which reveals that simple additive-dominance model is adequate to explain the variation present among generations (Table 2), which is further confirmed by non-significant chi square value of three parameter model of joint scaling test. In

three parameter model of joint scaling test, both additive and dominant parameters were significant, but the magnitude of additive gene effects was more than that of dominance gene effects which confirms that additive gene effects were found to contribute substantially in the inheritance of ascorbic acid content (Table 3). Whereas in cross Gy-14 × Pant Kheera-1, A and C components of scaling tests were significant but goodness of fit chi square test of simple additive dominance model was non-significant which means non-allelic interactions were not present and the three parameter model of joint scaling test was adequate to explain the variation present among the generations. In the best fit model of joint scaling test, both the additive and dominance effects were significant but the magnitude of additive effects was less than that of dominance effects which indicate the importance of dominance gene effects in the inheritance of the character.

In the cross Gy-14 × Punjab Naveen, significance of A and D components of scaling test clearly indicated the presence of all three type of non-allelic gene interactions *viz.* additive × additive (i), additive × dominance (j) and dominance × dominance (l) for the character (Table 2). Also the significant chi square value of three parameter model of joint scaling test confirmed the inadequacy of simple additive dominance model and presence of epistatic interactions. In the best fit model of joint scaling test, only additive gene effects were significant (Table 3). In the six parameter model, among the epistatic effects, all the three interaction parameters were significant. So the adequacy of best fit model could not be tested. The magnitude of dominance × dominance gene interaction was higher indicating its importance among the other interactions as presented in Table 3. Duplicate type of epistasis was present as indicated by opposite signs of [h] and [l].

In crosses Gy-14 × Punjab Naveen and Gy-14 × Pant Kheera-1, dominance gene action was prevalent which may be due to the dominance of increaser alleles indicating the usefulness of heterosis breeding. In cross Gy-14 × Punjab Naveen, significance of dominance × dominance gene effects coupled with duplicate type of epistasis indicates the usefulness of recurrent selection for the selection of desirable segregants. In cross Gy-14 × Pusa Uday, additive gene effect was present signifying the usefulness of pedigree method but none of the epistatic interactions were significant, so more generations need to be evaluated to exploit the trait. KAUR *et al.*, (2016) also reported the same.

Gene effects for mineral matter

Scaling test analysis of various generations from the all the three cross of cucumber revealed the absence of epistatic interactions as none of the components (A, B, C and D) of scaling test were significant which was confirmed by non-significant chi-square value of simple additive-dominance model (Table 2). Therefore, for all these crosses, mean value is constituted only by additive and dominance effects as non-allelic epistatic interactions are not present. In the best fit model of joint scaling test, merely the additive effects were significant which approves that additive gene effects were found to contribute significantly in the inheritance of the character (Table 3). This trait can be improved through the selection using pedigree method as there was occurrence of significant additive gene effects in the generation means. However, the additive effects had a negative sign for all crosses, indicating the dispersion of favourable alleles.

CONCLUSION

From the present experiment, it was concluded that characters such as total soluble solids and mineral matter were controlled by additive gene effects. Therefore, pedigree method can be used for improvement of these traits. However, for ascorbic acid content, both additive and non-additive genetic components were present and improvement of this trait can be done through selection of transgressive segregants using pedigree method followed by heterosis breeding.

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**STUDIJE O EFEKTIMA GENA ZA KARAKTERISTIKE KVALITETA KRSTAVCA
(*Cucumis sativus L.*) KORISĆENJEM GINOECIOUS RODITELJA**

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Izvod

Šest generacija (P1, P2, F1, F2, BC1P1 i BC1P2) krastavca razvijeno je ukrštanjem ginoecius roditelja (Gi-14) sa tri komercijalne sorte (Pusa Udai, Punjab Naveen i Pant Kheera-1) tokom februara-maja 2017. i septembra-decembra 2017. godine i ocenjivani su tokom februara-maja 2018. godine na Poljoprivrednom univerzitetu u Pendžabu, Indija, da bi se otkrila genetika svojstava kvaliteta kod krastavca. Iz ABCD testa skaliranja i tri parametrijska modela ispitivanja zajedničkog skaliranja, otkriveno je odsustvo nealelnih interakcija za ukupne rastvorljive čvrste materije, askorbinsku kiselinu u $Gi-14 \times Pusa Udai$ i $Gi-14 \times Pant Kheera-1$ i mineralne materije, poboljšanih izborom poželjnih segreganata, a potom pedigree metodom. Među epistatičkim interakcijama, u osobinama kao što je askorbinska kiselina u $Gi-14 \times Punjab Naveen$, interakcija dominacija \times dominacija bila je veća, pa se ove osobine mogu poboljšati heterozisom.

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