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Variability, correlation and path coefficient studies in F4 populations of Okra (*Abelmoschus esculentus* L. Moench) cross ok-2017-010 × Pusa Sawani

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Abstract
Variability, correlation and path coefficient analysis were undertaken in F_4 populations of okra (*Abelmoschus esculentus* L. Moench) derived from the cross OK-2017-010 × Pusa Sawani during Summer 2025 at the Department of Biotechnology and Crop Improvement (BCI), College of Horticulture, Bengaluru. A total of 11 families comprising 220 plants, two parents and five standard checks were evaluated in an Augmented Block Design for 14 yield and yield-contributing traits. High broad-sense heritability (h^2_{bs}) coupled with high genetic advance as percent mean (GAM) was recorded for total yield per plant (91.70%; 36.72%), days to 50% flowering (92.50%; 36.92%), number of fruits per plant (90.90%; 31.41%) and fruit diameter (86.80%; 35.66%), indicating the preponderance of additive gene action and the feasibility of direct selection for these traits. Number of fruits per plant exhibited the highest positive genotypic coefficient of variation (GCV = 25.99%) and phenotypic coefficient of variation (PCV = 26.77%), followed by total yield per plant (GCV = 28.61%; PCV = 29.44%). Correlation analysis revealed that number of fruits per plant (r = 0.898**) and number of branches per plant (r = 0.844**) had the strongest positive association with total yield per plant, while days to first flowering, plant height, fruit diameter, fruit length and number of seeds per fruit showed significant negative correlations with yield. Path coefficient analysis identified number of fruits per plant as the primary direct contributor to total yield (direct effect = 1.045), followed by number of seeds per fruit (0.649) and number of branches per plant (-0.145 with high indirect effects). These findings provide valuable insights for the improvement of okra yield through recurrent selection and family-based breeding in segregating populations.

Keywords: Okra, F4 population, heritability, genetic advance, correlation, path coefficient, yield components

Introduction
Okra [*Abelmoschus esculentus* (L.) Moench], belonging to the family Malvaceae, is one of the most widely cultivated warm-season vegetables in tropical, subtropical and semi-arid regions of the world. It is popularly known as 'Lady's finger' and is commercially grown for its tender, mucilaginous fruits, which are consumed fresh as well as processed. Okra is a nutritionally rich vegetable, providing significant amounts of protein (2.1 g/100 g), carbohydrates, dietary fibre, vitamins A, B and C, and essential minerals such as calcium, phosphorus and iron (Benchasri, 2012; Gemede *et al.*, 2015) [7, 13]. India is the leading producer of okra globally, accounting for approximately 70% of world production, with a cultivated area of about 0.51 million hectares and an annual production of 6.4 million metric tonnes (NHB, 2022).

Despite its economic importance, the average productivity of okra in India remains low at approximately 12.5 t/ha, which is considerably below its genetic potential (NHB, 2022). The major constraints limiting productivity include narrow genetic base of elite varieties, poor adaptability to diverse agro-climatic conditions, and susceptibility to biotic and abiotic stresses. Genetic improvement through systematic breeding approaches, particularly the exploitation of variability in segregating generations, is therefore critical for developing high-yielding varieties with desirable agronomic traits (Bello *et al.*, 2012; Akinyele and Osekita, 2006) [2, 8].

Understanding the nature and magnitude of genetic variability within breeding populations is a prerequisite for any crop improvement programme. Genetic variability parameters such as genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability in broad sense (h^2bs) and genetic advance as percent mean (GAM) provide essential information for estimating the heritable portion of total variation and predicting the response to selection (Burton and de Vane, 1953; Johnson et al., 1955) [9, 15]. High heritability combined with high genetic advance indicates the predominance of additive gene effects and suggests the effectiveness of direct selection (Panse and Sukhatme, 1957) [22].

Correlation studies reveal the degree of association among various traits and help identify indirect selection criteria for yield improvement (Dewey and Lu, 1959) [10]. However, correlation alone does not establish causation, and the relative direct and indirect contributions of each character to yield need to be assessed through path coefficient analysis, as outlined by Wright (1921) [28] and popularized in plant breeding by Dewey and Lu (1959) [10]. Path analysis partitions the correlation coefficient into direct and indirect effects, thereby identifying the most effective traits for inclusion in a selection index (Singh and Chaudhary, 1985) [26].

