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Statistical analysis of variances studies in segregating populations of okra (*Abelmoschus esculentus* L. Moench)

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Abstract

The present study aimed to assess the analysis of variance among F_3 and F_4 populations of okra (*Abelmoschus esculentus* (L.) Moench) derived from two crosses: OK-2017-010 $\times$ Pusa Sawani and OK-2017-010 $\times$ Varsha Uphar. Statistical variance analysis was conducted using the augmented block design for the F_3 populations and randomized complete block design (RCBD) for the F_4 populations. A total of fourteen agronomic traits were evaluated, including earliness (days to first flowering, days to 50% flowering), plant height, number of branches per plant, fruit size (length, diameter), number of fruits per plant, and total yield per plant. The analysis of variance revealed highly significant differences among the treatments in both F_3 and F_4 populations for all traits, indicating substantial genetic variability. The presence of significant variation across yield components, fruit quality traits, and plant architecture highlights the potential of these populations for the selection of superior genotypes. These findings provide a solid foundation for the advancement of promising segregants in okra breeding programs, with the ultimate goal of developing high-yielding, early-maturing, and improved-quality okra cultivars.

Keywords: Okra, *Abelmoschus esculentus*, F_3 and F_4 populations

Introduction

Okra (*Abelmoschus esculentus* L. Moench) is an important vegetable crop grown widely in tropical and subtropical regions for its nutritional and medicinal benefits. It is a rich source of vitamins, minerals, and dietary fibre, and plays a vital role in food security and nutrition (Kumar *et al.*, 2021) [4]. Despite its significance, okra breeding has faced challenges such as low genetic diversity, susceptibility to diseases, and yield constraints (Patel *et al.*, 2020) [5]. Therefore, exploring genetic variability in segregating populations is crucial for the development of improved varieties with enhanced yield, early maturity, and superior fruit quality. The use of variance analysis techniques, such as the augmented block design and randomized complete block design (RCBD), allows breeders to assess the genetic diversity and environmental stability of key agronomic traits (Verma *et al.*, 2022) [12].

Statistical analysis of variance was performed on fourteen key traits, including days to flowering, plant height, fruit dimensions, number of fruits, and total yield per plant, to assess treatment effects and determine the extent of genetic variation within the populations. Previous studies have emphasized the importance of such analyses in the identification of superior segregants for further selection and advancement in breeding programs (Sharma *et al.*, 2018; Gupta *et al.*, 2020) [10, 3]. By identifying significant genetic differences among the segregating populations, this study aims to contribute to the ongoing efforts to enhance the productivity and quality of okra through targeted breeding strategies. The findings will provide valuable insights for breeders in selecting high-performing genotypes for the development of new okra cultivars with improved agronomic traits.

Materials and Methods

The present investigation was carried out in the Department of Biotechnology and Crop Improvement, College of Horticulture, Bengaluru, to assess the statistical analysis of variance

in the F₃ and F₄ populations of OK-201-010 x Pusa Sawani and OK-2017-010 x Varsha Uphar. The F₃ consist of the 25 families from the both the cross along with the check Varsha Uphar, Pusa A4, Prabhani Kranti, Khasi Pragati and Arka Anamika along with the parents were analysed in Augmented block design the statistical analysis was done by using the R-STUDIO 4.4.1 (AUGMENTEDRBD) packages was used. The F₄ consist of the eleven segregant in cross OK-2017-010 x Pusa Sawani, and twelve segregants from OK-2017-010 x Varsha Uphar along with the checks Prabhani Kranti, Arka Anamika, Pusa A4 and parents analysed in Randomized Complete Block Design, the statistical analysis was done by using the GRAPES 1.0 from the Kerala Agriculture University. The observations were recorded from all the individual plants.

