

UTILIZING GYNOECIOUS CUCUMBER (*CUCUMIS SATIVUS* L.) INBREDS TO INVESTIGATE INHERITANCE OF GYNOECIUM, FRUIT YIELD AND ITS CONTRASTING TRAITS

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Kaur T., R. Kumar Dhall, P. Manchanda ,P.Kumari (2024). *Utilizing gynoeocious cucumber (cucumis sativus l.) inbreds to investigate inheritance of gynoeocium, fruit yield and its contrasting traits.* - Genetika, Vol 56, No.2, 255-269.

To determine the inheritance of fruit yield and its component traits in cucumber, three commercial monoecious varieties (Pusa Uday, Punjab Naveen and Pant Kheera-1) were crossed with gynoeocious parent (Gy-14) and developed six generations of each cross. The scaling test and the three-parameter model of the joint scaling test revealed the presence of epistasis for most of the traits. Duplicate epistasis was found in the majority of the traits, which will decrease the net gain from heterozygosity because of epistatic effects and dominance cancellation. The fruit weight in Gy-14 × Pant Kheera-1 showed a higher additive × dominance type among epistatic interactions, while fruit length in all crosses and fruit breadth in Gy-14 × Pant Kheera-1 showed a higher additive × additive type of interaction, indicating the use of pedigree method to improve these traits. Fruit diameter, fruit weight, number of fruits per plant and yield per plant in Gy-14 × Punjab Naveen, and fruit weight in Gy-14 × Pusa Uday were found to exhibit a higher dominance × dominance interaction. Consequently, these traits can be further enhanced through heterosis breeding in the corresponding crosses.

Keywords: Cucumber, Epistatis, Gene effects, Generation mean analysis, Gynoeocious

INTRODUCTION

Cucumber (*Cucumis sativus* L.) is an important cross pollinated cucurbit crop of the tropics and subtropics. Cucumber, originated in India, is usually monoecious in nature while gynoeocium is an important genetic mechanism that can be exploited for hybrid development. Three genes *F*, *M* and *A* are responsible for regulating the expression of sex in cucumber plant. The *M/m* gene governs bisexual flower expression, while the *F/f* gene controls the degree of female flower expression (YAMASAKI *et al.*, 2001; MIBUS and TATLIOGLU, 2004; LI *et al.*, 2008;

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LI *et al.*, 2009). The *M* locus regulates whether flowers are unisexual (*M*₋) or bisexual (*mm*), whereas the *F* locus affects the degree of femaleness (*FF*>*Ff*>*ff*). If a plant has homozygous recessive *aa* and *ff*, the *A* locus confers enhanced male inclination. In commercial cucumber production, the type and intensity of sex expression matter because variations in sex type and flowering can influence harvest date and relative yield. Due of dominant nature of gynoecious over monoecious trait, F₁ plants were discovered to be distinctly productive. Early phenotypic detection of gynoecious trait in breeding lines is challenging because environmental influences have a significant impact on the gynoecious characteristic. At an early stage of plant growth, identifying phenotypically pure gynoecious lines is a difficult but crucial endeavour. Therefore, understanding how both quantitative and qualitative features, including gynoecey, are inherited is crucial for utilizing effective breeding techniques to transfer desired genes. In F₁ hybrids created by crossing gynoecious × monoecious, the inheritance of gynoecious sex expression is controlled by various factors such as partial dominance (PERL-TREVESE and RAJAGOPALAN, 2006, multiple genes (LI *et al.*, 2012), single dominant gene (MIBUS and TATLIOGLU, 2004; MIAO *et al.*, 2011; PATI *et al.*, 2015; WIN *et al.*, 2015, JAT, 2016), oligogene with some background genes modified (SHENGJUM *et al.*, 2013). The introduction of gynoecious genes into commercial inbred lines has emerged as the main objective of cucumber breeders.

Cucumber yield, like that of all other crops, is the result of numerous genes interacting with the environment; hence, direct selection will not provide desired results. Selecting for yield components has been proposed as a way to boost fruit yield. Understanding how different traits are inherited in terms of additive and non-additive genetic variance is essential before beginning any breeding program. This will aid in efficiently organizing the hybridization and selection process to produce desired results. Understanding about gene action can be useful when choosing parents for hybridization programmes and when deciding on the best breeding technique to enhance the genetic makeup of different quantitative traits.

Generation mean analysis is one of the best techniques for estimating genetic parameters. It provides a general method for estimating parameters such as additive, dominance, additive x additive, additive x dominance, and dominance x dominance effects from the mean measurements of six generations (HAYMAN, 1958; JINKS and JONES, 1958). Although generation mean analysis has been widely applied to comprehend the impacts of genes in many crops, there aren't many reports on its application to comprehend the gene effects in cucumber. Because of this, the current study aims to determine the gene effects in the inheritance of fruit yield and its constituent traits in cucumber.