In segregating generations such as F4, families derived from biparental crosses may exhibit considerable genetic variability due to recombination and segregation. The F4 generation is particularly useful for evaluating genetic variability and family performance since sufficient fixation of alleles allows reliable estimation of genetic parameters (Allard, 1999) [4]. Studies on F4 and advanced generations of okra have reported substantial variability for yield and yield-attributing traits including fruit weight, number of fruits per plant, fruit length, and days to flowering (Aravindakumar *et al*., 2019; Patel *et al*., 2018; Singh *et al*., 2020; Kumar *et al*., 2021) [6, 16, 23, 27].

The cross OK-2017-010 × Pusa Sawani was made with the objective of combining the high-yielding ability and fruit quality traits of both parents. Pusa Sawani is a widely cultivated commercial variety known for its tender fruits and medium yield, while OK-2017-010 is an experimental line with superior fruit quality and branching characteristics. The F4 populations derived from this cross are expected to show transgressive segregants with desirable trait combinations. Therefore, the present investigation was undertaken to: (i) estimate the genetic variability parameters, broad-sense heritability, and genetic advance in F4 families; (ii) assess the association between yield and its component traits through correlation analysis; and (iii) determine the direct and indirect contributions of yield components to total yield per plant through path coefficient analysis.

Materials and Methods

1. Experimental Site and Genetic Material

The experiment was carried out at the experimental field of the Department of Biotechnology and Crop Improvement (BCI), College of Horticulture, Bengaluru (12.97°N, 77.56°E; altitude 920 m above mean sea level), University of Horticultural Sciences (UHS), Bagalkot, Karnataka, during the summer 2025 season. The experimental material consisted of F4 families derived from the biparental cross OK-2017-010 × Pusa Sawani, developed through successive selfing of F3 individuals. The F4 generation was employed to maximize allelic fixation and enable reliable estimation of genetic parameters within segregating families.

A total of 11 F4 families with a population size of 220 plants, along with two parents (OK-2017-010 and Pusa Sawani) and five standard checks viz., Kashi Pragati, Arka Anamika, Pusa A4, Varsha Uphar and Prabhani Kranti, were included in the study. Each family was represented by 20 plants, and all checks and parents were replicated across the experimental blocks.

2. Experimental Design and Agronomic Management

The F4 populations and checks were evaluated using an Augmented Block Design (ABD) (Federer, 1956) [12], comprising five blocks. The augmented design was chosen to accommodate a large number of test genotypes without replication while adjusting for block effects using replicated checks. Plants were spaced at 60 cm × 45 cm within and between rows to ensure optimal plant growth and to minimize inter-plant competition. All recommended agronomic package of practices prescribed by the University of Horticultural Sciences (UHS), Bagalkot, for okra cultivation in Karnataka were followed throughout the crop growth period (Anon., 2016) [5]. Standard plant protection measures including timely application of insecticides and fungicides were adopted to maintain healthy crop growth and to minimize losses due to pest and disease incidence.

3. Observations Recorded

Data were recorded on 14 quantitative traits: days to first flowering (DFF), days to 50% flowering (D50F), plant height (PH, cm), number of branches per plant (NBPP), number of nodes on the main stem (NNMS), internodal length (IL, cm), number of ridges on fruit surface (NR), fruit diameter (FD, cm), fruit length (FL, cm), stem girth (SG, cm), number of fruits per plant (NFPP), average fruit weight (AFW, g), number of seeds per fruit (NSF), and total yield per plant (TYPP, g). Observations were recorded on five competitive plants per family, and mean values were used for statistical analysis.

4. Statistical Analysis

Analysis of variance was computed as per the augmented block design procedure outlined by Federer (1956) [12] to test the significance of differences among genotypes and blocks. Genetic parameters including phenotypic variance (σ^2p), genotypic variance (σ^2g), environmental variance (σ^2e), phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), broad-sense heritability (h^2bs) and genetic advance as percent mean (GAM) were estimated as per Burton and de Vane (1953) and Johnson *et al*. (1955) [9, 15]. Phenotypic and genotypic correlation coefficients among pairs of traits were computed as per Al-Jibouri *et al.* (1958) [3]. Path coefficient analysis was performed to partition the correlation coefficients into direct and indirect effects as described by Dewey and Lu (1959) [10], using total yield per plant as the dependent variable. All computations were performed using GENRES statistical software (v. 9.1).

