Emirates Journal of Food and Agriculture. 2023. 35(6): 541-547
doi: 10.9755/ejfa.2023.v35.i6.3103
http://www.ejfa.me/

RESEARCH ARTICLE

Comparison of cotton (*Gossypium hirsutum*) hybrids and their non-transgenic in India

Kulvir Singh[1], **Sudhir Kumar Mishra**[2], **Manpreet Singh**[3], **Harjeet Singh Brar**[4], **Amarpreet Singh**[5]

[1]Principal Agronomist (Cotton), Punjab Agricultural University, Regional Research Station, Faridkot, Punjab, [2]Agrometeorologist, Punjab Agricultural University, Regional Research Station, Faridkot, Punjab, [3]Senior Agronomist (Cotton), Punjab Agricultural University, Regional Research Station, Abohar, Punjab, [4]Agronomist (Cotton), Punjab Agricultural University, Regional Research Station, Bathinda, Punjab, [5]Scientist (Agronomy), Central Institute for Cotton Research, Sirsa, India

ABSTRACT

It is still not clear whether differential response of *Bt* cotton and conventional non-*Bt* cotton genotypes in terms of growth, phenology and yield ability are hypothetical or realistic. This study investigated the response of three *Bt* cotton hybrids in comparison to their conventional non-transgenic version (near-isogenic lines) along with two locally adapted genotypes for growth, yield attributes, phenological characteristics and rooting behavior. Therefore, two experiments were conducted during *summer* season of year 2016 and 2017 to evaluate differences among 3 popular *Bt* cotton hybrids along with their non-*Bt* version. First field experiment was conducted as a pot study wherein shoot and root parameters of 3 *Bt* cotton hybrids (Ankur 3028, MRC 7017, Bioseed 6588) were compared with their non-*Bt* version along with 2 local checks (*i.e.,hirsutum* cotton Cv. F2228 and *arboreum* cottonCv. FDK124). Second field experiment evaluated growth, phenological characteristics, yield attributes and productivity potential of above mentioned *Bt* and non-*Bt* hybrids. Findings of pot experiment could not establish any significant difference among studied *Bt* and non-*Bt* hybrids for root and shoot characteristics. However, *arboreum* cotton FDK124 exhibited higher root length than all genotypes. Results of second experiment revealed significant differences for phenological characteristics, wherein *Bt* version of all the tested hybrids exhibited earliness for flowering initiation, 50 % flowering and days to maturity over their non-*Bt* version. Seed cotton yield (SCY) in all hybrids possessing *Bt* gene was significantly higher than their non-*Bt* version primarily due to higher bolls plant^{-1}. Studies conclude that introgression of *Bt* gene could not alter rooting parameters of evaluated cotton genotypes but significantly affected phenological stages by inducing earliness and higher SCY in *Bt* versions due to improved bolls plant^{-1}.

Keywords: *Bt* cotton; Near-isogenic lines; Phenology; Root dry matter; Seed cotton yield

INTRODUCTION

Cotton (*Gossypium hirsutum* L.) is an important crop being grown globally for fiber and oil. During 2020, it occupied nearly 32.1 m ha across the world and produced 113 m bales (170 kg each). India is leading country in terms of acreage and raw cotton production across the world. Indian cotton production during 2020-21 is estimated around 371 lakh bales from 130 lakh ha with a lint yield of 487 kg ha^{-1} (AICRP 2020-21). During the last two decades, Indian cotton has witnessed extraordinary progress in *Bt* cotton technology leading to development and release of new *Bt* hybrids. Such development has resulted into severe reduction in cultivation area under conventional (non-*Bt*) genotypes, while *Bt* hybrids experienced an unprecedented hike in acreage. As per Indian government report on status paper of Indian cotton during 2017, area under *Bt* cotton has touched to 93.14 percent of total cotton acreage within a period of 13 years (2002-03 to 2014-15) and it may increase further in near future.

