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Component Analysis of Genetic Variance in Okra (*Abelmoschus esculentus* L. (Moench)

M.I. Makdoomi[*], Kouser P. Wani, K. Hussain, Ambreen Nabi, Ajaz A. Malik, Ummaiyaih H. Masoodi and M. Mudasir Magray

[1]KVK, budgam, India
[2]Division of Vegetable Science, Sher-e-Kashmir University of Agricultural Sciences and Technology of Kashmir, Shalimar, Srinagar – 190 025 (J&K), India

*Corresponding author

A B S T R A C T

The estimates of components of genetic variation in okra revealed that additive component ($\hat{D}$) was significant for all traits i.e. days to first flowering, days to first pod picking, plant height, number of nodes, internodal length, pod length, pod girth, avg. pod weight, number of pods per plant, pod yield per plant (g), number of seeds per pod, 100 seed weight (g), seed yield per plant (g) and pod yield (t/ha). Both the components of dominance variance ($\hat{H}_1$ and $\hat{H}_2$) were significant for all the traits and were much higher in magnitude than the corresponding additive components ($\hat{D}$), thus revealing the importance of non-additive gene action in the inheritance of traits under study. Net dominance effect ($\hat{h}^2$) was found to be positive and significant for all traits except 100 seed weight in all the environments as well as in data pooled over environments. The $\hat{F}$ value was positive and significant for days to first flowering, days to first fruit picking, number of nodes, internodal distance, plant height, pod length, pod girth, number of pods per plant, pod yield per plant and seed yield per plant indicating the role of dominant alleles towards dominance variance and non significant for average pod weight, number of seeds per pod, 100 seed weight and pod yield revealing the role of recessive alleles towards dominance deviation.

Introduction

Okra or lady finger (*Abelmoschus esculentus* L. (Moench) is an annual vegetable crop grown from seed in tropical and subtropical parts of the world its tender green fruits are used as a vegetable and are generally marketed in fresh state, but sometimes in canned or dehydrated form the recent surge in widespread adoption of hybrids by farmers necessitates the development of new and higher yielding hybrids which are able to realise the high degree of economic heterosis. Several biometrical procedures are available for evaluation of parents and their crosses and to know the nature and magnitude of gene effects for expression of various metric traits. Diallel analysis as suggested by Griffing (1956) and Hayman (1954) are sufficient enough to generate basic information on

nature of inheritance of traits and to assess the combining ability of parents. It also helps to obtain information about genetic systems governing the inheritance of attributes to be improved, to assess the potential of different crosses and also to predict their performance in subsequent generations. It helps in formulating a coherent breeding methodology for crop improvement.

In the present study, diallel analysis over environments as proposed by Singh (1973) has been used to obtain information on combining ability, gene action and genetic parameters. Keeping all the facts under consideration, present investigation, involving a diallel crossing programme on ten diverse lines of okra, was initiated to generate information on the nature and magnitude of gene action for morphological, yield and yield attributing traits.

Materials and Methods

The present investigation entitled "Component analysis of genetic variance in okra [*Abelmoschus esculentus* L. (Moench)] was conducted during *Kharif* 2012 at three different locations viz., Vegetable Experimental Farm, SKUAST-Kashmir, Shalimar; Mountain Research Centre for Field Crops, Khudwani and Regional Research Station and Faculty Of Agriculture, Wadura..

The basic materials consisted of ten diverse genotypes of okra viz.SKBS-11, Pant bhindi, IC-117018, Azad Ganga, Parbhani kranti, Lam-1, GO-2, Red Bhindi, Arka Anamika and Pusa Sawani. Forty five F_1 crosses were generated through 10 x 10 diallel mating design at Vegetable Experimental Farm, Division of Vegetable Science, SKUAST-Kashmir, Shalimar during the year 2011. The final experimental materials consisting of ten parents and forty five F_1 crosses were evaluated during year 2012 at three locations.

At each location the experiment was laid out in completely randomized block design with three replications. The row to row and plant to plant spacing was maintained at 45 x 25 cm. Recommended package of practices were adopted to raise a healthy crop at all the locations

The observations like days to first flowering, days to first pod picking, plant height (cm), number of nodes, internodal length (cm), pod length (cm), pod girth (cm), avg. pod weight (g), number of pods per plant, pod yield per plant (g), number of seeds per pod, 100 seed weight (g), seed yield per plant (g) and pod yield (t/ha) were recorded.

