

15(5): 765-772(2023)

ISSN No. (Print): 0975-1130 ISSN No. (Online): 2249-3239

Exploring Variability, Heritability and Genetic Advances: Case study in Okra [*Abelmoschus esculentus* (L.) Moench] through Four Distinct Crosses in F₂

Parth Bagadiya^{1*}, Priya Patel², C.G. Intwala³, Jwala Pranati⁴, Vidyut Balar¹

 ¹Department of Genetics and Plant Breeding, B. A. College of Agriculture, Anand Agricultural University, Anand-388 110 (Gujarat), India.
 ²Department of Genetics and Plant Breeding, N. M. College of Agriculture, Navsari Agricultural University, Navsari-396 450 (Gujarat), India.
 ³Main Sugarcane Research Station, Navsari Agricultural University, Navsari-396 450 (Gujarat), India.
 ⁴Department of Genetics and Plant Breeding, Professor Jayashankar Telangana State Agriculture University, Rajendranagar, Hyderabad-500 030 (Andhra Pradesh), India.

(Corresponding author: Parth Bagadiya*) (Received: 20 March 2023; Revised: 16 April 2023; Accepted: 20 April 2023; Published: 20 May 2023) (Published by Research Trend)

ABSTRACT: The goal of the current research was to investigate the effects of different quantitative traits on fruit yield in F₂ populations of okra, including their genotypic and phenotypic coefficients, broad sense heritability, and genetic progress. This research material contained four crosses *viz.*, first cross (Arka Abhay × NOL 17-6), second cross (Arka Anamika × NOL 17-6), third cross (Arka Abhay × NOL 18-02) and fourth cross (AOL 10-22 × NOL 18-02) together with their parents, F₁ and the segregating F₂ population. Due to the involvement of the segregating F₂ generation, the crosses were examined in a nonreplicated manner. Twelve characters with varying degrees of variability were observed. The number of branches per plant at final harvest, followed by fruit yield per plant, internodal length, fruits per plant, and plant height at final harvest, were found to have the highest magnitudes of PCV and GCV. The study encountered various difficulties, including the difficulty of reliably quantifying trait heritability due to environmental factors, as well as the complexity of analysing the genetic improvements. Despite these obstacles, the research gives vital insights into the variability and genetic potential of Okra, helping to develop breeding programmes for this crop. Most of the traits in the four crossings showed substantial genetic advancement along with high heritability.

Keyword: Genetic advance, Heritability, GCV, PCV, Okra, Variability.

INTRODUCTION

Okra [Abelmoschus esculentus (L.)] is a significant crop that is planted all throughout the tropics and subtropics of the world. It is an annual crop from the Malvaceae family that is frequently cross pollinated. Okra takes 90 to 100 days to mature from seed to harvest. Typically, it is an annual plant. The stem is strong, upright, branching irregularly and ranges in height from 0.5 to 4.0 metres. Although the flowers are axillary and solitary, the leaves are alternate and often five lobed. Each of the okra flower's five white to yellow petals bears a scarlet or purple spot at the bottom. Its diameter ranges from 4 to 8 cm and it dries out in a day. Okra is farmed for its young, immature fruits and also its nonfibrous pods that contain spherical seeds (Bagadiya et al. 2022). Fruits of okra are useful for the control of goitre disease due to high iodine content (Chaudhary, 1979). According to reports from Chinese study, an alcohol extract from the leaves of Abelmoschus can reduce proteinuria, improve renal function, reduce oxygen free radicals, and treat renal tubular and interstitial disorders. Okra mucilage has been shown to increase blood volume and may be used to treat kidney disease, lower proteinuria and enhance renal function

(Siesmonsma and Koume 2004). The intricate nature of okra's reproductive biology and the influence of environmental factors can complicate the accurate assessment of heritability. Furthermore, analysing the genetic advances resulting from multiple crosses in the F₂ generation requires a comprehensive understanding of the underlying genetic mechanisms. Any crop plant can be improved to increase productivity by first choosing suitable genotypes from the current variants and then using the superior kinds in the breeding programme. All the characters under examination had a lot of variation, indicating that there is opportunity for advancement in the desired direction. High GCV, which just evaluates the level of genetic variability existing for a character, is insufficient to determine the heritable variation. The best representation of the advance to be predicted through selection would therefore be provided by GCV along with heritability estimates. Heritability, however, does not reflect genetic advancement; rather, it just reveals how successfully selection in germplasm can be done based on morphological performance. Heritability estimates are more accurate when paired with genetic advancement and trustworthy in foretelling increase in performance through simple selection. The degree of progress that can be made in one cycle of selection for improving the various features is predicted by estimates of genetic advancement.