Results and Discussion

1. Genetic Variability Parameters

The analysis of variance revealed significant differences among F_4 families for all the 14 traits evaluated, indicating the presence of substantial genetic variability in the population. The estimates of mean, range, GCV, PCV, h^2_{bs} and GAM for all traits are presented in Table 1.

Table 1: Estimation of genetic variability parameters in F4 populations of okra cross OK-2017-010 × Pusa Sawani

Traits	Mean	Min	Max	GCV (%)	PCV (%)	h²bs (%)	GAM (%)
Days to first flowering	35.26	32.75	39.75	6.84	7.33	87.10	13.16
Days to 50% flowering	45.97	42.50	48.50	18.63	19.37	92.50	36.92
Plant height (cm)	144.40	104.55	168.44	11.63	12.50	86.60	22.31
Number of branches	2.34	1.49	2.97	17.82	23.64	56.80	27.66
Number of nodes	16.88	14.90	21.50	9.11	10.53	74.80	16.22
Internodal length (cm)	7.33	5.62	9.09	12.60	14.30	77.60	22.86
Number of ridges on fruit surface	5.42	5.15	5.95	4.00	4.70	72.30	7.01
Fruit diameter (cm)	1.80	1.20	2.30	18.58	19.95	86.80	35.66
Fruit length (cm)	15.96	13.86	17.92	8.21	9.17	80.20	15.14
Stem girth (cm)	1.50	1.31	2.11	12.56	14.67	73.30	22.16

Number of fruits per plant	32.29	24.72	44.30	25.99	26.77	90.90	31.41
Average fruit weight (g)	15.33	12.03	18.80	9.11	9.68	88.60	17.68
Number of seeds per fruit	70.12	65.34	78.51	6.66	7.15	86.70	12.77
Total yield per plant (g)	499.15	346.38	711.99	28.61	29.44	91.70	36.72

GCV: Genotypic Coefficient of Variation; PCV: Phenotypic Coefficient of Variation; h²bs: Broad Sense Heritability; GAM: Genetic Advance as Percent Mean

Total yield per plant showed the highest GCV (28.61%) and PCV (29.44%) among all traits, followed by number of fruits per plant (GCV = 25.99%; PCV = 26.77%), days to 50% flowering (GCV = 18.63%; PCV = 19.37%) and fruit diameter (GCV = 18.58%; PCV = 19.95%). These high GCV and PCV values indicate substantial phenotypic and genotypic variability for these traits in the F4 population, which is consistent with earlier reports in okra (Aravindakumar *et al*., 2019; Kumar *et al*., 2021; Patel *et al*., 2018) [6, 16, 23]. A close correspondence between GCV and PCV values for most traits suggests minimal environmental influence on trait expression, which is favourable for selection (Lush, 1949) [18].

Low GCV and PCV values were recorded for days to first flowering (6.84%; 7.33%), number of ridges on the fruit surface (4.00%; 4.70%) and number of seeds per fruit (6.66%; 7.15%), suggesting limited genetic variation and possibly greater environmental sensitivity for these traits (Allard, 1999) [4]. The narrow range observed for the number of ridges (5.15–5.95) in the present study is in agreement with findings reported by Singh *et al*. (2020) and Akinyele and Osekita (2006) [2, 27], who noted that fruit ridges are a highly conserved morphological character in okra.

Broad-sense heritability (h²bs) estimates ranged from 56.80% (number of branches) to 92.50% (days to 50% flowering). High heritability (>80%) was recorded for days to 50% flowering (92.50%), total yield per plant (91.70%), number of fruits per plant (90.90%), average fruit weight (88.60%), days to first flowering (87.10%), number of seeds per fruit (86.70%), fruit diameter (86.80%) and plant height (86.60%). These high heritability values indicate that the phenotypic expression of these traits is largely governed by the genotype rather than the environment, and hence direct selection for these traits would be effective (Falconer and Mackay, 1996; Bello *et al*., 2012) [8, 11]. Moderate heritability was observed for number of nodes (74.80%), internodal length (77.60%), number of ridges (72.30%) and stem girth (73.30%), while number of branches showed relatively lower heritability (56.80%), suggesting that environmental influences are more pronounced for this trait.

