Original Research Article

Genetic variability studies in the interspecific derivatives (*S. indicum x S. mulayanum*) of sesame

Abstract

The present study aims to assess genetic variability for agronomic characters in the interspecific population developed by hybridization between *Sesamum indicum* (Swetha til) x *Sesamum mulayanum (*IC-43144-1). Experimental materials were raised during *late Kharif*-2023 at ICAR-Indian Institute of Oilseeds Research, Hyderabad. A total of 80 F_6 interspecific derivatives were evaluated along with four check varieties namely GT-10, Swetha Til, IC-43144-1 (*S. mulayanum*), CUMS-17 in Augmented Randomised Complete Block Design (ARCBD). Analysis of variance (ANOVA) revealed, significant variability in the interspecific derivatives for all the traits studied *viz.,* days for emergence, days for flowering initiation, days for flower session, days for maturity, plant height, number of primary branches per plant, total number of capsules per plant, capsule length, test weight, harvest index and seed yield per plant. The magnitude of phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) values were higher for the traits *viz*., total number of capsules per plant, harvest index, seed yield per plant, hence improvement through selection could be possible. Phenological traits such as days for emergence, plant height, number of primary branches per plant, total number of capsules per plant, harvest index and seed yield per plant exhibited a high heritability along with a high genetic advance as per cent of mean, indicating additive gene action in the expression of these traits. Simple phenotypic selection may be effective for improving these characters. So, the selection based on these traits should be prioritized in the selection process of interspecific hybrids of sesame breeding programme.

Keywords: *Augmented RCBD**,** heritability, interspecific derivatives, PCV, GCV, (S. indicum x S. mulayanum),*

INTRODUCTION

"Sesame (*Sesamum indicum* L.) is a diploid plant with 2n=2X=26 chromosomes. It is a self-pollinating crop that belongs to the Pedaliaceae family. It is commonly referred to as benni seed, simsim, til, and gingelly, sesame is one of the ancient oilseed crops believed to have originated in East Africa and India" [1]. "Sesame is regarded as one of the oldest oilseed

crops, is widely cultivated in Asia and Africa. Known as the "Queen of Oilseeds," it is valued for its high-quality oil content. The genus Sesamum consists of 30 "accepted" species and 17 species with "unresolved" status" [2]. "Asia has a rich diversity of cultivated sesame while Africa is prosperous in wild relatives" [3]. "Seeds are not only valuable for their nutritional and therapeutic benefits but also provide a significant source of oil (44–57%), proteins (18–25%), carbohydrates (13.5%), and ash (5%)" [4].

"Although genetic variation persists for agronomically important traits in sesame, production levels remain notably low in India. Traditional sesame landraces as well as related wild species are an important source of genetic diversity for breeders and form the backbone of agricultural production. Utilization of wild species of sesamum to create genetic variation is practiced by several workers. Pre breeding is a critical step in crop improvement to bring the wild alleles into cultivated genotypes. Wild relatives of sesame are important reservoir of useful genes and need to be exploited for sesame improvement. These wild species exhibit crossability with the cultivated gene pool to varying extents and can be utilized for transferring the desirable traits using conventional breeding approaches assisted with modern techniques" Singh *et al.* [5]. Biswas and Mitra [6] were successful in crossing *S. mulayanum, S. laciniatum with S. indicum*. Seed dormancy was absent in the F_1 hybrids of *S.indicum x S.mulayanum* and the inheritance of flower colour followed 9:3:3:1 ratio in F_2 population Tanesaka *et al*. [7]. Pre-fertilization barriers between *S. indicum* and *S.mulayanum* were absent Kulkarni *et al*. [8]. Development of interspecific populations and analysis of genetic variation for quality traits like lignans in sesame helps in developing genotypes with superior oil quality rich in lignans Pathak *et al*. [9]. Pre-breeding and understanding genetic variability within germplasm is essential for selecting and breeding high-yielding, high-quality cultivars to enhance production. The genetic variability present in the available germplasm may be utilized either for direct selection or for hybridization programme which involves a choice of potential parents that can produce progeny population out yielding the parents in a set of desirable characters i.e., characters related to yield. It is imperative to investigate variability in quantitative traits, considering genetic parameters such as genotypic and phenotypic variances, broad-sense heritability, and genetic advance.

