

GENERATION MEAN ANALYSIS OF UNADAPTED LANDRACES AND WILD RELATIVES OF CUCUMBER (*Cucumis sativus* L.) FOR EARLINESS AND DOWNY MILDEW

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The choice of breeding method for the genetic improvement of any crop largely depends on understanding the genetics and inheritance patterns of the traits involved. The knowledge pertaining to gene actions and interactions is likely to direct and strengthen the crop breeding programmes. With this objective the present investigation aims to elucidate the nature and magnitude of gene action associated for various earliness and disease trait through generation mean analysis (GMA) with six generations (P₁, P₂, F₁, F₂, B₁ and B₂) of two crosses involving three diverse parents of cucumber. The studies were undertaken at Experimental Research Farm of the Department of Vegetable Science, Dr YSP and UH&F Nauni, Solan, HP (India) under open field conditions. Experimental results revealed that non-allelic interactions were present for all the traits considered in both the crosses as evident from individual scaling and joint scaling test. In the inheritance of most of traits except a few, both additive and non-additive gene actions contribute significantly therefore, the breeding methods reciprocal recurrent selection/ bi-parental mating could be exploited for the improvements of the traits. Earliness traits *viz.*, node number bearing first female flower and days to first fruit set was mainly governed by dominance (h) and hence these characters can be improved through heterosis breeding. The duplicate type of epistasis influenced all traits in both cross-combinations; indicating the mild selection intensity in the earlier generations while intense in later generations.

Keywords: Bi-parental mating, duplicate epistasis, joint scaling test, non-allelic interactions, reciprocal recurrent selection, Scaling

INTRODUCTION

In India, from north Western Himalayan to southern peninsular region including riverbeds and floating gardens in Dal lake of Kashmir valley, cucumber (2n=2x=14) is widely

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grown as commercial salad crop. It is a low energy and high water content vegetable and also has soothing, cleansing and softening properties which are important for the cosmetics industry (YADAV *et al.*, 2012). In spite of its economic importance as a common vegetable consumed by many people in the country, not many suitable varieties are available for commercial cultivation. But very little scientific attention has been paid for the genetic improvement and commercial exploitation of this crop in our country. Moreover, the available open-pollinated cultivars have low yield potential, though the replacement of inbred lines/varieties by hybrids has remarkably increased yield, while the genetic gain rate has been reduced due to low genetic diversity within cultivated cucumber (KUMARI *et al.*, 2021). The genetic variation present in cultivated varieties of *Cucumis sativus* is not sufficient to solve the specific problems associated with its cultivation. Therefore, the incorporation of quantitatively inherited characters into commercially adapted cultivars from exotic/wild germplasm can be an effective way to obtain greater variation and response to selection. Information about the mode of genetic parameters, interactions and heritability different traits would be of immense help for a plant breeder to decide about the proper breeding procedure to be adopted and the characters on which the selection has to be made for genetic improvement of cucumber or any other crop. Gene action can vary from one population to another in the same crop and genetic studies are essential for a given genetic stock before we employ any breeding method for crop improvement. Out of various biometrical approaches available to estimate different genetic parameters, generation mean analysis, is an efficient tool involved first degree statistics and a simple but useful technique for characterizing gene effects for a polygenic character in interacting and non-interacting crosses which, it determines the presence and absence of non-allelic interactions. The first order statistics estimates are more robust and reliable than those of based on second order statistics. The greatest merit of generation mean analysis is that it helps in the estimation of epistatic gene effects namely additive \times additive (i), additive \times dominance (j) and dominance \times dominance (l). Therefore, present investigation was planned to derive information on the nature and magnitude of generation means and gene effects for earliness and disease trait (downy mildew) in two cross-combinations of cucumber.

MATERIALS AND METHODS

Description of experimental site and planting material used

The site where the research was conducted is situated at Nauni, about 14 km away from Solan city at an altitude of 1,270 meters above mean sea level lying between 35.5° North latitude and 77.8° East longitude. The farm area falls in the mid hill zone of Himachal Pradesh. Soil is sandy loam to clay loam comprising of sand (46.09 %), silt (32.12 %) and clay (25.01 %). The pH of the soil ranged from 6.85-7.04. The genetic material was comprised of 3 genetically diverse lines (LC-1-1, K-75 and *Cucumis hardwickii*). LC-1-1 is a local selection collected from mid-hills of Himachal Pradesh falls in foot hills of Shivalik regions in Western Himalaya. It bears fruits at early node like gynoeocious lines and very popular among the rural people of Himachal Pradesh. K-75 is a popular variety commercially grown in hilly regions bear light green crisp fruit released by Department of Vegetable Science, University of Horticulture and Forestry, Nauni-Solan, HP, India. *Cucumis hardwickii* is a wild relative of cucumber and is found in the natural habitats of Himalayan foothills of India. It characterizes with higher number

of lateral branches and sequential fruiting habit along with a resistant source against downy mildew disease which is considered useful for improving fruit yield.

