



Research Article

ESTIMATES OF GENETIC COMPONENT OF VARIANCES AND GENETIC RATIOS FOR EARLINESS AND YIELD ATTRIBUTING TRAITS IN CUCUMBER

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Received: March 28, 2018; Revised: April 03, 2018; Accepted: April 05, 2018; Published: April 15, 2018

Abstract- An experiment was undertaken to study the estimates of gene action of 28 F₁ hybrids involving 8 diverse parents in a half diallel fashion excluding reciprocals with three replications. Dominant variance was observed to be significant for all the traits viz., days to first female flower appearance, days to first fruit set, days to first fruit harvest, fruit length, fruit width, average fruit weight, no of fruits per plant and total yield while additive variance was significant for most of the traits except for number of fruits and total yield per plant indicating the importance of both additive and dominant variance for expression of the various traits in cucumber. However, dominance variance was observed to be higher than additive effect. The mean degree of dominance was also observed to be more than one for all the traits indicating over dominance except for average fruit weight which showed partial dominance. Narrow sense heritability was less than 50% for most of the traits except for fruit weight indicating predominance of non-additive gene action. It can be concluded that the traits which is governed by additive gene effect can be improved by pure line selection while traits where non-additive gene action is prevalent heterosis breeding can be adopted for its improvement.

Keywords- F₁ hybrids, Additive variance, Dominant variance, Narrow sense heritability, Cucumber.

Citation: Bhutia T.L., *et al.*, (2018) Estimates of Genetic Component of Variances and Genetic Ratios for Earliness and Yield Attributing Traits in Cucumber. International Journal of Genetics, ISSN: 0975- 2862 & E-ISSN: 0975-9158, Volume 10, Issue 3, pp.-373-375. DOI: <http://dx.doi.org/10.9735/0975-2862.10.3.373-375>

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Academic Editor / Reviewer: Dr Alok Kumar Yadav, Dr Manish K Singh

Introduction

Cucumber (*Cucumis sativus* L.) is one of the most popular and widely grown vegetable crops in the world, and one of the oldest vegetables cultivated by man [1]. In India, cucumber is being cultivated in an area of 71 thousand ha with the production of 1202 thousand MT [2]. It can be eaten raw as salad or cooked as vegetables. Cucumber has got cooling effect hence fruits are often used as cooling vegetable. It is ideal for people suffering from jaundice and prevents constipation. Cucumber fruit being rich in water content act as a moisturizer for the human body and reduce the body's need for water [3]. The knowledge of gene action involved in governing various traits is very important for formulation of any breeding programme. The success of selection mainly depends upon the extent of genetic variability present in it. If the variability in the genetic base is high then the magnitude of success in selection is also higher. Therefore, the present investigation was carried out to study the estimates of the gene action and its ratios.

Materials and methods

The present investigation was carried out at the research farm of Division of Vegetable Science, ICAR- Indian Agricultural Research Institute, New Delhi. The experimental material for the present study consisted of 8 promising and diverse lines / varieties of cucumber collected from different parts of the country namely P₁ (DC-77), P₂ (DC-70), P₃ (DC-83), P₄ (Pusa Uday), P₅ (Punjab Naveen), P₆ (DC-1), P₇ (Swarna Ageti) and P₈ (Kalyanpur Green). Twenty-eight F₁ hybrids were produced by crossing these eight parents in a half diallel

without reciprocals and these hybrids along with their parents were evaluated in a randomized block design with three replications. The crops were sown in rows of 1.5m × 60cm spacing between hills. All the recommended package of practices was followed. Five plants were taken for observation. Observation were recorded on eight quantitative traits viz., days to first female flower opening, days to first fruit set, days to first fruit harvest, fruit length (cm), fruit width (cm), average fruit weight (g), number of fruits per plant and fruit yield per plant (g). Gene action was studied by the diallel method of numerical approach given by [4]:

D = Component of variation due to additive effects of genes.

H₁ = Component of variation due to dominance effect of genes.

H₂ = H₁[1-(u-v)²]

Where,

u = Proportion of positive genes in the parents.

v = Proportion of negative genes in the parents where u + v =1.

