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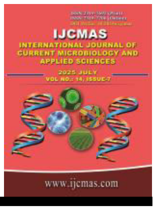

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Genetic Variability Studies for Seed Cotton Yield and Other Yield Attributes in the UASD *Bt*-78 Event Based F_2 Population of Cotton (*G. hirsutum* L.)

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ABSTRACT

Keywords

UASD cry-1Ac Bt-Cotton event-78, Analysis of variance, Leptokurtic, Variability, Heritability, Genetic advance as a percent of mean

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UASD *cry-1Ac Bt*-cotton event-78 is a novel event developed under the background of *G. hirsutum* L., RAH-100. In the present study early segregating F_2 population derived by selfing of F_1 of the cross, UASD *Bt*-78 × DHS-29 was evaluated for estimation of genetic variability for seed cotton yield and other yield attributes, during the *kharif*-2021 at Agricultural Research Station, Dharwad. For most of the traits, a wide range was observed in the segregating population, likewise analysis of variance also showed the presence of significant difference for the considered traits within the F_2 population and in between checks and F_2 segregants. Negatively skewed distribution was observed for the traits like seed cotton yield, plant height, average boll weight, number of bolls/plants and GOT, suggesting that mild selection is sufficient for improvement. All the yield attributes showed a leptokurtic distribution, suggesting that fewer genes control them. In the segregating population, moderate to higher to levels of variability (GCV and PCV) in association with higher per cent of heritability and genetic advance as a per cent of mean was recorded for most important traits such as seed cotton yield/plant, lint yield/plant, number of bolls/plant, number of sympodia/plant, plant height, number of monopodia/plant and sympodial length/plant, emphasising that simple selection in subsequent generations for improving these traits, as these traits are controlled by additive gene actions.

Introduction

Cotton (*Gossypium.spp*) is king of fiber, and an important crop for the sustainable economy of India. Nearly sixty million people depend on cotton cultivation, marketing, processing, and export for their livelihood. India is the only country to grow all the four cultivated species, including their intra-specific and inter-specific crosses. Cotton is grown on 318.80 lakh ha of land worldwide, yielding 242.70 lakh tonnes and a 763 kg/ha of productivity (ICAC, 2023-24). India ranks first with respect to area (125 lakh hectares) and second in production second in the world with 53.80 lakh tonnes, followed by China (55.90 lakh tonnes) with a productivity of 429 kg/ha. Gujarat, Telangana and Maharashtra, are the major cotton growing states (AICRP-2023-24). The entire global cotton supply chain in India has changed since the introduction of genetically modified cotton in 2002. The only genetically modified crop that has been approved for production is still *Bt* cotton. The GM hybrid cotton technology proved effective against the major bollworms. Over the course of two decades, the area planted to *Bt*-cotton has increased to over 95% of net crop area and soared up the Indian cotton production.

However, pink boll worms have developed resistance to BG-I (Dhurua and Gujar, 2011) and BG-II hybrids (Naik *et al.,* 2018 and Kranthi *et al.,* 2019) hybrids as a result of long-term cultivation of single event-based long duration hybrids. The transgenic technology with gene diversification pertaining to *cry* genes or use of hybrids/varieties derived from novel and more potential events would ensure the sustainability of the technology. The public sector *Bt*-cotton event of University of Agricultural Sciences Dharwad, UASD Event No-78 has been developed with *cry-1Ac* gene driven by double promoter. The transgene construct was obtained by International Centre for Genetic Engineering and Biotechnology, New Delhi. The event is in the genetic background of RAH-100, a released variety belonging to *G. hirsutum* L., with good agronomic characters. The expression of insecticidal Cry-protein in the different plant parts was found to be higher than BG-II, and consistent throughout entire crop growth (Manjunathswamy, 2014; Patil, 2019; Gangavati, 2022 and Manjula *et al.,* 2022). Different breeding strategies have been employed, to explore potential application of this unique event in the creation of *Bt*-cultivars, along with introgression of *cry-1Ac* gene, recombination of desirable yield attributing characters.

Hybridization followed by selfing is a key step in development of UASD *Bt*-78 event based homozygous lines, where in maximum segregation for any of the morphological characters is observed in the early segregating generations, and therefore assessing the amount of variation for a given trait is crucial for harnessing the available genetic variability for selection of desirable genotypes. The parameters of the population distribution include kurtosis and the coefficient of skewness. Skewness is a third-degree statistical tool that measures the degree of asymmetry in the population and also provides information about the nature of gene action (Fisher, 1932). A skewed distribution denotes the predominance of non-additive gene action, in which genes controlling such traits are largely dominant, regardless of their effect. A normal distribution is considered symmetrical if its skew value is zero, showing the prevalence of additive gene action.