Crossing programme

To ascertain the genetics of various horticultural traits, six generations (P₁, P₂, F₁, F₂, BC₁ & BC₂) of two crosses were developed by utilizing the three diverse parent's (LC-1-1, K-75 and *C. hardwickii*). Parental lines were intercrossed to produce two F₁ hybrids *viz.*, LC-1-1 × K-75 and LC-1-1 × *C. hardwickii* by using the recommended procedure of hand emasculation and pollination during *Kharif* season of 2015. Each F₁ was selfed to obtain F₂ seeds and simultaneously backcrossed to both the parents to produce BC₁ and BC₂ seeds during rainy season of 2016 in protected conditions.

Experimental layout

During *Kharif* season of 2017, the experimental material comprising of six generations (P₁, P₂, F₁, F₂, BC₁ & BC₂) of two crosses was evaluated in a randomized complete block design with three replications under natural farm conditions. Row to row and plant to plant spacing of 100 cm × 75 cm was kept in a plot having size 4.0 m × 3.0 m, which accommodated 16 plants per plot. The standard cultural practices as recommended in Package of Practices of Vegetable Crops were followed to raise the healthy crop stand (ANONYMOUS, 2016).

Data recording

The observation recorded were on ten randomly selected fruits per replication for earliness traits *viz.*, days to first flower appearance, node number bearing first female flower, days to first female flower appearance, days to first fruit set, days to first fruit picking and disease trait *i.e.* severity of downy mildew.

Disease severity for downy mildew was recorded by adopting 0-4 scale; where 0= no disease, 1=1-10 scattered small lesions per leaf and less than 25 per cent of leaf area turned yellowish, 2=11-20 scattered small lesions per leaf and yellowing covered >25-50 per cent of leaf area, 3=21-40 scattered or coalesced lesions per leaf and yellowing covered >50 per cent of leaf area, 4=more than 40 coalesced lesions per leaf, the infected area turned brown and died and yellowing covered >75 per cent of leaf area for downy mildew given by REUVENI (1983). Disease severity index (%) for downy mildew was calculated by using the formula:

$$\text{Disease severity index (\%)} = \frac{\sum(n \times v)}{Z \times N} \times 100$$

Where, n=number of leaves in each category, v=numerical value of each category, Z=numerical value of highest category and N=total number of leaves in sample

Statistical analysis of recorded data

The precise knowledge of additive, dominance and epistatic components of genetic variance for important metric traits is essential for achieving success in breeding programmes.

Generation mean analysis provides information on the relative importance of additive, dominance and non-allelic genetic interactions {additive \times additive (i), dominance \times dominance (j) and additive \times dominance (l)} effects to determining genotypic values of the individuals.

Simple scaling test

To test the adequacy of additive-dominance model, simple scaling tests (A, B, C and D) were carried out as described by HAYMAN and MATHER (1955). Significant deviation of A, B, C, D values from zero indicates the inadequacy of additive-dominance model and presence of epistasis justifying the use of six parameter model.

Joint scaling test

The main drawback of scaling test is that out of six populations only three or four are included in the test at a time. In order to overcome this problem another test, known as joint scaling test has been developed. This permits any combination of the six populations at a time. Moreover, joint scaling test also provides estimates of three genetic parameters, viz., m, d and h. This test also provides test for the model if more than three families are available.

Estimation of gene effects through six generations means

When simple additive-dominance model was inadequate, a weighted six parameter model which included digenic epistatic effects was fitted. Six parameter model was used to estimate the various gene effects including non-allelic interaction parameters i.e., additive \times additive (i), additive \times dominance (j) and dominance \times dominance (l) as described by JINKS and JONES (1958) and MATHER and JINKS (1982). The type of epistasis was determined only when (h) and (l) effects were significant, the same and opposite signs of these effects indicated complementary and duplicate epistasis, respectively (KEARSEY and POONI, 1996).