Results and Discussion

The pooled data estimates of components of genetic variance and their corresponding standard errors for the traits have been presented in the table 1.1 and 1.2 while as the proportion of related genetic parameters along with the estimates of average degree of dominance and heritability in narrow sense are presented in the table 2. The results are presented as follows:

Genetic variances are used for working out various genetic parameters. Six components of variance were worked out i.e., additive variance (D), dominance variance (H_1), proportion of positive and negative genes in parents (H_2), expected environmental component (E), mean of F_r over the array (F) and dominance effect (h^2).

These estimates were used to generate some genetic ratios i.e., average degree of dominance ($\hat{H}_1/\hat{D}$)$^{1/2}$, ratio of dominant and recessive genes in the parents [(4DH$_1$)$^{1/2}$ + F]/[(4DH$_1$)$^{1/2}$-F], the number of gene groups (h^2/H_2) and the proportion of positive and negative genes ($H_2/4H_1$).

Table.1.1 Estimates of components of genetic variation for various traits in Okra (*Abelmoschus esculentus* L. Moench)

Table-1.1: Estimates of components of genetic variation for various traits in Okra (*Abelmoschus esculentus* L. Moench)							
Components	**Days to first flowering**	**Days to first fruit picking**	**Number of nodes**	**Internodal distance**	**Plant height**	**Pod length**	**Pod Girth**
	Pooled	**Pooled**	**Pooled**	**Pooled**	**Pooled**	**Pooled**	**Pooled**
$\hat{D}$	8.95**±2.34*	11.62**±2.42	6.12**±1.05	0.95**±0.25	528.21**±40.34	0.61**±0.11	0.25**±0.04
$\hat{H}_1$	31.52**±7.12	29.94**±5.06	10.21**±2.16	2.51**±0.49	543.51**±86.45	4.93**±0.38	0.61**±0.12
$\hat{H}_2$	28.36**±3.64	29.83**±3.65	9.38**±1.76	1.95**±0.32	416.46**±72.67	2.95** ±0.52	0.61**±0.07
$\hat{h}^2$	5.12*± 2.12	7.16*± 3.57	4.67**±1.24	1.34**±0.31	348.21**±48.91	2.17**±0.32	0.24**±0.04
$\hat{F}$	8.62*± 4.28	10.81*±5.15	1.82*±0.42	1.41*±0.39	490.37**±92.58	0.58*±0.21	0.37* ±0.13
$\hat{E}$	0.25± 0.71	0.26±0.61	0.14±0.29	0.02±0.05	0.29±12.21	0.04 ±0.06	0.04 ±0.01

*,** significant at 5 and 1% level of significance

Table.1.2 Estimates of components of genetic variation for various traits in Okra (*Abelmoschus esculentus* L. Moench)

Table-1.2: Estimates of components of genetic variation for various traits in Okra (*Abelmoschus esculentus* L. Moench)							
Components	**Average pod weight**	**Number of pods plant⁻¹**	**Pod yield plant⁻¹**	**Number of seeds plant⁻¹**	**100 seed weight**	**Seed yield plant⁻¹**	**Total pod yield**
	Pooled	**Pooled**	**Pooled**	**Pooled**	**Pooled**	**Pooled**	**Pooled**
$\hat{D}$	0.62** ±0.27	5.67**±0.95	494.21*±200.34	65.25**±11.64	0.19**±0.03	315.01**±46.23	2.59*±1.16
$\hat{H}_1$	2.67**±0.62	10.36**±1.97	208*±48.21	180.36**±30.58	0.37**±0.07	634.25**±53.21	11.94**±2.61
$\hat{H}_2$	2.24**±0.54	8.67** ±1.72	127.32*±57.24	146.25**±23.95	0.29**±0.05	487.32**±81.24	10.61**±2.14
$\hat{h}^2$	2.64**±0.32	5.67**±1.09	124.25*±46.32	119.25**±17.85	0.07±0.04	152.32*±65.24	2.27*± 1.12
$\hat{F}$	0.96± 0.67	2.62*± 1.13	368.32**±46.31	42.36± 33.08	0.08±0.05	455.31**±119.82	1.71±2.58
$\hat{E}$	0.01±0.07	0.19±0.24	7.69± 6.21	0.41±4.36	0.01±0.01	1.38±11.24	0.06±0.31