If the frequency distribution curve for a trait is peaked on the left side, the population is said to be positively skewed and a peak on the right side indicates that the population is negatively skewed, positive skewness indicates complementary gene interactions, response to selection for such traits would be low, hence intense selection is required for enhancing the genetic gain. Whereas negative skewness suggests presence of duplicate (additive × additive) interactions, and mild selection is enough to maximize the genetic gain of such a trait (Poorni *et al.,* 1977). Kurtosis measures the peakness/sharpness of a probability distribution and provides the information about the number of genes governing the particular trait (Robson, 1956). Kurtosis is negative or close to zero (platykurtic) in absence of gene interaction and positive in presence of gene interaction (leptokurtic) (Nachimuthu *et al.,* 2014). A smaller proportion of genes regulate traits with a leptokurtic distribution, whereas a greater number of genes control traits with a platykurtic distribution (Poorni *et al.,* 1977). Studying the gene interactions is essential for improving the selection efficiency. In addition to genetic variability, understanding about heritability and genetic advance, determines the actual degree to which a character is transmitted to offspring. Therefore, a thorough understanding of the genetic parameters of the population is required to achieve the goal through appropriate breeding strategy. In this study, UASD *Bt*-78 event based early segregating (F_2) population, which was derived by crossing UASD *Bt*-78 with Dharwad hirsutum selection-29 was evaluated and genetic variability parameters were estimated for eleven morphological traits.

Materials and Methods

The present study was carried out at the Agricultural Research Station in Dharwad during the *Kharif*-2021, which is 668 meters above mean sea level and located at 15° 27ˈ30ˈˈ N latitude and 75° 00ˈ30ˈˈ E longitude. The experimental material consisting of the UASD *Bt*-78 event based early segregating (F_2) population derived from selfing of the F_1 hybrid of an intra-specific cross, UASD*Bt*-78 × DHS-29. In 15 blocks with an eight-meter row length, 600 F_2 plants were evaluated in the augmented randomized complete block design, with a 90 × 40 cm^2 spacing. Each block consisting of two rows of F_2 plants, one row each of parental lines, F_1 hybrid, and zonal *Bt*-check (CICR *Bt*-23). All the recommended agronomic package of practice undertaken at regular intervals (POP-2020). the statistical analysis was carried out based on the observations made on seed cotton yield of and ten yield-attributing traits, including the number of monopodia/plants, sympodial branches/plants, bolls/plants, average boll weight, plant height, seed index, lint index, lint yield/plant, and ginning outturn, using the "augmented RCBD" sub-package, which is built under the statistical analytical package "agricolae" in the "R" programming language. The following section provides a description of the findings from the analysis of variance, variability parameters such as genotypic and phenotypic coefficient variation (GCV and PCV), including heritability and genetic advance.

Analysis of variance

Analysis of variance was carried out according to Federer (1956). It also gives all possible paired treatment comparisons and significance levels (Prob >F) and critical difference between two checks, two test treatment (in a same block and different block separately) and in between test treatment and check treatment at five and one per cent level of significance (Table. 1)

Genetic variability parameters: The genotypic, phenotypic and environmental coefficient of variation was computed according to Burton and Devane (1953) as follows:

- **Genotypic coefficient of variation (GCV)**

$$= \frac{\sqrt{\delta_g^2}}{X} \times 100$$

- **Phenotypic coefficient of variation (PCV)**

$$= \frac{\sqrt{\delta_g^2} + \sqrt{\delta_e^2}}{X} \times 100$$

- **Environmental coefficient of variation (ECV)**

$$= \frac{\sqrt{\delta_e^2}}{X} \times 100$$

Where, $\sqrt{\delta_g^2}$ is the genotypic standard deviation

$\sqrt{\delta_g^2} + \sqrt{\delta_e^2}$ is the phenotypic standard deviation

$\sqrt{\delta_e^2}$ is the environmental standard deviation

X is the mean of the population

Sivasubramanian and Menon (1973) classified the genotypic coefficient of variation (PCV), phenotypic coefficient of variation (GCV) and environmental coefficient of variation (ECV) as follows.