Estimation of component of variance and heritability

The estimates of dominance ratio, narrow sense heritability, heterosis (mid-parent and better parent) and potence ratio were calculated using the following equation. These estimates were obtained by using corresponding generation variances.

Environmental variance (VE)	$= \frac{1}{4} [s^2P_1 + s^2P_2 + 2s^2F_1]$
Additive variance (VA)	$= [s^2F_2 - (s^2B_1 + s^2B_2)]$
Dominance variance (VD)	$= [(s^2B_1 + s^2B_2) - s^2F_2 - VE]$
Mid-parent heterosis (%)	$= [(\bar{F}1 - \overline{MP}) / \overline{MP}] \times 100$
Better parent heterosis (%)	$= [(\bar{F}1 - \overline{BP}) / \overline{BP}] \times 100$
Dominance ratio	$= 4VD / 2VA$
Narrow sense heritability (h^2n)	$= \frac{2s^2F_2 - (s^2BC_1 + s^2BC_2)}{s^2F_2}$

where s^2 , MP and BP represent the variance, mid-parent and better parent means, respectively.

RESULTS AND DISCUSSION

For various earliness and disease trait the nature of gene action was estimated with generation mean analysis by recording the data on six generations of two cucumber crosses. The mean performance of the six generations including P₁, P₂, F₁, F₂, BC₁ and BC₂ for different traits presented in Table 1. The values of individual scaling tests, joint scaling tests and estimates of gene effects namely m, d, h, i, j and l for different traits in two crosses were estimated (Table 2). The information on given estimates in genetic architecture of the various traits are essential for judicious selection of parents and breeding methodology. Though non-segregating generations consist of homogeneous population and the segregating generations consist of heterogeneous population, the number of plants analyzed was 10 plants for parents and F₁'s and 20 plants for F₂'s and back crosses in each replication.

Table 1. Estimates of different generations mean and their standard error for six quantitative traits in two crosses of cucumber

Traits	Generations					
	P ₁	P ₂	F ₁	F ₂	BC ₁	BC ₂
Days to first flower appearance						
Cross-I	47.34± 0.22	51.78 ± 0.18	42.66 ± 0.22	42.20 ± 0.15	45.77 ± 0.19	47.30± 0.14
Cross-II	47.34± 0.58	48.97 ± 0.16	44.26± 0.45	44.72± 0.20	46.83± 0.15	48.57± 0.22
Node number bearing first female flower						
Cross-I	4.12± 0.05	6.23± 0.15	3.26± 0.13	3.10± 0.095	4.05± 0.10	4.25± 0.27
Cross-II	4.12± 0.34	12.86 ± 0.10	7.39± 0.38	7.04± 0.05	7.59± 0.56	7.92± 0.06
Days to first female flower appearance						
Cross-I	49.52± 0.28	55.43 ± 0.38	45.11± 0.09	45.41± 0.21	46.20± 0.00	47.31± 0.22
Cross-II	49.52± 0.28	51.90± 0.25	47.83± 0.47	45.60± 0.09	45.50± 0.27	44.67± 0.42
Days to first fruit set						
Cross-I	52.89± 0.12	56.95± 0.13	55.42± 0.41	55.78± 0.31	56.93± 0.94	57.64± 0.25
Cross-II	52.89± 0.12	57.33± 0.43	54.89± 0.20	55.11± 0.19	56.90± 0.20	57.10± 0.05
Days to first picking						
Cross-I	59.82± 0.08	64.29± 0.15	61.71± 0.17	63.38± 0.46	63.50± 0.39	64.14± 0.13
Cross-II	59.82± 0.08	62.77± 0.11	59.63± 0.50	60.72± 0.22	61.54± 0.35	62.74± 0.16
Severity of downy mildew						
Cross-I	14.04 ± 0.07	90.64± 0.22	71.20± 1.11	57.88± 0.60	43.09± 0.15	83.16± 0.32
Cross-II	14.04± 0.07	4.11± 0.10	5.52± 0.01	5.05± 0.05	4.86± 0.23	5.89± 0.13

