Received: 09 Jan 2023 | Revised: 17 Jun 2023 | Accepted: 19 Jun 2023

Electronic Journal of Plant Breeding

Research Article

Genetic variability studies for yield and yield-related traits in F_2 populations based on UASD *Bt* Cotton Event No.78

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Abstract
Genetic variability for seed cotton yield and itscomponents were studied in three segregating F_2 populations of cotton (*Gossypium hirsutum*L.). Significant variation was recorded for major traits in all the three F_2 populations. Traits such as plant height (20 cm to 143 cm), bolls plant per plant (1 to 30), boll weight (2.0 g to 6.8 g) and seed cotton yield per plant (1.8 g to 115 g) exhibited wide range.High PCV and GCV estimates were recorded for all the traits under study except days to 50 *per cent* flowering and days to boll opening. High broad sense heritability and genetic advance over mean was observedin case of major yield attributing traits. Mid parent heterosis and inbreeding depression was significant for seed cotton yield per plant in the three F_2 populations. The results suggest that the variation generated in the F_2populations would be useful in selecting superior genotypes.

Keywords: Variability, Bt cotton, Heterosis, Inbreeding depression and *per se* performance

INTRODUCTION

Cotton is one of the most important commercial crops and has occupied importance since its historicdays. The history of cotton can be traced to domestication and the earliest evidence of the use of cotton in the old world is dated to 5500 BC.It is an industrial commodity of world wide importance and occupies superior place in Indian agriculture andeconomy by earning valuable foreign exchange. Cotton based textile industries provide the highest employment during production, processing, spinning,weaving, and marketing throughout the world. Cotton is a unique crop where many potential varieties have been developed and at the same time,the success of commercial exploitation of heterosis incotton is also seen.

Globally cotton is prone to most of the important pests *viz.*, American bollworm (*Helicoverpa armigera*), spotted bollworm(*Earias insulana*), and pink bollworms (*Pectinophora gossyypiella*). Among the bollworm complex *H. armigera* is the most dominant and difficult to control. In the recent past cotton transgenic events imparting resistance for bollworms have been developed using genetic recombination technology. At present more than 67events have been released all over the world. UASD Bt cotton Event No.78 is one such public sector event developed by UAS, Dharwad. The event carries Cry1Ac gene obtained from ICGEB, New Delhi, and has been confirmed to be significantly superior to Mon BG-II for cry toxin expression. The gene is in the genetic background of cultivar RAH-100, a released variety belonging to *Gossypium hirsutum* L. Presently the event is under biosafety trails (BRL). Development of Bt cotton varieties and hybrids using this potential event could be an alternative to Bt cotton hybrids that are released by MNC's andreduce farmer's financial burden.

Loci showing additive gene action will be having lesser influence of environment and thus respond positively to selection (Patil, 2014).Creation and assessment of genetic variability is pre-requisite for plantbreeders to exercise selection.The phenotypic and genotypic coefficients ofvariation were estimated to assess the extent of variabilityexisting for various traits. Heritability accompanied by estimates ofgenetic advance and genetic advance as per cent mean were also calculated to look into the heritable portion of the traits. The present investigation included evaluation of F_2 populations derived from three potential crossesderived from non Bt female parents with UASD Cry1Ac Bt cotton Event No.78 as male parent for variability parameters, heterosis and inbreeding depressionin segregating generations.

MATERIALS AND METHODS

Three F_2 populations developed by selfing of F_1s, derived from crossing three non Bt *hirsutum* inbred lines viz., DHS-114, DHS-121, DHS-108 as females with UASD Event No.78 as male parent, independently were used in the present study. UASD Bt cotton Event No.78 is a public sector event of UAS, Dharwad, developed with Cry1Ac gene from ICGEB, New Delhi and has been confirmed to be significantly superior over Mon BG-I and Mon BG-II for *Cry* toxin expression. The event is in the genetic background of cultivar RAH-100, a released variety belonging to *Gossypium hirsutum* L. The present investigation was conducted during *kharif,*2019, at Agricultural Research Station, Hebballi, University of Agricultural sciences, Dharwad . The F_2 seeds were sown in rows of 8 m length with spacing of 90 cm between rows and 40 cm between plants in augmented design along with two checks, namely Sahana and ARBH-813. The experiment proceeded in the augmented design with complete randomisation and consisted of twelve blocks (Fadhilah *et al*., 2022). All the agronomic management practices were followed according to recommended packages of practices. The biometrical observations on randomly selected five plants of each parent, checks, F_1s and individual plant observations in each F_2population of three crosses were recorded. The population size of three F_2 populations is presented below.