- Low: 0-10%
- Moderate: 10-20%
- High: > 20%

Heritability (H^2_{bs}): Heritability in broad sense refers to the heritable fraction of the total variation, which is nothing but the ratio of genotypic variance to phenotype variance, expressed in terms of per cent (Lush, 1940).

$$\textbf{Heritability } (H^2_{bs}) = \frac{\delta_g^2}{\delta_p^2} \times 100$$

Where, H^2_{bs} is heritability in broad sense

δ^2_g is genotypic variance and δ^2_p is phenotypic variance

Robinson *et al.,* (1949) given the classification for heritability of a character described as follows

- Low: 0-30%
- Moderate: 30-60%
- High: > 60%

Genetic advance (GA)

The transition in the population mean that is reflected in the next generation in the form of genetic advance, which depends mainly on the heritability(h_{bs}^2), high selection coefficient (i) and larger selection differential (S). GA can be estimated using following formula given by Bruton (1952).

$$GA = S\, H^2_{bs}.\, \sigma_p$$

Where, GA = Expected genetic advance
S = Selection differential (when selection intensity (i) = 0.05, then S = 2.063)

σ_p = Phenotypic standard deviation

$H^2_{b.s}$ = Heritability in broad sense.

Genetic advance as per cent of mean (GAM)

Genetic advance as a percent of mean is a measure of scale to compare with the other traits.

$$GAM = \frac{GA}{x} \times 100$$

Johnson *et al.,* (1955) classified the GAM as low (> 10%), moderate (10-20%) and high (<20 %)

Results and Discussion

Analysis of variance for eleven morphological traits in the UASD *Bt*-78 event based segregating F_2 population

Analysis of variance for seed cotton yield and other yield attributes showed a significant difference across F_2 plants and checks. The block effects were largely non-significant, confirming that blocks did not influence trait variation (Table 1). Traits like number of bolls/plants, seed cotton yield/plant, lint yield/plant and ginning outturn had large mean squares for checks and test vs. check, showing they can differentiate genotypes effectively. The combined genetic variance within the F_2 segregants and in between F_2 plants and checks was also significant for the considered traits.

The residual values were very low, indicating that the experiment had low error. Soomro *et al.,* (2010); Srour *et al.,* (2010); Mohankumar *et al.,* (2017); Vrinda *et al.,* (2018) and Roy *et al.,* (2019) recorded similar kind of results in the early segregating generations.

Mean performance of UASD *Bt*-78 F_2 segregants

The results pertaining to mean performance of F_2 segegants, parents and zonal *Bt*-check (CICR *Bt*-23), the estimates of coefficient of skewness and kurtosis and genetic parameters *viz*., genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), broad sense heritability (H^2_{bs}) and genetic advance over mean (GAM) for all the characters are furnished in Table. 2 and the frequency distribution graphs is presented in the Figure 1.

A wide range was observed for plant height with the minimum of 45.35 cm and maximum of 163.93 cm, with the lower mean of 99.20±0.74 cm, compared to parents (P_1-100.59 cm and P_2-117.47cm). The average number of monopodia/plants in P_1 P_2 and F_2 was 1.26, 2.42 1.18 ± 0.04 respectively with a moderate range of 0 to 4.92 was observed in the population. Number of sympodia/plant ranged from 10.88 to 25.27 and the mean number of sympodia in P_1 P_2 & F_2 was observed to be 22.29, 21.14 and 17.93±0.10 per plant respectively. Number of bolls/plants in the F_2 segregants was ranged from 10.98 to 30.03 with a lower mean of 20.60 ±0.14 bolls/plant than the parents (P1-24.4 and P2- 23.95) was observed. The average boll weight in P_1 P_2 & F_2 was 4.55g, 5.25g and 4.69 ±0.02 g/plant respectively, with a very narrow range (2.84 - 5.61 g/plant).

