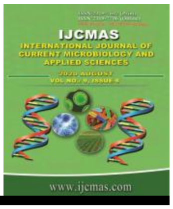
Int.J.Curr.Microbiol.App.Sci (2020) *9*(8): 3728-3732

International Journal of Current Microbiology and Applied Sciences
ISSN: 2319-7706 **Volume 9 Number 8 (2020)**
Journal homepage: http://www.ijcmas.com



Original Research Article https://doi.org/10.20546/ijcmas.2020.908.430

Genetic Analysis in Okra [*Abelmoschus esculentus* (L.) Moench] for Yield and its Contributing Traits

Ayushi Yadav, Aneeta Yadav* and Krishna Kumar Mishra

Faculty of Agricultural Sciences and Allied Industries, Rama University,
Mandhana, Kanpur (U.P.)-209217, India

**Corresponding author*

ABSTRACT

An experiment was undertaken on thirty eight genotypes of okra [*Abelmoschus esculentus* (L.) Moench] to determine the genetic variability, heritability and genetic advance in all genotypes. The wide range of variability was observed among eight characters of all genotypes. The phenotypic coefficient of variance (PCV) was generally higher than their respective genotypic coefficient of variance, thus revealing the role of environmental factors. The genotypic and phenotypic coefficient of variability were high for The genotypic and phenotypic coefficient of variability were high for edible yield per plant (91.78% and 306.85% respectively), plant height (65.12% and 177.56% respectively), number of seeds per fruit (21.07% and 33.92% respectively) and days to 50 % flowering (8.33% and 13.31% respectively) which indicates that maximum amount of variability present in the genotypes for these characters which would be amenable for further selection. High heritability (>70 %) coupled with high genetic advance (>25 %) as per cent of mean was observed for fruit diameter (71.10 % and 27.59 % respectively), indicating predominance of additive genetic component in governing of these traits and improvement of these traits through simple selection would be rewarding. It also indicates predominance additive gene action. Thus, there is immense scope for improving these characters through direct selection. Moderate heritability (>50 %) coupled with high genetic advance (>25 %) as per cent of mean was observed for number of branches per plant (52.40 % and 45.95 % respectively), number of fruit per plant (52.60 % and 27.87 respectively) and fruit length (51.20 % and 26.24 % respectively). This indicates the importance of additive effects for this trait and selection may be rewarding.

Keywords

Genetic variability, Heritability, Genetic advance and okra

Article Info

Accepted:
28 July 2020
Available Online:
10 August 2020

Introduction

Okra *(Abelmoschus esculentus (L.) Moench)* is commonly known as bhindi or lady's finger belonging to family Malavacesae having chromosome no is 2n = 130, 2n = 8x = 72 or 144. Okra is extensively grown in tropical, sub-tropical and warm areas of the world. It is a powerhouse of variable nutrients and because of this okra has a prominent position among all the vegetables in India. The experiment was conducted to estimate genetic variability, which is important for any breeding program for crop improvement or selection. An attempt was made to evaluate 38 genotypes (24 hybrids along with their parents (12 lines and 2 testers)) for different characters. The experiment was conducted with certain objectives to evaluate the *per se* performance of parents and their hybrids for some important characters, determining the magnitude of the genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV), heritability and genetic advance for yield and its component characters under the study.

Materials and Methods

The experiment was conducted at Research Farm, Faculty of Agricultural Sciences and Allied Industries, Rama University, Kanpur in the year 2019-20. The genotypes used in the experiment shows geographical as well as morphological diversity, which is the pre-requisite for any breeding programme. The experiment material consists of total 38 genotypes (24 hybrids from 12 lines and 2 testers), listed in Table 1. Randomized block design was used for experimentation. The observation were recorded for different traits *viz.,* days to 50% flowering, plant height (cm), number of branches/plant, length of fruit (cm), diameter of fruit (cm), number of seeds per fruit, number of fruits per plant and edible fruit yield per plant (g). The variances and corresponding standard errors of the mean were computed from the deviations of the individual values (Panse and Sukhatme, 1978). The observed values were subjected to genetic analysis.

Results and Discussion

Analysis of variance due to parents and hybrids for eight characters are presented in Table 2. ANOVA shows significant difference among hybrids for all the characters except plant height. The coefficient of variability, heritability and genetic advance estimates were estimated for eight characters and have been presented in Table 3. The characters under study are denoted as per following:

DFF- days to 50% flowering, PH- plant height (cm), NBPP- number of branches per plant, NFP- number of fruits per plant, FL- fruit length (cm), DF-fruit diameter (cm), SPF- number of seeds per fruit, EYPP- edible fruit yield per plant (g).