UASD-78 based F_2 populations used in the present investigation

S. No.	Cross	F_2 population size
1	DHS-114 × UASD Cry1Ac transgenic Event No.78	227
2	DHS-121 × UASD Cry1Ac transgenicEvent No.78	136
3	DHS-108 × UASD Cry1Ac transgenicEvent No.78	127

Statistical Analysis:The mean and variances were analyzed based on the formula given by Singh and Chaudhary (1977). The genotypic and phenotypic coefficient of variation was computed according to Burton and Devane (1953). Classification of Phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) as low (< 10 %), moderate (10 - 20 %), and high (> 20 %) was performed as per the suggestion of Shivasubramanian and Menon (1973). The heritability percentage was classified as low (0-30%), moderate (30–60%), and high (> 60%) (Robinson *et al*.,1949). The Genetic advance was computed as per Robinson *et al*. (1949). The genetic advance as *per cent* of mean was categorized as low (up to 10 per cent), moderate (10 to 30 per cent) and high (>30 per cent) (Johnson *et al*., 1955). Magnitude of heterosis in F1 hybrids over mid-parent for each character was calculated using the formula given by Hallauer and Miranda (1981).Inbreeding depression in each of the F_2 populations was assessed using the formula, Inbreeding Depression (%) = $[F_2\text{-}F_1 / F_1] \times 100$.

Increase in mean F_1performance over the mean performance of the mid parent:

$$\text{Relative heterosis} = \frac{\overline{F1} - \overline{MP}}{\overline{MP}} \times 100$$

The significance of heterosis was tested using the formula suggested by Wynne *et al*. (1970)

$$\text{'t' for relative heterosis} = \frac{\overline{F1} - \overline{MP}}{\sqrt{(3/2r)\sigma 2e}}$$

Where,
r = number of replication
σ^2_e = error mean square obtained from ANOVA

Significance for inbreeding depression can be assessed as follows:

$$t = \frac{\overline{F1} - \overline{F2}}{SEd}$$

$SEd = \sqrt{SE_1^2 + SE_2^2}$
where SE_1, SE_2 are standard error of F_1 and F_2respectively
SEd = Standard Error of difference.

The calculated't' value should be compared with table t value at error df. If calculated t value is greater than the table value, and then it can be concluded that significant heterosis exist in this cross.

RESULTS AND DISCUSSION

Assessment of genetic variability: An insight into the magnitude of variability present in a crop is of utmost importance as it provides the basis for effective selection. The variability can be utilized either for direct selection or for a hybridization program which involves a choice of potential parents to develop potential hybrids. Effective selection on the phenotypic basis is feasible through the improvement of genetic variability along with the heritability of a character. Heritability (h^2) measures the genetic portion of variability, while the expected genetic advance as percent of mean (GAM) measures the amount of progress that could be expected with selection for a trait.

Significant variation was detected among gentoypesfor all the traits considered in the study in the three F_2populations, except for seed yield per plant in F_2 population of cross DHS-121 × Event No. 78 and number of bolls per plant in F_2 population of cross DHS-108 × Event No. 78 (**Table 1a, 1b and 1c**). Genetic variability parameters estimated for different quantitative traits in three F_2 populations are presented in **Tables 2a, 2b and 2c**.

Table 1a. Sum of squares obtained for yield and yield related traits of F_2 population of cross DHS 114 × UASD Event No.78

Source	Df	ABW	DFF	DOP	NBP	NMP	NSP	PH	SCY
Treatment (ignoring blocks)	228	1.53**	134.95**	173.66**	33.94**	0.99*	25.62*	546.15*8	486.18*
Check	1	0.35 ns	36.96 ns	448.62**	26.00 ns	6.5**	55.54*	775.54**	80.33 ns
Test vs Check	1	15.04**	5321.28**	12964.61**	578.78**	1.32 ns	1334.53**	10440.64**	9614.47**
Treatment: Test	226	1.47**	112.43**	115.85**	31.57**	0.97 ns	19.69 ns	501.35**	447.58 ns
Block (eliminating treatments)	12	0.28 ns	83.70**	125.13**	4.18 ns	0.49 ns	51.93**	61.93 ns	131.23 ns
Residuals	12	0.11	16.88	25.53	8.5	0.33	9.79	26.46	195.31