MATERIALS AND METHODS

Location and climatic conditions

The current research was carried out at Vegetable Research Farm, Department of Vegetable Science, Punjab Agricultural University, Ludhiana, India. Ludhiana is situated at an elevation of 247 meters above mean sea level and at latitude 30°54' North and longitude 75°48' East. This region experiences chilly winters with sporadic ground frost from mid-December to mid-February, and hot summers with desiccating winds from April to June. This area receives 700 mm of rainfall on average a year, most of which falls between July and mid-September during the monsoon season.

Plant material

The plant material consisted of gynoecious line Gy-14 (female parent) and three commercial monoecious varieties i.e. Pusa Uday, Punjab Naveen and Pant Kheera-1 (male parent).

Development of F₁, F₂ and back cross

During first season, the seeds of parents were sown in crossing block and F₁'s (Gy-14 × Pusa Uday, Gy-14 × Punjab Naveen and Gy-14 × Pant Kheera-1) were developed at Vegetable Research Farm, Department of Vegetable Science, Punjab Agricultural University, Ludhiana. The parents were also selfed to raise the crop for next year. The gynoecious parent, Gy-14 was selfed by inducing male by spraying it with silver thiosulphate. The seed of parents and F₁ of each cross was harvested separately. During second season, the F₁ hybrids were sown along with parents in polyhouse throughout rainy season in order to produce F₂ and backcross (BC₁P₁ and BC₁P₂) generations. During the third season, all the six generations (P₁, P₂, F₁, F₂, BC₁P₁ and BC₁P₂) were evaluated during summer season under open field conditions.

Experimental method and Cultural practices

The nursery of all the six generations were raised in plug trays in the first week of January, 2018 using 3:1:1 ratio of cocopeat: perlite: vermiculite. The seedlings were transplanted in the first week of March, 2018 in open field conditions on both sides of raised bed (2.0 meter wide) by keeping plant to plant spacing of 45 cm. For better growth and development, 40 kg N, 20 kg P₂O₅ and 20 kg K₂O per acre were used when the seeds were sown in two parallel bans 15 cm away from the bed mark. The first irrigation was applied immediately after transplanting and subsequently irrigations were applied second or third day of sowing. The crop was irrigated at 3-5 days interval depending upon the temperature. During the initial stage, seedlings were infected with red pumpkin beetle which were controlled by spraying Decis 2.8 (Deltamethrin 2.8 EC) @ 1.5/litre of water. The hand weeding was done in the furrows one month after transplanting and thereafter 20 kg N per acre is applied in the furrows and earthing up was done one day after application of nitrogen. The downy mildew was managed by spaying Ridomil gold (4% Metalaxyl-M and 64% WP Mancozeb) @ 2g per litre of water. Randomized Complete Block Design (RCBD) with three replications was used to set up the experiment. Single plants, 10 of each parent (P₁ and P₂), F₁, 20 of each backcross (BC₁P₁ and BC₁P₂) and 40 of each of the three crosses of F₂ plants were used to record the data on yield and yield attributing traits.

Observations recorded

The various fruit parameters recorded were fruit length (space between the stem end and blossom end of fruit, measured with the help of a scale and expressed in centimetres), fruit diameter (measured from the middle of the fruit with the help of a Vernier Caliper and expressed in centimetres), fruit weight (g) and number of fruits per plant (number of fruits per plot obtained from each harvest were added and divided by number of plants per plot). The fruit yield per plot obtained from each picking was added and divided by number of plants per plot to estimate fruit yield per plant (kg).

Statistical analysis for inheritance of yield and yield attributing traits

For all the traits, the generation means analysis of the six populations (P_1 , P_2 , F_1 , F_2 , B_1 and B_2) was used to estimate the gene effects as suggested by MATHER (1949), JINKS and JONES (1958) and HAYMAN (1958). For statistical analysis, the data of individual plants for different traits were employed. By averaging all of the plants in each replication, the generation mean of each generation was calculated. To check the presence of significance of genetic variability within the generations (F_2 and back crosses) and between different generations under investigation, the individual as well as combined data from all the generations was subjected to analysis of variance. The test of existence or absence of epistasis is required for the evaluation of genetic effects and further aids in selecting the analytical approach. The scaling test (A, B, C, D) provided by MATHER (1949) and HAYMAN and MATHER (1955) used to test for the presence of epistasis was estimated using the observed means of the six generations and their standard errors. The significance of any one of the A, B, C or D scaling tests revealed the presence of non-allelic interactions (epistasis).

