



Estimation of epistasis and genetic components of variance for different traits in cucumber (*Cucumis sativus*)

REENA KUMARI^{1*}, RAMESH KUMAR¹ and MEENU GUPTA¹

Dr Y S Parmar University of Horticulture and Forestry, Nauni, Solan, Himachal Pradesh 173 230, India

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ABSTRACT

To estimate epistasis and components of genetic variance a study was carried out during 2016 and 2017 at Experimental Research Farm of Department of Vegetable Science, Dr YSP UH & F Nauni, Solan, (HP) and data were recorded for different qualitative and quantitative traits using triple test cross (TTC) analysis of an inter-varietal cross LC-1-1 × K-75 of cucumber (*Cucumis sativus* L.). Three testers of cucumber named LC-1-1, K-75 and their F_1 (LC-1-1 × K-75) were crossed to 15 inbred lines for detecting the additive, dominance and epistatic components of genetic variance. Good quantum of genetic variability has been generated through triple test cross progenies with respect to different traits studied as revealed by the significant analysis of variance. TTC analysis revealed that overall epistasis and j+l type component were found to be significant for majority of the traits except fruit breadth and total soluble solids. Further, experimental results showed that (i) type of epistasis were also significant for majority of the traits under study. The components of genetic variance were estimated using analysis of variance for sums and differences revealed the importance of both additive (D) as well as dominance (H) components of genetic variance in controlling various traits and showed partial dominance except over dominance for fruit breadth and severity of downy mildew. Therefore, kind of genetic variance revealed from triple test cross can be exploited by intermating selected individuals in early segregating generations with delayed selection in later generations, or recurrent selection followed by pedigree method to exploit both additive and non-additive components along with epistasis in cucumber.

Keywords: Additive, Cucumber, Dominance, Epistasis, Genetic variance, Triple test cross

The elucidation of genetic components of variance is an important pre-requisite for efficient management of available genetic variability and formulation of breeding programme. Cucumber (*Cucumis sativus* L.) is the most extensively cultivated cucurbitaceous vegetable. In spite of extensive cultivation, economic importance and consumption of cucumbers as a common vegetable by many people in the country, very little attention has been paid for its genetic improvement by using genetically superior parents. It is an allogamous crop and its yield and yield contributing traits are mostly controlled polygenically. In order to initiate any such crop improvement programme, it is essential to gain genetic information on the breeding material, especially about the components of genetic variance, viz. additive, dominance and epistasis (Tai 1979). Several biometrical methods are available for obtaining information on the nature of genetic variation. Although the generation mean analysis is commonly used to detect the epistasis and estimate the components of genetic variance

(Hayman and Mather 1955) but it involves the analysis of first degree statistics the estimates of which are less reliable. The North Carolina Design- III (NCD-III) of Comstock and Robinson (1952) in which homozygous parents are crossed and F_2 plants are back crosses to each of the parents provides reliable estimate of additive and dominance components, but it assumes no epistasis. Kearsley and Jinks (1968) extended this concept and included back cross to the F_1 generation. This type of experiment was called Triple Test Cross (Jinks *et al.* 1969) and it is modified by many other workers (Jinks and Perkins 1970). It is most efficient method for detection and estimation of epistatic provides unbiased estimates of genetic variation. Triple test cross analysis provides unambiguous test for the presence of epistasis regardless of gene frequencies, degree of inbreeding and linkage relationship. Very meager information is available in the literature on estimation of triple test cross analysis for different metric traits in cucumber. Therefore, the present study was carried out to detect epistasis and components of genetic variance by employing the analysis of second degree statistics in an inter-varietal cross of cucumber.

MATERIALS AND METHODS

The experimental site is located at Nauni, Solan, at an altitude of 1270 m amsl lying in the mid hill zone of

Present address: ¹Dr Y S Parmar University of Horticulture and Forestry, Nauni, Solan, Himachal Pradesh. *Corresponding author e-mail: reena.sarma92@gmail.com.