MATERIALS AND METHODS

The research was carried out at the Main Sugarcane Research Station, Navsari Agricultural University, Navsari-396450, during the kharif-2020 season. Navsari is located at an elevation of 11.98 m above mean sea level and is geographically located at 20°37' N latitude and 72°54' E longitude. The soil has a pH of 7.3 to 7.5 and is medium black. The growing seasons' weather was typical and ideal for crop growth. A planting distance of 60×30 cm was maintained. Cultural recommendations for okra were followed. Experimental material consisted of four crosses viz., first cross (Arka Abhay × NOL 17-6), second cross (Arka Anamika \times NOL 17-6), third cross (Arka Abhay \times NOL 18-02) and fourth cross (AOL 10-22 \times NOL 18-02) together with their parents, F_1 and the segregating F₂ population. The following characters were observed in ten plants from each parent, twenty plants from the F_1 generation, and one hundred plants from the F_2 generation. The days to first flowering, days to first picking, number of branches per plant, fruit length (cm), fruit weight (g), fruit girth (cm), plant height (cm), fruit yield per plant (g) and days to last picking were all recorded.

Based on the formula provided by Singh and Chaudhary (1977), the mean and variances were examined. The range for a certain character was represented by the minimum and maximum value based on specific plant observations. Based on mean and variance derived using data from unreplicated treatments, genotypic and phenotypic variances and coefficients of variance were determined. According to Burton and DeWane (1953), the genotypic and phenotypic coefficient of variance was calculated. Heritability, in its broadest definition, is the proportion of genetic variation to total population variance. It was calculated using Allard's formula (1960). According to what Johnson *et al.* (1955) suggested, genetic advance was calculated as a percentage over the mean.

RESULTS AND DISCUSSION

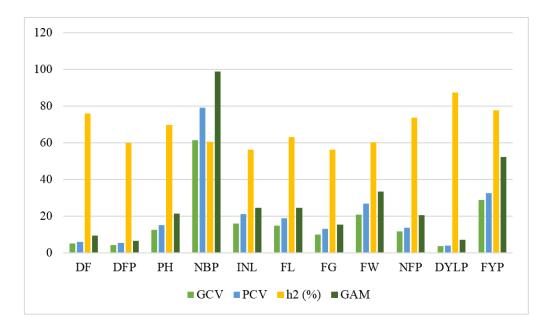
The variables used to measure variability, include range, mean, GCV, PCV, heritability, and genetic progress as a percentage mean for all eleven traits under study in respect to 100 plants of F_2 population is presented in Table 1, 2, 3 and 4 for all the four crosses, respectively. The range of values showed an excellent opportunity for breeders to pick appropriate basic material for further improvement. The mean character values are crucial in character selection. Graphical representation of GCV, PCV, $h^2(bs)$ and GAM for all the four crosses is shown in Graph 1, 2, 3 and 4 respectively.

In all four crosses, the high magnitude of GCV and PCV was seen for the number of branches per plant while specifically, in first cross for fruit yield per plant (28.74 and 32.59), fruit weight (20.97 and 27.00) and in second cross for fruit length (20.66 and 23.45) respectively. The high magnitude of PCV and GCV for the aforementioned characters demonstrated greater phenotypic and genotypic diversity within the F2 segregating populations and suggested that phenotypic selection may be used to improve these characters. Similar findings of higher GCV and PCV were reported by Kumar et al. (2012), Syullah et al. (2018) and Kumari et al. (2017) for number of branches per plant; Chandramouli et al. (2016), Deepanshu and Abdul (2017) and Singh et al. (2020) for fruit yield per plant; Adewusi and Adeweso (2018) for fruit weight and fruit length.

GCV and PCV were found to be of moderate for plant height (12.54 and 15.02), number of fruits per plant (11.71 and 13.63) and fruit length (14.93 and 18.77) in first cross, while internode length (14.99 and 19.24), fruit weight (10.86 and 12.02) and number of fruits per plant (12.42 and 14.89) in second cross whereas internode length (10.19 and 14.25), fruit length (12.67 and 18.72), fruit weight (12.61 and 15.48) and number of fruits per plant (13.85 and 17.32) in third cross and internode length (13.71 and 17.07), fruit length (13.26 and 18.33), plant height (10.31 and 15.21) and fruit weight (12.28 and 14.92) in fourth cross respectively, which indicates that environment has a significant impact on traits.