Table 1b. Sum of squares obtained for yield and yield related traits of F_2 population of cross DHS 121 × UASD Event No.78

Source	Df	ABW	DFF	DOP	NBP	NMP	NSP	PH	SCY
Treatment (ignoring blocks)	135	1.69**	371.75**	444.05**	61.61*	0.95*	17.19*	725.69**	707.61 ns
Check	1	0.47 ns	39.38 ns	400.15**	0.96 ns	5.54**	2.46 ns	465.38**	1376.79 ns
Test vs Check	1	12.85**	9370.57**	18700.17**	2133.97**	2.51*	231.83	26838.25**	14279.17**
Treatment: Test	133	1.61**	306.59**	306.59**	46.48 ns	0.91*	15.68*	531.31**	600.54 ns
Block (eliminating treatments)	12	0.3 ns	75.04**	128.54**	37.43 ns	0.51 ns	4.88 ns	52.87 ns	53.36 ns
Residuals	12	0.17	16.97	25.57	23.38	0.37	5.54	38.13	378.65

Table 1c. Sum of squares of variance for yield and yield related traits of F_2 population of cross DHS 108 × UASD Event No. 78

Source	Df	ABW	DFF	DOP	NBP	NMP	NSP	PH	SCY
Treatment (ignoring blocks)	128	0.76**	215.22**	272.02**	41.08 ns	1.04*	43.58**	934.44**	407.61**
Check	1	0.3ns	39.38 ns	400.15**	0.96 ns	5.54**	2.46 ns	465.38**	169.06 ns
Test vs Check	1	17.8**	4397.81	11308.14**	1891.29**	2.34*	1135.19**	7774.61**	19455.15**
Treatment: Test	126	0.63**	183.42**	183.42**	26.71 ns	0.99*	35.24**	883.88**	258.33*
Block (eliminating treatments)	12	0.3 ns	75.04**	128.54**	33.79 ns	0.51 ns	4.88 ns	52.87 ns	94.11 ns
Residuals	12	0.13	16.97	25.57	23.38	0.37	5.54	38.13	107.49

** = significant at 1% probability level, *= significant at 5% probability level

ns: Non significant; Df: Degree of freedom; ABW: Average boll weight (g); DFF: Days to 50 *per cent* flowering; DOP: Days to boll opening; BP: Number of bolls per plant; NMP: Number of monopodia per plant; NSP: Number of sympodia per plant; PH: Plant height (cm); SCY: Seed cotton yield per plant (g)

Table 2a. Genetic variability parameters for yield and yield attributing traits in segregating F_2 population of the cross DHS-114 × Event No. 78

Character	DHS-114 × Event No. 78								Mean values	
	Mean ± SE	Range	Variance	PCV (%)	GCV (%)	h^2 (%)	GA	GAM (%)	P1	P2
Days to 50 per centflowering	126.60 ± 0.7	106-158	112.25	8.36	7.74	84.99	18.59	14.72	117.4	124.8
Days to boll opening	161.60 ± 0.6	141-193	115.3	6.40	5.22	77.96	17.31	10.73	126.7	135.4
Plant height (cm)	74.77 ± 1.4	20-143	501.3	30.0	29.27	94.72	43.76	58.76	54.4	84.8
Number of monopodia per plant	1.33 ± 0.06	0-5	0.96	71.66	58.03	65.58	1.33	96.95	0.6	1.2
Number of sympodia per plant	17.5 ± 0.29	5-30	19.60	25.19	17.86	50.30	4.60	26.14	12.8	19.2
Number of bolls per plant	9.86 ± 0.55	1-30	31.27	57.89	49.49	73.08	8.47	87.27	11	17
Average boll weight(g)	3.44 ± 0.27	2.0-6.8	1.47	37.1	35.69	92.52	2.32	70.82	3.6	4.53
Seed cotton yield per plant(g/plant)	29.75 ± 0.72	2.3-115	447.5	71.00	53.68	56.36	24.60	83.14	33.5	73.5

Table 2b. Genetic variability parameters for yield and yield attributing traits in segregating F_2 population of the cross DHS-121 × Event No. 78

