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Study of the transgressive segregants in the F_4 population of Okra for yield and its contributing traits

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Abstract
The study was conducted during the *Kharif* season of 2024 at the College of Horticulture, Bengaluru, Karnataka, India, focusing on the okra population derived from the cross OK-2017-010 × Varsha Uphar. Among the segregants, a notable frequency was observed for key traits: 40.42% of segregants exhibited increased numbers of branches, 50.42% showed increased numbers of nodes and 55% displayed earlier days to first flowering. The simultaneous transgressive segregant shows the highest for the combined favorable attributes, including a higher number of nodes, increased branches and number of fruits per plant, which collectively contributed to its enhanced productivity. Significantly, the transgressive segregant identified as "T" recorded the highest yield increase, achieving a remarkable 64.21% improvement compared to the parent. The findings underscore the potential of transgressive segregants for achieving substantial yield improvements in okra through the synergistic enhancement of critical traits, emphasizing their value in breeding programs aimed at maximizing genetic gain.

Keywords: Transgresive segregants, yield, Superior, okra

Introduction
Okra (Abelmoschus esculentus), a globally significant crop, is valued for its agricultural and nutritional contributions. Traditionally, breeding efforts in okra have focused on improving yield, fruit quality, and disease resistance (Kumar *et al*., 2018) [7]. However, the underutilized potential of transgressive segregation, where offspring exceed parental phenotypes in certain traits, offers new avenues for crop enhancement. Johannsen (1903) [5] highlighted this phenomenon as crucial in developing superior genotypes across various plant species. Harnessing this genetic mechanism in okra could lead to groundbreaking advances in yield and quality.
Through the exploration of diverse okra germplasm, this study seeks to identify transgressive segregants with exceptional performance. Phenotypic transgression often results from the recombination of advantageous alleles from genetically diverse parents (Paterson *et al*., 1991) [11], making it a powerful tool in breeding programs. Key traits such as plant height, fruit weight, fruit number, and flowering time play a pivotal role in analyzing the genetic architecture of promising genotypes (Singh *et al*., 2015) [14]. Early-generation segregants like F2, F3, and F4 exhibit heightened variability due to their broader genetic base, making them ideal for identifying unique and superior individuals (Mallikarjun and Savitramma, 2017).

Materials and methods
The field research was carried out at the Department of Biotechnology and Crop Improvement College of Horticulture Bengaluru, GKVK, crosses, *viz*, OK-2017-010 X Varsha Uphar, were evaluated using an Randomized Complete Block design with two replications.
From each replication at random 120 plants F_4 generation a total population of 240 individuals and plot were tagged for recording observations on nine characters *viz*., plant height (cm), inter nodal length, number of nodes on main stem, number of branches per plant, days to flowering, fruit length (cm), fruit weight (g), number of fruits per plant, yield per plant (g).
The procedure given by Panse and Sukhatme (1995) [10] was followed for performing the statistical analysis. Transgressive segregants were estimated by calculating the threshold value (T.V.) by the following formula.
$T.V = \bar{A}^{(+)} + 1.96 \times \sigma \bar{A}^{(+)}$
Where, $\bar{A}^{(+)}$ and $\sigma \bar{A}^{(+)}$ are the mean and standard deviation of the Increasing parent, respectively. The individuals who transgressed this threshold limit were considered the transgressive segregants.

Results and Discussion
Top Desirable Segregants in F4 Populations Based on Combination of Traits from the Cross OK-2017-010 × Varsha Uphar.
The best-performing desirable segregants displayed remarkable genetic potential for trait improvement in both yield and fruit quality, from the cross OK-2017-010 × Varsha Uphar, in terms of yield and quality traits are shown in Table 1.