To determine the kind of gene effects, the generation means were analysed. The [m], [d], and [h] parameters of a three-parameter model (simple additive dominating model) known as joint scaling tests, which were introduced by CAVALLI (1952), were estimated to produce a test for the model's goodness of fit. The adequacy of the simple additive dominance model (mean, additive, and dominance effects) was determined by χ^2 test. Whenever, χ^2 value was not significant, additive dominant model fit well to estimate the genetic effects. The significance of [d] highlights the presence of additive genetic effects and points towards the improvement through selection. The significance of [h] highlights the presence of dominant genetic effects and points towards the improvement through heterosis breeding. However, if calculated χ^2 value was significant, epistatic interactions were present for that trait. The interactions were also estimated using a six-parameter model.

Significant estimates of χ^2 for some quantitative traits suggested the existence of epistasis (inadequacy of additive-dominance model). Following the confirmation of the presence of epistasis, the data were subjected to the joint scaling test, or six parameter model, as suggested by MATHER and JINKS (1982). This included new estimates of m, [d], and [h] as well as non-allelic interactions ([i], [j], and [l] parameters). The t-test was used to determine the significance of the genetic parameters (m, [d], [h], [i], [j], and [l]). Because the degrees of freedom in the full six-parameter model were lowered to zero, the chi-square adequacy test could not be performed. However, using chi-square test, if the estimation of the six parameters revealed that one or two interaction parameters were not significant, those parameters were removed, and the remaining parameters were re-estimated in addition to the adequacy of the model.

Statistical analysis for Inheritance of gynoecium

For qualitative traits, the observed data of six generations were subjected to χ^2 test in order to find goodness of fit as per Mendelian ratios of F_2 and backcross generations as suggested by PANSE and SUKHATME (1985).

The χ^2 distribution in F_2 , BC_1P_1 and BC_1P_2 was used for phenotypic classes as:

$$\chi^2 = \frac{(O - E)^2}{E} \quad \text{at } 2-1=1 \text{ d.f. for each } F_2 \text{ and backcross}$$

Where O = Observed frequency

E = Expected frequency

RESULTS AND DISCUSSION

Generation mean of all traits

While the F_1 means of all three crosses exceeded both of their corresponding parental means for the number of fruits per plant and the yield of marketable fruits per plant, indicating over-dominance for these two traits (Table 1), the mean values of the F_1 of all three crosses were intermediate between their respective parental means, suggesting partial dominance for fruit length, fruit diameter, and fruit weight.

Table 1 Generation means of different cucumber hybrid combinations

Crosses	Generations						M.P.
	P ₁	P ₂	F ₁	F ₂	B ₁	B ₂	
Fruit length (cm)							
GY-14 × Pusa Uday	10.560 ±0.225	16.111 ±0.279	15.447 ±0.239	11.956 ±0.218	12.973 ±0.251	14.927 ±0.169	13.335
GY-14 × Punjab Naveen	10.560 ±0.225	17.746 ±0.279	15.191 ±0.188	12.218 ±0.253	13.094 ±0.217	15.260 ±0.144	14.153
GY-14 × Pant Kheera-1	10.560 ±0.225	19.037 ±0.322	16.108 ±0.331	13.448 ±0.220	13.728 ±0.239	16.586 ±0.284	14.798
Fruit diameter (cm)							
GY-14 × Pusa Uday	5.634 ±0.154	4.959 ±0.142	5.152 ±0.152	4.941 ±0.090	5.250 ±0.148	4.814 ±0.074	5.296
GY-14 × Punjab Naveen	5.634 ±0.154	5.322 ±0.103	5.725 ±0.105	5.368 ±0.088	5.493 ±0.087	5.205 ±0.056	5.478
GY-14 × Pant Kheera-1	5.634 ±0.154	4.882 ±0.079	5.426 ±0.131	4.973 ±0.077	5.283 ±0.103	5.030 ±0.084	5.258
Fruit weight (g)							
GY-14 × Pusa Uday	153.162 ±2.381	260.151 ±2.566	230.905 ± 4.292	213.633 ±2.893	207.763 ±2.786	239.112 ±2.636	206.656
GY-14 × Punjab Naveen	153.162 ±2.381	265.305 ±3.620	233.979 ±3.461	217.007 ±2.456	211.462 ±2.508	241.342 ±1.452	209.233
GY-14 × Pant Kheera-1	153.162 ±2.381	264.266 ±3.834	228.846 ±2.611	219.466 ±2.355	208.398 ±3.896	236.403 ±2.272	208.714
Number of fruits per plant							
GY-14 × Pusa Uday	8.200 ± 0.327	5.400 ±0.340	8.700 ±0.300	7.725 ±0.196	8.250 ±0.204	6.650 ±0.310	6.800
GY-14 × Punjab Naveen	8.200 ±0.327	5.700 ±0.367	9.000 ±0.333	7.950 ± 0.193	7.900 ±0.280	6.450 ±0.246	6.950
GY-14 × Pant Kheera-1	8.200 ±0.327	5.900 ±0.348	8.600 ±0.340	7.625 ±0.188	7.650 ±0.274	6.700 ±0.341	7.050
Yield of marketable fruits per plant (g)							
GY-14 × Pusa Uday	1239.647±41.30	1386.096±80.42	1979.704±46.23	1622.288±34.92	1695.304±44.14	1574.628 ±78.11	1312.871
GY-14 × Punjab Naveen	1240.809±45.69	1490.757±89.19	2076.509±54.15	1695.147±31.22	1647.599±52.60	1538.932 ±57.26	1365.202
GY-14 × Pant Kheera-1	1240.810±45.69	1541.509±90.50	1942.008±60.33	1648.346±36.13	1563.335±40.47	1559.621 ±71.08	1390.578