Owing to several morphological, genetical and yield traits, crop cultivars perform differently under similar types of soil, fertility conditions and environment. Such variability in the phenotype is manifested by the genotypes resulting into phenotypic expression by varied gene expressions (Gul et al. 2014). Despite massive adoption of *Bt* cotton by growers because of higher profit expectation, there is rising concern that transgenic cotton may affect nutrient cycling in the agro ecosystem by releasing *Bt* toxins into the environment. Farmer's also apprehend that rooting behavior of *Bt* and non-*Bt* cotton is different and often complain about poor rooting of *Bt* cotton plants as compared to traditional cotton genotypes. Consequently,

***Corresponding author:**
Kulvir Singh, Principal Agronomist, Punjab Agricultural University, Regional Research Station, Faridkot- 151203,
E-mail: kulvir@pau.edu

Received: 13 September 2022; **Accepted:** 21 May 2023

certain physiological disorders such as leaf reddening and parawilt have also been primarily reported to be associated with *Bt* cotton only (Hosmath et al. 2012).

Although lot of studies have evaluated the environmental impact of transgenic crops (O'Callaghan et al. 2005), little studies have investigated the phenology, rooting characteristics and seed cotton yield. Transgenic plants may modify root rhizosphere by affecting plant residual quality in the soil (Dunsfield and Germida, 2004). Shen et al. (2006) elucidated that enzymatic (*dehydrogenase*) activity among different *Bt* and non-*Bt* cotton versions is dependent upon crop cultivars. Reduced microbial activity in the *Bt* cotton system confirmed that soil fauna and flora may be either killed or prohibited by released toxins (Masto et al. 2006). Pindi and Sultana (2013) also observed significant variations in soil rhizosphere microbial population in fields having transgenic *Bt* cotton over conventional cotton. Several studies have indicated that growing *Bt* cotton genotypes may affect the soil properties (Velmourougane et al. 2013 and Zhang et al. 2014), and performance of the crops following cotton (Zaman et al. 2015) to differential release and consequently absorption of *Bt* toxins. However, it is presumed that cultivating non-*Bt* cotton genotypes might not exert such ill impact as *Bt* toxins are absent.

Despite sufficient literature on *Bt* cotton studies as indicated above, only little documented information on phenology and rooting pattern and yield behavior is available on the comparison of *Bt* cotton genotypes with their recommended non-*Bt* cotton versions (Arshad et al. 2009). However, different workers have given opposing opinions. For instance, Dhillon and Sharma (2013) reported that *Bt* versions outperformed their non-*Bt* version for SCY but Pray et al. (2001) reported lower yield of *Bt* cotton genotypes as compared with non-*Bt* versions. Martins et al. (2008) also verified significant differences in growth of *Bt* and non-*Bt* plants.

Thus, there is a lack of information on comparison of transgenic and non-transgenic *Bt* cotton hybrids as for as their phenology, root characteristics and SCY is concerned. Moreover, documented information about the rooting patterns, while comparing a pair of near-isogenic lines (NILs) of *Bt* and non-*Bt* cotton is scarce. In comparison to temperate zones, most of Indian soils have poor soil fertility characteristics with low organic C and poor nitrogen content. Consequently, soil response to *Bt* crops might be different in India over what is that reported elsewhere. This study hypothesize that *Bt* cotton might express significant variations in comparison to its non-*Bt* counterpart for various characteristics and this might affect their phenology and productivity levels. Accordingly, yield potential of different *Bt* cotton genotypes and their non-*Bt* versions may not be similar under field conditions and therefore necessitates location specific investigations.

Therefore, main objective of study was

(i) To assess growth, yield parameters and phenological characteristics of *Bt* and non-*Bt* cotton hybrids of 3 near-isogenic lines (NILs).
(ii) To study the rooting pattern, physiological traits and yield behavior of three popular *Bt* hybrids and their non-*Bt* cotton counterparts differing only by the presence of the cry1Ac gene.
(iii) To compare agronomic characters, yield of Bt genotypes with conventional genotypes (local checks) to visualize differences.