 Table 1: Range, mean and variance components, GCV, PCV, h_{bs}^2 and GAM for different characters in okra (Arka Abhay × NOL 17-6).

a	Traits	Range	Mean	Variance comp	oonents	~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~				
Sr. no.				$\sigma_{\rm p}^2$	σ_{g}^{2}	σ_e^2	GCV %	PCV %	h ² (%)	GAM %
1.	DF	43.00-59.00	53.51	10.31	5.38	4.94	5.23	6.00	76.03	9.39
2.	DFP	49.00-66.00	60.02	10.30	5.23	5.07	4.14	5.35	60.06	6.62
3.	PH	63.00-136.00	99.57	223.80	147.54	76.27	12.54	15.02	69.67	21.56
4.	NBP	0.00-2.00	1.10	0.75	0.39	0.37	61.62	79.13	60.65	98.85
5.	INL	3.50-8.40	5.79	1.51	0.89	0.63	15.94	21.26	56.25	24.63
6.	FL	7.50-16.20	11.53	4.69	2.58	2.11	14.93	18.77	63.30	24.48
7.	FG	4.10-7.10	5.21	0.47	0.26	0.22	9.92	13.21	56.32	15.33
8.	FW	5.10-19.00	11.16	9.08	5.50	3.59	20.97	27.00	60.29	33.54
9.	NFP	9.00-21.00	15.12	4.24	2.79	1.46	11.71	13.63	73.74	20.71
10.	DYLP	68.00-99.00	94.61	14.07	10.23	3.85	3.71	3.97	87.43	7.14
11.	FYP	64.90-323.00	170.21	3077.80	2306.68	771.13	28.74	32.59	77.73	52.19



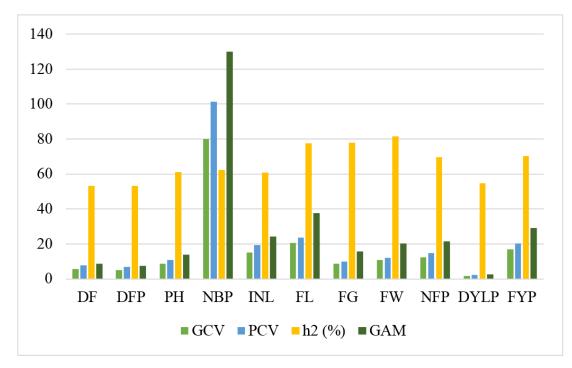
Graph 1: GCV, PCV, h_{bs}^2 and GAM for quantitative characters in F₂ progenies in first cross of Okra (Arka Abhay × NOL 17-6).

Since GCV indicates the heritable portion of total variation, which is needed for a breeder it would be more helpful for analysing the diversity observed in several traits for okra genotypes. This relates to an earlier report of Thulasiram et al. (2017) and Adewusi and Adeweso (2018) for plant height; Saleem et al. (2018) for fruit length; Makhdoomi et al. (2018), for internode length; Kumari et al. (2017) and Singh et al. (2020) for fruit weight; Thulasiram et al. (2017), Singh et al. (2017), Kumari et al. (2017), Saleem et al. (2018) and Verma et al. (2018) for number of fruits per plant. Days to first flowering, days to first picking, and days to last picking all revealed low magnitudes for GCV and PCV in all the four crosses, while fruit girth in second cross (8.59 and 9.74) and third cross (7.08 and 9.08) respectively. The most likely explanation may be that these abilities exhibit phenotypic plasticity, which is the primary source of variation other than genetic diversity. These findings also demonstrated that selection is inefficient for these qualities due to their limited genetic diversity. Similar outcomes were attained by Saleem *et al.* (2018) and Syullah *et al.* (2018) for days to first flowering; Chandramouli *et al.* (2016) and Kumar *et al.* (2020) for days to first picking; Priyanka *et al.* (2018) for days to last picking; Karthika and Maheshwari (2019) and Makhdoomi *et al.* (2018) for fruit girth.