The present study is aimed to understand the extent of genetic variation for agronomic characters in the population developed through interspecific hybridization of sesame (*S. indicum* and S. *mulayanum*).

MATERIALS AND METHODS

The present investigation was carried out at ICAR - Indian Institute of Oilseeds Research Rajendranagar, Hyderabad during late *kharif,* 2023. The experiment was laid out in augmented block design with 84 germplasm accessions including four check varieties namely GT-10, Swetha Til, IC-43144-1 (*S. mulayanum)*, and CUMS-17. The genotypes were sown by following a spacing of 45 cm between the rows and 15 cm between the plants. The recommended agronomical practices and plant protection measures were adopted for raising a good crop. The observations were recorded on five randomly taken plants for eleven quantitative traits *viz*., days for emergence, days for flowering initiation, days for flower session, days for maturity, plant height, number of primary branches per plant, total number of capsules per plant, capsule length, test weight, harvest index and seed yield per plant. Analysis of variance (ANOVA) was calculated for eleven quantitative traits by using the formula given by Federer *et al.* [10]. The genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were estimated by using the formula given by Burton and de Vane [11]. Heritability in broad sense (h2b) was estimated according to the formula suggested by Johnson *et al.* [12] and Hanson *et al*. [13]. Genetic advance in absolute unit (GA) and percent of the mean (GAM), assuming selection of superior 5% of the genotypes was estimated in accordance with the methods illustrated by Johnson et al. [12]. All the statistical analysis were done in R program version 0.1.7.9000 using augmented RCBD package developed by Aravind *et al.* [14].

RESULTS AND DISCUSSION

The analysis of variance for ARCBD experimental design is presented in (**Table-1a and 1b**). In the present study, analysis of variance showed that significant mean sum of squares for all traits for different sources of variation. The source of variation for entries (excluding blocks) were found to be significant for all the traits analysed *viz*., days for emergence, days for flowering initiation, days for flower session, days for maturity, plant height, number of primary branches per plant, total number of capsules per plant, capsule length, test weight, harvest index and seed yield per plant. This indicated the presence of sufficient amount of genetic variability among the genotypes for all the traits. Similarly, a wide range of variation for the majority of the traits was reported by Kumar *et al.* [15] and Kumar *et al.* [16] in sesame.

The critical difference (CD) (**Table 2**) for any two test treatments of the different blocks showed marginally higher values than the same two test treatments for the same blocks.

The highest value of coefficient of variation (C.V) was found in case of seed yield per plant (13.19), followed by number of primary branches per plant (9.76), total number of capsules per plant (8.07), capsule length (7.44), harvest index (6.15), Plant height (5.22), while, days for maturity (3.53), test weight (2.72) and days for flower session (1.90) had lower C.V values.

Descriptive statistics such as mean, range, standard deviation, standard error, coefficient of variation, skewness and kurtosis for the quantitative traits studied are presented in (**Table 2**). Significant coefficient of variation for the traits indicated the variability present in the interspecific derivatives. The range of variation for days for emergence is 4 to 6 days with the mean value of 4, days for flowering initiation ranges from 33 to 46 days with the mean value of 39, days for flower session ranges from 62 to 85 days with the mean value of 75 days, days for maturity ranges from 83 to 110 days with the mean value of 96 days, Likewise, the characters plant height ranged from 90.79 to 194.87 cm with the mean value of 132.12 cm, number of primary branches per plant ranged from 3 to 10 with the mean value of 7, total number of capsules per plant ranged from 16 to 124 with the mean value 58, capsule length ranged from 1.80 to 3.49 cm with the mean value of 2.63, seed yield per plant ranged from 1.56 to 10.19 g with the mean value of 5.48 g, test weight ranges from 2.39 to 3.45 g with the mean value 3.0 g, and harvest index ranges from 6.31 to 35.83 % with the mean value 17.33 % also showed adequate variation in the interspecific population. Maximum variation for traits like total number of capsules per plant, plant height and lowest for days for emergence, capsule length, test weight was observed. Vamshi *et al*. [17] reported low variation for in capsule length and test weight among the advanced breeding lines derived from *S.indicum* crosses.