Results and Discussion

Statistical Assessment of Variance in F₃ Populations

The statistical assessment of variance in the F₃ populations derived from the crosses OK-2017-010 x Pusa Sawani and OK-2017-010 x Varsha Uphar reveals significant differences for all the fourteen traits under investigation. The application of the augmented block design ensured robust analysis and precise identification of the genetic variation within these populations. This variation is critical for the progress of okra breeding programs aimed at developing superior cultivars with enhanced agronomic traits.

Cross OK-2017-010 x Pusa Sawani

In the F₃ populations of OK-2017-010 x Pusa Sawani, significant variation was observed among the treatments across all fourteen characters, including key traits such as days to first flowering, days to 50% flowering, plant height, number of branches per plant, fruit size (length and diameter), number of fruits per plant, and total yield per plant presented in Table 1. This suggests that these traits are influenced by

genetic factors rather than environmental variability, making this population a valuable resource for selection. The genetic variability for earliness and yield components, particularly the number of fruits and fruit size, highlights the potential of specific segregants in contributing to early maturity and higher yields, which are critical breeding targets in okra improvement programs.

The presence of significant differences across traits related to plant architecture (e.g., plant height, number of branches, and stem girth) and reproductive attributes (e.g., number of fruits and seeds per plant) suggests that the population contains considerable genetic diversity similar findings with the Prakash *et al.* (2022) ^[6], Akotar *et al.* (2010) ^[2], and Singh *et al.* (2017) ^[9]. This diversity offers opportunities for breeders to select desirable genotypes that combine favourable traits, ultimately leading to the development of high-yielding okra varieties with superior agronomic performance.

Cross OK-2017-010 x Varsha Uphar

Similarly, the analysis of variance for the F₃ populations of OK-2017-010 x Varsha Uphar revealed significant differences for all fourteen characters, further emphasizing the presence of genetic variation within this cross presented in Table 2. Traits such as plant height, days to flowering, fruit dimensions, and yield-related parameters exhibited substantial variability among the treatment diversity, similar to the findings of Prakash *et al.* (2022) ^[6], Akotar *et al.* (2010) ^[2], and Singh *et al.* (2017) ^[9]. This variability is crucial for identifying superior segregants that can be advanced to the next generation. The significant differences observed in traits such as fruit length, diameter, and average fruit weight are particularly important for okra breeding, as these characteristics directly influence marketability and consumer preference. Additionally, the variation in total yield per plant across the segregants indicates the potential for selecting high-yielding lines from this population.

Table 1: Statistical analysis of variance for earliness growth and yield parameters in the F₃ populations of the cross OK-2017-010 x Pusa Sawani in Okra

Source	Treatment (ignoring Blocks)	Treatment: Check	Treatment: Test	Treatment: Test and Test vs. Check	Block (eliminating Treatments)	Residuals
Degrees of freedom	31	4	26	27	4	16
Days to first flowering	5.52 *	4.23	5.96 *	4.92 *	2.35	1.99
Days to 50% flowering	9.79 **	6.80 **	10.43 **	8.49 **	0.20	0.38
Plant height (cm)	378.39 **	17.84	453.90 **	378.59 **	11.65	8.48
Number of branches	0.11 **	0.15 **	0.11 **	0.11 **	0.03	0.01
Number of nodes	8.74 **	23.79 **	6.37 **	4.53 **	0.06	0.10
Inter nodal length (cm)	3.07 **	0.82	3.29 **	3.22 **	0.53	0.65
Number of ridges	0.25 *	0.22	0.26 *	0.19 *	0.49 **	0.09
Fruit diameter(cm)	3.37 **	1.59	3.47 **	3.14 **	0.95	0.68
Fruit length (cm)	0.09 **	0.17 **	0.07 **	0.08 **	0.01	0.01
Stem girth (cm)	0.01 **	0.01 **	0.01 **	0.01 **	0.00	0.00
Number of fruits per plant	26.42 **	5.55	12.42 *	26.01 **	10.13	5.29
Average fruit weight (g)	4.60 **	3.88 **	4.70 **	4.24 **	1.22	0.73
Number of seeds per fruit	101.84 **	8.14 *	114.63 **	115.30 **	17.92	29.50
Total yield per plant (g)	9687.07 **	8960.60 **	5030.92 **	9184.84 **	356.02	476.43