T: demonstrated superior yield performance with 1303.5 g per plant, 20 nodes, a fruit diameter of 1.54 cm, 16.5 g mean fruit weight, and a total fruit count of 79. Flowering occurred early, with the first flowers appearing in 28 days. M: yielded 630.27 g per plant, with 15 nodes, a 1.64 cm fruit diameter, 13.41 g mean fruit weight, and 47 fruits. Flowering started in 47 days. L: recorded a yield of 633.5 g per plant, with 15 nodes, a 1.65 cm fruit diameter, 18.1 g mean fruit weight, and 35 fruits, with flowers appearing in 35 days. D: achieved a yield of 633.04 g per plant, with 20 nodes, a 1.54 cm fruit diameter, 15.44 g mean fruit weight, and 41 fruits. Flowering commenced on day 41. O: yielded 636.83 g per plant, with 15 nodes, a 1.44 cm fruit diameter, 14.81 g mean fruit weight, and 43 fruits, with flowering occurring on day 33.

The observed variations in yield and fruit quality traits among the segregants from the cross OK-2017-010 × Varsha Uphar can be attributed to the genetic diversity and complementary traits inherited from the parental lines. The superior performance of segregant T, which exhibited the highest yield (1303.5 g per plant) and an impressive fruit count, likely stems from favorable gene combinations influencing traits like early flowering (28 days) (Nimbalkar, 2018 and Meena, 2011) [8, 9] and efficient nutrient utilization. Early flowering not only shortens the vegetative phase but also allows for an extended fruiting period, contributing to higher overall yield Preddep *et al*., 2003 observed in cotton. In contrast, the relatively lower yield of segregants M, L, D, and O may result from genetic limitations in their ability to optimize key traits simultaneously, such as fruit weight and node count. Segregants M and D, for instance, displayed delayed flowering (47 and 41 days, respectively), which might have reduced their fruiting duration, thereby limiting yield potential (Kavya, 2019) [6]. Meanwhile, segregants L and O showed higher fruit weights, suggesting a trade-off between fruit size and total fruit count (Guddamath *et al*., 2012).

Environmental factors and potential interactions between genotype and environment might also play a role in shaping these differences. The parental combination appears to have introduced variability in traits like fruit diameter, mean fruit weight, and flowering time, indicating the importance of selecting desirable combinations during breeding to achieve a balance of yield and quality (Kumar *et al*., 2018 and Meena 2011) [7, 8]. These results highlight the genetic potential for crop improvement, emphasizing the critical role of selecting superior segregants for further breeding programs. For the qualitative traits, Plant M exhibited dark green fruits, while all the remaining plants showed green tender fruits. The fruits across all plants were characterized by weak pubescence and featured five ridges on their surface, contributing to their distinct textural qualities (Girar and Deshmukah, 2002).

Simultaneous Transgressive Segregant

The Simultaneous Transgressive segregant were the combination of of the traits were analysed, in that the combination of number of nodes, fruit length, fruit weight, and number of fruits per plant showed of 23 plant, followed by number of branches per plant and fruit weight 18 individuals, number of nodes along with number of fruits per plant 17 and plant height with number of fruits had 16 plants (Table 2). The observed combinations in simultaneous transgressive segregants reflect the inheritance of complementary and favorable alleles from both parents, leading to enhanced trait performance. The high number of segregants (23) combining traits like nodes, fruit length, fruit weight, and fruit count suggests polygenic inheritance, where multiple genes contribute cumulatively to these traits. Traits like branches and fruit weight (18 segregants) or plant height and fruit count (16 segregants) involve trait-specific gene interactions and potential pleiotropic effects (Aminu *et al*., 2007; Singh *et al*., 2015) [14]. These patterns highlight the genetic complexity of quantitative traits, with transgressive segregation allowing the expression of superior phenotypes beyond the parental range through novel allele combinations (Sogland *et al*., 2009).

Desirable segregants in the F4 population of the two biparental crosses in okra

The desirable segregants study showed that the percentage of highest transgressive segregants was seen in the cross OK-2017-010 × Varsha Uphar showed the highest frequencies for fruit diameter (15.41%), number of fruits per plant (27.91%), and days to first flowering (55%).

