Original Research Article

Diallel analysis to investigate the nature of gene action in okra[*Abelmoschus esculentus* (L.) Moench]

ABSTRACT

In a diallel scheme excluding reciprocal was adopted in okra to develop 45 F_1 hybrids in *Rabi*season 2020 and the hybrids along with 10 parents were evaluated complete randomized block design in *Kharif* 2020. The additive components (D) of genetic variance was found to be highly significant for days to first flowering, days to 50% flowering**, node at first flower appear**, number of branches per plant and plant height (cm) at harvesting. The estimates of dominant components *viz.*$\hat{H}_1$,$\hat{H}_2$ and $\hat{h}^2$ were evaluated which $\hat{H}_1$ and $\hat{H}_2$ were find to be highly significant for all the characters. Dominance components ($\hat{h}^2$) were found in few characters *viz.* days to first flowering, number of fruit per plant, fruit weight, fruit length, fruit diameter, 100 seed weight, fruit yield per plant and fruit yield quintal per hectare suggested the role of dominance components for this traits. Near about fifty percent traits was showed significant value in environment component. The average degree of dominance was more than one for all the characters showed over dominance.

Key Word: Additive components, dominant components, diallel analysis, gene action.

UNDER PEER REVIEW

INTRODUCTION

Okra (*Abelmoschus esculentus* L. (Moench) is an economically important vegetable crop grown in the tropical and sub-tropical parts of the world. This crop is suitable for cultivation as a garden crop as well as in large commercial farms. It is one of the most widely known and utilized species of the family Malvaceae (Naveed *et al.*, 2009). Okra/lady's finger is a powerhouse of valuable nutrients. Due to its high soluble fiber content in the form of gum and pectin, it helps to lower serum cholesterol and the risk of heart diseases. Okra mucilage has medicinal applications when used as a plasma replacement or blood volume expander. Okra has several potential health beneficial effects for some of the important human diseases like cardiovascular diseases, type 2 diabetes, digestive diseases and some cancersRomdhane*et al.* (2020).In India, okra is cultivated in Uttar Pradesh, Bihar, Orissa, West Bengal, Andhra Pradesh, Karnataka and Assam (Benchasri*et al.*, 2012). A good knowledge of the nature and inheritance of economically important quantitative traits will help to develop a more pragmatic breeding prgramme. Diallel analysis is a useful tool for getting a quick overview of the gene action involved in the inheritance of various quantitative traits.Several hybrids have been released by public as well as private sectors for its commercial cultivation. The area under F_1 hybrids is growing fast, which has helped to enhance the production and productivity of this crop.Different researchers(Adenji and Kehinde, 2007),Verma&Sood (2015) andBhatt *et al.* (2015) have investigated the nature of gene action on several biometric traits in okra.However, the mode of action of genes differs from germplasm to germplasm. Consequently, the study was conducted to elucidate the nature and extent of gene action involved in the inheritance of fruit yield and their constituents.

MATERIAL AND METHODS

The investigation on gene action involved in inheritance ofyield and yield attributing traitsin okra was carried out at the Vegetable Research Farm, Department of Vegetable Science, Banda University of Agriculture and Technology, Banda, Uttar Pradesh. The experimental farm situated in 24º 53'-25º 55' N latitudes and 80º 07'-81º 34' E longitudes.Experiment was done during *rabi* season by providing good agronomic practices to keep the crop in good condition. The material for experimentation comprised of 10 distinct genotypes and 45 F_1 hybrids**. The observations were recorded on randomly selected five plants in each replication of F_1s and their parents.** The selected plants were tagged and properly labeled before flowering for taking observations, *viz.* Days to first flowering, Days to 50% flowering, Plant height (cm), Number of branches per plant, Node at which first flower Appear, Internodal length (cm), Number of nodes per plant, Number of fruits per plant, Fruit yield per plant (g), Fruit yield ($q\ ha^{-1}$), Fruit length (cm), Fruit diameter (cm), Fruit weight (g), Days to edible fruit maturity, Number of seeds per fruit, Seed weight per fruit, 100-Seed weight and Seed yield per plant. Genetic parameter *viz.*, D, H_1, H_2, h^2 and E and the standard ratios of these genetic parameters were worked out by component of variance methods, using second degree statistics and error mean square (Hayman, 1954).