Scaling and Joint Scaling test*Fruit length*

The presence of epistatic interactions was shown by the significance of one or more scaling test components (A, B, C, D) in each of the three crossings (Table 2).

Table 2. Scaling test for different characters

Character	Cross	Scales				
		A	B	C	D	
Fruit length	GY-14 × Pusa Uday	-0.062 ±0.600	-1.703 ±0.500**	-9.741 ±1.057**	-3.988 ±0.531**	
	GY-14×Punjab Naveen	0.437 ±0.524	-2.418 ±0.444**	-9.815 ±1.137**	-3.917 ±0.569**	
	GY-14 × Pant Kheera-1	0.788 ±0.623	-1.974 ±0.731**	-8.020 ±1.169**	-3.417 ±0.576**	
	Fruit diameter	GY-14 × Pusa Uday	-0.286 ±0.367	-0.483 ±0.255	-1.134 ±0.515*	-0.183 ±0.244
Fruit diameter	GY-14×Punjab Naveen	-0.374 ±0.255	-0.637 ±0.185**	-0.933 ±0.449*	0.039 ±0.204	
	GY-14 × Pant Kheera-1	-0.495 ±0.289	-0.248 ±0.227	-1.476 ±0.439**	-0.367 ±0.203	
	Fruit weight	GY-14 × Pusa Uday	31.460 ±7.425**	-12.832 ± 7.266	-20.591 ±14.826	-19.609 ±6.941**
	Fruit weight	GY-14×Punjab Naveen	35.783 ±6.542**	-16.599 ±5.789**	-18.396 ± 12.773	-18.790 ±5.703**
GY-14 × Pant Kheera-1		34.788 ±8.556**	-20.306 ±6.493**	2.744 ±11.678	-5.869 ±6.521	
Number of fruits per plant		GY-14 × Pusa Uday	-0.400 ±0.602	-0.800 ±0.768	-0.100 ±1.094	0.550 ±0.540
		GY-14×Punjab Naveen	-1.400 ±0.729	-1.800 ±0.698**	-0.100 ±1.131	1.550 ±0.536**
	GY-14 × Pant Kheera-1	-1.500 ±0.723*	-1.100 ±0.838	-0.800 ±1.122	0.900 ±0.577	
	Yield of marketable fruits per plant	GY-14 × Pusa Uday	171.257 ±107.879	-216.544 ±181.704	-95.999 ±190.361	-25.356 ±113.706
GY-14×Punjab Naveen		-22.121 ±126.843	-489.402 ±154.940**	-103.998 ±193.309	203.762 ±99.728*	
GY-14 × Pant Kheera-1		-56.147 ±110.817	-364.274 ±179.009*	-72.950 ±213.842	173.736 ±109.145	

Furthermore, the joint scaling test's three-parameter model's substantial chi square value indicated the existence of epistatic interactions and the insufficiency of the basic additive-dominance model (as χ^2 value was significant) in explaining the variation observed between generations (Table 3). Both the dominant and additive effects were significant, with the dominance impact being larger than the additive, according to the three parameter model of the

joint scaling test. However, because all three types of epistatic interactions were significant, it was not possible to assess the suitability of the best fit model. Nonetheless, the additive \times additive gene interaction had a greater magnitude, suggesting its significance concerning the remaining interactions. Different signs of [h] and [l] components depict duplicate type of epistasis. For improvement of this trait selection of transgressive segregates using pedigree method can be employed to get longer fruits as additive \times additive genetic variance is present. Positive value of additive \times additive component indicates the association of favourable alleles. Similar findings were also given by BASAVARAJESHWARI *et al.* (2014); MUNSHI *et al.* (2006) and CHOUDHARY and SINGH (2010). Duplicate type of epistasis suggested that selection should be mild in earlier generations and intense in later generations.