Himachal Pradesh. The experimental material for the present study consisted of 45 triple test cross (TTC) progenies of LC-1-1 and K-75 developed according to the crossing plan proposed by Kearsay and Jinks (1968). Fifteen plants were randomly selected from F_2 population of cross LC-1-1 $\times$ K-75, designated as 15Pi lines and crossed to their respective tester namely L_1 (LC-1-1), L_2 (K-75) and L_3 (F_1 of LC-1-1 and K-75) during 2016. These 45 TTC families along with 15 F_2 selected plant progenies, their parents (P_1 and P_2) and F_1 were evaluated in a completely randomized block design, in three replications during 2017. Each progeny were grown in double row of 4 m length accommodated at least 16 plants with inter and intra row spacing of 100 cm $\times$ 50 cm. The standard cultural practices for raising a healthy crop of cucumber as recommended in the Package of Practices for Vegetable Crops, published by the Directorate of Extension Education, UHF, Nauni, Solan (Anonymous 2016) have been followed to raise healthy crop of cucumber. Observations were recorded on 10 plants in each entry per replication for various horticultural traits, viz. days to first female flower opening, node number bearing first female flower, days to marketable maturity (days), number of marketable fruits per plant, harvest duration (days), fruit length (cm), fruit breadth (cm), average fruit weight (g), yield per plant (kg), total soluble solids ($^{\circ}$ B), incidence of fruit fly (%) and severity of powdery and downy mildew (%). The statistical analysis of the data was carried out using MS-Excel, SPAR 2.0 statistical package of Indostat, Hyderabad.

RESULTS AND DISCUSSION

Test for the detection of epistasis: The data recorded on 45 triple test cross families were subjected to triple test cross analysis to estimate different components of genetic variance. The perusal of analysis of variance for the triple test cross indicated that mean squares due to crosses were significant for all the traits which suggested the presence of sufficient variability in the triple test cross progenies for use in recombination breeding. Epistasis being an integral component of genetic variation and ignorance of presence of the epistasis would lead to the biased estimates of additive and dominance components of variation. Further, the significance of mean squares due to epistasis revealed the presence of epistasis for majority of the traits under study except, fruit breadth and total soluble solids, where epistasis was found to be non-significant or observed to be absent. The significant estimates of epistasis may be the result of the involvement of different alleles due to heterozygous state of the lines. The presence of epistasis had been detected for majority of the traits in the present set of materials underlined the importance of additive and dominance components of variance which would have been biased if procedure assuming no epistasis had been employed (Barona *et al.* 2012). Further, partitioning of mean sum of square due to epistasis into 'i' and 'j+l' interaction showed the significant presence of additive $\times$ additive (i) type of epistasis for majority of the traits except number of marketable fruits per plant, fruit breadth, average fruit weight

and total soluble solids. On the other hand, the presence of additive $\times$ dominance (j) type along with dominance $\times$ dominance (l) type components were noticed significant for almost all the traits except fruit breadth and total soluble solids. Therefore, it is clear from the results that epistasis is an integral component of genetic variation and should not be ignored while formulating breeding programme to improve commercially important traits. If the presence of epistasis is ignored, information of inter allelic interactions may be lost and one may get biased estimates of additive and dominance components which may lead to wrong conclusions. The presence of significant epistasis, i.e. additive $\times$ additive (i), dominance (j) and dominance $\times$ dominance (l) in the inheritance for yield and yield contributing traits in present study in cucumber are in consonance with Shahi *et al.* (2010) by following triple test cross in cucumber. Similar results have also been reported by Panda and Singh (2014) in okra, Kumari *et al.* (2017) in brinjal and Kumari *et al.* (2018) in brinjal by following triple test cross method.

Estimation of additive and dominance components

Analysis of variance: The analysis of variance for sums ($\bar{L}_{1i} + \bar{L}_{2i} + \bar{L}_{3i}$) and differences ($\bar{L}_{1i} - \bar{L}_{2i}$) which provides a direct test for the detection of additive and dominance genetic components has been presented in Table 1. Further, the perusal of the data revealed that the mean squares due to sums ($\bar{L}_{1i} + \bar{L}_{2i} + \bar{L}_{3i}$) were significant for all the traits except fruit breadth and total soluble solids, whereas, mean squares due to differences ($\bar{L}_{1i} - \bar{L}_{2i}$) were significant for all the traits except number of marketable fruits per plant, yield per plant and total soluble solids. The significance of mean squares due to the sums and differences provide a direct test of significance of additive (D) and dominance (H) components of variation.

