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HARNESSING GENETIC VARIABILITY AND TRANSGRESSIVE SEGREGATION IN A DOUBLE CROSS F_2 POPULATION OF OKRA (*ABELMOSCHUS ESCULENTUS* L. MOENCH) FOR INBRED LINE DEVELOPMENT

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ABSTRACT

The present investigation was carried out to evaluate genetic variability and to identify transgressive segregants in the F_2 population derived from the double cross hybrid BDCH 9 in okra (*Abelmoschus esculentus* (L.) Moench). The study was conducted during summer 2025 at the Botany Garden, Department of Genetics and Plant Breeding, University of Agricultural Sciences, Dharwad. A total of 300 F_2 plants derived from BDCH 9 (SCH 1 × SCH 10) were evaluated for twelve quantitative traits related to yield. Wide phenotypic variation was observed for most of the characters indicating substantial genetic variability. High phenotypic and genotypic coefficients of variation along with high heritability and genetic advance were observed for fruit yield per plant, number of fruits per plant and average fruit weight suggesting predominance of additive gene action. Several transgressive segregants exceeding the population mean were identified for important yield traits. The elite segregant P 378 exhibited the highest yield advantage over the population mean. The results indicated that the F_2 population of BDCH 9 possesses considerable variability and provides valuable material for selection of superior inbred lines in okra breeding programs.

Key words : Okra, genetic variability, double cross hybrid, transgressive segregation, F_2 population.

Introduction

Okra (*Abelmoschus esculentus* (L.) Moench), belonging to the family Malvaceae, is an important vegetable crop widely cultivated in tropical and subtropical regions of the world. It is primarily grown for its tender green fruits which are rich in vitamins, minerals and dietary fiber, making it an important component of human nutrition. India is the leading producer of okra globally and contributes a significant share to world production. Despite its wide cultivation and economic importance, productivity of okra in several regions remains below its potential, highlighting the need for developing improved cultivars with higher yield and better adaptability.

Okra is a partially cross-pollinated crop with natural outcrossing ranging from 4 to 19 per cent, mainly mediated by insect pollinators. This biological characteristic facilitates genetic recombination and the generation of variability through hybridization. Development of superior inbred lines is essential for hybrid breeding programs aimed at exploiting heterosis for yield improvement. Segregating populations generated from hybridization serve as valuable sources of genetic variability from which desirable recombinants can be selected.

F_2 populations derived from double cross hybrids are of considerable importance in crop improvement programs because they involve recombination of alleles from four different parental lines, thereby generating broader genetic variability compared to single cross combinations. This increased genetic diversity results in wider phenotypic variation and enhances the probability of identifying superior recombinants in segregating generations. Such populations exhibit extensive genetic segregation and recombination, enabling breeders to effectively explore the available variability for different quantitative traits. Estimation of genetic parameters such as phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability and genetic advance provides valuable insights into the nature of genetic control of these traits and the effectiveness of selection. An important phenomenon frequently observed in segregating populations is transgressive segregation, where some individuals exhibit phenotypic values beyond the range of their parents due to the accumulation of favorable alleles from both parents. Identification of such transgressive segregants is highly valuable for crop improvement, as these superior individuals can serve as promising candidates for selection and further advancement in breeding programs aimed at developing improved inbred lines and high-yielding hybrids.

Considering the importance of genetic variability and the potential of double cross–derived populations for generating superior recombinants, the present investigation was undertaken to evaluate genetic variability and to identify superior transgressive segregants in the F_2 population derived from the double cross hybrid BDCH-9 in okra.

Materials and Methods

The experiment was conducted during summer 2025 at the Botany Garden, Department of Genetics and Plant Breeding, University of Agricultural Sciences, Dharwad, India. The F_2 population derived from the double cross hybrid BDCH 9 (SCH 1 × SCH 10) consisting of 300 plants was evaluated under an unreplicated design with a spacing of 60 × 30 cm. Observations were recorded on twelve quantitative traits including days to first flowering, plant height, number of primary branches per plant, number of internodes, internodal length, fruit length, fruit diameter, average fruit weight, number of fruits per plant, number of seeds per fruit, test weight and fruit yield per plant.

Mean, variance and standard deviation were calculated for each trait. Genetic variability parameters such as phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability (broad sense) and genetic advance were estimated using standard biometric procedures. Transgressive segregants were identified as plants exceeding the population mean plus one standard deviation (Mean + SD) for yield and yield related traits.

Results and Discussion

Genetic variability

The F_2 population of BDCH-9 exhibited wide variation for most of the characters studied, indicating the presence of substantial genetic variability (Table 1). High PCV and GCV values were observed for fruit yield per plant, number of fruits per plant and average fruit weight, indicating considerable genetic variability and good scope for selection. Similar findings of high phenotypic and genotypic variability for yield and its contributing traits in okra segregating populations have been reported earlier by Shanthakumar and Salimath (2010), Raval *et al*. (2018), Rathod *et al*. (2019b) and Srivarsha *et al*. (2022), who observed high PCV and GCV values for yield and related traits indicating the presence of substantial genetic variability and the predominance of additive gene action.