Fruit diameter

The magnitude and signs of all the three interaction parameters were found to be vary from cross to cross showing lot of variability for the character. In cross Gy-14 \times Pusa Uday, among scaling test, only one component of scaling test i.e. C component was recorded to be significant (Table 2) but the joint scaling test's three-parameter model's chi square goodness of fit was non-significant, indicating that there were no epistatic interactions and that the data could be described by a simple additive dominance model (Table 3). The additive effects were significant in the joint scaling test best fit model, suggesting their significance in the inheritance of this trait. As none of the epistatic interactions were significant, therefore, more generations need to be evaluated for this cross.

The presence of non-allelic interactions is indicated by the significance of scaling test components in the crosses Gy-14 \times Pant Kheera-1 and Gy-14 \times Punjab Naveen (Table 3). Further significance of chi square value for goodness of fit of simple additive dominance model suggests that differences among generation means could not be explained on basis of three parameter model. In cross Gy-14 \times Punjab Naveen, both dominance and additive gene action were significant but value of dominance component was higher. Among digenic interactions only dominance \times dominance gene effect was significant which can be exploited through heterosis breeding for further improvement in the trait. Duplicate type of epistasis was observed for this trait pertaining to the opposite signs of dominance [h] and dominance \times dominance [l]. Both dominance and additive gene effects were significant in the Gy-14 \times Pant Kheera-1 cross, however the dominance effects were greater than the additive effects. In digenic interactions, the presence of only additive \times additive type of epistatic interaction governing the trait was found, that can be exploited by using pedigree method followed by selection for improvement in the character. Similar findings were also reported by MALAV *et al.* (2018), SHARMA *et al.* (2000) and TIWARI *et al.* (2011).

Fruit weight

Scaling test analysis of various generations in all the three crosses revealed the existence of epistatic interactions and the shortcomings of the basic additive dominance model due to significance of atleast one of the components of scaling tests (Table 2). Furthermore, significant chi square value of three parameter model of joint scaling test indicated that simple additive dominance model was not adequate to explain the variation among generations (Table

3). The joint scaling test's three-parameter model revealed that this trait's dominance and additive effects were both significant with dominance effects higher in magnitude than additive except in cross Gy-14 × Pant Kheera-1, where additive effects were higher in magnitude. The appropriateness of the best fit model could not be verified because, among the epistatic effects in the six parameter model, all three interaction parameters were significant in the crosses Gy-14 × Pusa Uday and Gy-14 × Punjab Naveen. The dominance × dominance gene interaction had a greater magnitude, suggesting its significance in relation to the other interactions. The presence of duplicate epistasis was revealed by the opposing indications of [h] and [l]. Due to a significant and greater dominance gene effect, heterosis breeding can be used to improve this trait. Whereas in cross Gy-14 × Pant Kheera-1, the presence of only additive × dominance type of epistatic interaction was found to be governing the trait which suggests utilizing both the heterosis breeding and pedigree technique to choose desirable segregants in order to improve the trait. The findings confirm those of VIDHYA and KUMAR (2014), MOUSHUMI and SIROHI (2006), RAI *et al.* (2018).

Number of fruits per plant

In crosses Gy-14 × Pusa Uday and Gy-14 × Pant Kheera-1, non-significance of all the components (A, B, C and D) of scaling tests indicated the absence of epistasis (i.e. presence of only additive or dominance effects) (Table 2). Also, non-significant chi square value of simple additive-dominance model revealed the adequacy of three parameter model of joint scaling test to explain the variation present among generations. Both dominance and additive effects were significant in the best fit model of the joint scaling test, however the dominance effects were greater in size than the additive effects which may be due to the dominance of increaser alleles indicating the usefulness of heterosis breeding for improvement in the trait (Table 3). But in cross Gy-14 × Punjab Naveen, the significance of B and D components of scaling test revealed non-allelic interactions and the three-parameter model's failure. Further, the inadequacy of simple additive dominance model to explain the variation among different generations was indicated by significant chi-square value of simple additive-dominance model. The three parameter model of joint scaling tests showed that this trait had both dominance and additive effects; however, the degree of dominant gene action was greater. In digenic interactions, only two interaction parameters i.e. additive × additive [i] and dominance × dominance [l] were significant in the six parameter model, but dominance × dominance effect had higher magnitude. Opposite signs of dominance effect and dominance × dominance effect indicated duplicate type of epistasis for this character. The significance of dominance × dominance gene effects when combined with duplicate epistasis type suggests that recurrent selection is beneficial in identifying desirable segregants. The results were in accordance with KUMAR *et al.* (2013), RAI *et al.* (2018), MISHRA *et al.* (2015), TIWARI *et al.* (2011).

Yield of marketable fruits per plant

The lack of epistasis in the crosses Gy-14 × Pant Kheera-1 and Gy-14 × Pusa Uday was revealed by the non-significance of all the scaling tests components (A, B, C, and D) (Table 2). Also, non-significant chi square value of three parameter model of joint scaling test revealed adequacy of

three parameter model and absence of epistasis (Table 3). So for this cross the mean value is constituted by only additive and dominance effects as non- allelic interactions are absent.