Frequency distribution of different quantitative traits was presented in **Figure-1**. The traits like plant height, total number of capsules per plant, harvest index showed positive skewness. It indicates that more proportion of genotypes are found at lower end of distribution. Selection of these genotypes will improve the positively skewed traits. Negative skewness was observed for days for maturity and test weight. Distribution of DFI, DFS, CL, and SYP exhibited mesokutic distribution, indicating uniform or normal distribution for these traits among the interspecific derivatives, while test weight showed negative kurtosis indicating, tailed towards lower values than the mean and harvest index showed positive kurtosis which was tailed towards higher value than the mean. This results are in agreement with the distribution results of advance breeding lines of *S. indicum* by Vamshi *et al*. [17].

(Table 3). Estimation of variance, coefficients of variability, heritability and genetic advance as per cent of mean (GAM).

The value of Phenotypic Coefficient of Variation (PCV) ranged from 4.74 for days for flowering initiation to 37.7 for seed yield per plant, while Genotypic Coefficient of variation (GCV) varied from 3.95 for days to maturity to 36.67 for harvest index. Higher magnitude of both PCV and GCV was recorded for total number of capsules per plant (37.5) and (36.5), seed yield per plant (37.7) and (35.36) and harvest index (37.26) and (36.67). Similar results of high PCV and GCV for total number of capsules per plant, seed yield per plant were reported by Roy *et al.* [18], Srikanth and Ghodke [19], Thouseem *et al*. [20] and harvest index by Takele and Abera [21]. Moderate estimates were recorded for days for emergence (15.26), plant height (15.36) and (14.46) and number of primary branches per plant (16.93) and (13.83). Similar results had been reported for plant height by Durodola *et al*. [22]. Further Low estimates were recorded for days for flowering initiation (6.12) days for maturity (5.27) and (3.95) and days for flower session (4.74), and (4.35) and test weight (7.6), and (7.09). Similar results were reported by Ranjithkumar *et al.* [23] and Manepalli [24] for days to maturity and days for flowering initiation. Zeinalzadeh [25] reported for test weight. The trait capsule length recorded moderate PCV (10.68) coupled with low GCV (7.71). These results are in agreement with those of Abate and Mekbib [26] and Kant *et al.* [27]. In the present study, values of PCV were higher for all traits than corresponding GCV but a very little difference between PCV and GCV were noticed for all the traits, indicating that these were less affected by environment and selection could be effective for further improvement of these traits.

High heritability (broad sense) was observed for the traits viz., days for emergence (100), days for flowering initiation (100), days for flower session (84.2), plant height (88.56), number of primary branches per plant (66.68), total number of capsules per plant (94.74%), seed yield per plant (87.95), test weight (87.04), harvest index (96.83). These findings are in agreement with Gayathri [28]. Remaining traits such as days for maturity (56.13) and capsule length (52.11) exhibited moderate estimates of heritability (broad sense) reported by Abate and Mekbib [26]. This suggested that the phenotypes were the true representative of their genotypes for these characters and selection based on phenotypic value could be reliable.