RESULTS AND DISCUSSIONS

The findings on the additive genetic effects were recordedpositive and significant for characters *viz.*days to first flowering, days to 50% flowering, node at first flower appear, number of branches per plant and plant height (cm) at harvesting indicating high transmissibility in the progeny.

Therefore, it was conformed that direct selection in okra for such traits willbe useful which is conformed with the findings of Devi *et al.* (2020), Verma and Sood (2015), Bhatt *et al.* (2015) and Kumar *et al.* (2014). Among all the charactersthe F value (mean for over arrays) observed significant only for days to 50% flowering, node at first flower appear and plant height (cm) at harvesting (table-1) implying that dominant alleles were preponderance for these traits in the parents (Table 1). The estimates of components of variation due to dominance (H_1) and proportion of dominance due to positive and negative genes (H_2) showed the importance of non-additive gene effects than additive gene effects in controlling the expression of all eighteen characters i.e. days to first flowering, days to 50% flowering, node at first flower appear, edible fruit maturity, node number/plant, internodal length, plant height, number of fruits per plant, fruit weight, fruit length, fruit diameter, number of seeds per fruit, seed weight per fruit, 100-Seed weight, seed yield per plant, fruit yield per plant and fruit yield quintal per hectare these characters magnitude of dominance effect is more compare to the additive component, hence solution may be practiced in the segregating population and also intermating of selected plants in segregating population or recurrent selection may be practiced to improve the yield (Table 2).

UNDER PEER REVIEW

The estimated mean degree of dominance $(H_1/D)^{1/2}$ estimate was more than one for all traits indicating repulsive phase linkage or over dominance. Which is accordance withVachhani and Shekhat (2008), Solankey*et al.* (2012) and Mrinmoy*et al.* (2013).

The proportion of total dominant to recessive alleles $[(4D\hat{H}_1)^{1/2} + F/ (4D\hat{H}_1)^{1/2} - F]$pooled over all the parents also indicated unequal frequency of dominant and recessive genes with more number of dominant genes in all the traits except for internodal length (cm), fruit yield per plant and fruit yield quintal per hectare have predominance of recessive alleles. So it can be assumed that the parents used were carrying more of recessive than dominant alleles for the above traits.

The unequal distribution of alleles over loci is obtained by the ratio of $H_2/4H_1$, which is estimate of uv. The uv estimates were in range of 0.15 to 0.24.

The proportion of genes with positive and negative effects in the parent is less than 0.25 for all eighteen characters indicates positive and negative alleles at the loci exhibiting dominance were not in equal proportions of the parents of interest.Similar results were finding in line with **Vachhani&Shekhat (2008) Ramesh *et al.* (2017) and Paul *et al.*, (2017). If** the proportion was equal to 0.25 it indicates that the positive and negative alleles at the loci are in equal proportion in the parents. The knowledge of number of gene groups responsible for a particular character is important for the genetic progress through selection. The ratio of number of gene group was low for most of all the characters under studies excluding number of branch per plant, fruit length (cm) and seed yield per plantindicating that a few genes or group of genes generally controlled the inheritance of particular trait.

The estimates of sum of dominance effect over all loci (h_2) were positive and significant for days to first flower, number of fruit per plant, fruit weight (g), fruit length (cm), fruit diameter, 100-seed weight, fruit yield per plant and fruit yield quintal per hectare.Similar results were found by Hamada *et al.*, (2015), Devi *et al.* (2020) and Vekariya*et al.* (2020).Consequently, in this study, both additive and non-additive genetic components were important in fruit yield and inheritance of those components, with non-additive genetic effects predominant. Accordingly, it is suggested that improvement of fruit yield and its characteristics in okra can be achieved by breeding methods such as selective diallel mating followed by selection in the advanced generation. The positive correlation coefficient (r) between parental order of dominance (Wr + Vr) and parental measurement (Yr) showed positive results for all the characters indicated that the excess for recessive gene for these traits in the parental population. For rest of the characters including days to edible fruit maturity, number of node per plant, fruit diameter (cm), number of seed per fruit and seed weight per fruit was negative which indicated preponderance of dominant gene in the parents. The value of $t^2$was found significant for all the eighteen characters indicated the validity of the hypothesis of assumption of diallel cross analysis.