MATERIALS AND METHODS

Experimental design and procedure

The field and pot experiments were conducted at Research farm of Punjab Agricultural University, Regional Station, Faridkot, India, during *Kharif* seasons of year 2016 and 2017. First field experiment has been conducted in pots made of PVC pipes (7 ft long having a radius of 9 inches). The experiment having 8 treatments was arranged in randomized complete block design in 3 replications. It comprised of 3 *Bt* cotton hybrids [BG (*Bollgard*) II] along with their non-*Bt* versions and two local popular varieties of cotton *i.e.* *arboreum* cotton (FDK124) and *hirsutum* cotton (F2228). A total of 216 pots were arranged in 6 rows (*i.e.* 36 pots row^{-1}) established at a distance of 75 cm within pots as well as rows to facilitate normal operations and randomly arranged by adopting the randomized complete block design (Fig. 1). A total of 9 pots per genotype constituted one replication for periodical studies. The treatments included a total of 8 genotypes viz. 3 *Bt* (BGII) cotton hybrids and their non-*Bt* versions *i.e.* Ankur 3028 *Bt* (Pot #

Fig 1. The arrangement of cotton genotypes in the pot experiment.

1-27), Ankur 3028 non-*Bt* (Pot #28-54), MRC 7017 *Bt* (Pot #55-81), MRC 7017 non-*Bt* (Pot #82-108), Bioseed 6588 *Bt* (Pot #109-135), Bioseed 6588 non-*Bt* (Pot #136-162), one local *hirsutum* cotton Cv.F2228(Pot #163-189) and one local *arboreum* cotton Cv.FDK 124 (Pot #190-216) having three replications for each treatment. Various growth, and root related observations were recorded at 60, 90 and 120 days after sowing (DAS) from 5 plants per replication (Singh et al. 2019). For root studies, first pot was dug out the from the field with the help of a spade and then plant roots in that pot were extracted by exposing the whole plant to a jet of pressurized water to remove the intact soil without breaking or injuring the root (Fig. 2). Then shoot and root biomass was recorded with a digital weighing machine, while root length and shoot length was measured with a graduated scale.

In the second field experiment, seeds of 3*Bt* and their non-*Bt* cotton hybrid versions were sown in a planting geometry of 67.5 x 75 cm during May months of year 2016 and 2017 to compare their growth, yield and phenological characters.

Weather parameters, initial soil status and measurements

The details of weather parameters have been given in Fig 3. A peak temperature of 39.6ºC has been recorded on June 2016, while May (40.4ºC) remained the hottest month in 2017. The soil of experimental site was loamy sand in texture with pH 8.4, normal (EC 0.20 ds m^{-1}; OC 0.51%), medium in available P (20.2 kg ha^{-1}) and high in K (750 kg ha^{-1}). The data pertaining to various growth parameters like plant height, monopods and sympods $plant^{-1}$was measured from 5 plants selected at random in each plot. Various yield attributes like bolls $plant^{-1}$ and boll weight were measured from 10 plants selected at random in each plot.

Statistical analysis

The data from both experiments was statistically analyzed to evaluate the effect of *Bt* hybrids *vis-à-vis* non-*Bt* hybrids on various parameters and compared at 5% level of significance by following statistical package, CPCS-1 software developed by Punjab Agricultural University, Ludhiana.

Fig 2. The washing of cotton plants with pressurized water jet to extract intact roots without damage in the pot experiment.

RESULTS AND DISCUSSION

Shoot length and shoot dry matter of cotton genotypes in Pot Experiment

The data in Table 1 revealed significant differences among evaluated genotypes for shoot length (SL) and shoot dry matter (SDM) at all the observation stages during both study years. The SL improved at a slower rate from 60 to 90 DAS but increased sharply at 120 DAS. However, in lieu of tested *Bt* and their non-*Bt* versions, differences within all near-isogenic lines (NILs) were variable without any trend. For instance, during 2016 SL at 60 DAS (days after sowing) was statistically similar for MRC 7017*Bt* (35.5 cm) and MRC 7017non-*Bt* (35.5 cm) and also for Bioseed 6588*Bt* (41.0 cm) and Bioseed non-*Bt* (42.5 cm). However in case of Ankur 3028*Bt* (44.5 cm), SL was significantly higher than Ankur 3028non-*Bt* (36.7cm). Pooled data at 60 DAS further indicated that except for Ankur 3028, all tested hybrids exhibited similar SL between *Bt* and their non-*Bt* versions. However, at 60 DAS it was significantly higher in case of FDK124 (52.3cm) over rest of the genotypes. The SL at 90 and 120 DAS varied non-significantly for year 2016 and 2017 and also under pooled means. SL was maximum in case of F2228 at 90 DAS, while at 120 DAS, Ankur 3028*Bt* exhibited higher value (71.0 cm).