The high genetic advance (GA) was recorded in traits viz., plant height (37.08), total number of capsules per plant (43.04), while capsule length (0.3), test weight (0.41) were recorded low genetic advance (GA). Genetic advance as per cent of mean (GAM) was observed high for days for emergence (31.48), plant height (28.07), number of primary branches per

plant (23.29), total number of capsules per plant (73.3), seed yield per plant (68.41) and harvest index (74.44). These findings are similar with Sahu *et al.* [29] and Vamshi *et al.* [17] for plant height, number of primary branches per plant and total number of capsules per plant. Moderate GAM was observed for days for flowering initiation (12.63), capsule length (11.48) and test weight (13.66). Low GAM was observed for days for flowering session (8.24) and days for maturity (6.11) respectively. Pavani *et al.* [30] also reported low GAM for days for maturity.

Heritability and genetic advance, when considered together would be more reliable and useful in predicting the resultant effects of selection Johnson *et al*. [12]. High heritability coupled with high genetic advance as percent of mean was observed for six traits viz., days for emergence, plant height, number of primary branches per plant, total number of capsules per plant, seed yield per plant, harvest index indicating that these traits which may be attributed to the preponderance of additive gene action and possess high selective value and thus, selection pressure could profitably be applied on these traits for their rationale improvement. These results were in agreement with those of Divya *et al.* [31], Khuntia *et al*. [32], Thouseem *et al*. [20] for plant height, number of primary branches per plant, total number of capsules per plant, seed yield per plant and harvest index by Hassen *et al* [33] and Mahla *et al* [34].

PCV, GCV, heritability in broad sense and Genetic advance as per cent of mean (GAM) should be considered together while assessing the effect of selection than single parameter alone. Mohanty *et al.* [35] reported high PCV, GCV, heritability and genetic advance as per cent of mean for harvest index and seed yield per plant as observed in the present investigation.

CONCLUSION

Pre-breeding is a very important step in crop improvement which involves inflow of wild alleles into the cultivated species. The present study involving interspecific derivatives developed from cultivated *Sesamum indicum* and wild species *Sesamum mulayanum* gives an insight to the extent of genetic diversity created in the sesame crop using wild species. This studies aims to identify and characterize variations in agronomic traits related to seed yield. The present study, strongly indicates, significant variability among the interspecific derivatives developed using wild species *S.mulayaanum*, for all traits studied. The results of this study can be used by the sesame researchers for developing improved high yielding sesame genotypes. High heritability along with high genetic advance as percent of mean in the traits *viz*., days for emergence, plant height, number of primary branches per plant, total number of capsules per plant, seed yield per plant, harvest index were with the predominance of additive type of gene

action predicting genetic gain under selection than heritability estimates alone and suggesting that these characters can be improved by simple selection among the interspecific derivatives.

Disclaimer (Artificial intelligence)

Option 1:

Author(s) hereby declare that NO generative AI technologies such as Large Language Models (ChatGPT, COPILOT, etc) and text-to-image generators have been used during writing or editing of manuscripts.

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Table-1a. Analysis of variance for treatment adjustment of eleven agronomic traits for different source of variation.

ANOVA - treatment adjusted												
Source of variation	df	DE	DFI	DFS	DM	PH	NPB	TCP	CL	TW	HI	SYP
Block (ignoring Treatments)	3	1.2 **	0.54 **	38.18**	51.36*	347.15**	2.28*	1746.20**	0.25*	0.03**	113.27**	25.27**
Treatment (eliminating Blocks)	83	0.68 **	8.96**	21.96**	45.05*	392.93**	1.6*	697.2**	0.11*	0.07**	72.33**	3.62**
Treatment: Check	3	4 **	91.67**	200**	360.17**	235.18*	8.25**	3502.06**	1.04**	0.48**	433.7**	11.97**
Treatment: Test and Test vs. Check	80	0.55 **	5.86 **	15.29**	33.23*	398.85**	1.35*	592.01**	0.08 ns	0.06**	58.78**	3.31**
Residuals	9	0	0	2	11.44	47.14	0.47	25.56	0.04	0.01	1.32	0.51

Significance levels: ns(non-significant) P > 0.05; * P <= 0.05; ** P <= 0.01, d.f. degrees of freedom,

DE-Days for emergence, DFI-Days for flowering initiation, DFS-Days for flower session, DM-Days for maturity, PH-Plant height (cm), NPB-Number of primary branches per plant, TCP-Total number of capsules per plant, CL-Capsule length (cm), TW-Test weight (g), HI- Harvest index (%), SYP-Seed yield per plant (g).