The magnitude of PCV was higher than that of GCV for all the traits revealing little influence of the environment in the expression of these traits. The high ratio of GCV and PCV indicate that some of the characters were influenced by the environment. The genotypic and phenotypic coefficient of variability were high for edible yield per plant (91.78% and 306.85% respectively), plant height (65.12% and 177.56% respectively), number of seeds per fruit (21.07% and 33.92% respectively) and days to 50 % flowering (8.33% and 13.31% respectively) which indicates that maximum amount of variability present in the genotypes for these characters which would be amenable for further selection. Characters like fruit diameter (0.08% and 0.11% respectively), number of branches per plant (0.38% and 0.72% respectively), fruit length (2.47% and 4.82% respectively) and number of fruits per plant (3.59% and 6.83% respectively) indicated limited variability in the genotypes under evaluation. This necessitates need for generation of new variability for these characters.

Heritability itself provides no clear indication about the amount of genetic improvement that is expected to come out from selection of individual genotype, estimation of heritability without genetic advance will not be of practical value, hence knowledge of genetic advance as per cent of mean coupled with heritability becomes more useful to work out an effective selection criteria. Genetic advance as per-cent of mean is the improvement in the mean of the selected family over the base population. High heritability (>70 %) coupled with high genetic advance (>25 %) as per cent of mean was observed for fruit diameter (71.10 % and 27.59 % respectively), indicating predominance of additive genetic component in governing of these traits and improvement of these traits through simple selection would be rewarding.

Table.1 List of genotypes used for genetic analysis in okra

S. No.	Parents	Genotypes
Lines (females)		
1	L1	Pusa Sawani
2	L2	P-7
3	L3	K.S- 312
4	L4	A-Abhaya
5	L5	Prabhani Kranti
6	L6	V.R.O – 6
7	L7	B.O- 2
8	L8	K.S – 325
9	L9	K.S – 326
10	L10	K.S- 443
11	L11	K.S- 445
12	L12	K.S- 447
Testers (Males)		
13	T1	A.B-1
14	T2	A.B-2
15-26	L1 to L12 × AB 1	Hybrids
27-38	L1 to L12 × AB 2	Hybrids

Table.2 Analysis of variance

	MSS								
	DF	**DFF**	**PH(cm)**	**NBPP**	**NFP**	**FL(cm)**	**DF(cm)**	**SPF**	**EYPP(g)**
Replication	2	28.18*	1179.04**	0.17	15.79	28.08***	0.071	0.542	1105.18*
Hybrids	23	29.36***	268.17	1.40***	12.46***	9.66***	2.21***	63.740***	624.01*
Line effect	11	39.72	346.42	1.88	19.15*	16.92**	0.15	79.943	556.41
Tester effect	1	37.56	296.06	3.12	9.39	2.21	0.11	171.125	1870.69
Line x tester	11	18.25**	187.39	0.77*	6.06	3.08	0.27***	37.792*	578.29
Error	46	6.60	166.13	0.35	3.95	2.97	0.02	16.25	321.01
Total	71	14.58	227.79	0.69	7.04	5.84	0.07	31.30	444.26

* Significant at 5 % probability level, **Significant at 1 % probability level, *** Significant at 0.1 % probability level

Table.3 Genetic parameters for different traits in okra

Traits	ECV (%)	GCV (%)	PCV (%)	Heritability h² (Broad Sense) (%)	Genetic Advance	Genetic Advancement as % of Mean
DFF	4.98	8.33	13.31	62.60	6.03	13.87
PH(cm)	112.44	65.12	177.56	36.70	12.90	11.36
NBPP	0.34	0.38	0.72	52.40	1.17	45.95
NFP	3.24	3.59	6.83	52.60	3.63	27.87
FL(cm)	2.35	2.47	4.82	51.20	2.97	26.24
DF(cm)	0.03	0.08	0.11	71.10	0.62	27.59
SPF	12.85	21.07	33.92	62.10	9.55	18.87
EYPP(g)	215.06	91.78	306.85	29.90	13.83	6.79

Moderate heritability (>50 %) coupled with high genetic advance (>25 %) as per cent of mean was observed for number of branches per plant (52.40 % and 45.95 % respectively), number of fruit per plant (52.60 % and 27.87 respectively) and fruit length (51.20 % and 26.24 % respectively). This indicates the importance of additive effects for this trait and selection may be rewarding.