The data on shoot dry matter revealed significant variation only at 90 and 120 DAS, while only trivial differences were evident at 60 DAS for year 2016 and 2017 (Table 1). However, pooled data depicted significant differences at all the observational periods. The rate of SDM growth was initially slow from 60 to 90 DAS but it was relatively faster at 120 DAS. There was no clear cut trend to disclose that SDM of *Bt* versions remained higher than their non-*Bt* versions. For instance, pooled data indicated that at 60 DAS, SDM in case of Ankur 3028 *Bt* (19.6g) remained better than Ankur 3028 non-*Bt* (15.9g). The trend was almost similar in case of MRC 7017*Bt* (16.0g) over MRC 7017 non-*Bt* (14.8g), but differences were at par. Martins et al. (2008) and Rosolem et al.(2019) also observed non-significant differences for dry matter production by leaves, leaf area index and total dry matter production among studied *Bt* and non-*Bt* cotton plants. Contrarily, SDM was numerically higher under Bioseed 6588 non-*Bt* (19.9g) over that of Bioseed 6588 *Bt* (18.2g).Therefore, it was hard to establish a pattern owing to differential behavior of various cotton genotypes.

Root length and root dry matter of cotton genotypes in Pot Experiment

Root characteristics is an important factor which can govern rhizosphere biochemistry and thereby nutrients transformation. Release through root exudates is prime source of *Bt*-toxin in soil from transgenic crops. The data in Table 2 revealed significant differences among evaluated genotypes for root length (RL) and root dry matter (RDM) at different observation stages during both study years. During 2016, RL was significantly higher for *arboreum* cotton genotype FDK124 (49.5cm). However, MRC7017*Bt* exhibited lowest value (37.9cm). Interestingly, RL between same *Bt* and non-*Bt* versions was not statistically different and values were near identical with *hirusutum* genotype F2228 (39.4cm). A similar trend has been observed at 90 and 120 DAS, where FDK124 maintained its superiority by exhibiting higher RL in comparison to all other tested genotypes. Also, during 2016, RL of F2228 (57.0cm) at 90 DAS was superior as compared to all *Bt* and non-*Bt* hybrids. A close view at 120 DAS during 2016 also revealed that RL of all *Bt* and non-*Bt* hybrids gradually improved from 90 to 120 DAS and became at par with F2228.A similar pattern was evident for most of the observational periods during 2017, where FDK124 exhibited significantly higher RL. For instance, RL of FDK124 was 56.2, 91.0 and 104.0 cm at 60, 90 and 120 DAS, respectively. The pooled values further revealed that FDK124 always recorded higher RL over rest of the genotypes at all observational periods, whereas F2228 could exhibit better value only at 90 DAS but at par value for 60 and 120 DAS (Table 2).It was observed that RL in case of F2228 exhibited negligible improvement from 90 to 120 DAS, whereas in contrast all other genotypes recorded a constant improvement even upto 120 DAS. The data on RDM elucidated significant differences at most of the observational periods. Bioseed 6588 non-*Bt* exhibited significantly higher values in comparison to its *Bt* version and rest of the genotypes during both study years. However, except for Bioseed 6588, all other genotypes exhibited statistical similar values within *Bt* and non-*Bt* versions in agreement with Sarkar et al.(2009) who reported that root dry weight within *Bt* and non-*Bt* versions was not statistically different however root volume at 90 and 120 days remained higher over non-*Bt* cotton.