As environment plays its role by interacting with genotype in order to give a particular phenotype so heritability estimates in broad sense which contains total genetic variability not additive affect alone therefore, it could not be a true representation of the genotype's genetic potential. As a result, a high heritability in combination with a significant genetic progress as a percentage of the mean can explain the frequency of additive genes. Additionally, given that these traits were controlled by additive genes, it predicts a stronger response for the selection of high yielding genotypes.

 Table 2: Range, mean and variance components, GCV, PCV, h_{bs}^2 and GAM for different characters in okra (Arka Anamika × NOL 17-6).

	Traits	Range	Mean	Variance	compone	nts				
Sr. No.				σ_p^2	σ_{g}^{2}	σ_e^2	GCV %	PCV %	h ² (%)	GAM %
1	DF	44.00-61.00	52.65	16.95	10.40	6.56	5.69	7.82	53.01	8.54
2	DFP	50.00-68.00	59.00	15.85	8.43	7.42	4.93	6.75	53.26	7.41
3	PH	67.00-118.00	93.00	102.86	54.61	48.25	8.52	10.91	61.03	13.71
4	NBP	0.00-2.00	0.83	0.71	0.38	0.32	79.97	101.39	62.21	129.94
5	INL	3.90-7.90	5.72	1.20	0.66	0.55	14.99	19.24	60.73	24.07
6	FL	6.80-16.60	12.35	8.39	6.47	1.93	20.66	23.45	77.60	37.49
7	FG	4.80-6.80	5.89	0.32	0.21	0.12	8.59	9.74	77.84	15.62
8	FW	9.50-14.60	12.22	2.16	1.16	0.99	10.86	12.02	81.64	20.22
9	NFP	8.00-22.00	15.06	5.02	2.97	2.06	12.42	14.89	69.63	21.35
10	DYLP	90.00-98.00	92.86	4.58	2.71	1.88	1.71	2.31	54.79	2.60
11	FYP	102.40-275.00	184.18	1384.87	875.68	509.19	16.93	20.20	70.23	29.23



Graph 2: GCV, PCV, h_{bs}^2 and GAM for quantitative characters in F₂ progenies in second cross of Okra (Arka Anamika × NOL 17-6).

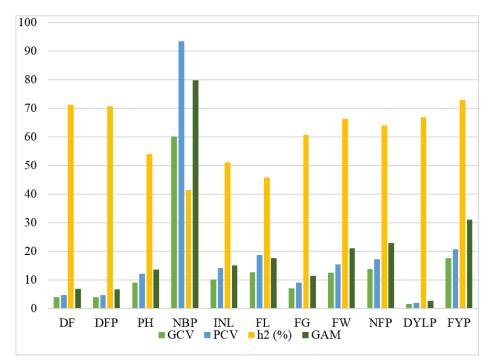
High heritability in conjunction with a high genetic advance as a percentage of the mean was observed for traits viz., plant height (69.67 and 21.56), number of branches per plant (60.65 and 98.85), fruit length (63.30 and 24.48), fruit weight (60.29 and 33.54), numbers of fruits per plant (73.74 and 20.71) and fruit yield per plant (77.73 and 52.19) in first cross respectively while, number of branches per plant (62.21 and 129.94), internode length (60.73 and 24.07), fruit length (77.60 and 37.49), fruit weight (81.64 and 20.22), numbers of fruits per plant (69.63 and 21.35) and fruit yield per plant (70.23 and 29.23) in second cross respectively. High heritability in conjunction with a high genetic advance as a percentage of the mean was recorded for characters like fruit weight (66.33 and 21.15), numbers of fruits per plant (63.95 and 22.82) and fruit yield per plant (72.89 and 31.08) in third cross and number of branches per plant (66.15 and 109.31), internode length (64.47 and 22.67), fruit weight (67.75 and 20.82),

numbers of fruits per plant (60.38 and 25.47) and fruit yield per plant (65.95 and 30.74) in fourth cross respectively. This suggests the presence of additive genes, and as a result, there is a lot of room for strengthening these traits through simple selection. This relates to an earlier reports of Alam et al. (2020) and Temam et al. (2020) for plant height; Khatik et al. (2012), Nwangburuka et al. (2012) and Sravanthi (2016), for number of branches per plant; Sravanthi (2016) and Temam et al. (2020) for internode length; Agbowuro et al. (2019) and Temam et al. (2020) for fruit length; Bello et al. (2015) and Temam et al. (2020) for fruit weight; Saleem et al. (2018), Adewusi and Adeweso (2018), and Alam et al. (2020) for number of fruits per plant; Bello et al. (2015), and Temam et al. (2020) for fruit yield per plant, therefore direct selection for these characters will be valuable for improvement.