*and** indicate significance of values at p = 0.05 and p = 0.01, respectively

Table 2: Statistical analysis of variance for earliness, growth and yield parameters in the F₃ populations of the cross OK-2017- 010 × Varsha Uphar in okra

Source	Treatment (eliminating Blocks)	Treatment: Check	Treatment: Test	Treatment: Test and Test vs. Check	Block (eliminating Treatments)	Residuals
Degrees of freedom	31	4	26	27	4	16
Days to first flowering	1.81	1.62	2.14 *	1.85	2.31	0.90
Days to 50% flowering	4.44 **	6.44 **	2.67 *	4.12 **	0.54	0.86
Plant height (cm)	536.70 **	414.89 **	583.96 **	556.19 **	1.53	5.01
Number of branches	0.08 **	0.03	0.10 **	0.09 **	0.01	0.02
Number of nodes	10.52 **	21.13 **	10.27 **	8.82 **	0.09	0.13
Inter nodal length (cm)	5.80 **	11.87 **	3.80 **	4.83 **	1.04	0.51
Number of ridges	0.20 *	0.21	0.13	0.20 *	0.67 **	0.08
Fruit diameter(cm)	0.73 **	0.93 **	0.38 **	0.69 **	0.06	0.11
Fruit length (cm)	0.11 **	0.00	0.02 **	0.12 **	0.00	0.00
Stem girth (cm)	1.18 **	0.02	1.50 **	1.37 **	0.01	0.01
Number of fruits per plant	29.01 *	6.96	24.87 *	32.53 **	26.64	9.53
Average fruit weight (g)	8.61 **	3.77 **	10.46 **	9.39 **	0.25	0.45
Number of seeds per fruit	94.79 **	8.71	154.27 **	108.56 **	37.03	24.72
Total yield per plant (g)	17455.17 **	318.05 *	17657.94 **	20197.11 **	3580.33 **	603.02

*and** indicate significance of values at p = 0.05 and p = 0.01, respectively

Implications for Breeding Programs

The significant variation in both crosses reflects the genetic diversity present in the F₃ populations, which is essential for effective selection in early segregating generations. The ability to identify superior genotypes based on key traits such as earliness, fruit quality, and yield potential highlights the effectiveness of the augmented block design in assessing genetic variability while controlling environmental effects. For okra breeders, this analysis provides valuable insights into the potential of specific crosses to contribute to the development of improved okra cultivars. The identification of significant treatment effects across multiple traits demonstrates that these populations harbour sufficient genetic variability for further selection and advancement to subsequent generations. This variability forms the foundation for selecting superior lines that exhibit a combination of desirable traits, such as early maturity, increased yield, and enhanced fruit quality.

Statistical Analysis of Variance in F₄ Populations

The analysis of variance (ANOVA) conducted for the F₄ populations of both crosses OK-2017-010 × Pusa Sawani and OK-2017-010 × Varsha Uphar revealed highly significant differences among the treatment groups for all fourteen parameters studied. This result indicates substantial genetic variation among the evaluated populations, which is crucial for selecting superior lines in the breeding program.

Cross OK-2017-010 × Pusa Sawani

In the case of the cross OK-2017-010 × Pusa Sawani, the significant differences observed among the treatments, including the segregating F₄ populations, the parents, and the four checks, suggest considerable genetic diversity is present within the population in Table 3. This diversity offers a strong foundation for selecting desirable traits related to yield and its attributing factors. Highly significant treatment effects typically reflect the influence of genetic factors over environmental conditions, which reinforces the potential for identifying superior genotypes within these similar results found in the studies of Adeolua and Kehinde (2011)^[1], Simon *et al.* (2013)^[8] and Reddy *et al.* (2012)^[11]. The results also suggest that specific segregants in the F₄ generation are likely to exhibit promising agronomic traits, enhancing the potential for further selection in subsequent generations.