Whereas, Cross-I= LC-1-1 × K-75, Cross-II= LC-1-1 × *C. hardwickii*

Mean performance of the evaluated hybrids

Results of the mean values and their standard errors of the six generation of two crosses for different traits have been presented in Table 1. The significant variations were observed for the traits determining the earliness of a hybrid showed relatively significant wide range of

genetic variability for most studied traits, namely, days to first flower appearance (Cross-I =42.66 days and cross II=44.26 days); node number bearing female flower (Cross-I =3.26 and cross II=7.39); days to first female flower appearance (Cross-I =45.11 days and cross II=47.83 days); days to first fruit set (Cross-I =55.42 days and cross II=54.89 days); days to first fruit picking (Cross-I =61.71 days and cross II=59.63 days) and for severity of downy mildew (Cross-I =71.20 % and cross II=5.52 %). The F_1 hybrids performed better than their respective parents in desired direction in both the crosses except for node number bearing first female flower in cross II, days to first picking in cross I and severity of downy mildew in cross I and II showed inferior performance compared to either of parents (P_1 or P_2 or both).

Scaling, joint scaling for inadequacy of the genetic model

The data presented in Table 2 (scaling test) showed that significance of any of the four scales namely A, B, C, D in both the crosses revealed the presence non-allelic interaction. So additive-dominance model was found inadequate for both crosses which are further supported by significant value of joint scaling test for all the traits in both the crosses. For earliness trait *viz.*, days to first flower appearance scale namely A, B, D in cross I and A, B, C, D in cross II; for node number bearing first female and days to first female flower appearance flower scales A, B, C and D scale in both the crosses; days to first fruit set all the four scales in cross I and A, B, D in cross II; days to first fruit picking scale A, B, C in cross I and A, B, D in cross II and for severity of downy mildew A, B, C scales in cross I and all the four scales in cross II was found significant respectively. Further we analyzed the data for joint scaling test to accommodate the data within three parameter model to evaluate adequacy of simple additive-dominance model. Chi-square test was conducted to assess the goodness of fit of this model. The significant of chi-square values for all the traits studied indicated the inadequacy of additive-dominance model for both crosses under study and epistatic-digenic interaction was found to be a suitable fit. Therefore, six generation model was used to estimate the types of gene effects for these traits.

Gene action and epistasis effects

In the present study, scaling test and joint scaling test were found to be significant for all the traits under study. This indicates that higher order interaction (inter allelic interactions) plays an important role in the expression of a trait, and additive-dominance alone will not be adequate to deal with such traits (DEVI *et al.*, 2023). Under such conditions, available populations are forwarded to next generations to arrive at the best fit model. Digenic non allelic interaction model with six parameters, namely m, d, h, i, j and l portrayed that the epistatic interaction model sufficiently explained the gene action in the most of the studied traits. The result revealed (Table 2) that mean effects (m) was highly significant for all the studied traits in both the crosses. The classification of gene interaction depends on the magnitude and sign of the estimates of dominance (h) and dominance \times dominance (l) effects, when there are many pairs of interacting genes (MATHER and JINKS, 1982). The sign associated with the estimates of additive effects (d) and dominance effects (h) indicates the parent who concentrates the highest number of genes or positive alleles. For trait days to first flower appearance significant additive (d) gene effect was observed in negative desirable direction in both interacting crosses along with higher magnitude of dominant (h) effect but with positive sign than the additive effect (d).

Table 2. Estimates of scaling test and gene effects from generation mean analysis for different traits of earliness and severity of downy mildew of two crosses of cucumber