UNDER PEER REVIEW

It was suggested that the heterosis breeding might be advantageous for improvement of yield and its component traits in okra. The findings are similar to that ofAyesha *et al.* (2017) and Devi *et al.*(2020).

Abbreviations

Symbols	**Descriptions**	**Symbols**	**Descriptions**
$\hat{D}$	(Additive effect)	$(\hat{H}_1/\hat{D})^{1/2}$	(Mean degree of dominance)
$\hat{H}_1$	(Dominance effect)	$\hat{H}_2/4\hat{H}_1$	(proportion of gene with +/- effects in parents)
$\hat{H}_2$	(Dominance including asymmetry of +/- effect of genes)	$(4\hat{D}\ \hat{H}_1)^{1/2} + \hat{F}/(4\hat{D}\ \hat{H}_1)^{1/2} - \hat{F}$	(Proportion of dominant and recessive genes in parents)
$\hat{F}$	(Mean Fr Over arrays)	$\hat{h}^2/\hat{H}_2$	(Number of genes groups)
$\hat{E}$	(Environmental component)	R	(Correlation coefficient)

Conclusion

Form this studies it is concluded that both the additive and non-additive conflicts were initiate to be primein genetic control of all eighteen quantitative and associated characters in okra. The adoption of a population improvement technique, like diallel selective mating or mass selection with simultaneous random mating, can allow in the release of new varieties of okra with higher yields.

UNDER PEER REVIEW

Table-1 Estimates of components of variation and their related statistics in 10 x 10 diallel crosses for Days to First Flowering, Days to 50% Flowering, Node at first flower appear, Days to Edible Fruit Maturity, Number of Node/Plant, Internodallength (cm), Number ofBranches/ Plant, Plant height(cm) atHarvesting and No. of fruit / plant of okra

Components of variation and related statistics	Days to First Flowering	Days to 50% Flowering	Node at first flower appear	Days to Edible Fruit Maturity	Number of Node/Plant	Internodal length (cm)	Number of Branches/ plant	Plant height (cm) at harvesting	No. of fruit / plant
$\hat{D}$	3.45* ± 1.27	6.85* ± 1.29	0.89* ± 0.16	1.65 ± 3.94	1.41 ± 1.96	0.14 ± 0.18	0.12* ± 0.03	229.97* ± 49.63	1.96 ± 2.47
$\hat{H}_1$	14.54* ± 2.7	15.43* ± 2.74	2.52* ± 0.35	21.17* ± 8.39	25.4* ± 4.18	1.64* ± 0.38	0.53* ± 0.07	1002.58* ± 105.65	45.15* ± 5.25
$\hat{H}_2$	11.6* ± 2.29	10.06* ± 2.33	1.47* ± 0.3	18.2* ± 7.13	23.95* ± 3.55	1.48* ± 0.33	0.51* ± 0.06	867.72* ± 89.79	41.19* ± 4.47
$\hat{F}$	4.76 ± 2.93	10.94* ± 2.97	1.74* ± 0.38	4.15 ± 9.09	1.17 ± 4.53	-0.15 ± 0.42	0.04 ± 0.08	287.79* ± 114.52	2.08 ± 5.69
$\hat{h}^2$	3.54* ± 1.54	1.77 ± 1.56	0.07 ± 0.2	2 ± 4.77	1.6 ± 2.38	0.07 ± 0.22	-0.01 ± 0.04	59.31 ± 60.1	10.07* ± 2.99
$\hat{E}$	2.04* ± 0.38	1.23* ± 0.39	0.08 ± 0.05	4.36* ± 1.19	1.52* ± 0.59	0.1 ± 0.05	0.03* ± 0.01	9.28 ± 14.96	1.95* ± 0.74
$(\hat{H}_1/\hat{D})^{1/2}$	2.05	1.5	1.68	3.58	4.25	3.44	2.14	2.09	4.8
$\hat{H}_2/4\hat{H}_1$	0.2	0.16	0.15	0.22	0.24	0.23	0.24	0.22	0.23
$(4\hat{D}\ \hat{H}_1)^{1/2} + \hat{F}/(4\hat{D}\ \hat{H}_1)^{1/2} - \hat{F}$	2.01	3.27	3.76	2.08	1.22	0.72	1.18	1.86	1.25
$\hat{h}^2/\hat{H}_2$	0.31	0.18	0.05	0.11	0.07	0.04	-0.01	0.07	0.25
R	0.52	0.67	0.3	-0.28	-0.07	0.22	0.71	0.68	0.29
t^2	0.74	4.53	0.02	6.54	5.65	4.46	0.14	0.42	0.05