Character	DHS-121× Event No. 78								Mean values	
	Mean ± SE	Range	Variance	PCV (%)	GCV (%)	h^2 (%)	GA	GAM (%)	P1	P2
Days to 50 percentflowering	130.79 ± 1.5	103-165	304.30	13.39	13.01	94.47	34.12	26.09	126.4	124
Days to boll opening	165.42 ± 1.4	138-200	298.6	10.590	10.13	91.66	33.11	20.02	139.8	141
Plant height(cm)	86.79 ± 2.02	35-134	547.43	26.56	25.59	92.82	44.14	50.86	65.4	85
Number of monopodia per plant	1.31 ± 0.08	0-4	0.90	73.00	56.10	59.06	1.16	88.94	0.8	1.6
Number of sympodia per plant	18.07 ± 0.34	5-25	15.56	21.91	17.62	64.64	5.28	29.22	13.4	19
Number of bolls per plant	9.47 ± 0.70	1-28	44.68	71.74	50.58	49.70	6.99	73.56	12	17.6
Average boll weight(g)	3.42 ± 0.28	2.1-5.8	0.94	39.25	37.08	89.22	2.34	72.25	3.4	4.51
Seed cotton yield per plant(g/plant)	26.87 ± 0.88	1.8-96.5	589.28	91.21	55.44	36.95	18.68	69.52	39.3	74.2

Table 2c. Genetic variability parameters for yield and yield attributing traits in segregating F_2 population of the cross DHS-108 × Event No. 78

Character	DHS-108 × Event No. 78								Mean values	
	Mean ± SE	Range	Variance	PCV (%)	GCV (%)	h^2 (%)	GA	GAM (%)	P1	P2
Days to 50 *per centf*lowering	124.33 ± 1.2	106-160	181.97	10.89	10.38	90.75	25.36	20.39	116	123
Days to boll opening	159.58 ± 1.1	141-195	175.6	8.50	7.88	86.06	24.04	15.09	124	139
Plant height(cm)	70.80 ± 2.99	20-138	883.6	41.99	41.08	95.69	58.69	82.89	82.6	83
Number of monopodia per plant	1.95 ± 0.08	0-2	0.98	50.95	40.25	62.41	1.28	65.60	1.2	1
Number of sympodia per plant	14.18 ± 0.52	2-28	34.96	41.86	38.42	84.27	10.32	72.76	17.8	18
Number of bolls per plant	10.13 ± 0.53	1-26	26.71	51.03	43.24	84.73	8.75	86.45	11.3	18
Average boll weight(g)	3.10 ± 0.25	2.0-6.6	0.62	25.50	22.65	78.86	1.29	41.49	3.5	4.50
Seed cotton yield per plant(g/plant)	24.48 ± 0.67	2-88	257.31	65.65	50.16	58.39	19.36	79.08	36.8	75.5

Plant height exhibited wide variability in all the three F_2 populations. The phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV)were high in all three populations for the trait plant height. F_2 population of the cross DHS-108 × Event No. 78 exhibited highest PCV (41.99 %) and GCV (41.08 %). These results are in accordance with the findingsof Neelam and Potdukhe (2002),Choudki*et al*. (2012), Jawahar and Patil (2017) and Kumar and Katageri (2017)who observed high estimates of PCV and GCV for plant height. The Highest h^2_{bs} (95.69 %) was recorded in the F_2 population of cross DHS-108 × Event No. 78, F_2 populations of crosses DHS-114 × Event No. 78 and DHS-121 × Event No. 78 recorded 94.72 % and 92.82 % heritability, respectively for the trait plant height. Genetic advance as per cent over mean (GAM) was high in all three F_2 populations. Our results were in accordance with Jawahar and Patil (2017) and Kumar and Katageri (2017) who recorded high heritability and genetic advance in their F_2populations of cotton. The above results suggest that high variation is present in the population for the trait plant height to carry out selection. High heritability and genetic advance for the trait indicates the trait is governed by additive genes and response for selection is effective.