Table 3: Range, mean and variance components, GCV, PCV, h_{bs}^2 and GAM for for different characters in
okra (Arka Abhay × NOL 18-02).

Sr. No.		_		Variance components						
	Traits	Range	Mean	$\sigma_{\rm p}^2$	σ_{g}^{2}	σ_e^2	GCV %	PCV %	h ² (%)	GAM %
1	DF	50.00-59.00	55.14	6.65	3.77	2.88	3.95	4.68	71.35	6.87
2	DFP	55.00-66.00	61.99	8.23	5.01	3.23	3.89	4.63	70.71	6.74
3	PH	67.00-121.00	93.93	131.60	68.22	63.39	8.98	12.21	54.09	13.61
4	NBP	0.00-2.00	0.86	0.65	0.23	0.41	60.25	93.52	41.50	79.95
5	INL	3.80-8.10	6.03	0.74	0.37	0.37	10.19	14.25	51.10	15.00
6	FL	6.50-16.00	12.04	5.08	2.71	2.37	12.67	18.72	45.80	17.66
7	FG	4.60-6.90	5.85	0.28	0.16	0.12	7.08	9.08	60.77	11.36
8	FW	7.69-18.60	13.05	4.08	2.88	1.20	12.61	15.48	66.33	21.15
9	NFP	6.00-17.00	12.75	4.88	3.00	1.87	13.85	17.32	63.95	22.82
10	DYLP	94.00-102.00	97.45	3.64	1.91	1.74	1.60	1.96	66.91	2.70
11	FYP	61.20-248.20	165.36	1171.72	775.87	395.85	17.67	20.70	72.89	31.08

Biological Forum – An International Journal 15(5): 765-772(2023)



Graph 3: GCV, PCV, h_{bs}^2 and GAM for quantitative characters in F_2 progenies in third cross of Okra (Arka Abhay × NOL 18-02).

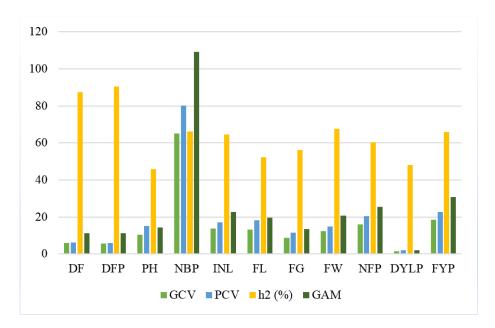
Characters were found to have high heritability and low genetic advance as a percentage of the mean for days to first flowering (76.03 and 9.39), days to first picking (60.06 and 6.62) and days to last picking (87.43 and 7.14) in first cross and also in third cross for same traits i.e., days to first flowering (71.35 and 6.87), days to first picking (70.71 and 6.74) and days to last picking (66.91 and 2.70) respectively, which signifies presence of dominance and epistatic gene action. The high heritability is not of the genotypic effect rather due to favourable environment effect and selection might not be rewarding for such traits. This result was in close proximity to that of Sravanthi (2016) and Saleem *et al.* (2018) for days to first flowering; Saleem *et al.* (2018)

and Priyanka *et al.* (2018) for days to first picking and days to last picking.

High heritability in conjunction with moderate genetic advance as per cent of mean was recorded for characters like plant height (61.03 and 13.71) and fruit girth (77.84 and 15.62) in second cross while, fruit girth (60.77 and 11.36) in third cross and days to first flowering (87.43 and 11.23) and days to first picking (90.46 and 11.20) in fourth cross respectively, shows that non-allelic gene interactions are involved in regulating these traits. This result was in close proximity to that of Khatik *et al.* (2012) and Alam *et al.* (2020) for days to first flowering; Khatik *et al.* (2012) and Maurya *et al.* (2019) for plant height; Maurya *et al.* (2019) and Alam *et al.* (2020) for days to first picking.

Table 4: Range, mean and variance components, GCV, PCV, h_{bs}^2 and GAM for for different characters in
okra (AOL 10-22 × NOL 18-02).