Table-1b : Analysis of variance for block adjustment of eleven agronomic traits for different source of variation.

		ANOVA - block adjusted										
Source	df	DE	DFI	DFS	DM	PH	NPB	TCP	CL	TW	HI	SYP
Treatment (ignoring Blocks)	83	0.72**	8.98**	23.33**	46.76*	405.14 **	1.65 *	756.94 **	0.12 *	0.07 **	76 **	4.52 **
Treatment: Check	3	4**	91.67**	200 **	360.17**	235.18 *	8.25 **	3502.06 **	1.04 **	0.48 **	433.76 **	11.97 **
Treatment: Test	79	0.57**	5.85**	12.66 **	26.09 ns	411.93 **	1.42 *	486.14 **	0.08 ns	0.05 **	41.67**	4.27 **
Treatment:Test vs. Check	1	2.85**	8.27**	336.67**	740.03**	378.08 *	0.13 ns	13914.8 **	0.28 *	0.37 **	1714.5 **	1.66 ns
Block (eliminating Treatments)	3	0 ns	0 ns	0.33 ns	3.83 ns	9.56 ns	0.92 ns	93.23 ns	0.1 ns	0.01 ns	11.71 **	0.61 ns
Residuals	9	0	0	2	11.44	47.14	0.47	25.56	0.04	0.01	1.32	0.51

Significance levels: ns(non-significant) P > 0.05; * P <= 0.05; ** P <= 0.01, d.f. degrees of freedom,

DE-Days for emergence, DFI-Days for flowering initiation, DFS-Days for flower session, DM-Days for maturity, PH-Plant height (cm), NPB-Number of primary branches per plant, TCP-Total number of capsules per plant, CL-Capsule length (cm), TW-Test weight (g), HI- Harvest index (%), SYP-Seed yield per plant (g).

Table 2. Critical difference and Coefficient of Variation

	Critical difference										
Comparison	DE	DFI	DFS	DM	PH	NPB	TCP	CL	TW	HI	SYP
Control Treatment Means	0.00	0.00	2.26	5.41	10.98	1.1	8.09	0.31	0.13	1.84	1.15
Two Test Treatments (Same Block)	0.00	0.00	4.52	10.82	21.96	2.2	16.17	0.62	0.26	3.67	2.29
Two Test Treatments (Different Blocks)	0.00	0.00	5.06	12.1	24.56	2.46	18.08	0.69	0.29	4.11	2.57
A Test Treatment and a Control Treatment	0.00	0.00	4	9.57	19.41	1.94	14.3	0.55	0.23	3.25	2.03
Descriptive statistics											
Mean	4.94	39.50	75.04	96.85	132.12	7.03	58.80	2.63	3.00	17.33	5.48
Std. Error	0.08	0.28	0.42	0.59	2.20	0.14	2.74	0.04	0.03	0.78	0.24
Std. Deviation	0.77	2.53	3.83	5.42	20.16	1.28	25.10	0.36	0.24	7.13	2.23
Min	4.00	33.00	62.25	83.00	90.79	3.63	16.11	1.80	2.39	6.31	1.56
Max	6.00	46.00	85.75	110.00	194.87	10.62	124.31	3.49	3.45	35.83	10.19
CV	0.1	0.06	1.90	3.53	5.22	9.76	8.07	7.44	2.72	6.15	13.19
Skewness	0.10 ^{ns}	0.00 ^{ns}	0.36 ^{ns}	-0.77**	0.58*	0.05 ^{ns}	0.59*	0.09 ^{ns}	-0.53*	1.03**	0.28 ^{ns}