F_r = The covariance of additive and dominance effects in a single array.

F = The mean of F_r over the arrays.

h² = Dominance effect (as the algebraic sum over all loci in heterozygous phase in all crosses

Genetic ratios calculated were;

($\hat{H}/\hat{D}$)^{1/2} = Mean degree of dominance

($\hat{H}_2/4\hat{H}_1$) = The proportion of genes with positive and negative effects in parents

[(4 $\hat{D}\hat{H}_1$)^{1/2} + $\hat{F}$]/ [(4 $\hat{D}\hat{H}_1$)^{1/2} - $\hat{F}$] = The proportion of dominant and recessive genes in the parents

$\hat{h}^2/\hat{H}_2$ = The number of groups of genes which control the character and exhibited

dominance

$\hat{h}^2(ns)$ = Heritability (narrow sense)

Results and Discussion

The estimates of genetic components of variation and genetic ratios for eight different quantitative traits are presented in [Table-1] and [Table-2] which has been described in details below:

Days to first female flower opening

The estimates of genetic component of variation for days to first female flower opening, i.e., D, H_1 , H_2 and h^2 were highly significant. The value of additive

component of variance (2.31) was more than dominant component of variance (2.28), indicating the role of over-dominance. The environmental component of variance (E) was insignificant and did not play any role in expressing this trait. The $(H/D)^{1/2}$ value was 1.01 which is >1 , showing over-dominance for this trait. The $[(4D H_1)^{1/2} + F / (4D H_1)^{1/2} - F]$ was less than 0.25 i.e. 0.16 which shows asymmetrical distribution of genes in the parents. Genetic ratio of dominant and recessive gene as indicated by $[(4D H_1)^{1/2} + F / (4D H_1)^{1/2} - F]$ was 4.43 which indicated excess of dominant gene while the no of gene groups which control the character (h^2 / H_2) and exhibited dominance was 1.01. Narrow sense heritability being 49.84%, (less than 50%) showed preponderance of non-additive gene action.

Table-1 Estimate of genetic components of variation for eight quantitative traits

Genetic parameters	Days to first female flower opening	Days to first fruit set	Days to first fruit picking	Fruit length (cm)	Fruit width (cm)	Average fruit weight (g)	No. of fruits per plant	Total yield/plant (g)
D (Additive effect)	2.28** ±0.23	2.15** ±0.28	2.16** ±0.28	2.43** ±0.55	0.03** ±0.01	1768.87** ±258.42	0.31 ±0.33	60939.50 ±34763.40
F	0.21 ±0.54	1.12 ±0.68	2.24** ±0.67	6.56** ±1.30	-0.01 ±0.02	865.79 ±610.61	1.84* ±0.80	140398.80 ±82142.90
H_1 (Dominance effect)	2.31** ±0.53	2.16** ±0.66	5.47** ±0.65	4.54** ±1.26	0.10** ±0.02	1609.20** ±594.06	6.11** ±0.77	455052.50** ±79916.20
H_2	1.55** ±0.46	2.12** ±0.57	2.62** ±0.56	4.26** ±1.10	0.10** ±0.02	1438.56** ±516.83	2.82** ±0.67	359398.17** ±69526.90
H^2	1.56** ±0.46	2.67** ±0.38	3.78** ±0.38	0.09 ±0.74	0.01 ±0.01	389.94 ±346.61	3.15** ±0.45	1413063.40** ±46267.70
E	1.04 ±0.11	0.19* ±0.09	1.05** ±0.09	0.50** ±0.18	0.03** ±0.01	84.28 ±86.14	0.22* ±0.11	463.70 ±11587.00

* & **, significance at 1% and 5% probability, respectively

Table-2 Estimate of various genetic ratios for eight quantitative traits.