Estimation of genetic components of variance: The estimates of additive (D), dominance (H) and covariance of sums and differences and average degree of dominance $(H/D)^{1/2}$ for different groups of traits are presented in Table 2. The estimates of mean squares due to sums (measuring D component) and differences (measuring H component) revealed that additive (D) genetic components were significant for all the traits except fruit breadth and total soluble solids whereas, dominance (H) genetic components were significant for all the traits except number of marketable fruits per plant, yield per plant and total soluble solids which indicated the importance of both components in controlling these traits. The preponderance of additive variance for most of the traits indicated the relative importance of fixable type of gene action in their inheritance. However, non-fixable type of gene action was more important for fruit breadth and severity of downy mildew due to high magnitude of dominance component. The preponderance of both additive and non-additive gene action for fruit yield and most of its component traits are in accordance with generation mean analysis (Rai *et al.* 2018), North Carolina Design-II (Golabadi *et al.* 2017) and contrary to the reports of earlier workers who have reported the preponderance of non-

Table 1 Analysis of variance for sums ($L_{11}+L_{21}+L_{31}$) and differences ($L_{11}-L_{21}$) for 45 triple test cross progenies for different horticultural traits in cucumber

Source of variation	df	Days to first female flower opening	Node number bearing first female flower	Days to marketable maturity	Number of marketable fruits per plant	Harvest duration	Fruit length	Fruit breadth	Average fruit weight	Yield per plant	Total soluble solids	Incidence of fruit fly	Severity of powdery mildew	Severity of downy mildew
Sums	14	47.99*	5.67*	47.76*	2.89*	30.90*	18.33*	0.85	10228.43*	3.71*	0.89	31.18*	12.15*	12.32*
Sum × Replication	28	3.29	1.27	3.44	1.22	1.65	1.52	0.45	1194.46	0.93	0.47	1.20	1.05	0.38
Differences	14	44.51*	4.90*	44.89*	1.13	12.54*	12.26*	1.29*	517.11*	1.85	0.40	24.02*	4.45	18.31*
Differences × Replication	28	2.50	1.27	2.46	1.74	2.66	0.92	0.47	1108.72	0.90	0.41	1.58	1.13	0.60

* Significant at 5 per cent level of significance

Table 2 Estimates of genetic parameters for 45 triple test cross progenies for different horticultural traits in cucumber

Source of variation	Days to first female flower opening	Node number bearing first female flower	Days to marketable maturity	Number of marketable fruits per plant	Harvest duration	Fruit length	Fruit breadth	Average fruit weight	Yield per plant	Total soluble solids	Incidence of fruit fly	Severity of powdery mildew	Severity of downy mildew
D	59.60*	5.86*	59.09*	2.23*	39.00*	22.41*	0.52	12045.29*	3.71*	0.56	39.97*	14.80*	15.92*
H	56.02*	4.85*	56.57*	-0.82	13.17*	15.12*	1.09*	5415.19*	1.27*	-0.02	29.83*	4.42*	23.62*
(H/D) ^{1/2}	0.97	0.91	0.98	-	0.58	0.82	1.45	0.67	0.58	-	0.87	0.55	1.22
R	-0.34	-0.36	-0.34	0.12	0.56	-0.10	0.41	0.44	0.64*	-0.38	-0.31	-0.70*	-0.04

* Significant at 5 per cent level of significance

additive gene action for fruit yield and most of its component by following diallel analysis (Chirani *et al.* 2011). However, in contradiction to non-additive gene action for fruit yield and most of its component through line $\times$ tester and diallel mating design by afore mentioned workers, the limited report of Shahi *et al.* (2005) in cucumber and Mallikarjun *et al.* (2017) in okra, for both the additive and non-additive gene action through triple test cross for these traits supports the results of present study. This, in addition, also signifies the reliability of triple test cross mating design in precisely determining the gene action of biometrical traits.

Average degree of dominance (H/D)^{1/2}: The higher estimates of additive (D) than dominance (H) resulted into value of degree of dominance less than unity indicating partial dominance for most of the traits namely, days to first female flower opening, node number bearing first female flower, days to marketable maturity, number of marketable fruits per plant, harvest duration, fruit length, average fruit weight, yield per plant, incidence of fruit fly, and severity of powdery mildew highlighting the relative importance of additive gene action for these traits. In contrast values of degree of dominance more than unity recorded for fruit breadth and severity of downy mildew only indicated that greater role played by dominance (over) gene effects in their general expression (Table 2). The greater magnitude of additive gene action and existence of partial dominance in cucumber for majority of traits has also been reported by Shahi *et al.* (2005) by following triple test cross analysis.

It is concluded that triple test cross analysis exhibited additive, dominance and epistasis gene actions were important in determining the inheritance of different characters. Under such a situation triple test cross mating as well as mating of selected plants in early segregating generations could be attempted for developing potential populations having optimum levels of homozygosity and heterozygosity. Although, transgressive segregants can also be isolated by attempting alternative intermating and subsequent handling of segregating generations in order to obtain high yielding and stable lines in cucumber where all the three kinds of gene effects are present.

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