Further differences between local genotypes *i.e.,* F2228 and FDK124 were also non-significant and could not establish any trend. However, root system of *arboreum* cotton (FDK124) was found to be better than all other studied genotypes. Hence, it may be concluded that root system

Table 1: Shoot parameters of cotton genotypes in pot study

Genotypes	Shoot length (cm)									Shoot dry matter (g plant $^{-1}$)								
	2016			2017			Pooled			2016			2017			Pooled		
	DAS (days after sowing)																	
	60	90	120	60	90	120	60	90	120	60	90	120	60	90	120	60	90	120
Ankur 3028 *Bt*	44.5	49.3	66.2	50.2	56.5	75.7	47.3	52.8	71.0	18.35	22.98	44.36	20.9	26.4	50.2	19.6	24.7	47.3
Ankur 3028 non-*Bt*	36.7	43.3	65.0	41.5	49.5	74.5	39.1	46.3	69.7	14.86	24.50	38.61	17.0	28.2	43.6	15.9	26.3	41.1
MRC 7017 *Bt*	35.5	43.0	60.6	40.0	49.2	69.0	37.7	46.1	64.8	14.99	19.78	33.08	17.1	22.8	37.3	16.0	21.3	35.2
MRC 7017 non-*Bt*	35.5	46.0	52.5	40.0	53.0	59.7	37.7	49.5	56.1	13.82	22.58	28.40	15.7	25.9	32.5	14.8	24.2	30.4
Bioseed 6588 *Bt*	41.0	55.6	61.5	46.5	63.7	70.5	43.7	59.7	66.0	17.03	34.90	46.13	19.5	40.2	52.3	18.2	37.5	49.2
Bioseed6588 non-*Bt*	42.5	49.4	64.8	48.0	56.5	74.2	45.2	53.1	69.5	18.56	29.51	40.90	21.2	33.8	46.3	19.9	31.6	43.6
F2228	39.7	57.0	61.6	45.2	65.2	70.7	42.5	61.1	66.1	16.00	32.85	45.20	18.2	37.8	51.4	17.1	35.3	48.3
FDK124	49.0	55.4	64.3	55.7	63.5	73.7	52.3	59.5	69.0	15.55	25.84	30.58	17.8	29.6	34.5	16.7	27.7	32.5
LSD (p=0.05)	5.6	NS	NS	6.4	NS	NS	4.1	NS	NS	NS	7.7	9.0	NS	8.8	10.3	2.7	5.7	6.6

Table 2: Root parameters of cotton genotypes in pot study

Genotypes	Root length (cm)									Root dry matter (g plant $^{-1}$)								
	2016			2017			Pooled			2016			2017			Pooled		
	DAS (days after sowing)																	
	60	90	120	60	90	120	60	90	120	60	90	120	60	90	120	60	90	120
Ankur 3028 *Bt*	41.1	46.8	56.5	46.7	53.7	67.2	43.9	50.2	62.0	5.34	6.18	13.04	6.05	7.05	15.7	5.70	6.61	14.3
Ankur 3028 non-*Bt*	39.6	43.5	59.3	45.0	49.7	70.5	42.5	46.6	65.0	4.38	7.70	14.18	5.70	8.80	17.0	4.66	8.25	15.6
MRC 7017 *Bt*	37.9	42.8	45.4	42.7	49.0	53.7	40.3	45.8	49.6	4.43	6.58	11.46	5.02	7.50	13.8	4.72	7.03	12.6
MRC 7017 non-*Bt*	39.8	45.9	53.0	45.2	52.2	63.0	42.6	49.1	58.0	4.61	6.35	12.20	5.22	7.25	14.7	4.92	6.80	13.4
Bioseed 6588 *Bt*	41.4	45.8	59.3	47.2	52.5	70.5	44.3	49.1	64.8	5.83	7.50	19.03	6.57	8.62	23.2	6.20	8.06	21.1
Bioseed6588 non-*Bt*	38.8	46.9	54.8	44.0	53.2	64.7	41.3	50.1	59.7	7.41	10.91	22.00	8.42	12.4	26.4	7.92	11.6	24.2
F2228	39.4	57.0	58.8	44.7	65.5	70.0	42.1	61.2	64.5	4.73	9.45	21.25	5.37	10.8	25.7	5.05	10.1	23.5
FDK124	49.5	79.8	87.5	56.2	91.0	104.0	52.8	85.3	95.7	6.33	8.08	18.83	7.20	9.27	22.7	6.76	8.67	20.7
LSD (p=0.05)	6.3	9.0	9.9	7.3	10.0	11.9	4.6	6.5	7.5	1.7	1.7	NS	1.8	1.9	NS	1.2	1.2	6.4