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

Crosses	Components							Epistasis
	m	d	h	χ^2	i	j	l	
Fruit length								
GY-14 × Pusa Uday	5.359±1.077**	-2.776±0.179**	16.299±2.587*	90.640	7.976±1.062**	1.641±0.704*	-6.211±1.608**	D
GY-14 × Punjab Naveen	6.319±1.152**	-3.593±0.179**	14.725±2.620*	92.512	7.834±1.138**	2.855±0.633**	-5.853±1.543**	D
GY-14 × Pant Kheera-1	7.965±1.168**	-4.238±0.196**	13.791±2.917*	64.165	6.834±1.151**	2.762±0.839**	-5.648±1.889**	D
Fruit diameter								
GY-14 × Pusa Uday	5.186±0.092**	0.377±0.085**	-0.277±0.175	8.169	-	-	-	-
GY-14 × Punjab Naveen	5.502±0.089**	0.218±0.068**	-0.862±0.325**	13.890	-	-	1.086±0.317**	D
GY-14 × Pant Kheera-1	4.523±0.201**	0.340±0.072**	0.911±0.302**	11.503	0.716±0.218**	-	-	-
Fruit weight								
GY-14 × Pusa Uday	167.438±13.992*	-	121.314±33.33	35.054	39.219±13.882	44.292±8.430**	-57.847±21.333**	D
GY-14 × Punjab Naveen	171.654±11.609*	-	119.089±27.24	56.134	37.580±11.405	52.382±7.236**	-56.764±17.250**	D
GY-14 × Pant Kheera-1	209.716±1.985**	55.996±2.206**	20.472±3.432*	30.530	-	51.161±9.525**	-	-
Number of fruits per plant								
GY-14 × Pusa Uday	6.715 ±0.203**	1.418 ± 0.196**	1.848 ±0.374**	1.582	-	-	-	-
GY-14 × Punjab Naveen	10.079 ±1.098**	1.311 ±0.205**	-7.438	11.814	-3.136	-	6.358 ±1.866**	D
GY-14 × Pant Kheera-1	6.873 ±0.210**	1.073 ±0.209**	1.356 ±0.398**	5.431	-	-	-	-
Yield of marketable fruits per plant								
GY-14 × Pusa Uday	1292.026±37.990	-28.260±38.983	696.152±63.12	5.335	-	-	-	-
GY-14 × Punjab Naveen	1773.308±205.65	124.974±50.109	615.846±552.8	12.440	407.525±199.4	467.281±185.01	919.047±366.221*	D
GY-14 × Pant Kheera-1	1353.285±42.246	112.551±41.586	554.952±74.83	4.538	-	-	-	-

* P=0.05%, ** P=0.01%

Both dominance and additive parameters were significant in the joint scaling test's three-parameter model, with dominance gene action having greater magnitude than additive. The cross Gy-14 × Punjab Naveen revealed non-allelic interactions and the failure of the three parameter model, as indicated by the significant B and D components of the scaling test (Table 2). The simple additive-dominance model was also confirmed to be inadequate by the significant value of chi-square test of three parameter model of joint scaling test. Only the additive effects were shown to be significant in the joint scaling test best fit model, suggesting their significance in trait inheritance. All three of the digenic interactions—additive × additive [i], additive × dominance [j], and dominance × dominance effects [l]—were significant in the six parameter model (Table 3). So, it was not possible to evaluate the best fit model's adequacy. Compared to other epistatic interactions, the dominance × dominance epistatic interaction has a greater magnitude. Different [h] and [l] indications indicate duplicate type of epistasis. More improvement in this trait can be achieved by heterosis breeding because of the greater magnitude of dominance and the dominance × dominance kind of interaction. Several breeders also analysed generation means for yield per plant and reported the presence of dominance gene effects controlling the trait (KUMAR *et al.*, 2013; MUNSHI *et al.*, 2006; RAI *et al.*, 2018).