Genetic parameters	Days to first female flower opening	Days to first fruit set	Days to first fruit picking	Fruit length (cm)	Fruit width (cm)	Average fruit weight (g)	No. of fruits per plant	Total yield/plant (g)
$(H/D)^{1/2}$	1.01	1.01	1.59	1.37	1.84	0.95	4.47	2.73
$(H_2/4H_1)$	0.16	0.24	0.11	0.23	0.24	0.22	0.11	0.20
$[(4DH_1)^{1/2} + F / (4DH_1)^{1/2} - F]$	4.43	3.34	4.96	159.17	0.83	1.69	1.56	2.46
(h^2 / H_2)	1.01	1.25	1.41	0.02	0.10	0.27	1.12	3.93
Heritability % (Narrow sense)	49.84	42.62	12.52	28.90	10.72	62.07	48.81	9.26

Days to first fruit set

Genetic component variances such as D, H_1 , H_2 , H^2 and E were significant for days to first fruit set while F was non-significant. The value of H_1 (2.16) was more than D (2.15), suggesting the role of over-dominance. The average degree of dominance $(H/D)^{1/2}$ (1.01) was >1 showing over-dominance for this trait. Asymmetrical distribution of positive and negative allele was observed as the value was 0.24 showing dominance. The proportion of dominant and recessive gene as indicated by $[(4D H_1)^{1/2} + F / (4D H_1)^{1/2} - F]$ was 3.34 which indicated excess of dominant gene while h^2 / H_2 was 1.25. Narrow sense heritability being 42.62% indicates the predominance of non-additive gene action.

Days to first fruit harvest

Result pertaining to the estimates of D, H_1 , H_2 , H^2 , F and E were highly significant. The value of H_1 (5.47) was greater than D (2.16), indicating role of dominance alleles in the parent. The positive F value (2.24) indicated presence of dominant alleles in the parents. The mean degree of dominance being 1.59 indicating over-dominance. The proportion of genes with positive and negative effects ($H_2/4 H_1$) in the parents was 0.11, indicating asymmetrical distribution. The proportion of dominant and recessive genes $[(4D H_1)^{1/2} + F / (4D H_1)^{1/2} - F]$ in the parents was 4.96, while the group of dominant genes (h^2 / H_2) was 1.41. Narrow sense heritability being low (12.52%), exhibited the predominance of non-additive gene action.

Fruit length (cm)

For fruit length, the estimated value of D, H_1 , H_2 , E and F were highly significant whereas H^2 was non-significant. The value of H_1 (4.54) was more than D (2.43), exhibiting non-additive gene action. The positive F value indicated predominance of dominant alleles in parents. The average degree of dominance $(H_1/D)^{1/2}$ was 1.37, indicating over-dominance. The proportion of genes with positive and negative effects ($H_2/4 H_1$) in parents was 0.23 with asymmetrical distribution. The proportion of dominant and recessive genes $[(4D H_1)^{1/2} + F / (4D H_1)^{1/2} - F]$ in parents was 159.17 indicating excess of dominant gene in the parents whereas the number of genes (h^2 / H_2) which controlled the trait and exhibit dominance was 0.02. Low narrow sense heritability i.e., 28.90% indicates predominance of non-additive gene action for this particular trait.

Fruit width (cm)

The values for additive variance, dominance variance, environmental variance, H_1 and H_2 were significant while F and H^2 were non-significant for fruit diameter. Non-additive gene action played a major role as the value of dominance effect (0.10) was greater than additive effect (0.03). The negative value of F indicated that the recessive alleles were more frequent in parents. The mean degree of dominance $(H_1/D)^{1/2}$ being 1.84 exhibited over-dominance. The ratio of genes with positive and negative effects ($H_2/4 H_1$) in the parents was noted to be 0.24, indicating asymmetrical distribution. Prevalence of excess recessive gene in the parents as the genetic ratio was less than 1 (0.83) while the number of dominant exhibiting

genes (h^2/H_2) was 0.10. Low values of narrow sense heritability (10.72%) exhibited the prevalence of non-additive type of gene action.

Average fruit weight (g)

For average fruit weight, the estimated value of D, H_1 and H_2 were highly significant while other parameters viz. h^2 , E and F were non-significant. The estimated value of H_1 (1609.20) was less than D (1768.87) which revealed that additive genes were more than non-additive genes. Positive value of F indicated predominance of dominant alleles. The mean degree of dominance (H_1/D) $^{1/2}$ being 0.95 suggesting partial dominance. Similar result was reported by [5] in cucumber. The proportion of genes with positive and negative effects ($H_2/4H_1$) was 0.22, which denotes asymmetrical distribution at loci. The proportion of dominance and recessive genes $[(4D H_1)^{1/2} + F / (4D H_1)^{1/2} - F]$ was 1.69 whereas the number of group of genes exhibiting dominance and controlling trait was 0.27. High narrow sense heritability (62.07%) exhibited additive type of gene action for expression of this trait.