of *Bt* and non-*Bt* cotton genotypes was almost identical. Therefore, lesser root development in case of *Bt* hybrids in comparison to their non-*Bt* counterparts could not be scientifically established from the obtained results. There was no evidence of changed root patterns in studied cotton hybrids as being influenced by the presence of *Bt* gene and therefore, a differential response could not be evident in close agreement with Rosolem et al.(2019).

Growth and phenological parameters of cotton genotypes in field experiment

The data in Table 3 indicated significant differences among evaluated genotypes for different growth and phenological parameters during both study years. Tested genotypes could not differentiate significantly for plant height and monopods plant^{-1} within their *Bt* and non-*Bt* versions in accordance with Hebbar et al. (2007) who observed trivial differences for plant height among *Bt* hybrids and non-*Bt* versions. However, pooled data revealed higher plant height (159.1 cm) under Bioseed 6588 non-*Bt*, while MRC7017*Bt* (124.8cm) recorded least.

Significant variation among tested genotypes was also evident for various phenological stages. Irrespective of *Bt* or non-*Bt* version, Bioseed 6588 took significantly higher number of days to achieve flowering initiation, 50 % flowering and days to maturity, while Ankur 3028 required least days for acquiring the various phenological stages. It was also observed that *Bt* versions of all the hybrids took significantly lesser number of days to flowering initiation and 50 % flowering in line with findings of Hlophe and Mavuso (2018) who reported early flowering in JKCH 1947*Bt* (85 days) and JKCH 1050*Bt* (86 days) cotton hybrids as compared to Alba Plus QM 301 Non-*Bt* (106 days). Pooled values revealed that Ankur 3028 *Bt,* MRC7017 *Bt* and Bioseed 6588 *Bt* took 69.0,73.6 and 80.6 days to initiate flowering, while their non-*Bt* versions took significantly higher number of days *i.e.,* 71.6,78.0 and 84.0 days, respectively. Similarly, days to 50% flowering were also significantly higher under Non-*Bt* versions with a value of 102.8, 107.1 and 111.5 for Ankur 3028 non-*Bt,* MRC 7017 non-*Bt* and Bioseed6588 non-*Bt,* respectively. These findings are supported by Hlophe and Mavuso (2018) who observed that JKCH1947*Bt* (102 days) and JKCH1050 *Bt* (106 days) took lesser number of days to achieve 50% flowering as compared to Alba Plus QM 301Non-*Bt* (159 days).Present findings also get support from Li et al. (2015) who reported that different genetic makeup and/or genetic changes could lead to differential physiology characters and might be utilized to explore the potential impact of transgenic cotton. In this study, days to maturity were higher by 4.4, 3.3 and 3.3 for Ankur 3028 non-*Bt,* MRC 7017 non-*Bt*andBioseed6588 non-*Bt,* in comparison to their non-*Bt* versions, respectively (Table 3).This indicated that owing to earlier and relatively faster flowering pattern, plant maturity was hastened in *Bt* versions over that of respective non-*Bt* versions (Hofs et al. 2006).

Yield parameters and seed cotton yield (SCY) of cotton genotypes in field experiment

The data on different yield parameters and SCY exhibited significant differences among tested genotypes. Although, sympodial branches plant^{-1} and boll weight varied trivially among *Bt* and non-*Bt* versions of similar genotypes but bolls plant^{-1} varied significantly. Since SCY is primarily dependent on yield contributing characters like boll weight and bolls plant^{-1} and hence the study of interrelationship of such characters and their relationship with yield is essential.