Monopodiaper plant and sympodia per plant in cotton are vegetative and reproductive branches, respectively. A higher number of sympodia per plant are desirable so that it can bear more bolls. In the present study, the F_2 population of cross DHS-121 × Event No. 78 exhibited the highest mean (18.07) for sympodia per plant. Moderate to high PCV and GCV was recorded for both traits in all the three F_2populations with minimum influence of environment. Medium to high heritability coupled with highGAM was observed for both the traitsin all the three F_2populations. Our results were in accordance withSoomro *et al*. (2008) BalochandLakho(2002), Majjiga*et al*. (2018) and Joshi and Patil (2018) who recorded high heritability coupled with high genetic advance for sympodia per plant.Mean for umber of bolls per plant was higher in F_2 population of the cross DHS-114 × Event No. 78 (10.13).High PCV and GCV estimates along with moderate to high heritability coupled with high GAM for boll number were observed for allthree F_2 populations. Similar results including significant genetic variances, moderate to high heritability estimates coupled with high GAM for boll number per plant in upland cotton was observed by Naveed *et al*. (2004), Soomro*et al*. (2008),Dhamayanathi*et al*. (2010) andRanganath*et al*. (2013). Hussain *et al*. (2000) and Mushtaq *et al*. (2011)also reported high genotypic variability, GAM and heritability estimates for number of bolls per plant.

The highest boll weight of 6.8g was recordedin F_2 population of cross DHS-114 × Event No. 78. High PCV and GCV were found for boll weight with minimun influence by environment. While, heritability was high in the three F_2 populations and GAM was also found high.The results suggests that direct selection based on boll weight would be feasible to obtain higher yield in cotton. Similar results were reported by Krishnarao and Mary (1990), Kaushik *et al*. (2006), Laxman and Ganesh (2003), Gururajan and Sundar (2004), Neelima*et al*. (2005), Tuteja*et al*. (2006), Kale *et al*.(2007), Sakthi *et al*. (2007), Neelima and Chenga (2008)and Ranganath*et al*. (2013). On the other handMajjiga*et al*. (2018) recorded low PCV and GCV in both main and ratoon F_2 populations.

All the three F_2 populations recorded wide range of variability for seed cotton yield. Highest seed cotton yield of 115 g per plant was observed. High estimates of PCV, GCV and heritability coupled with high GAM were observed in all the three F_2 populations.

In the present study, high heritability for most of the traits indicated that large proportion of phenotypic variance was contributed by genotype and selection based on the phenotypic expression would be reliable for improvement of those traits. High GAM was observed for most of the important traits in the study. High GAM indicates that the traits are governed by more number of additive genes and the traits are less influenced by environment.

Comparison of mean performance between F_1 hybrids with F_2populations and parents: The *per se*performance of F_1 hybrids, F_2 populations and their parents is represented in **Table 3**. Seed cotton yield of the female parents ranged from 33.5g to 39.3g whereas, the male parent recorded 73.5g. Mean performance of F_1 hybrids of cross DHS – 114 × Event No.78 recorded higher mean values for all the traits including seed cotton yield followed by F_1 hybrid of crossDHS – 108 × Event No.78.These results are in accordance with earlier reported results by Soomro and Kalhoro (2000) and Basamma*et al*. (2009).Thus, female lines*viz*., DHS – 114 and DHS-108 were found to be better combiners with Event No. 78 todevelop potential Bt crosses.

Heterosis and Inbreeding depression: The data on mid parent heterosis of F_1hybrids and the percentage of inbreeding depression in F_2generation for all the traits are presented in **Table 4.**

Mid parent heterosis was non-significant for the traits under consideration in the F_2 population of cross DHS 114 × Event No.78. Whereas, F_2 populations of cross DHS 121 × Event No.78 and DHS 108 × Event No.78 recorded significant heterosis for all the traits except number of monopodia per plant and average boll weight.

F_2 population of cross DHS 114 × Event No.78 exhibited non significant mid parent heterosis (26.2%) for seed cotton yield followed by F_2 population of cross DHS 108 × Event No.78 which exhibited significant mid parent heterosis (17.2 %) and F_2 population of cross DHS 121 × Event No.78 also recorded significant heterosis of 3.1 *per cent*. Both the F_2 populations of crosses DHS 121

Table 3. Comparison of mean performance of parental genotypes, their F_1 hybrids and F_2 populations for yield and yield related traits in three crosses