Sr. No.	Traits	Range	Mean	Variance	nts	GCV	PCV		GAM	
				$\sigma_{\rm p}^2$	σ_{g}^{2}	σ_e^2	%	%	h ² (%)	%
1	DF	55.00-69.00	63.2	15.52	13.67	1.85	5.83	6.23	87.43	11.23
2	DFP	60.00-76.00	70.15	17.79	16.22	1.57	5.72	6.01	90.46	11.20
3	PH	59.00-124.00	95.21	209.74	111.29	98.45	10.31	15.21	45.94	14.40
4	NBP	0.00-2.00	1.01	0.66	0.37	0.28	65.24	80.22	66.15	109.31
5	INL	3.50-8.10	5.99	1.04	0.59	0.46	13.71	17.07	64.47	22.67
6	FL	4.20-14.70	10.75	3.89	2.08	1.81	13.26	18.33	52.35	19.77
7	FG	4.20-6.80	5.79	0.45	0.23	0.22	8.66	11.54	56.34	13.39
8	FW	8.00-15.60	12.28	3.36	2.05	1.30	12.28	14.92	67.75	20.82
9	NFP	7.00-17.00	12.64	6.69	4.19	2.50	15.91	20.47	60.38	25.47
10	DYLP	95.00-105.00	98.82	4.55	2.42	2.14	1.50	2.16	48.22	2.14
11	FYP	70.7-265.20	154.04	1215.07	739.19	475.88	18.38	22.63	65.95	30.74



Graph 4: GCV, PCV, h_{bs}^2 and GAM for quantitative characters in F₂ progenies in fourth cross of Okra (AOL 10-22 × NOL 18-02).

Moderate heritability in conjunction with moderate genetic advance as per cent of mean was observed for fruit girth (56.32 and 15.33) in first cross while, plant height (54.09 and 13.61), internode length (51.10 and 15.00) and fruit length (45.80 and 17.66) in third cross and plant height (45.94 and 14.40), fruit length (52.35 and 19.77) and fruit girth (56.34 and 13.39) in fourth cross respectively which explains how both additive and non-additive gene action affects how certain traits are inherited so, in order to get rewarding results methods like progeny selection or any other modified procedures for selection which would exploit the additive gene effects should be used. This relates to an earlier report of Priyanka et al. (2018) for plant height; Maurya et al. (2019) and Alam et al. (2020) for fruit length Maurya et al. (2019) for fruit girth.

Moderate heritability in conjunction with low genetic advance as per cent of mean was recorded for days to first flowering (53.01 and 8.54), days to first picking (53.26 and 7.41) and days to last picking (54.79 and 2.60) in second cross and days to last picking (48.22 and 2.14) in fourth cross respectively which reveals that environment effect is playing an important role and selection would be not effective. Adewusi and Adeweso (2018) found comparable results for days to first flowering.

CONCLUSION

The results of the current study showed that the PCV was larger than the matching GCV for all of the characteristics, suggesting that there may be some degree of genotype-environment interaction. Strong genetic advance as a percentage of mean and high heritability estimations gives us idea about the governance of additive genes for the characters. It also suggests selection would be rewarding for high yielding genotypes as those characters mentioned above were

governed by additive genes. Thus, we should focus on those yield attributing characters which is giving higher response of high estimates of heritability along with high genetic advance.

FUTURE SCOPE

Okra [Abelmoschus esculentus (L.) Moench] being a highly nutritious vegetable that is rich in fibre, vitamins and minerals and is an excellent source of antioxidants is a tropical and subtropical vegetable crop that is widely grown around the world. By investigating the phenotypic diversity present in okra cultivars and landraces we can conduct comprehensive field trials to assess traits such as yield, fruit quality, disease resistance, abiotic stress tolerance and nutritional content. Analysing the variation in these traits and desirable identify superior genotypes with characteristics. Assessing the variability of okra genotypes in response to changing climatic conditions we can study the adaptive traits and stress tolerance mechanisms in different genotypes to identify those that are better suited to withstand climate change-induced challenges such as heat stress, drought and disease outbreaks.

Abbreviations: DF: Days to first flowering; FL: Fruit length; FYP: Fruit yield per plant; DFP: Days to first picking; FG: Fruit girth; GCV: Genotypic coefficient of variation; PH: Plant height; FW: Fruit weight; PCV: Phenotypic coefficient of variation; NBP: Number of branches per plant; NFP: Number of fruits per plant; hbs²: Heritability (Broad sense); INL: Internode length; DYLP: Days to last picking; GAM: GA as per cent of mean (%).