Number of fruits per plant

Estimates of genetic component of variation viz. H_1 , H_2h^2 were highly significant while E and F were only significant whereas additive variance was non-significant. The value of H_1 (6.11) was more than D (0.31) indicating more prevalence of dominant genes. The positive value of F suggested predominance of dominant alleles in the parents. The mean degree of dominance (H_1/D) $^{1/2}$ was 4.47 revealing the role of over-dominance. The gene proportion with positive and negative effects ($H_2/4 H_1$) was 0.11 exhibiting dominance suggesting asymmetrical distribution at the loci. The proportion of dominant and recessive genes $[(4D H_1)^{1/2} + F / (4D H_1)^{1/2} - F]$ was 1.56 indicating excess of recessive gene whereas the number of group of genes (h^2/H_2) which showed dominance was 1.12. Narrow sense heritability was observed to be less than 50% (48.81%) indicated non-additive gene action.

Total yield per plant (g)

The result pertaining to components of genetic variation for this trait revealed that the estimate of H_1 , H_2 and h^2 were highly significant while other parameters viz. D, E and F were non-significant. The value of H_1 (455052.50) was greater than D (60939.50), indicating the presence of more dominant genes than additive ones. The positive value of F showed preponderance of dominant allele. The value of (H_1/D) $^{1/2}$ was more than one (2.73) indicating over-dominance. The proportion of genes with positive and negative effects ($H_2/4 H_1$) in parents was found to be 0.20, which denoted asymmetry at loci showing dominance. The proportion of dominance and recessive genes $[(4D H_1)^{1/2} + F / (4D H_1)^{1/2} - F]$ was 2.46 indicating excess of dominant genes in the parents. The number of group of genes (h^2/H_2) exhibiting dominance and controlling the character was 3.93. Very low values of narrow sense heritability (9.26%) indicated that non-additive gene action played an important role in inheritance of this trait.

The dominant and additive, both the variances were predominance component governing the expression of all the traits studied. Similar was also reported by [6] in bottle gourd. However, the dominance components were higher than the additive component for most of the traits. These results are in conformity with [7, 8, 9]. In the present investigation, the predominance of non-additive gene action and low narrow sense heritability for most of the yield attributing characters suggesting the importance of heterosis breeding in cucumber. Similar was reported by [5, 10].

Conclusion

Gene action studies are very important for formulating any breeding programme to know the inheritance of the traits. Genetic component analysis in the present study revealed that earliness, yields and its attributing traits are largely controlled by non-additive gene action hence heterosis breeding method can be used for improving these traits. Similarly, narrow sense heritability was also found to be less than 50% for all the traits except for average fruit weight indicating prevalence of dominance effects suggesting the importance of heterosis breeding in the present materials.

Application of research: Gene action studies can be applied for deciding the breeding method to improve a particular trait of a cucumber

Research Category: Breeding

Abbreviations:

g: gram
cm: centimeter
D : Component of variation due to additive effects of genes.
 H_1 : Dominance variance component of variation due to dominant effect
 H_2 : Symmetry and asymmetry of alleles
F: Mean of F_r over the array being the covariance of additive and non-additive effects in the r^{th} array
E: Environmental variance

***Data analysis software package:** SAS 9.4.

Acknowledgement / Funding: Author thankful to the Division of Vegetable Science, ICAR-Indian Agricultural Research Institute, Pusa, New Delhi, 110012 for providing necessary facilities to carry out the study.

***Research Guide or Chairperson of research:** Dr. A.D. Munshi

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Research project name or number: PhD Thesis

Author Contributions: All author equally contributed

Author statement: All authors read, reviewed, agree and approved the final manuscript

Conflict of Interest: None declared

Ethical approval: This article does not contain any studies with human participants or animals performed by any of the authors.

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