Bolls plant^{-1} not only varied among different genotypes but their number was also higher under *Bt* version than respective non-*Bt* genotype (Luqman et al. 2015; Hlophe and Mavuso, 2018). Pooled data revealed a boll count of 62.4, 48.0, and 46.6 for Bioseed 6588 *Bt*, Ankur 3028 *Bt* and MRC7017 *Bt,* while the value for respective non-*Bt* version was significantly reduced *i.e.* 55.7, 36.2, and 39.1 plant^{-1}. Hosmath et al.(2004) also reported higher bolls plant^{-1}in *Bt* cultivars over respective non-*Bt* cotton cultivars. Consequently, SCY under tested *Bt* versions remained significantly higher than non-*Bt* version (Dhillon and Sharma, 2013).

In present study, *Bt* cotton hybrids resulted in higher SCY over their non-*Bt* counterpart in conformity with Hosmathet al.(2012) who observed almost double yield (2483 kg ha^{-1}) for Neeraja (BG II) *Bt* as compared to its non-*Bt* cotton version (1131 kg ha^{-1}), respectively indicative

Table 3: Growth and phenological parameters of cotton genotypes in field experiment

Genotypes	Plant height at maturity (cm)			Monopodial branchesplant^{-1}			Days to flowering initiation			Days to 50% flowering			Days to maturity		
	2016	2017	pooled	2016	2017	pooled	2016	2017	pooled	2016	2017	pooled	2016	2017	pooled
Ankur 3028 *Bt*	120.8	135.8	128.3	2.88	3.04	2.96	68.0	70.0	69.0	98.0	100.6	99.3	167.3	172.0	169.6
Ankur 3028 non-*Bt*	121.6	136.6	129.1	2.66	2.94	2.80	70.6	72.6	71.6	101.3	104.3	102.8	171.6	176.3	174.0
MRC 7017 *Bt*	119.6	130.5	124.8	3.13	3.03	3.08	72.6	74.6	73.6	102.3	105.3	103.8	170.0	174.6	172.3
MRC 7017 non-*Bt*	125.0	133.0	129.0	3.24	3.36	3.30	77.0	79.0	78.0	106.0	108.3	107.1	173.3	178.0	175.6
Bioseed 6588 *Bt*	144.7	166.7	155.7	3.15	3.22	3.18	79.6	81.6	80.6	106.6	109.6	108.1	178.6	183.3	181.0
Bioseed6588 non-*Bt*	149.1	169.1	159.1	3.06	3.08	3.07	83.0	85.0	84.0	110.0	113.0	111.5	182.0	186.6	184.3
LSD (p=0.05)	16.8	15.1	10.6	NS	NS	0.28	1.1	1.1	0.72	2.3	2.2	1.5	1.8	1.8	1.2

Table 4: Seed cotton yield and yield attributes of cotton genotypes in field experiment

Genotypes	Sympodial branches plant^{-1}			Bolls plant^{-1}			Bolls weight (g)			Seed cotton yield (kg ha^{-1})			Plant stand ha^{-1}		
	2016	2017	pooled	2016	2017	pooled	2016	2017	pooled	2016	2017	pooled	2016	2017	pooled
Ankur 3028 *Bt*	21.1	23.2	22.1	43.9	52.1	48.0	3.55	3.52	3.54	2207	2352	2280	18849	18462	18655
Ankur 3028 non-*Bt*	19.6	21.9	20.7	34.5	37.9	36.2	3.47	3.48	3.48	1673	1798	1735	18300	18687	18493
MRC 7017 *Bt*	19.3	20.0	19.7	42.3	51.0	46.6	3.79	3.83	3.81	2045	2266	2156	18666	18972	18819
MRC 7017 non-*Bt*	20.3	20.2	20.2	37.7	40.5	39.1	3.86	3.87	3.86	1786	1864	1825	18208	18176	18192
Bioseed 6588 *Bt*	23.8	24.3	24.0	60.8	64.0	62.4	3.62	3.60	3.61	2583	2694	2638	18849	18612	18730
Bioseed6588 non-*Bt*	25.5	25.3	25.4	56.6	54.7	55.7	3.58	3.74	3.66	2193	2310	2252	18300	18827	18563
LSD (p=0.05)	3.91	2.07	2.07	7.8	8.0	5.2	NS	NS	0.21	241	345	197	NS	NS	NS