A wide range was observed for sympodial length/plant ranging from 10.16 to 52.79 cm with mean of 24.64 ± 0.28 cm, which was intermediate to the parents (P_1-21.76 cm and P_2 -27.79 cm). A narrow range (7.29 - 15.79 g) was observed for the seed index, the F_2 segregants (10.68 ± 0.04 g) were having bolder seeds than the parents (P_1-9.29 g and P_2- 10.55g). The average lint yield of the F_2 segregants (31.32 ± 0.29 g/plant) was low as compared to the parents (P_1 - 39.49 and P_2 - 45.23 g/plant), with a wide range of 15.15 to 57.75 g/plant. A moderate range was observed for lint index (3.06 - 9.29 g) and the F_2 mean (5.96±0.03 g) was intermediate to parents (P_1 - 5.72 g and P_2- 6.50 g). The mean ginning outturn of F_2 segregants (35.80 ± 0.33 %) was lower than the parents (P_1 - 38.09 % and P_2 - 38.14 %) with the minimum of 22.66% and maximum of 44.64%. The mean seed cotton yield of F_2 segregants (87.62 ±0.76 g/plant) was much lower than the parental means (P_1 -103.69 g and P_2 - 118.62 g) with the lowest seed cotton yield weighed to be about 37.97 grams and highest was about 151.41 grams per plant. Nine transgressive segregants were identified from the segregating population for seed cotton yield, in which percent transgression ranged from 3.86 % (F_2-429) to 27.92 % (F_2-56) over the non-*Bt* better parent. Vekariya *et al.,* (2017) also recorded wide range for the traits like plant height, number of bolls/plants, ginning outturn, and seed cotton yield, while narrow range for boll weight, seed index and lint index.

The segregating F_2 population showed positively skewed distribution for the traits such as number of monopodia/plant, number of sympodia/plant, sympodial length/plant, seed index, lint yield/plant and lint index, for which stringent selection is required for maximizing the genetic gain as these are governed by complementary gene action. Preetha and Raveendren, (2008) also observed positive skewness for number of sympodia/plant. For the remaining traits like plant height, number of bolls/plants, average boll weight, ginning outturn and seed cotton yield/plant negatively skewed distribution was observed, prevailing the duplicate gene interactions, hence mild selection is enough for quick genetic gain.

Leptokurtic distribution was observed for all the considered traits, indicating that all the traits under study are governed by fewer number of genes, in agreement with results obtained by Preetha and Raveendren, (2008) for plant height, number of sympodia, boll weight and seed cotton yield.

Estimates of genetic variability parameters

Higher percent of genotypic and phenotypic coefficient of variation (>20) was observed for traits *viz,* number of monopodia/plant (PCV- 84.87 and GCV- 84.53), sympodial length/plant (PCV-29.46 and GCV-27.72), lint yield/plant (PCV-23.44 and GCV- 22.22) and seed cotton yield/plant (PCV- 21.79 and GCV- 21.09).

Furthermore, these attributes can be enhanced through simple selection because the environmental coefficient of variation low.The obtained results are in agreement with Riaz *et al.,* (2019); Adeela *et al.,* (2021); Thirumal *et al.,* (2021); Shailaja *et al.,* (2023) and Shilpa *et al.,* (2023).

Moderate levels of phenotypic and genotypic coefficient of variation (10 % - 20%) was observed for number of bolls/plant (PCV-17.93 and GCV-17.89), plant height (PCV-18.96 and GCV-16.36), number of sympodia/plant (PCV-15.15 and GCV- 15.02) and lint index (PCV-12.73 and GCV-10.77), which can be exploited through stringent selection (Figure. 2).

Similar findings were also recorded by Thirumal *et al.,* (2021) and Ravindra kumar *et al.,* (2022). Lower percent of variation (<10) was observed for average boll weight (PCV- 8.12 and GCV- 6.16), seed index (PCV-8.96 and GCV-7.62) and ginning outturn (PCV- 9.12 and GCV-7.20) as parental lines were less diverse for these traits.

Low variability for average boll weight was also recorded by Gnanasekaran *et al.,* (2020), for seed index by Soomro *et al.,* (2010) and Srour *et al.,* (2010), and for ginning outturn by Hampannavar *et al.,* (2020).

High heritability combined with high GAM was observed for the traits *viz*., number of monopodia/plant (99.68% and 180.53), sympodial length/plant (88.57% and 53.82), lint yield/plant (89.89% and 43.47), seed cotton yield/plant (93.67% and 42.10), plant height (74.45% and 29.13), number of bolls/plant (99.49% and 36.81), number of sympodia/plant (98.23% and 30.71) and lint index (71.53% and 18.79) (Table 3 and Figure. 3).