Table 3: Statistical analysis of variance for growth, earliness and yield parameters in the F₄ populations of the cross OK-2017-010 × Pusa Sawani in okra

Source of variation	Treatment	Replication	Error
Degrees of freedom	15	1	15
Days to first flowering	12.5**	0.01	0.86
Days to 50% flowering	69.30**	7.03	2.70
Plant height (cm)	0.50**	0.05	0.13
Number of branches	5.52**	1.08	0.80
Number of nodes	4.94*	2.04	0.25
Inter nodal length (cm)	0.11**	0.01	0.02
Number of ridges	3.86**	0.61	0.43
Fruit diameter(cm)	0.24**	0.02	0.02
Fruit length (cm)	0.02**	3.78	0.01
Stem girth (cm)	55.98**	0.67	2.65
Number of fruits per plant	4.154**	0.001	0.25
Average fruit weight (g)	607.83**	9.74	43.48
Number of seeds per fruit	46.9*	0.11	3.33
Total yield per plant (g)	18047.86**	1.02	784.91

*and** indicate significance of values at p = 0.05 and p = 0.01, respectively

Table 4: Statistical analysis of variance for growth, earliness and yield parameters in the F₄ populations of the cross OK-2017-010 × Varsha Uphar in okra

Source of variation	Treatment	Replication	Error
Degrees of freedom	16	1	16
Days to first flowering	16.85**	1.61	1.62
Days to 50% flowering	49.59**	2.38	3.57
Plant height (cm)	0.22**	0.12	0.06
Number of branches	16.76**	0.02	1.02
Number of nodes	7.38**	0.06	0.24
Inter nodal length (cm)	0.03**	0.002	0.002
Number of ridges	3.76**	2.21	0.34
Fruit diameter(cm)	0.07**	0.0004	0.02
Fruit length (cm)	0.01**	0.0001	0.0002
Stem girth (cm)	44.90**	0.042	0.3
Number of fruits per plant	28.36**	22.91	10.46
Average fruit weight (g)	871.49**	18.07	21.05
Number of seeds per fruit	28.36**	22.91	10.46
Total yield per plant	10706.87**	59.92	527.36

*and** indicate significance of values at p = 0.05 and p = 0.01, respectively

Cross OK-2017-010 × Varsha Uphar

Similarly, the variance analysis for the F₄ populations derived from the cross OK-2017-010 × Varsha Uphar showed

significant differences across all fourteen parameters Furnished in Table 4. This indicates the presence of considerable genetic variability within this population as well, which is essential for effective selection similar results were found in the studies of Adeoluwa and Kehinde (2011)^[1], Simon *et al.* (2013)^[8] and Reddy *et al.* (2012)^[11]. The significant variation observed among the treatments, including the segregants, parents, and checks, points to the genetic potential of this population to contribute to okra improvement programs, especially for traits related to yield, disease resistance, and plant vigour.

General Implications for Breeding Programs

The identification of highly significant differences among the treatments across both crosses underscores the effectiveness of the Randomized Complete Block Design (RCBD) in controlling environmental variability and accurately estimating genetic variation. This, in turn, provides breeders with robust data for the selection of superior genotypes.

The genetic variability observed in these F₄ populations is crucial for enhancing important traits in okra, including yield and resilience to environmental stressors. These findings suggest that there is ample scope for selecting high-performing lines that could contribute to the development of superior okra cultivars with improved yield potential and other agronomically valuable traits.

Conclusion

Statistical variance analysis of the F₃ populations of both crosses, OK-2017-010 × Pusa Sawani and OK-2017-010 × Varsha Uphar reveals substantial genetic variation across key agronomic traits. Similarly, the significant treatment effects across both crosses demonstrate the presence of meaningful genetic variability in the F₄ populations, which is a critical requirement for the continued progress of okra breeding programs. This provides a strong basis for the selection of promising segregants that can be advanced in future breeding efforts aimed at developing superior okra varieties.

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