Author Contributions. Parth Bagadiya conducted the experiment. Parth Bagadiya, Priya Patel and Jwala Pranati collected all the phenotypic data. C. G. Intwala provided the material for research and also helped to meet the required agronomic practices. Parth Bagadiya, Priya Patel and Balar 770

Bagadiya et al.,

Biological Forum – An International Journal 15(5): 765-772(2023)

Vidyut analysed the data. Parth Bagadiya wrote the manuscript. All authors have done the proof reading.

Acknowledgement. The authors are gratuitous towards the Main Sugarcane Research Station, Navsari Agricultural University, Navsari, Gujarat, India for providing the seeds of Arka Abhay, Arka Anamika, NOL 17-6 and NOL 18-02, as well as the committee members and also would like to specially mention Department of Genetics and Plant Breeding, N.M.C.A., Navsari, for providing the required resources and guidelines for the research.

Conflict of Interest. The authors declare that they have no conflicts of interest.

REFERENCES

- Adewusi, O. F. and Adeweso, S. O. (2018). Genetic variability and heritability studies in west african okra (Abelmoschus caillei (A. Chev. Stevels). Journal of Experimental Agriculture International, 28(5), 1-8.
- Agbowuro, G. O., Salami, A. E., Awoyemi, S. O., Ogunwale, G. I., Kehinde-Fadare, A. F. and Olajide, O. O. (2019). Genetic variations, heritability and genetic advance studies among okra accessions grown in different agro-ecological zones in Nigeria. *International Journal of Food Science and Agriculture*, 3(1), 130-135.
- Alam, K., Singh, M. K., Kumar, M., Singh, A., Kumar, V., Ahmad, M. and Keshari, D. (2020). Estimation of genetic variability, correlation and path coefficient in okra (*Abelmoschus esculentus* (L.) Moench). *Journal* of Pharmacognosy and Phytochemistry, 9(5), 1484-1487.
- Allard, R. W. (1960). Principles of Plant Breeding. John Wiley and Sons.
- Bagadiya, P. G., Intwala, C. G., Patel, P. and Usadad, J. S. (2022). Assessment of the correlation and path analysis with association of growth and yield characteristics in okra [Abelmoschus esculentus (L.) Moench].
- Bello, O. B., Aminu, D., Gambo, A., Azeez, A. H., Lawal, M., Ali, I. and Abdulhamid, U. A. (2015). Genetic diversity, heritability and genetic advance in okra (*Abelmoschus esculentus* (L.) Moench). *Bangladesh Journal of Plant Breeding and Genetics*, 28(2), 25-38.
- Burton, G. W. and DeWane, E. M. (1953). Estimating heritability in fall fescue (*Festuaca cirunclindcede*) from replicated clonal material. *Agronomy Journal*, 45, 478-481.
- Chandramouli, B., Shrihari, D., Rao, A. V. D. D. and Rao, M. P. (2016). Studies on genetic variability, heritability and genetic advance in okra (*Abelmoschus esculentus* (L.) Moench) genotypes. *Plant Archives*, 16(2), 679-682.
- Chaudhary B. (1979). Vegetables. National Book Trust of India, 184-488.
- Deepanshu and Abdul, S. (2017). Genetic variability, heritability and correlation coefficient in okra (*Abelmoschus esculentus* (L.) Moench) in Allahabad agroclimatic conditions. *Plant Archives*, 17(2), 1597-1602.
- Johnson, H. W., Robinson, H. F. and Comstock, R. E. (1955). Genotypic and phenotypic correlation in soybean and their implications in selection. *Agronomy Journal*, 47, 477-483.
- Karthika, N. and Maheswari, T. (2019). Genetic variability, heritability and genetic advance in okra (*Abelmoschus* esculentus (L.) Moench). Annals of Plant and Soil Research, 21(1), 98-99.