Genetic advance as percent mean (GAM) is considered a more reliable indicator of the type of gene action governing a trait when interpreted in conjunction with heritability. In the present study, days to 50% flowering recorded the highest GAM (36.92%), followed by total yield per plant (36.72%), fruit diameter (35.66%), number of fruits per plant (31.41%) and number of branches (27.66%). These traits exhibited high heritability along with high GAM, which suggests preponderance of additive gene action and indicates that phenotypic selection would be productive in subsequent generations (Johnson *et al*., 1955; Singh and Chaudhary, 1985) [15, 26]. Similar observations of high heritability and high genetic advance for number of fruits per plant and total yield in okra were reported by Reddy *et al*. (2013), Kumar *et al*. (2021) and Rashwan (2011) [16, 24, 25]. Traits such as days to first flowering (13.16%), number of ridges (7.01%) and number of seeds per fruit (12.77%) exhibited high heritability but low GAM, indicating that non-additive genetic effects (dominance and epistasis) may be contributing to the expression of these traits, and thus selection for these characters may not be very effective in early segregating generations (Panse and Sukhatme, 1957) [22].

2. Correlation Analysis

The phenotypic and genotypic correlation coefficients among 14 yield and yield-attributing traits in the F_4 populations are presented in Table 2. The genotypic correlations were generally higher in magnitude than the corresponding phenotypic correlations, indicating strong inherent genetic associations among traits and relatively small masking effect of environment (Al-Jibouri *et al*., 1958; Bello *et al*., 2012) [3, 8].

Table 2: Correlation coefficients among yield and its attributing traits in F4 populations of okra cross OK-2017-010 × Pusa Sawani

	DFF	D50F	PH	NBPP	NNMS	IL	NR	FD	FL	SG	NFPP	AFW	NSF	TYPP
DFF	1	0.721**	0.347*	-0.108	-0.130	0.582**	0.034	0.865**	0.475**	0.319*	-0.74**	0.360*	0.979**	-0.540**
D50F		1	0.077	-0.856**	0.038	0.115	0.264*	0.470*	0.369*	0.55**	-0.593**	0.430*	0.724**	-0.401*
PH			1	-0.523**	-0.360*	0.167	0.032	0.387*	0.352*	-0.097	-0.629**	-0.154	0.330*	-0.644**
NBPP				1	0.208	-0.590**	0.089	-0.931**	-0.733**	-0.441*	0.954**	-0.315*	-0.085	0.844**
NNMS					1	0.074	-0.292*	-0.242	-0.077	-0.413*	0.307*	-0.337*	-0.195	0.142
IL						1	-0.250	0.499**	-0.010	-0.082	-0.105	-0.081	0.502**	-0.027
NR							1	0.070	-0.164	0.321*	-0.294*	0.538**	0.064	-0.051
FD								1	0.591**	-0.036	-0.681**	0.139	0.910**	-0.569**
FL									1	0.007	-0.651**	0.096	0.642**	-0.634**
SG										1	-0.297*	0.509**	0.270*	-0.073
NFPP											1	-0.210	-0.704**	0.898**
AFW												1	0.416*	0.254*
NSF													1	-0.496**
TYPP														1

** Significant at 1% level of probability; * Significant at 5% level of probability. DFF: Days to first flowering; D50F: Days to 50% flowering; PH: Plant height; NBPP: Number of branches per plant; NNMS: Number of nodes on main stem; IL: Internodal length; NR: Number of ridges; FD: Fruit diameter; FL: Fruit length; SG: Stem girth; NFPP: Number of fruits per plant; AFW: Average fruit weight; NSF: Number of seeds per fruit; TYPP: Total yield per plant.

Total yield per plant showed highly significant positive correlation with number of branches per plant (r = 0.844**) and number of fruits per plant (r = 0.898**), while average fruit weight showed a weak but positive association (r = 0.254*). These positive correlations indicate that selection for increased branching and higher fruiting potential would simultaneously improve overall yield. The strong association between number of fruits per plant and total yield has been consistently reported in okra breeding literature (Muluken *et al*., 2015; Nwangburuka *et al*., 2012; Adeniji *et al*., 2007) [1, 19, 21], and affirms the pivotal role of this trait as a primary yield determinant.