Yield of marketable fruits per plant

The lack of epistasis in the crosses Gy-14 × Pant Kheera-1 and Gy-14 × Pusa Uday was revealed by the non-significance of all the scaling tests components (A, B, C, and D) (Table 2). Also, non-significant chi square value of three parameter model of joint scaling test revealed adequacy of three parameter model and absence of epistasis (Table 3). So for this cross the mean value is constituted by only additive and dominance effects as non-allelic interactions are absent. Both dominance and additive parameters were significant in the joint scaling test's three-parameter model, with dominance gene action having greater magnitude than additive. The cross Gy-14 × Punjab Naveen revealed non-allelic interactions and the failure of the three parameter model, as indicated by the significant B and D components of the scaling test (Table 2). The simple additive-dominance model was also confirmed to be inadequate by the significant value of chi-square test of three parameter model of joint scaling test. Only the additive effects were shown to be significant in the joint scaling test best fit model, suggesting their significance in trait inheritance. All three of the digenic interactions—additive × additive [i], additive × dominance [j], and dominance × dominance effects [l]—were significant in the six parameter model (Table 3). So, it was not possible to evaluate the best fit model's adequacy. Compared to other epistatic interactions, the dominance × dominance epistatic interaction has a greater magnitude. Different [h] and [l] indications indicate duplicate type of epistasis. More improvement in this trait can be achieved by heterosis breeding because of the greater magnitude of dominance and the dominance × dominance kind of interaction. Several breeders also analysed generation means for yield per plant and reported the presence of dominance gene effects controlling the trait (KUMAR *et al.*, 2013; MUNSHI *et al.*, 2006; RAI *et al.*, 2018).

Inheritance of gynoeocious sex expression

In the present experiment to study the genetics of gynoeocious sex expression using the classical Mendelian ratio, cucumber plants were divided into two sex expression categories:

gynoecious and monoecious. For this study, F₂ and backcross generations of all the three crosses were subjected to chi square (χ^2) analysis. The current experiment's findings agreed with those of LOU *et al.* (2007); MIAO *et al.* (2011); WIN *et al.* (2015); PATI *et al.* (2015) and JAT (2016).

Gy-14 × Pusa Uday : The fact that every plant in the F₁ generation was gynoecious indicates that gynoecy predominates over monoecy. In the F₂ population, 25 plants displayed gynoecious, whereas 15 plants displayed monoecious behavior. This clearly showed an excellent fit to a Mendelian ratio, i.e., 3 (gynoecious): 1 (monoecious), with a probability of 0.068 and a chi-square value of 3.33 (Table 4). By examining the backcross population {(Gy-14 × Pusa Uday) × Pusa Uday}, which had 12 gynoecious and 8 monoecious plants in a ratio of 1:1 ($\chi^2 = 0.80$ P = 0.371), the monogenic dominant hypothesis was further supported. When Gy-14 is employed as the gynoecious line, the chi-square goodness of fit study showed that the gynoecious trait is controlled by monogenic dominance.

Table 4. Chi-square (χ^2) analysis of F₂ and backcross population derived from different crosses for inheritance of gynoecious sex expression in cucumber

Generation	Total number of plants	Observed ratio		Expected ratio	χ^2 -value	P value
		Gynoecious Plant	Monoecious Plant			
Six generations of "Gy-14 × Pusa Uday"						
P ₁ (Gy-14)	10	10	0	-	-	-
P ₂ (Pusa Uday)	10	0	10	-	-	-
F ₁ (Gy-14 × Pusa Uday)	10	9	1	-	-	-
F ₂	40	25	15	3:1	3.33	0.068
B ₁ {(Gy-14 × Pusa Uday) × Gy-14}	20	20	0	-	-	-
B ₂ {(Gy-14 × Pusa Uday) × Pusa Uday}	20	12	8	1:1	0.80	0.371
Six generations of "Gy-14 × Punjab Naveen"						
P ₁ (Gy-14)	10	10	0	-	-	-
P ₂ (Punjab Naveen)	10	0	10	-	-	-
F ₁ (Gy-14 × Punjab Naveen)	10	10	0	-	-	-
F ₂	40	27	13	3:1	1.20	0.273
B ₁ {(Gy-14 × Punjab Naveen) × Gy-14}	20	20	0	-	-	-
B ₂ {(Gy-14 × Punjab Naveen) × Punjab Naveen}	20	13	7	1:1	1.80	0.179
Six generations of "Gy-14 × Pant Kheera-1"						
P ₁ (Gy-14)	10	10	0	-	-	-
P ₂ (Pant Kheera-1)	10	0	10	-	-	-
F ₁ (Gy-14 × Pant Kheera-1)	10	10	0	-	-	-
F ₂	40	26	14	3:1	2.13	0.144
B ₁ {(Gy-14 × Pant Kheera-1) × Gy-14}	20	20	0	-	-	-
B ₂ {(Gy-14 × Pant Kheera-1) × Pant Kheera-1}	20	14	6	1:1	3.20	0.074

Gy-14 × Punjab Naveen: Every plant in the F₁ progeny displayed gynoecious sex expression. In F₂ generation, 27 plants showed gynoecious behaviour and 13 plants showed monoecious behaviour, which perfectly fit to 3:1 (gynoecious: monoecious) Mendelian segregation ratio $\chi^2 = 1.20$, $P = 0.273$ indicating the monogenic dominant control of gynoecious sex expression. The frequency distribution of gynoecious and monoecious plants of back cross progenies were also tested for their best fit with classical Mendelian ratios (*i.e.* 1:1 in back cross progenies with a monoecious parent). In the B₂ generation (*Gy-14 × Punjab Naveen*) × Punjab Naveen, 13 plants showed gynoecious and 07 were monoecious. The χ^2 value indicated a good fit to 1:1 ratio ($\chi^2 = 1.80$ $P = 0.179$) (Table 4.15). Consequently, this population's results demonstrated that gynoecey is controlled by single dominant gene in nature. Similar results were also corroborated by MIAO *et al.* (2011); PATI *et al.* (2015); WIN *et al.* (2015), JAT (2016).