***, ** Significant at 5 per cent and 1 per cent probabilitylevels,respectively.**

UNDER PEER REVIEW

Table-2 Estimates of components of variation and their related statistics in 10 x 10 diallel crosses for Fruit Weight (g), Fruit Length (cm), Fruit diameter (cm), No. of Seeds per fruit, Seed Weight Per Fruit, 100-Seed Weight, Seed Yield Per Plant (g), Fruit yield per plant (g) and Fruit yield quintal per hectare of okra

Components of variation and related statistics	Fruit Weight (g)	Fruit Length (cm)	Fruit diameter (cm)	No. of Seeds per fruit	Seed Weight Per Fruit	100-Seed Weight	Seed Yield Per Plant (g)	Fruit yield per plant (g)	Fruit yield quintal per hectare
$\hat{D}$	3.56 ± 5.55	0.23 ± 0.14	0.01 ± 0.01	2.97 ± 10.54	0.1 ± 0.11	0.09 ± 0.19	16.54 ± 32.42	610.44 ± 369.97	188.4 ± 114.19
$\hat{H}_1$	68.73* ± 11.82	1.55* ± 0.3	0.08* ± 0.01	92.63* ± 22.43	1.29* ± 0.24	2.97* ± 0.4	253.64* ± 69.02	6133.55* ± 787.51	1893.03* ± 243.06
$\hat{H}_2$	60.18* ± 10.05	1.28* ± 0.25	0.06* ± 0.01	83.06* ± 19.06	1.04* ± 0.2	2.39* ± 0.34	219.22* ± 58.66	5642.27* ± 669.3	1741.41* ± 206.57
$\hat{F}$	8.36 ± 12.81	0.28 ± 0.32	0.02 ± 0.02	3.3 ± 24.31	0.17 ± 0.25	0.38 ± 0.43	21.74 ± 74.81	-298.87 ± 853.63	-92.24 ± 263.46
$\hat{h}^2$	38.32* ± 6.72	2.94* ± 0.17	0.03* ± 0.01	22.02 ± 12.76	0.15 ± 0.13	1.43* ± 0.23	-5.83 ± 39.26	5093.82* ± 448	1572.14* ± 138.27
$\hat{E}$	1.38 ± 1.67	0.3* ± 0.04	0.01* ± 0	4.09 ± 3.18	0.06 ± 0.03	0.09 ± 0.06	21.39* ± 9.78	124.39 ± 111.55	38.39 ± 34.43
$(\hat{H}_1/\hat{D})^{1/2}$	4.39	2.58	3.1	5.58	3.66	5.61	3.92	3.17	3.17
$\hat{H}_2/4\hat{H}_1$	0.22	0.21	0.2	0.22	0.2	0.2	0.22	0.23	0.23
$(4\hat{D}\ \hat{H}_1)^{1/2} + \hat{F}/(4\hat{D}\ \hat{H}_1)^{1/2} - \hat{F}$	1.73	1.62	2.38	1.22	1.66	2.11	1.4	0.86	0.86
$\hat{h}^2/\hat{H}_2$	0.64	2.3	0.5	0.27	0.14	0.6	-0.03	0.9	0.9
R	0.15	0.57	-0.01	-0.01	-0.38	0.42	0.26	0.62	0.62
t^2	4.53	0.79	0.12	12.77	1.18	22.25	3.76	1.70	1.70

***, ** Significant at 5 per cent and 1 per cent probabilitylevels,respectively.**

UNDER PEER REVIEW

REFERENCE

Adenji, O.T. and Kehinde, O.B. (2007). Combining ability and genetic components for length and width of pod in west African okra (*Abelmoschus caillei,A. Cheo. Stevels*). *J. of Agronomy.,* **6**(1):131-136.