Highly significant negative correlations with total yield per plant were observed for days to first flowering (r = -0.540**), plant height (r = -0.644**), fruit diameter (r = -0.569**), fruit length (r = -0.634**) and number of seeds per fruit (r = -0.496**). The negative association of plant height with yield may suggest that taller plants in this population tend to allocate more resources toward vegetative growth at the expense of reproductive output (Rashwan, 2011) [24]. The negative correlation between fruit size traits (fruit diameter and fruit length) and total yield suggests a trade-off between individual fruit size and number of fruits produced per plant, a common phenomenon in vegetable crops where smaller fruits tend to be produced in larger quantities (Adeniji *et al*., 2007) [1].

Among inter-trait associations, days to first flowering exhibited a strong positive correlation with days to 50% flowering (r = 0.721**), fruit diameter (r = 0.865**) and number of seeds per fruit (r = 0.979**), indicating that early-flowering genotypes may also produce fruits with larger diameter and more seeds. Number of fruits per plant showed a highly significant positive correlation with number of branches per plant (r = 0.954**), confirming that branching capacity strongly determines fruiting potential. Number of branches per plant was negatively associated with fruit diameter (r = -0.931**) and fruit length (r = -0.733**), reinforcing the inverse relationship between fruiting number and individual fruit size (Bello *et al*., 2012; Kumar *et al*., 2021) [8, 16].

3. Path Coefficient Analysis

The phenotypic path coefficient analysis for total yield per plant in the F_4 populations is presented in **Table 3**. The residual effect was 0.421, indicating that approximately 57.9% of the variation in total yield was explained by the traits included in the analysis, while the remaining variation may be attributed to other unmeasured factors or interactions.

Table 3: Phenotypic path coefficient analysis for yield and yield attributing traits in F4 populations of okra cross OK-2017-010 × Pusa Sawani

	DFF	D50F	PH	NBPP	NNMS	IL	NR	FD	FL	SG	NFPP	AFW	NSP	TYPP
DFF	0.052	-0.104	-0.025	0.16	0.017	0.013	0.007	-0.505	-0.035	-0.064	-0.773	0.083	0.635	-0.54
D50F	0.038	-0.145	-0.006	0.124	-0.005	0.003	0.053	-0.274	-0.028	-0.11	-0.62	0.099	0.47	-0.401
PH	0.018	-0.011	-0.072	0.076	0.047	0.004	0.006	-0.226	-0.026	0.019	-0.658	-0.035	0.214	-0.644
NBPP	-0.058	0.124	0.038	-0.145	-0.027	-0.013	0.018	0.544	0.055	0.088	0.998	-0.072	-0.704	0.844
NNMS	-0.007	-0.006	0.026	-0.03	-0.131	0.002	-0.059	0.141	0.006	0.083	0.32	-0.077	-0.126	0.142
IL	0.03	-0.017	-0.012	0.085	-0.01	0.023	-0.051	-0.291	0.001	0.017	-0.109	-0.019	0.326	-0.027
NR	0.002	-0.038	-0.002	-0.013	0.038	-0.006	0.202	-0.041	0.012	-0.064	-0.307	0.124	0.041	-0.051
FD	0.045	-0.068	-0.028	0.135	0.032	0.011	0.014	-0.584	-0.044	0.007	-0.712	0.032	0.59	-0.569
FL	0.025	-0.053	-0.025	0.106	0.01	0	-0.033	-0.345	-0.075	-0.001	-0.68	0.022	0.417	-0.634
SG	0.017	-0.079	0.007	0.064	0.054	-0.002	0.065	0.021	-0.001	-0.2	-0.311	0.117	0.175	-0.073
NFPP	-0.039	0.086	0.045	-0.138	-0.04	-0.002	-0.059	0.398	0.049	0.06	1.045	-0.048	-0.457	0.898
AFW	0.019	-0.062	0.011	0.046	0.044	-0.002	0.109	-0.081	-0.007	-0.102	-0.22	0.23	0.27	0.254
NSP	0.051	-0.105	-0.024	0.157	0.025	0.011	0.013	-0.531	-0.048	-0.054	-0.736	0.096	0.649	-0.496

Bold diagonal values denote direct effects. DFF: Days to first flowering; D50F: Days to 50% flowering; PH: Plant height; NBPP: Number of branches per plant; NNMS: Number of nodes on main stem; IL: Internodal length; NR: Number of ridges; FD: Fruit diameter; FL: Fruit length; SG: Stem girth; NFPP: Number of fruits per plant; AFW: Average fruit weight; NSP: Number of seeds per fruit; TYPP: Total yield per plant.