High heritability coupled with moderate genetic advance as per cent of mean indicates non-additive gene action. As high heritability was being exhibited due to favourable influence of environment rather than genotype and selection for such traits may not be rewarding. No such case was observed under study.

Moderate heritability (>60 %) coupled with low genetic advance (less than 20 %) as per cent of mean was observed for days to 50% flowering (62.60 % and 13.87 % respectively) and number of seeds per fruit (62.10 % and 18.87 % respectively) indicating non-additive gene action and selection for such traits may not be rewarding.

In conclusion the estimates of phenotypic coefficient of variation (PCV) were higher than genotypic coefficient of variation (GCV) for all the characters. The genotypic and phenotypic coefficient of variability were high for edible yield per plant followed by plant height, number of seeds per and days to 50 % flowering which indicates that maximum amount of variability present in the genotypes for these characters which would be amenable for further selection. Moderate variation was noted in case of fruit diameter, number of branches per plant, fruit length and number of fruits per plant. The occurrence of moderate values for these parameters reveals reasonable scope of improvement through selection. Fruit weight exhibited low value of GCV and PCV and likely to show less response under selection. Heritability in broad sense ranged from 29.90% to 71.10%. High heritability with high genetic advance was reported for fruit diameter, number of branches per plant, number of fruit per plant and fruit length, indicating predominance of additive genetic component in governing of these traits and improvement of these traits through simple selection would be rewarding. In future, these experimental results may prove very useful for development of high yielding genotypes in okra.

References

Ali, H.A., M.H.Z. Eldekashy and A.A. Helay (2013). Combining ability and heterosis studies for yield components in some cultivars of okra (*Abelmoschus esculentus* L. Moench). *American Eurasian. J. agri. Environ. Sci.*, 13(2): 162-167.

Chaudhary, D.R., Jagmohan Kumar, P. Vidyasagar and S.K. Sharma (1991). Line × Tester analysis of combining ability of okra. *South Indian Hort.*, 39(6): 198-204.

Mehta, D.R., Dhaduk, L.K. and Patel, K.D. (2006). Genetic variability, correlation and path analysis studies in okra (*Abelmoschus esculentus* L. Moench). *Agric. Sci. Digest*, 26(1): 117-124.

Nagesh, G.C., R. Mulge, V. Rathod, L.B. Basavaraj and S.M. Mahaveer (2014). Heterosis and combining ability studies in okra (*Abelmoschus esculentus* L. Moench) for yield and quality parameters. *The Bioscan.*, 9(4): 1717-1723.

Pawar, V.Y., Poshiya, V. K. and Dhaduk, H. L.(1999). Heterosis studies in okra (*Abelmoschus esculentus* (L.) Moench). *G.A.U. Res. J.*, 25(1): 26-31.

Prakash, M., Kumar, M.S., Saravanan, K., Kannan, K. and Ganesan, J. (2002). Line x Tester analysis in okra. *Ann. Agril. Res.*, 23(2): 233-37.

Pravin Kumar Sharma, D. P. Mishra and Amit Pandey (2016). Genetic variability studies for yield and its contributing traits in okra [*Abelmoschus esculentus* (L.) Moench]. *Journal of Applied and Natural Science* 8 (3): 1634 – 1637.

Reddy, M.T., Kadiyala, H., Mutyala, G., Reddy, K.C., Begum H., Reddy, R.S.K. and Babu J.D. (2012). Genetic analysis for yield and its components in okra (*Abelmoschus esculentus* (L.) Moench). *Songklanakarin J. Sci. Tech.*, 34 (2): 133-141.

S. Abinaya, K.R. Saravanan*, P. Thangavel, R. Madhubala and K.R. Pushpanathan. (2020). Studies and heterosis and combining ability analysis in Okra (*abelmoschus esculentus* moench.) *Plant Archives.*, 20(I): 1340-1342.

Singh, B., Pal, A.K. and Singh, S. (2006). Genetic variability and correlation analysis in okra [*Abelmoschus esculentus* (L) Moench]. *Indian Journal of Horticulture*, 63(3): 281-285.

Yassin, G.M. and Anbu, S. (1997). Variability studies in bhendi. *South Indian Hort.* 45: 13-15.

How to cite this article:

Ayushi Yadav, Aneeta Yadav and Krishna Kumar Mishra. 2020. Genetic Analysis in Okra [*Abelmoschus esculentus* (L.) Moench] for Yield and its Contributing Traits. *Int.J.Curr.Microbiol.App.Sci.* 9(08): 3728-3732. doi: https://doi.org/10.20546/ijcmas.2020.908.430