These traits are governed by additive gene actions hence can be improved by simple selection. Abbas *et al.,* (2014); Monish *et al.,* (2018); Vrinda *et al.,* (2018); Lokeshkumar *et al.,* (2018), and Adeela *et al.,* (2021) recorded similar results for number of monopodia/plant, Ahasan *et al.,* (2019) and Meena (2022) for sympodial length/plant, Ravindra kumar *et al.,* (2022); Erande *et al.,* (2014); Parmar *et al.,* (2015) and Riaz *et al.,* (2019) for lint yield/plant. Roy *et al.,* (2019); Kumbhar *et al.,* (2020); Thirumal *et al.,* (2021) and Shailaja *et al.,* (2023) for seed cotton yield/plant and Dhivya *et al.,* (2014); Anjani *et al.,* (2020) and Parre *et al.,* (2021) for lint index recorded similar results.

High heritability with modest GAM values were recorded for seed index (72.37% and 13.38), ginning outturn (62.37% and 11.73). Moderate heritability with low GAM was observed for average boll weight (57.53 % and 8.28). These traits are most likely to be governed by both additive and non-additive gene actions therefore can be improved by other efficient breeding methods like ear to row method. The obtained results are in agreement with Mohankumar *et al.,* (2017); Lokeshkumar *et al.,* (2018); Adeela *et al.,* (2021) and Shailaja *et al.,* (2023) for seed index. Aarati *et al.,* (2018) and Joshi *et al.,* (2018) for ginning outturn, and Vekariya *et al.,* (2017) for average boll weight.

In conclusion in the present study on “Genetic variability studies in the UASD *Bt*-78 F_2 population of cotton”, moderate to higher levels of variability (GCV & PCV) in association with higher per cent of heritability and genetic advance as a percent of mean was observed for the traits *viz.,* seed cotton yield/plant, lint yield/plant, number of bolls/plant, number of sympodia/plant, plant height, number of monopodia/plant and sympodial length/plant. Since these traits are governed by additive gene actions, they can be optimized through simple selection.

Table.1 Analysis of variance for augmented randomized complete block design (Un-replicated Trials)

Source of variation	Degrees of freedom	Sum of squares	Mean sum of squares	F ratio	Logic
Entries(a)	a-1	aSS	MSSa	MSSa/MSSe	S/ NS
Blocks(b)	b-1	bSS	MSSb	MSSb/MSSe	S/NS
Checks	c-1	cSS	MSSc	MSSc/MSSe	S/ NS
Varieties	v-1	vSS	MSSv	MSS/MSSe	S/ NS
Checks vs Varieties	1	cvSS	MSScv	MSScv/MSSe	S/ NS
Blocks vs Checks	1	bcSS	MSSbc	MSSbc/MSSe	S/ NS
Error	(c-1) (b-1)	eSS	MSSe	-	
Total	N-1	tSS			

Where,

- a= total number of entries
- b = total number of blocks
- c= number of check genotypes
- v= total number of test varieties
- eSS =sum of square of entries
- cSS=sum of square of checks
- vSS= sum of square of varieties
- tSS = total sum of square
- MSSe= Error mean sum of square

Table.2 Analysis of variance for eleven quantitative traits in the UASD *Bt*-78 event-based segregating (F_2) populations of the cross, UASD *Bt*-78 × DHS-29

Source	Df	Mean Sum of Squares										
		PH	**NMP**	**NSP**	**NBP**	**ABW**	**SLP**	**SI**	**LYP**	**LI**	**GOT**	**SCY**
Entries (ignoring Blocks)	603	339.58**	1.13**	9.41**	16.43**	0.17**	51.07**	1.19**	78.86**	0.73**	11.09**	501.28**
Blocks (eliminating treatments)	14	14	0.68^{ns}	0.01**	0.21^{ns}	0.25**	0.00^{ns}	0.35^{ns}	0.00^{ns}	0.30^{ns}	0.01^{ns}	0.21^{ns}
Test (F_2 plants)	599	353.87**	1.08**	7.38**	13.64**	0.15**	52.69**	0.92**	53.88**	0.58**	10.65**	364.51**
Checks	3	1025.64**	6.46**	330.59**	478.17**	6.70**	103.55**	25.66**	3911.22**	32.48**	245.53**	21372.54**
Test vs. Check	1	6553.00**	26.45**	482.58**	532.65**	0.07^{ns}	1.81^{ns}	111.21**	4433.49**	24.10**	0.18^{ns}	27470.64**
Test and Test vs. Check	600	336.15**	1.10**	7.80**	14.12**	0.14**	50.80**	1.07**	59.70**	0.57**	9.92**	396.93**
Residuals	42	90.41	0.00	0.13	0.07	0.06	6.02	0.25	5.45	0.16	4.01	23.09