Ayesha, Revanappa, D. S., Hadimani, H. P., and Siddappa, R., (2017). Nature of gene action in okra [*Abelmoschus esculentus* (L.) Moench] through diallel analysis. *International journal of current microbiology and applied science*,**6**(10):256-260.

Benchasri, S. (2012). Okra (*Abelmoschus esculentus* (L.) Moench) as a valuable vegetable of the world. *Ratarstvoipovrtarstvo,* **49**(1): 105-112.

Bhatt, J. P., Kathiria, K. B., Christian, S. S., & Acharya, R. R. (2015). Combining ability studies in okra [*Abelmoschus esculentus*(L.) Moench] for yield and its component characters. *Electronic Journal of Plant Breeding,* **6**(2): 479-485.

Devi, K. A., Kumar, P.S., Saravanan, K., Suganthi, K. A. and Sabesan, T. (2020). Studies on gene action in bhindi [*Abelmoschus esculentus* (L.) Moench]. *Plant archives,* **20**(9):2020.

Hamada, M., El-Aziz, A., &Zaater, M. (2015). Nature of gene action for some economic traits and combining ability in several geneotypes of okra. *Journal of Agricultural Chemistry and Biotechnology*, **6**(3): 53-63.

Hayman's B. I. (1954). The analysis of variance in diallel crosses. *Biometrics*, 10:235-244.Mrinmoy, D., Asif, M., Venkatesha, K. T., & Kumar, K. V. (2013). Nature of gene action in okra through diallel analysis. *Asian Journal of Bio Science,* **8**(1): 145-146.

Naveed, A., Khan, A. A. and Khan, I. A. (2009). Generation mean analysis of waterstress tolerance in okra (*Abelmoschus esculentus* L.). *Pakistan Journal ofBotany*,**41**: 195205.

Paul, T., Desai, R. T., & Choudhary, R. (2017). Genetic architecture, combining ability and gene action study in okra [*Abelmoschus esculentus* (L.) Moench]. *Int. J. Curr. Microbiol. App. Sci,* **6**(4): 851-858.

Rameshkumar, D., Gunasekar, R., & Sankar, R. (2017). Gene action studies for quantitative and qualitative traits in okra (*Abelmoschus esculentus* (L.) Moench). *IJCS,* **5**(5): 2309-2312.

UNDER PEER REVIEW

Romdhane, M. H., Chahdoura, H., Barros, L., Dias, M. I., Corrêa, R. C. G., Morales, P.& Ferreira, I. C. (2020). Chemical composition, nutritional value, and biological evaluation of Tunisian okra pods (*Abelmoschus esculentus* L. Moench). *Molecules*, **25**(20):4739.

Solankey, S. S., Singh, R. K., Singh, S. K., Singh, D. K., Singh, V. P., & Singh, P. (2012). Nature of gene action for yield and yield attributing traits in okra [*Abelmoschus esculentus* (L.) Moench]. *Asian J. Hort*, **7**(2):321-323.

Vachhani, J. H., &Shekhat, H. G. (2008). Gene action in okra (*Abelmoschus esculentus* (L.) Moench). *Agric. Sci. Digest*, **28**(2): 84-88.

Vekariya, R. D., Patel, A. I., Modha, K. G., Kapadiya, C. V., Mali, S. C., & Patel, A. A. (2020). Estimation of Heterosis, Gene Action and Combining Ability over Environments for Improvement of Fruit Yield and its Related Traits in Okra [*Abelmoschus esculentus* (L.) Moench]. *Int. J. Curr. Microbiol. App. Sci*, **9**(9): 866-881.

Verma, A., &Sood, S. (2015). Gene action studies on yield and quality traits in okra (Abelmoschus esculentus (L.) Moench). *African Journal of agricultural research*, **10**(43): 4006-4009.

UNDER PEER REVIEW