Traits →	Days to first flower appearance		Node number bearing first female flower		Days to first female flower appearance		Days to first fruit set		Days to first picking		Severity of downy mildew	
	C-I	C-II	C-I	C-II	C-I	C-II	C-I	C-II	C-I	C-II	C-I	C-II
Gene effects ▼												
A	1.53 [±] 0.29	2.06 [±] 0.46	0.72 [±] 0.14	3.73 [±] 0.71	-2.24 [±] 0.22	-6.36 [±] 0.44	5.55 [±] 1.11	6.01 [±] 0.30	5.46 [±] 0.46	3.64 [±] 0.50	-2.40 [±] 0.53	-9.85 [±] 0.27
B	0.15 [±] 0.23	3.91 [±] 0.37	-1.00 [±] 0.33	-4.41 [±] 0.24	-5.92 [±] 0.34	-10.44 [±] 0.57	2.91 [±] 0.38	1.99 [±] 0.28	2.29 [±] 0.20	3.07 [±] 0.35	-57.86 [±] 0.52	2.14 [±] 0.16
C	-15.65 [±] ± 0.45	-5.93 [±] 0.77	-4.45 [±] 0.28	-3.52 [±] 0.50	-13.56 [±] 0.56	-14.69 [±] 0.62	2.43 [±] 0.85	0.43 [±] 0.57	5.98 [±] 1.08	1.01 [±] 0.78	-59.24 [±] 0.85	-8.99 [±] 0.14
D	-8.67 [±] ± 0.22	-5.95 [±] 0.27	-2.09 [±] 0.20	-1.42 [±] 0.33	-2.70 [±] 0.28	1.04 [±] 0.31	-3.01 [±] ± 0.66	-3.78 [±] 0.25	-0.89 [±] 0.58	-2.85 [±] 0.34	0.51 [±] 0.55	-0.64 [±] 0.16
χ ²	1807.65 [*]	490.17 [*]	363.54 [*]	636.98 [*]	730.40 [*]	623.18 [*]	74.11 [*]	499.78 [*]	264.73 [*]	130.77 [*]	16270.49 [*]	5946.00 [*]
[m]	42.20 [±] ± 0.08	44.72 [±] 0.11	3.10 [±] 0.05	7.04 [±] 0.03	45.40 [±] 0.12	45.60 [±] 0.05	55.78 [±] ± 0.18	55.11 [±] 0.11	63.38 [±] 0.26	60.72 [±] 0.13	14.21 [±] 0.21	5.05 [±] 0.03
[d]	-1.53 [±] ± 0.14	-1.74 [±] 0.15	-0.197 [±] 0.17	-0.33 [±] 0.33	-1.12 [±] 0.15	0.83 [±] 0.29	-0.71 [±] 0.56	-0.21 [±] 0.11	-0.65 [±] 0.24	-1.19 [±] 0.22	-3.07 [±] 0.36	-1.03 [±] 0.15
[h]	10.44 [±] ± 0.46	8.00 [±] 0.63	2.26 [±] 0.41	1.77 [±] 0.71	-1.97 [±] 0.58	-4.95 [±] 0.68	6.52 [±] 1.35	7.34 [±] 0.53	1.42 [±] 1.16	4.02 [±] 0.74	-32.66 [±] 1.11	-2.28 [±] 0.33
[i]	17.34 [±] ± 0.43	11.91 [±] 0.55	4.18 [±] 0.40	2.84 [±] 0.66	5.39 [±] 0.56	-2.07 [±] 0.61	6.03 [±] 1.33	7.57 [±] 0.50	1.77 [±] 1.53	5.69 [±] 0.68	-1.02 [±] ± 1.11	1.28 [±] 3
[j]	0.69 [±] 0.32	-0.92 [±] 0.46	0.86 [±] 0.34	4.07 [±] 0.69	1.84 [±] 0.40	2.02 [±] 0.61	1.32 [±] 1.13	2.01 [±] 0.37	1.54 [±] 0.48	0.28±0.45	27.13 [±] 0.74	-6.00 [±] 0.33
[l]	19.03 [±] ± 0.71	-17.88 [±] 0.98	-3.91 [±] 0.72	-2.16 [±] 1.40	2.77 [±] 0.81	18.84 [±] 1.31	14.49 [±] ± 2.41	-15.57 [±] 0.75	-9.52 [±] 1.44	-12.40 [±] 1.18	61.28 [±] 1.69	6.43 [±] 0.63
Epistasis	Duplicate	Duplicate	Duplicate	Duplicate	Duplicate	Duplicate	Duplicate	Duplicate	Duplicate	Duplicate	Duplicate	Duplicate

Whereas C-I=LC-1-1 × K-75 and C-II=LC-1-1 × *Cucumis hardwickii*

Among the interaction the magnitude of dominance × dominance (l) was greater than all other gene effects and also was in desirable direction which indicates the earliness. The value of (h) and (l) put together is more than that of additive (d) and tend to overpower additive effects and implies the preponderance of all the three types of gene action for this trait. Earlier, TIWARI *et al.*, (2011) reported additive, dominance and additive × dominance gene effects for days to first flowering in case of cucumber. For node number bearing first female flower additive (d) gene effects were found to be non-significant in both the crosses and only dominant (h) gene effect with positive signs was significant for both the crosses. Among the epistatic components, all the three effect (i), (j), (l) was significant in cross I and (i), (j) genetic effect in cross II. DEVI *et al.*, (2023) and TOMAR *et al.*, (2008) reported dominance gene action for the trait in cucumber. Due to predominance of dominant genes, heterosis breeding and recurrent selection can be useful to get lines with female flowers at early nodes. Both the additive (d) and dominant (h) gene effect was found to be significant in trait days to first female flower appearance. The absolute magnitude of dominance (h) effects was greater than additive (d) effects and in negative direction. The magnitude of interaction was greater than the gene effects and dominance × dominance (l) effects was highly significant but with positive