PH: Plant height, NMP: Number of monopodia/plant, NSP: Number of sympodia/plant, NBP: Number of bolls/plants, ABW: Average boll weight, SLP: Sympodial length/plant, SI: Seed index, LYP: Lint yield/plant, GOT: Ginning outturn, LI: Lint index and SCY: Seed cotton yield/plant

Table.3 Descriptive statistics and estimates of genetic variability parameters for eleven quantitative traits in the UASD *Bt*-78 event-based segregating (F_2) population of the cross, UASD *Bt*-78 x DHS-29

Traits	F_2 Mean ± SEm	CV (%)	UASD *Bt*-78 (Check-1) mean	DHS-29 (Check-2) mean	F_1 hybrid (Check-3) mean	CICR *Bt*-23 (Check-4) mean	Minimum	Maximum	Skewness	Kurtosis	PV	GV	EV	GCV (%)	PCV (%)	ECV (%)	H^2_{bs} (%)	GA	GAM (%)
PH	99.20 ±0.74	9.52	117.47	100.59	117.47	100.59	45.35	163.93	-0.05	3.11	353.87	263.47	90.41	16.36	18.96	9.58	74.45	28.89	29.13
NMP	1.18 ± 0.04	4.80	1.26	2.42	1.26	2.42	0.00	4.92	0.46	2.67	1.08	1.07	0.00	87.65	87.79	5.00	99.68	2.13	180.53
NSP	17.93 ±0.10	2.00	22.29	21.14	22.29	21.14	10.88	25.27	0.02	2.68	7.38	7.25	0.13	15.02	15.15	2.02	98.23	5.51	30.71
NBP	20.60 ±0.14	1.26	24.43	23.95	24.43	23.95	10.98	30.03	-0.25	2.57	13.64	13.57	0.07	17.89	17.93	1.28	99.49	7.58	36.81
ABW	4.69 ± 0.02	5.29	4.55	5.25	4.55	5.25	2.84	5.61	-0.49	4.23	0.15	0.08	0.06	6.16	8.12	5.29	57.53	0.45	9.64
SLP	24.64 ±0.28	9.93	21.76	27.79	21.76	27.79	10.16	52.79	0.74	3.74	52.69	46.66	6.02	27.72	29.46	9.96	88.57	13.26	53.82
SI	10.68 ±0.04	4.76	9.29	10.55	9.29	10.55	7.29	15.79	0.63	6.12	0.92	0.66	0.25	7.62	8.96	4.71	72.37	1.43	13.38
LYP	31.32 ±0.29	7.28	39.49	45.23	39.49	45.23	15.15	57.75	0.34	3.06	53.88	48.44	5.45	22.22	23.44	7.45	89.89	13.61	43.47
LI	5.96 ± 0.03	6.87	5.72	6.50	5.72	6.50	3.06	9.29	0.47	5.42	0.58	0.41	0.16	10.77	12.73	6.80	71.53	1.12	18.79
GOT	35.80 ±0.13	5.60	38.09	38.14	38.09	38.14	22.66	44.64	-0.36	3.87	10.65	6.64	4.01	7.20	9.12	5.59	62.37	4.20	11.73
SCY	87.62 ±0.76	5.36	103.69	118.62	103.69	118.62	37.97	151.41	-0.09	2.94	364.51	341.42	23.09	21.09	21.79	5.48	93.67	36.89	42.10

Traits : PH - Plant height, NMP –Number of monopodia/plant, NSP –Number of sympodia/plant, NBP – Number of bolls/plant, BW- Average boll weight, SLP : Sympodial length/plant, SI :Seed index, LYP :Lint yield/plant, LI : Lint index, GOT-Ginning outturn, and SCY: Seed Cotton yield/plant

Figure.1 Graphs showing frequency distribution for eleven quantitative traits in the UASD *Bt*-78 event based F_2 segregants of the cross, UASD *Bt*-78 × DHS-29