Gy-14 × Pant Kheera-1: Given that every plant in the F₁ generation was gynoecious, gynoecey is clearly dominant over monoecy. 26 plants in the F₂ population displayed gynoeceum, whereas 14 plants displayed monoecious behavior. This suggested a strong fit to a Mendelian ratio of 3:1 (gynoecious: monoecious), with a probability of 0.144 and a chi-square value of 2.13 (Table 4). The back cross generation B₂ {(Gy-14 × Pant Kheera-1) × Pant Kheera-1}, which had 12 gynoecious and 8 monoecious plants, further supported the monogenic dominating model with a strong fit into the Mandelian ratio of 1:1 ($\chi^2 = 0.80$ $P = 0.371$). The chi-square goodness of fit study makes it abundantly evident that a monogenic dominant gene controls gynoecey.

CONCLUSIONS

The study's overall findings demonstrated the importance of additive, epistatic, and dominant components in the majority of crosses for various quantitative traits. From the present experiment, it was concluded that fruit length and fruit diameter were controlled by additive gene effects and individual plant selection can be used for improvement of these traits. However, dominance gene action was observed for fruit weight and it can be improved through biparental mating and recurrent selection breeding method. Epistatic components, however, were not significant in two of the three total crosses for the number of fruits per plant or the yield of marketable fruits per plant. However, in one cross with both of these characters, both additive and non-additive genetic components were present, and selecting transgressive segregants followed by heterosis breeding can improve these traits. The evaluation of various gene effects served as a test for gene action and helped decipher the genetic makeup of various traits. As also noted in the current study, the estimations derived from each cross may differ in degree from one another and may not be relevant to the parental population. Consequently, while choosing a breeding strategy and doing selection, each cross needs to be taken into account separately.

ACKNOWLEDGEMENTS

The Punjab Agricultural University in Ludhiana, Punjab, India, the parent university, provided financial support for the research project.

Received, October 10th, 2023

Accepted April 25th, 2024

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**KORIŠĆENJE GINOECIJSKIH LINIJA KRSTAVCA (CUCUMIS SATIVUS L.)
ZA ISTRAŽIVANJE NASLEĐENJA GINOECIJUMA, PRINOSA PLODA I NJEGOVIH
KONTRASTNIH OSOBINA**

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Izvod

Da bi se utvrdilo nasleđe prinosa ploda i njegovih komponentnih osobina u krstavcu, tri komercijalne jednodomne sorte (Pusa Udai, Punjab Naveen i Pant Kheera-1) su ukrštene sa ginodomnim roditeljem (Gy-14) i razvile su šest generacija svakog ukrštanja. Test skaliranja i triparametarski model testa skaliranja otkrili su prisustvo epistaze za većinu osobina. Duplikat epistaze je pronađen u većini osobina, što će smanjiti neto dobitak od heterozigotnosti zbog epistatičkih efekata i otkazivanja dominacije. Težina ploda u Gy-14 × Pant Kheera-1 pokazala je veći aditivni × dominantan tip među epistatičkim interakcijama, dok su dužina ploda u svim ukrštanjima i širina ploda u Gy-14 × Pant Kheera-1 pokazali veći aditivni × aditivni tip interakcije, što ukazuje na upotrebu pedigre metode za poboljšanje ovih osobina. Utvrđeno je da prečnik ploda, težina ploda, broj plodova po biljci i prinos po biljci u Gy-14 × Punjab Naveen i težina ploda u Gy-14 × Pusa Udai pokazuju veću interakciju dominacije × dominacije. Shodno tome, ove osobine mogu biti dodatno poboljšane putem odgovarajućih ukrštanja. Utvrđeno je da prečnik ploda, težina ploda, broj plodova po biljci i prinos po biljci u Gy-14 × Punjab Naveen i težina ploda u Gy-14 × Pusa Udai pokazuju veću interakciju dominacije × dominacije. Shodno tome, ove osobine mogu biti dodatno poboljšane putem heterozisnog uzgoja u odgovarajućim ukrštanjima.

Primljeno 10.X.2023.

Odobreno 25. IV 2024.