The presence of higher PCV compared to GCV for most of the characters indicated the influence of environmental factors on trait expression, though the relatively smaller differences between PCV and GCV suggested that genetic factors predominantly governed these traits. Similar observations were reported by Kumar and Kumar (2019) and Farooq khan *et al*. (2023) in okra genotypes, indicating that yield and yield-related traits exhibit considerable variability and can be effectively improved through selection.

Transgressive segregation in the F_2 population of BDCH-9

A substantial level of transgressive segregation was observed in the F_2 population of the double cross hybrid BDCH-9 for fruit yield and several yields contributing traits, indicating effective recombination of favorable alleles from the parental lines involved in the cross. Transgressive segregants were identified based on the criterion of mean ± one standard deviation (SD). The results of which are presented in Table 2.

Among the characters studied, days to first flowering recorded the highest proportion of transgressive segregants (82.00%), suggesting good scope for isolating early maturing genotypes. A relatively higher frequency of transgressive segregants was also observed for number of primary branches per plant (27.67%), internodal length (21.67%), number of internodes on the main stem (19.00%) and number of fruits per plant (17.33%), indicating considerable variability for plant architecture and yield components.

For the economically important trait fruit yield per plant, 53 plants (17.67%) were identified as transgressive segregants exceeding the population mean + SD value. Among them, P-378, P-370, P-393, P-102 and P-337 emerged as superior genotypes with enhanced yield performance, demonstrating the potential of the BDCH-9 F_2 population for selection of elite recombinants and development of high yielding inbred lines in okra breeding

Table 1 : Genetic variability parameters for 12 traits in BDCH-9 F_2 population.

Trait	Mean±SD	Range		PCV (%)	GCV (%)	Heritability (h^2_{bs})	GAM
		Min	Max				
Days to first flowering	50.37± 3.81	39.00	56.00	7.57	7.01	85.65	13.36
Plant height	79.95±18.19	20.00	145.00	22.74	19.64	74.59	34.95
Primary branches/plant	2.97±0.92	1.00	6.00	30.96	22.75	53.99	34.43
Internodes	13.90± 2.86	5.00	22.00	20.55	17.16	69.76	29.53
Internodal length	5.55±1.45	2.00	12.00	26.14	20.40	60.90	32.79
Fruit length	15.33± 2.65	6.77	22.17	17.27	15.65	82.06	29.20
Fruit diameter	1.87±0.26	1.02	2.62	13.68	10.54	59.30	16.72
Average fruit weight	30.29± 8.03	8.00	58.67	26.50	25.07	89.49	48.86
Fruits/plant	13.44± 4.13	2.00	26.00	30.74	25.14	66.91	42.36
Seeds/fruit	38.65± 8.10	16.33	66.00	20.97	15.33	53.43	23.08
Test weight	4.37±1.21	1.00	7.80	27.72	22.85	67.98	38.82
Fruit yield/plant	406.68±163.18	56.00	988.00	40.12	36.37	82.17	67.92

Table 2 : Frequency of transgressive segregants for fruit yield per plant and its attributing traits in F_2 population of cross BDCH-9 of Okra.

Characters	Number of plants at (Mean±1SD)	Percent of transgressive segregants (%)	Top 10 lines
Days to first flowering	246	82.00	P-196, P-123, P-125, P-170, P-282, P-120, P-177, P-273, P-296, P-110
Plant height (cm)	47	15.67	P-163, P-337, P-225, P-147, P-386, P-154, P-193, P-325, P-153, P-146
Number of primary branches per plant	83	27.67	P-102, P-272, P-373, P-111, P-121, P-135, P-147, P-153, P-154, P-158
Number of internodes on main stem	57	19.00	P-109, P-337, P-147, P-106, P-124, P-128, P-144, P-173, P-193, P-155
Internodal length (cm)	65	21.67	P-146, P-132, P-154, P-121, P-171, P-115, P-101, P-102, P-108, P-118
Fruit length (cm)	47	15.67	P-153, P-253, P-241, P-394, P-246, P-383, P-301, P-196, P-170, P-303
Fruit Diameter (cm)	39	13.00	P-228, P-306, P-351, P-398, P-367, P-378, P-397, P-394, P-260, P-310
Average fruit weight (g)	37	12.33	P-288, P-260, P-351, P-394, P-298, P-367, P-398, P-253, P-355, P-371
Number of fruits/plant	52	17.33	P-102, P-378, P-147, P-186, P-310, P-155, P-163, P-193, P-357, P-177
Number of seeds/fruit	48	16.00	P-364, P-159, P-397, P-149, P-356, P-353, P-366, P-370, P-298, P-373
Test weight (g)	45	15.00	P-182, P-164, P-113, P-132, P-184, P-188, P-363, P-369, P-135, P-207
Fruit yield per plant (g)	53	17.67	P-378, P-370, P-393, P-102, P-337, P-191, P-397, P-147, P-155, P-185

programs.