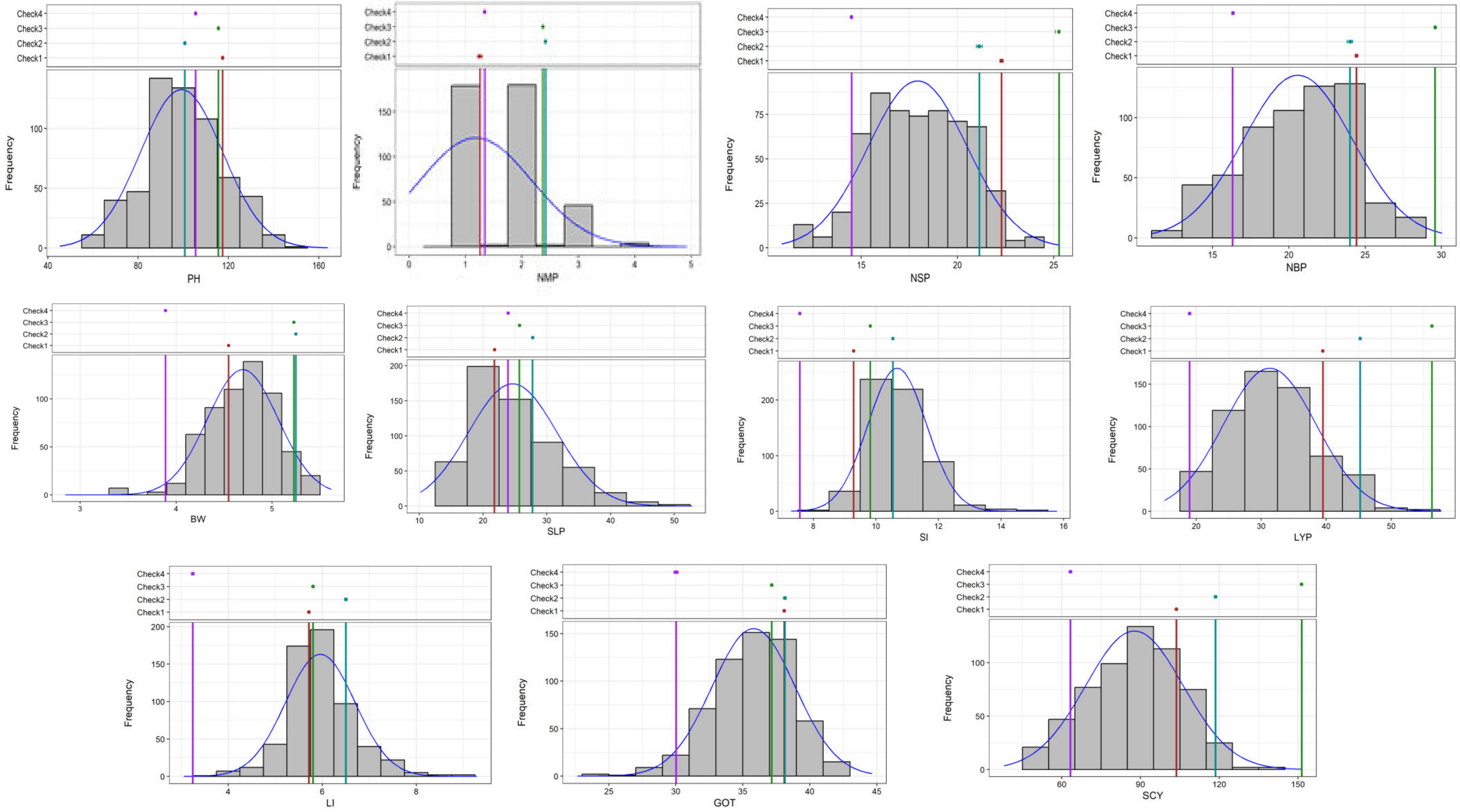


Figure.2 Estimates of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) in the UASD *Bt*-78 event based F_2 segregants of cross, UASD *Bt*-78 × DHS-29