values and similar findings were also reported by SHAHI *et al.* (2005). For days to first fruit set, only dominant (h) gene effect was found to be significant for both the crosses. Among the epistatic components, all the three effects (i), (j) and (l) was significant in both the crosses. The genic component dominance \times dominance (l) effect was higher and in desirable direction in both the crosses. DEVI *et al.* (2023) and TIWARI *et al.* (2011) in cucumber also reported that earliness traits *viz.*, node number bearing first female flower and fruit set governed mainly by dominance (h) effects and dominance \times dominance (l). Hence heterosis breeding followed by effective selection procedure would be rewarding for improving this particular trait. For days to first fruit picking both additive (d) and dominant (h) gene effect was found to be significant in both the crosses. Among the epistatic components, all the three effect (j) and (l) was significant in cross I and (i), (l) genetic effect in cross II. But the magnitude of dominance \times dominance (l) effects was higher and in desirable direction for both the crosses contributing to earliness. SANANDIA *et al.* (2010) also reported additive (d), dominance (h) and additive \times dominance (j) gene effects and all the three types of non-allelic interaction in sponge gourd. For downy mildew both the additive (d) and dominant (h) gene effect was found to be significant in both the crosses in desirable direction. Additive component of variance is higher in magnitude with negative direction and dominant with positive sign in LC-1-1 \times K-75 whereas the dominance effects were significantly higher in magnitude with desirable negative direction in LC-1-1 \times C. *hardwickii*. And among epistatic interaction (j) and (l) in cross I and all the three (i), (j) and (l) were found significant in cross II. The magnitude of dominance \times dominance (l) effects was higher and significantly negative in LC-1-1 \times K-75 and significantly positive in cross LC-1-1 \times C. *hardwickii*. Similar results were reported by SHASHIKUMAR *et al.* (2010) in muskmelon plants for resistance to downy mildew.

For all the traits studied both the crosses showed duplicate type of epistasis because dominance (h) and dominance \times dominance (l) gene effects displayed opposite signs. Since none of signs of (h) were similar to the (l) type of epistasis, it was concluded that no complementary type of interaction was present in the genetic control of the studied traits. Our results were in contradictory to previous studies who reported complementary type of gene action for earliness and fruit traits. Duplicate type of non-allelic gene interaction for most of studied traits further confirms the prevalence of dominance effects. Also, the manifestation of duplicate epistasis by different crosses for traits studied revealed that this kind of epistasis generally hinders the improvement through selection as it decrease the variation in F₂ and subsequent generations. So the selection should be delayed until a high level of gene fixation (additive component) is achieved.

Components of variance

Estimates of additive, dominance, environmental components of variance, dominance ratio, mid and better parent heterosis, potence ratio and narrow sense heritability are presented in Table 3. Dominance ratio for all the traits was more than unity except for days to first flower appearance in LC-1-1 \times K-75 and days to first fruit picking in both the crosses indicated the importance of dominance gene effects. The earliness traits have had very low mid-parent heterosis, whereas severity of downy mildew showed significant higher negative mid-parent heterosis in comparison. The significant negative better parent heterosis was highest for downy

mildew (Table 3). In cross LC-1-1 \times K-75 for days to first female flower appearance, narrow sense heritability was moderate and low for other traits in both the crosses.