Kurtosis	1.73**	3.30 ns	4.18*	3.86 ns	3.41 ns	2.87 ns	2.70 ns	2.62 ns	2.89 ns	3.63 ns	2.32 ns

CD-Critical difference, CV-Coefficient variation, DE-Days for emergence, DFI-Days for flowering initiation, DFS-Days for flower session, DM-Days for maturity, PH-Plant height (cm), NPB-Number of primary branches per plant, TCP-Total number of capsules per plant, CL-Capsule length (cm), TW-Test weight (g), HI- Harvest index (%), SYP-Seed yield per plant (g).

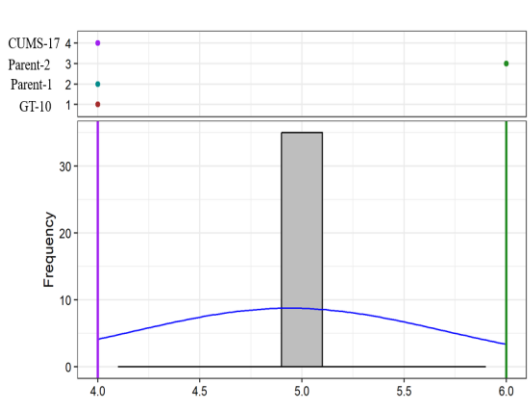
Table 3. Estimation of variance, coefficients of variability, heritability and genetic advance as per cent of mean (GAM) for eleven agronomic traits.

Trait	Mean	PV	GV	EV	GCV		PCV		ECV	hBS		GA	GAM	
					Values	Category	Values	Category		Values	Category		Values	Category
DE	4.94	0.57	0.57	0	15.26	Medium	15.26	Medium	0	100	High	1.56	31.48	High
DFI	39.5	5.85	5.85	0	6.12	Low	6.12	Low	0	100	High	4.99	12.63	Medium
DFS	75.04	12.66	10.66	2	4.35	Low	4.74	Low	1.88	84.2	High	6.18	8.24	Low
DM	96.85	26.09	14.64	11.44	3.95	Low	5.27	Low	3.49	56.13	Medium	5.91	6.11	Low
PH	132.12	411.93	364.8	47.14	14.46	Medium	15.36	Medium	5.2	88.56	High	37.08	28.07	High
NPB	7.03	1.42	0.94	0.47	13.83	Medium	16.93	Medium	9.78	66.68	High	1.64	23.29	High
TCP	58.8	486.14	460.58	25.56	36.5	High	37.5	High	8.6	94.74	High	43.09	73.3	High
CL	2.63	0.08	0.04	0.04	7.71	Low	10.68	Medium	7.39	52.11	Medium	0.3	11.48	Medium
TW	3	0.05	0.05	0.01	7.09	Low	7.6	Low	2.74	87.04	High	0.41	13.66	Medium
HI	17.33	41.67	40.35	1.32	36.67	High	37.26	High	6.63	96.83	High	12.9	74.43	High
SYP	5.48	4.27	3.75	0.51	35.36	High	37.7	High	13.09	87.95	High	3.75	68.41	High

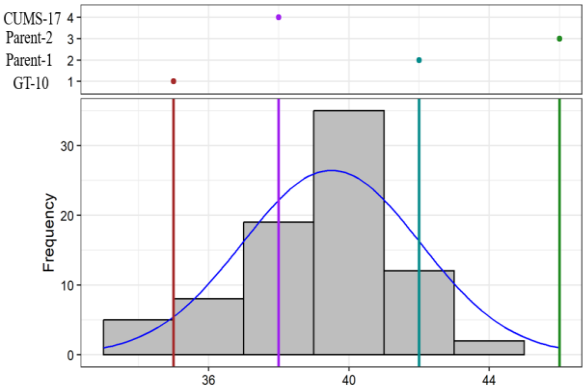
PV-Phenotypic Variance, GV-Genotypic Variance, EV-Environmental Variance, GCV-Genotypic Coefficient Variation, PCV-Phenotypic Coefficient Variation, hBS -Heritability in a Broad Sense, GA-Genetic Advance and GAM-Genetic Advance Mean