Parent/hybrid	Generation	Days to 50 *per cent* flowering	Plant height (cm)	Number of monopodia per plant	Number of Sympodia per plant	Number of bolls per plant	Average boll weight (g)	Seed cotton yield (g/plant)
DSH-114	-	117.4	54.4	0.6	12.8	11.0	3.6	33.5
DSH-121	-	126.5	65.4	0.8	13.4	12.0	3.4	39.3
DSH108	-	116.0	82.6	1.2	17.8	11.3	3.5	36.8
EVENT NO. 78 (P2)	-	124.8	84.8	1.2	19.2	17.0	4.5	73.5
DHS – 114 × Event No.78	F_1	108.0	67.0	1	20.0	18.0	4.5	67.5
	F_2	126.4	74.8	1.3	17.6	9.6	3.2	28.8
DHS – 121 × Event No.78	F_1	112.0	83.0	1.5	23.0	15.8	4.4	63.5
	F_2	131.1	87.3	1.3	18.0	9.0	3.2	26.4
DHS – 108 × Event No.78	F_1	116.0	69.0	1.7	17.5	17.0	4.25	65.8
	F_2	124.6	71.1	1.9	14.1	9.7	3.1	23.7

Table 4. Estimation of heterosis in F_1 hybrids and inbreeding depression in F_2 populations for yield and yield related traits

S. No	Days to 50 per cent flowering	Plant height (cm)	Number of monopodia per plant	Number of Sympodia per plant	Number of bolls per plant	Average boll weight (g)	Seed cotton yield (g/plant)
DHS114 × UASD Cry1Ac Bt cotton Event No.78							
Mid parent heterosis	-10.8	-3.7	11.1	25.0	28.6	4.9	26.2
Inbreeding depression	17.1	11.6	33.9	-12.0	-46.6	-24.0*	-57.4*
DHS – 121 × UASD Cry1Ac Bt cotton Event No.78							
Mid parent heterosis	-10.5*	10.4*	25.0	42.0*	6.8*	11.3	3.1*
Inbreeding depression	17.0*	5.1*	-14.9	-21.5*	-43.1*	-26.8	-55.0*
DHS – 108 × UASD Cry1Ac Bt cotton Event No.78							
Mid parent heterosis	-2.9*	-16.7*	54.5	-2.2*	29.7*	6.3	17.2*
Inbreeding depression	7.4*	3.1*	14.4	-19.7*	-49.1*	-27.4	-63.9*

* = Significant at 5 % probability level

× Event No.78 and DHS 108 × Event No.78 recorded significant heterosis for traits such as plant height, number of symposia per plant, number of bolls per plants. In accordance with our results, Khan *et al.* (2017) also recorded significant mid parent heterosis for seed yield per plant in F_2s of crosses CIM-554 × CIM-499 and CIM-554 × CIM-707.

To assess decline in performance from F_1 to F_2, the extent of inbreeding depression was estimated. High inbreeding depression was observed for seed cotton yield in all the three F_2 populations. Significant inbreeding depression was recorded for traits such as average boll weight and seed cotton yield per plant for the cross DHS 114 × Event No.78. The other two populations exhibited significant inbreeding depression for all the traits considered in the study except number of monopodia per plant and seed cotton yield per plant. Contrasting our results Khan *et al*. (2017) recorded non- significant inbreeding depression for seed cotton yield per plant. In the study, the high heterosis was found to be associated with high inbreeding depression for all the traits.

The results were in confirmation with those of Wang and Pan (1991) and Khan (2007). Khan *et al*. (2017) reported maximum inbreeding depression of -68.89% in the cross

CIM-554 × CIM-446, which exhibited heterosis 36.6 per cent in F_1 generation.The F_1 hybrids with higher seed cotton yield would be tested further for their yield stability against commercial checks. The F_2 individual plants with higher seed cotton yield per plant coupled with minimum open boll damage would be advanced to next generations to identify good segregants. Further, the development of Bt varieties would be aimed from the superior segregants selected. The study of heterosis and inbreeding depression in F_1 and F_2 generation would help to eliminate the plant exhibiting higher inbreeding depression at early evaluation. The female line that recorded high heterobeltiosis and low inbreeding depreesion suggests that the particular line is a better combiner with the Bt cotton Event No. 78. The superior genotypes selected from the population that is exhibiting significantheterobeltiosis and non significant inbreeding depression would be advanced to further generation in developing Bt cotton varieties or can be utilised as parent in further introgression breeding.

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