Table 3. Variance components, dominance ratio, heterosis, potence ratio and heritability estimates for traits of earliness and disease trait in two crosses of cucumber

Trait	V _A		V _D		V _E		DR		HM(%)		HB(%)		PR		h _a ²	
	C-I	C-II	C-I	C-II	C-I	C-II	C-I	C-II	C-I	C-II	C-I	C-II	C-I	C-II	C-I	C-II
DTFFA	-0.03	-0.03	-0.01	-0.16	0.05	0.19	0.80	3.27	-13.92	-8.10	-9.89	-6.51	3.11	4.78	-0.63	0.23
NNBFFF	-0.07	-0.32	0.06	0.24	0.01	0.07	1.27	1.24	-37.07	-12.98	-20.89	79.43	1.81	0.25	-7.04	-119.53
DTFFFA	-0.02	-0.24	-0.04	0.09	0.06	0.15	1.90	1.90	-14.03	-5.68	-8.90	-3.41	2.49	2.42	0.50	-28.50
DTFFS	-0.27	0.00	-0.51	-0.17	0.78	0.18	1.96	1.96	-13.06	-9.13	-9.72	-9.04	3.54	57.31	-1.87	0.96
DTFP	-0.14	-0.32	0.03	0.31	0.11	0.02	0.63	0.63	-15.86	-10.88	-14.12	-10.17	7.04	13.77	-3.81	-5.57
SDM	-0.27	-0.07	0.25	0.06	0.02	0.00	1.36	1.36	-70.56	-39.21	-6.0	34.20	1.03	-0.72	-1.06	-26.70

CONCLUSION

The experimental results showed that as a consequence of higher magnitude of interactions, the non-fixable gene effects were higher than the fixable. Additionally, duplicate epistasis was observed for all traits across both cross-combinations. In these crosses, selection intensity is expected to be mild in the earlier generations and more intense in the later generations, reflecting the progression of selection over time. In crosses exhibiting high magnitudes of dominance gene effects and dominance \times dominance interactions, the presence of duplicate epistasis complicates their exploitation. In such scenarios, methods involving repeated crossing, such as diallel selective mating or biparental mating, can be effectively employed. Dominance gene effects (h) can be effectively harnessed through heterosis breeding, while additive effects can be successfully utilized via selection. Therefore, intermating among selected individuals to break undesirable linkages, followed by selection in subsequent generations, is likely to yield positive results. This study indicates that the nature and magnitude of gene effects influencing the inheritance of various traits differ depending on the breeding material used in different crosses. Consequently, a specific breeding strategy must be tailored for each cross to achieve significant improvements in particular traits. Therefore, due to the presence of all gene actions, namely, additive, dominant and epistasis, reciprocal recurrent selection is the best suited strategy to meet the need of yield improvement.

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**ANALIZA SREDNJE VREDNOSTI GENERACIJA NEADAPTIRANIH LOKALNIH
POPULACIJA I DIVLJIH SRODNICA KRASTAVCA (*Cucumis sativus* L.)
ZA RANOSTASNOST I PEPELNICU**

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Izvod

Za genetsko poboljšanje bilo kog useva, metod oplemenjivanja koji treba usvojiti zavisi uglavnom od razumevanja genetike i nasleđa uključenih u osobine. Znanje koje se odnosi na delovanje i interakcije gena će verovatno usmeriti i ojačati programe oplemenjivanja useva. Ovo istraživanje ima za cilj da razjasni prirodu i veličinu delovanja gena povezanih za različite osobine ranostasnosti i bolesti kroz analizu srednje vrednosti generacije (GMA) sa šest generacija (P1, P2, F1, F2, B1 i B2) dva ukrštanja koja uključuju tri različita roditelja krastavca. Studije su sprovedene na Eksperimentalnoj istraživačkoj farmi Odeljenja za nauku o povrću, dr YSP i UH&F Nauni, Solan, HP (Indija) u uslovima otvorenog polja. Eksperimentalni rezultati su otkrili da su nealelne interakcije bile prisutne za sve osobine koje su razmatrane u oba ukrštanja, što je vidljivo iz individualnog skaliranja i testa zajedničkog skaliranja. U nasleđivanju većine osobina osim nekoliko, i aditivna i neaditivna dejstva gena značajno doprinose, stoga, metode oplemenjivanja recipročna rekurentna selekcija/bi-roditeljsko ukrštanje mogu se iskoristiti za poboljšanje osobina. Osobine ranostasnosti tj. broj čvorova koji nose prvi ženski cvet i dane do prvog zametanja plodova, uglavnom su vođene dominacijom (h) i stoga se ove osobine mogu poboljšati kroz heterozis oplemenjivanje. Takođe, dupli tip epistaznog efekta je kontrolisao sve osobine u obe unakrsne kombinacije, što sugeriše blagi intenzitet selekcije u ranijim generacijama, dok je intenzivan u kasnijim generacijama.

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