Table 1: List of top desirable segregants of F4 selected based on a combination of traits from the cross, OK-2017-010 × Varsha Uphar

Sl. No.	Plant No.	NBPP	NNMS	FL (cm)	FD (cm)	AFW (g)	NFPP	DFF	FC	FP	NRPP	TYPP (g)
1	T	5*	20*	16.11	1.54	16.5*	79*	28*	G	W	5	1303.5*
2	M	3*	15	14.15	1.64	13.41	47*	35*	DG	W	5	630.27*
3	L	2*	15	16.44	1.65	18.1*	35*	35*	G	W	5	633.5*
4	D	3*	20*	16.6	1.54	15.44*	41*	34*	G	W	5	633.04*
5	O	4*	15	15.64	1.44	14.81	43*	33*	G	W	5	636.83*
Checks (Mean of parents)												
P1	OK-2017-010	1.49	16.55	15.83	2.30*	15.29	27.80*	39.75*	G	W	5.20	425.11*
P2	Varsha Uphar	2	17.95*	18.81*	2.00	14.99*	31.30*	40.65	G	W	5	466.52

NBBP: Number of branches per plant NNMS: Number of nodes FL: Fruit length FD: Fruit diameter AFW: Average fruit weight NFPP: Number of fruits per plant DFF: Days to first flowering FC: Fruit colour FP: Fruit pubescence NRPF: Number of ridges per fruit TYPP: Total yield per plant DG: Dark green G: Green LG: Light green PLG: Purple light green W: Weak pubescence

Table 2: Number of simultaneous transgressive segregants for yield in combination with other characters in three crosses of Okra

Character combinations Fruit yield with	Number of segregants
PH+NN+NBP+DF+FW+NFF	1
PH+NN+DF+FL+FW+NFP	2
PH+NN+NBP+FW+NFP	4
PH+NN+FL+FW+NFP	2
NBP+DF+FL+FW+NFP	3
PH+NN+FL+NFP	1
PH+NN+FW+NFP	3
PH-NN+NBP+NFP	6
PH+NN+FL+FW	2

PH-NBP+FL+FW	6
PH-NBP+FW+NFP	2
PH+FL+FW+NFP	11
NN+FL+FW+NFP	23
NBP+DF+FW+NFP	0
NBP+FL+FW+NFP	4
PH+NN+FW	4
PH+NN+NFP	1
PH NBP+NFP	6
PH+FW+NFF	3
NN NBP+NFP	2
NN+FL+FW	6
NN+FW+NFP	9
NBP+FL+FW	2
NBP+FL-NFP	4
NBP-FW+NFP	3
FL+FW+NFP	2
PH+NN	9
PH+FW	11
PH+NFP	16
NN+NFP	17
NBP+FW	18
NBP+NFP	14
FL+FW	4
FW+NFP	3
Total simultaneous transgressive segregants	204

NBP: Number of branches per plant, PH: Plant height, NN: Number of nodes, FL: Fruit length, FW: Fruit weight, NFP: Number of fruits per plant, NN: Number of nodes and DF: Diameter of fruit

Table 3: Desirable segregants in the F4 population of the two biparental crosses in okra

Sl. No.	**F3populations**	**Total number of individuals**	**Desirable Segregants**							
			NBPP (%)	NNMS (%)	FL (%)	FD (%)	AFW (%)	NFPP (%)	DFF (%)	TYPP (%)
2	OK-2017-010 × Varsha Uphar	240	40.42 (97)	50.42 (121)	13.75 (33)	13.75 (33)	12.92 (31)	22.08 (53)	55.00 (132)	26.25 (63)

() Values in the parenthesis are the number of desirable segregants

NBPP	Number of branches per plant	NNMS	Number of nodes per plant
FD	Fruit diameter	FL	Fruit length
AFW	Average fruit weight	NFPP	Number of fruits per plant
TYPP	Total yield per plant	DFF	Days to first flowering

Conclusion

The transgressive segregants may be due to the complementary gene action, the identified lines from the F_4 populations were used to carry out another season to check their performance and however the fruit weight, fruit length and number of fruits were major traits for consideration and the combination of the number of nodes, fruit length, fruit weight and number of fruits per plant showed best combination.

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