Further evaluation of the top fifteen transgressive segregants (Table 3) for fruit yield revealed that these plants significantly outperformed both the parental hybrids SCH-1 (124.72 g plant^{-1}) and SCH-10 (116.12 g plant^{-1}) as well as the standard check Indam Madhuri (588.91 g plant^{-1}). Among them, P-378 emerged as the most superior genotype, recording a fruit yield of 988.00 g plant^{-1}, representing a 67.77% increase over the standard check. Similar occurrence of transgressive segregants for yield and its component traits in F_2 populations of okra has been reported by Nimbalkar and Totre (2018) and Nimbalkar (2023).

These elite segregants also exhibited superior performance for several yield contributing traits such as plant height, number of internodes, average fruit weight and number of fruits per plant, indicating that transgressive segregation resulted in the simultaneous improvement of multiple traits. Similar observations regarding the effectiveness of double cross derived populations in generating wider variability and superior recombinants have also been reported by Katagi *et al.* (2014) and Guddadamath *et al.* (2011a) in okra.

Table 3 : Top fifteen F_2 transgressive segregants for fruit yield per plant in double cross hybrid BDCH-9 of Okra.

Rankings	**Plant number**	**DF**	**PH**	**PB**	**NI**	**IL**	**FL**	**FD**	**AFW**	**NFP**	**NSF**	**TW**	**FYP**	***Per cent* increase**
1	P-378	46	100	2	17	5	17.50	2.46	43.0	26	48.00	5	988.00	67.77
2	P-370	47	97	4	13	7	16.00	1.86	25.0	20	55.67	5.6	940.00	59.62
3	P-393	51	74	3	10	5	17.17	2.03	38.3	16	36.00	4.6	906.67	53.96
4	P-102	53	91	6	14	8	16.67	1.86	32.67	26	37.00	2.8	849.33	44.22
5	P-337	46	135	5	22	6	18.17	2.20	33.0	20	45.33	3	833.33	41.50
6	P-191	54	93	4	18	7	16.83	2.20	40.67	20	36.67	4.6	813.33	38.11
7	P-397	53	97	2	10	6	13.83	2.37	36.7	15	58.33	6.6	810.00	37.54
8	P-147	49	127	5	21	3	17.00	1.95	33.00	24	32.00	1.6	792.00	34.49
9	P-155	52	70	3	19	4	18.33	2.12	35.00	22	39.00	4.2	770.00	30.75
10	P-185	53	70	2	17	5	18.00	2.12	42.67	18	33.33	4.4	768.00	30.41
11	P-154	50	120	5	18	10	14.33	2.20	38.33	20	44.33	4	766.67	30.18
12	P-153	50	112	5	18	4	22.17	2.20	46.00	16	29.67	2.6	736.00	24.98
13	P-357	49	98	4	11	3	16.67	1.61	29.0	22	52.33	5.6	726.00	23.28
14	P-198	54	100	3	14	7	17.67	2.20	39.33	18	34.33	4.4	708.00	20.22
15	P-117	53	58	2	16	3	15.77	1.95	35.33	20	40.33	5.2	706.67	20.00
	SCH-1	43.40	63.20	1.60	12.80	6.40	18.16	2.01	10.06	16.73	57.22	5.11	124.72	
	SCH-10	45.33	70.83	1.67	12.00	5.83	18.82	2.00	9.20	17.42	51.90	5.61	116.12	
	Indam Madhuri	45	84.33	2	21.33	3.66	20.8	2.25	19.42	29.33	63.11	6.06	588.91	
	Standard Deviation (SD)	3.81	18.19	0.92	2.86	1.45	2.65	0.26	8.03	4.13	8.10	1.21	163.18	

Overall, the presence of several high yielding transgressive segregants demonstrates the considerable breeding potential of the BDCH-9 F_2 population and these superior plants can be advanced through pedigree selection for the development of improved inbred lines and high yielding hybrids in okra breeding programs.

Conclusion

The F_2 population derived from the double cross hybrid BDCH-9 exhibited substantial genetic variability for fruit yield and its component traits, indicating the effectiveness of double cross–derived populations in generating broader variability in okra. High PCV, GCV, heritability and genetic advance for key traits such as fruit yield per plant, number of fruits per plant and average fruit weight suggested the predominance of additive gene action and good scope for selection. A considerable level of transgressive segregation was observed for several traits, particularly fruit yield per plant (17.67%), indicating the presence of superior recombinants. Among them, P-378, P-370, P-393, P-102 and P-337 emerged as promising genotypes with higher yield performance. These elite segregants can be further advanced through pedigree selection for the development of superior inbred lines and high-yielding hybrids in okra breeding programs.

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