*, ** significant at 5 and 1% level of significance

Table.2 Proportion of related genetic parameters of variation for maturity and yield attributing traits in okra (*Abelmoschus esculentus* L. Moench) (pooled)

S.No.	Proportion	$[\dfrac{\hat{H}_1}{\hat{D}}]^{1/2}$	$\dfrac{\hat{H}_2}{4\hat{H}_1}$	$\dfrac{KD}{KR}$	$\dfrac{\hat{h}^2}{\hat{H}_2}$	Heritability (n.s)
1	Days to first flowering	1.87	0.22	2.16	0.18	0.25
2	Days to first fruit picking	1.59	0.24	2.47	0.24	0.26
3	Plant height	1.014	0.191	2.713	0.49	0.437
4	Number of nodes	1.329	0.220	1.256	0.68	0.548
5	Internodal distance	1.568	0.191	2.198	0.83	0.559
6	Pod length	2.694	0.251	1.739	0.73	0.485
7	Pod girth	1.593	0.191	2.425	0.39	0.151
8	Average pod weight	2.009	0.221	1.175	1.17	0.249
9	Number of pods plant^{-1}	1.291	0.237	1.269	0.65	0.527
10	Pod yield plant^{-1}	2.546	0.229	1.417	0.61	0.269
11	Number of seeds pod^{-1}	1.632	0.218	1.452	0.81	0.449
12	100 seed weight	1.694	0.202	1.419	0.24	0.486
13	Seed yield plant^{-1}	2.261	0.203	2.357	0.31	0.566
14	Pod yield	2.418	0.229	0.566	0.21	0.328

Perusal of data pooled over environments indicated that additive genetic variance component ($\hat{D}$) was significant for all traits under study. Measures of dominance components ($\hat{H}_1$ and $\hat{H}_2$) were significant for all the traits. These results indicated the involvement of both additive and dominance components in the inheritance of these traits. However, the magnitude of dominance components, in general, was higher than the corresponding additive component. This suggests the greater role of dominance component in the inheritance of these traits. Similar observations were also reported by Vachhani and Shekhat (2008) and Shashank *et al.,* (2012). A preponderance of dominant gene action over the additive one was also observed for all traits. Vachhani and Shekhat (2008) observed similar gene action for yield and its attributing traits. Asymmetrical distribution of genes with positive and negative effects in the parents was observed in all traits in the present study. In such a situation, the non-additive genetic variance could be justified by either the dominance or the over dominance effects of genes in heterozygous position. The net dominance effects (h^2) was significant and positive for all traits, suggesting significant high dominance effects in the heterozygote over all loci and positive direction of dominance for these traits. (F) values were found to be positive and significant for days to first flowering, days to first fruit picking, number of nodes, internodal distance, plant height, pod length, pod girth, number of pods per plant, pod yield per plant and seed yield per plant, depicting higher frequency of dominant alleles in the parents with respect to these traits. For rest of traits, (F) values were positive but non significant, depicting the relative frequency of dominant and recessive alleles in the parents was proportionally equal. Vachhani and Shakhat (2008) reported similar observations in a diallel cross of okra. The average degree of dominance ($\hat{H}_1 / \hat{D}$)$^{1/2}$ was greater than unity in all characters, indicating over dominance in the expression of these traits.

The estimate of $(H_2/4H_1)$ was less than 0.25 in all traits, revealing asymmetrical distribution of genes in parents with respect to these traits. The value of KD/KR ratio was greater than unity in all traits, indicating excess of dominant alleles as compared to recessive alleles. The estimate of (h^2/H_2) was greater than 0.50 for number of nodes, internodal distance, pod length, average pod weight, number of pods per plant, pod yield per plant and number of seeds per pod, indicating greater proportion of dominant genes/ gene groups for these traits, whereas for rest of the traits, the valve was less than 0.50 indicating greater proportion of recessive genes. The heritability (n.s.) estimates for days to first flowering, days to first pod picking, pod girth, average pod weight, pod yield per plant was low(10-25%); whereas for rest of traits, heritability (n.s.) estimates were medium(30-55%). The low to medium heritability (n.s.) indicated the major role of non-additive gene action in the inheritance of most of the characters and limited scope of their improvement through straight selection. Similar results were also reported by Srivastava *et al.,* (2008), Indurani *et al.,* (2002) and Vachhani and Shekhat (2008).

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