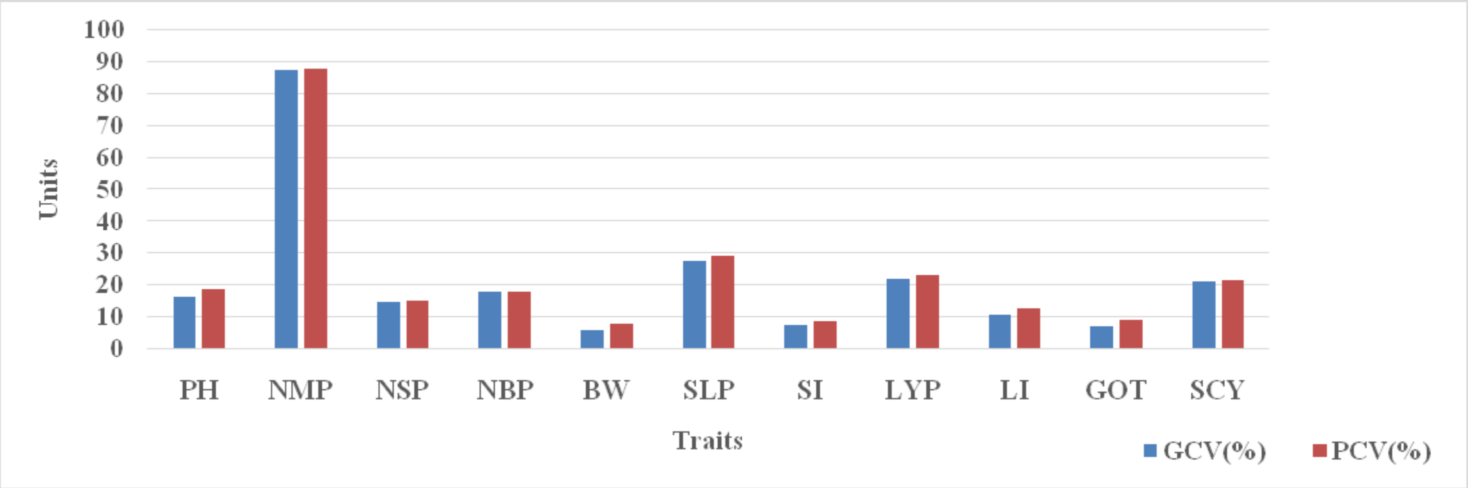
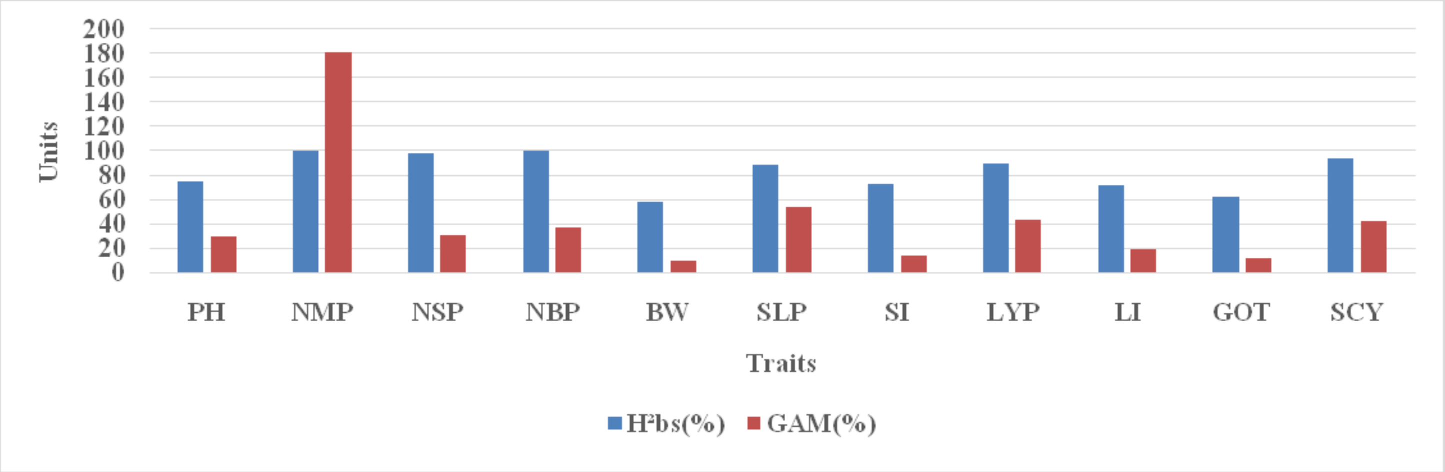


Figure.3 Estimates of broad sense heritability and genetic advance as a percent of mean in the UASD *Bt*-78 event based F_2 segregants



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Author Contributions

Pushpa M Aralikatti: Conceived the original idea and designed the model and wrote the manuscript. and the computational framework and analysed the data.; Manjula S Maralappanavar: Designed the model, Data Curation, Review & Editing.; Basavraj D Biradar: Visualization and Supervision.; Siddharudha B Patil: Review & Editing.; S. Md. Akbar: Review & Editing

Data Availability

The datasets generated during and/or analyzed during the current study are available from the corresponding author on reasonable request.

Declarations

Ethical Approval Not applicable.

Consent to Participate Not applicable.

Consent to Publish Not applicable.

Conflict of Interest The authors declare no competing interests.

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