DE-Days for emergence, DFI-Days for flowering initiation, DFS-Days for flower session, DM-Days for maturity, PH-Plant height (cm), NPB-Number of primary branches per plant, TCP-Total number of capsules per plant, CL-Capsule length (cm), TW-Test weight (g), HI- Harvest index (%), SYP-Seed yield per plant (g).

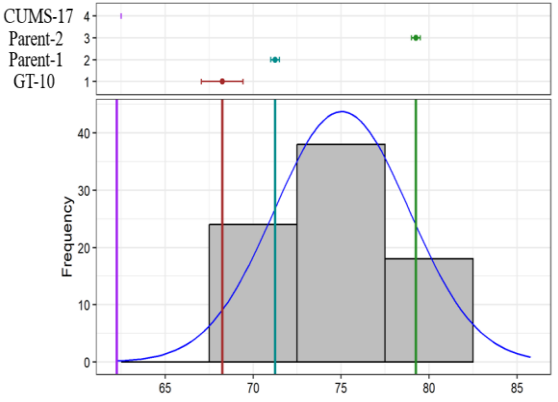
Fig 1. Estimation of frequency distribution of quantitative traits in sesame



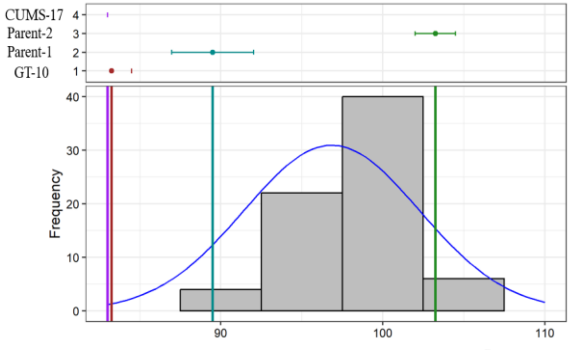
Days for emergence