- Khatik, K. R.; Chaudhary, R. and Khatik, C. L. (2012). Heritability, genetic advance and correlation coefficient in F₁ generation of okra (*Abelmoschus esculentus* (L.) Moench). *Asian journal of horticulture*, 7(2), 405-408.
- Kumar, P., Singh, K. V., Singh, B., Kumar, S. and Singh, O. (2012). Genetic variability, heritability and genetic advance in okra (*Abelmoschus esculentus* (L.) Moench). *Annals of Horticulture*, 5(1), 69-73.
- Kumar, Y., Singh, V. B., Gautam, S. K., Kumar, V. and Singh, V. (2020). Studies on genetic variability, heritability and genetic advance for fruit yield and its contributing traits in okra (*Abelmoschus esculentus* L. Moench). *The Pharma Innovation Journal*, 9(10), 351-354.
- Kumari, M., Solankey, S. S., Akhtar, S. and Neha, P. (2017). Assessment of genetic variability and character association in okra genotypes for yield and contributing characters. *Journal of Applied and Natural Science*, 9(3), 1825-1830.
- Makhdoomi, M. I., Wani, K. P., Jabeen, N., Nabi, A., Afroza, B., Hussain, K. and Singh, P. K. (2018). Variability analysis in okra (*Abelmoschus esculentus* (L.) Moench). Journal of Pharmacognosy and Phytochemistry, 7(2), 177-180.
- Maurya, V. K. and Yadav, G. C. (2019). Studies on extent of variability, heritability and genetic advance in okra (Abelmoschus esculentus (L.) Moench). Journal of Pharmacognosy and Phytochemistry, 8(1), 1779-1782.
- Nwangburuka, C., Denton, O., Kehinde, O., Ojo, D. and Popoola, A. (2012). Genetic variability and heritability in cultivated okra (*Abelmoschus esculentus* (L.) Moench). Spanish Journal of Agricultural Research, 10(1), 123-129.
- Priyanka, D. V., Reddy, M. T., Begum, H., Sunil, N. and Jayaprada, M. (2018). Studies on genetic variability, heritability and genetic advance in genotypes of okra (Abelmoschus esculentus (L.) Moench). International Journal of Current Microbiology and Applied Sciences, 7(5), 401-411.
- Saleem, A. M., Amjad, M., Ziaf, K. and Shahbaj, T. S. (2018). Characterization of okra (Abelmoschus esculentus) genotypes for fruit firmness, other horticultural traits and heritability studies. International Journal of Agriculture and Biology, 20(2), 345-352.
- Siesmonsma, J. S. and Kouame, C. (2004). Vegetables. In: Plant resources of tropical Africa 2 (Grubben GJH & Denton OA Eds.) PROTA Foundation, Wageningen, *Agriculture and Biology Journal of North America*, 4(5), 532-538.
- Singh, A. K., Singh, D. K., Singh, N. K., Kushwaha, M. L. and Maurya, S. K. (2020). Genetic analysis in okra under tarai region of Uttarakhand. *International Journal of chemical studies*, 8(1), 2767-2770.
- Singh, N., Singh, D. K., Pandey, P., Panchbhaiya, A. and Rawat, M. (2017). Correlation and path coefficient studies in okra (*Abelmoschus esculentus* (L.) Moench). *International Journal of Current Microbiology and Applied Sciences*, 6(7), 1096-1101.
- Singh, R. K., & Chaudhary, B. D. (1977). Biometrical methods in quantitative genetic analysis. Biometrical methods in quantitative genetic analysis.
- Sravanthi, U. (2016). Studies on Variability, Heritability and Genetic Advance in Okra (Abelmoschus esculentus (L.) Moench.). International Journal of Current Microbiology and Applied Sciences, 6(10), 1834-1838.

Bagadiya et al.,

- Syullah, K., Sani, M. N. H., Nasif, S. O., Parvin, S., Rony, M. M. H., Islam, M. S. and Hossain, M. S. (2018).
 Genetic Variability, Heritability, Character Association and Morphological Diversity in Okra (Abelmoschus esculentus (L.) Moench). International Journal of Plant & Soil Science, 25(6), 1-11.
- Temam, N., Mohamed, W., and Aklilu, S. (2020). Agro morphological Characterization and Evaluation of

Okra (*Abelmoschus esculentus* (L.) Moench) Genotypes for Yield and Other Variability Components at Melkassa, Central Ethiopia. *MOJ Ecology & Environmental Sciences*, 5(2), 80-87.

Thulasiram, L. B., Bhople, S. R., Srikanth, M. and Nayak, B. R. (2017). Genetic variability and heritability studies in okra (*Abelmoschus esculentus* (L.) Moench). *Plant Archives*, 17(2), 907-910.

How to cite this article: Parth Bagadiya, Priya Patel, C.G. Intwala, Jwala Pranati and Vidyut Balar (2023). Exploring Variability, Heritability and Genetic Advances: Case study in Okra [*Abelmoschus esculentus* (L.) Moench] through Four Distinct Crosses in F₂. *Biological Forum – An International Journal*, *15*(5): 765-772.