Number of fruits per plant exerted the highest direct positive effect on total yield per plant (direct effect = 1.045), which was also reflected in its high positive correlation with yield (r = 0.898**), confirming that this trait directly and genuinely contributes to yield improvement. This finding is in agreement with Reddy *et al*. (2013), Nwangburuka *et al*. (2012) and Ige *et al*. (2011) [14, 21, 25], who consistently reported number of fruits per plant as the most important yield-determining trait in okra. Number of seeds per fruit also recorded a direct positive effect (0.649) on yield, despite its negative phenotypic correlation (-0.496**), suggesting that the negative correlation is largely a consequence of indirect effects mediated through other traits such as fruit diameter and days to first flowering (Singh and Chaudhary, 1985) [26].

Number of branches per plant had a high positive indirect contribution through number of fruits per plant (0.998) despite its negative direct effect (-0.145), resulting in a strongly positive net correlation with yield (r = 0.844**). This underscores the importance of number of fruits per plant as a mediating variable through which branching exerts its influence on yield. Similar patterns have been reported by Lal *et al*. (2015) and Aravindakumar *et al*. (2019) [6, 17], who noted that the indirect effects via number of fruits per plant often override the direct effects of branching traits.

Days to first flowering, despite showing a high negative phenotypic correlation with yield (r = -0.540**), had a low direct effect (0.052) on yield. Its negative correlation was largely mediated through indirect effects via number of fruits per plant (-0.773) and fruit diameter (-0.505), suggesting that early flowering genotypes in this cross tend to produce more, but smaller fruits. Plant height exhibited a low direct effect (-0.072) but exerted significant negative indirect effects through number of fruits per plant (-0.658), resulting in a high negative correlation with yield (r = -0.644**). These results indicate that plant height per se is not a reliable direct selection criterion for yield improvement in this cross.

Average fruit weight recorded a moderate direct positive effect (0.230) on yield with a weak positive correlation (r = 0.254*), suggesting that selection for heavier individual fruits could contribute incrementally to yield improvement without adversely affecting number of fruits per plant. This is particularly relevant in the context of developing okra varieties for fresh market and processing industries where fruit quality and size are important commercial attributes (Gemede *et al*., 2015; Benchasri, 2012) [7, 13]. Fruit length and fruit diameter exhibited negative direct effects (-0.075 and -0.584, respectively) and negative correlations with yield, implying that emphasis on these traits in selection may inadvertently reduce yield, possibly due to the trade-off between fruit size and number of fruits per plant (Muluken *et al*., 2015) [19].

Overall, path analysis suggests that selection emphasis should be placed on number of fruits per plant as the primary selection criterion, supported by number of branches per plant and average fruit weight as secondary traits. Simultaneously, attention should be given to reducing days to flowering and maintaining optimum plant height to maximize yield potential in advanced segregating families of the cross OK-2017-010 × Pusa Sawani.

Conclusion

The F_4 families derived from the cross OK-2017-010 × Pusa Sawani showed significant variability for all traits studied. High heritability coupled with high GAM for total yield per plant, days to 50% flowering, number of fruits per plant and fruit diameter indicates the preponderance of additive gene action, suggesting that direct phenotypic selection would be effective for these traits in subsequent generations. Correlation analysis highlighted number of fruits per plant and number of branches per plant as the most important positive associates of yield. Path coefficient analysis confirmed number of fruits per plant as the primary direct contributor to total yield, with number of seeds per fruit and average fruit weight as secondary contributors. Based on these findings, selection for genotypes combining high number of fruits per plant, more branches, early flowering and optimum fruit size would be the most efficient breeding strategy to develop superior okra varieties from this cross. Superior F_4 families with desirable trait combinations identified in this study could be advanced to F_5 and beyond for line development and eventual variety release.

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