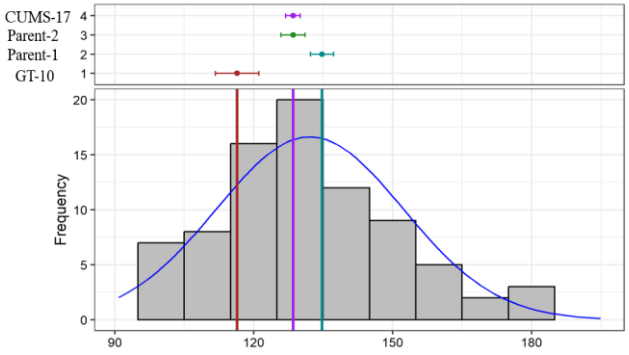


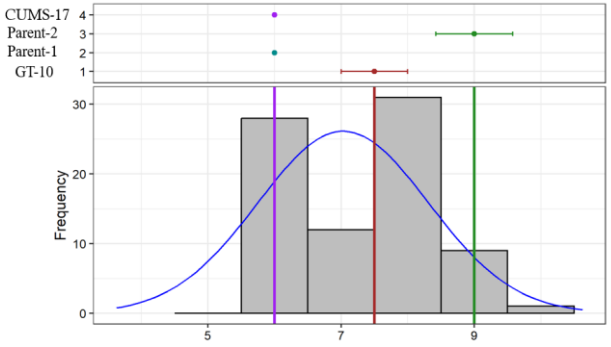
Days for flower initiation



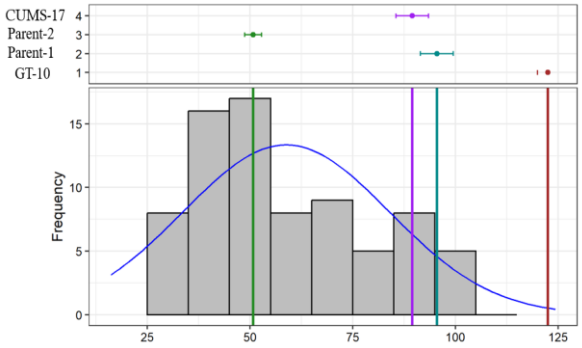
Days for flower session



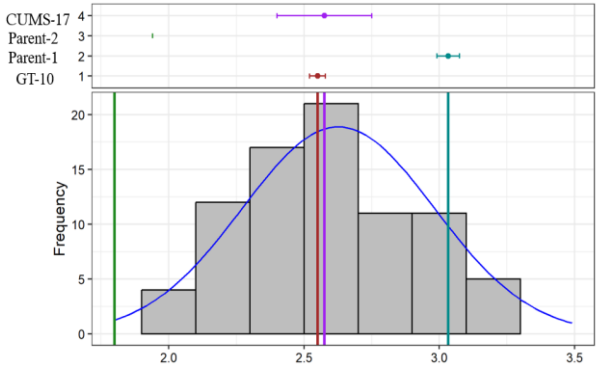




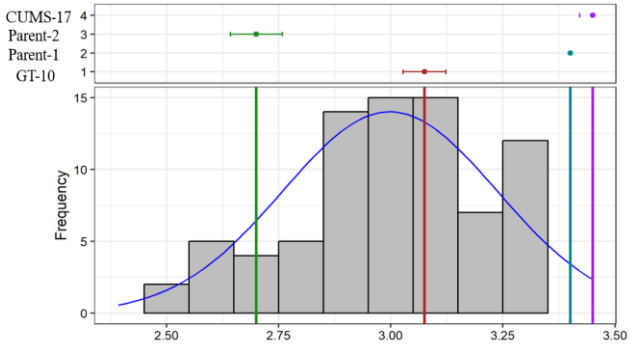
Days for maturity



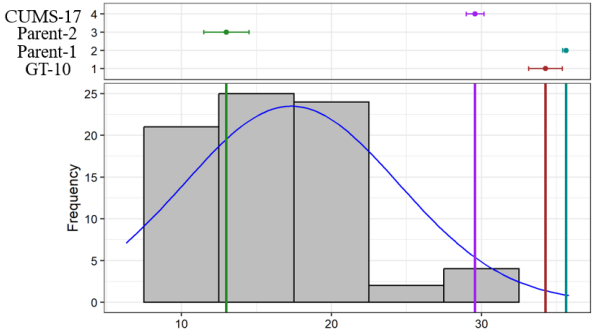
Plant height



Number of primary branches per plant



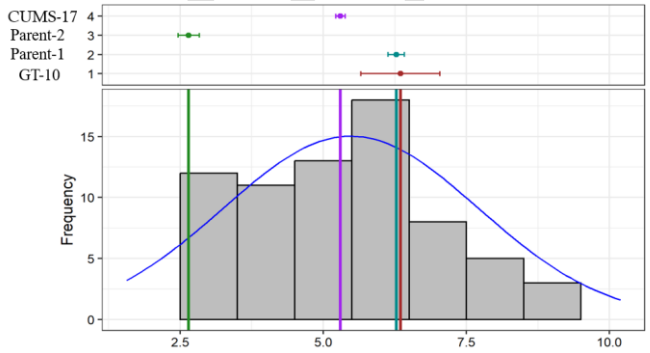
Total number of capsules per plant



Capsule Length

Test weight

Harvest Index



Seed yield per plant