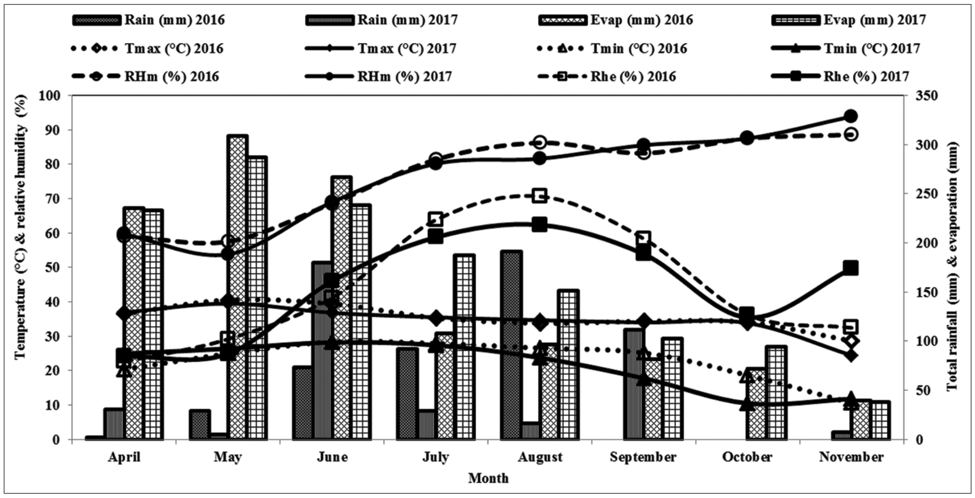

Fig 3. Prevailing weather conditions (temperature, relative humidity, rainfall, and evaporation) at study site during 2016-2017.

of higher SCY under *Bt* genotypes. Hosmath et al. (2012) also observed that *Bt* hybrids (BGI and BGII) were better yielders (1978 kg ha^{-1}) as compared to their non-*Bt* versions (1258 kg ha^{-1}). However, in our studies significantly higher SCY was observed for Bioseed 6488*Bt* (2638 kg ha^{-1}) followed by Ankur 3028 *Bt* (2280kg ha^{-1}) and MRC7017 *Bt*(2156 kg ha^{-1}). It was observed that yield was higher by 31.4,18.1 and 17.1 % under Ankur 3028 *Bt,* MRC7017 *Bt* and Bioseed 6588 *Bt* over their non-*Bt* versions primarily owing to statistically higher boll number plant^{-1}. Hlophe and Mavuso (2018) observed that *Bt* genotypes out yielded non-*Bt* genotypes in Swaziland. Non-significant variation among tested genotypes for plant stand indicated that yield differences were solely due to different treatments (Table 4).

Based upon the above said observations, there is sufficient evidence to conclude that rooting pattern is akin in various *Bt* and their Non-*Bt* cotton counterparts in present study. Sanaullah et al.(2016) also summarized that the cultivation of *Bt*-cotton expressing *cry1Ac* could not exert any negative effect on metabolic, microbial population, and soil nutrient dynamics. Similarly, Ahamd et al.(2017) could not find significant variation on soil physico-chemical properties among transgenic *Bt*cotton over that of non-*Bt* cotton. However, we could establish that SCY in all cotton hybrids possessing *Bt* gene was significantly higher than their non-*Bt* version owing to higher bolls plant^{-1}.

CONCLUSION

Present study investigated the response of 3*Bt* cotton hybrids in comparison to their conventional non-transgenic version (near-isogenic lines) for growth, yield attributes and phenological parameters. Pot studies elucidated that introgression of *Bt* gene could not modify rooting characteristics of evaluated cotton genotypes, though *arboreum* cultivar (FDK124) exhibited relatively higher root length. However, presence of *Bt* gene significantly affected various phenological stages by inducing earliness in flowering and days to maturity. Higher yield in *Bt* hybrids over respective non-*Bt* version sowing to improved bolls plant^{-1} has been evident. Nevertheless, yield increments under *Bt* versions over respective non-*Bt* version would be sufficient enough to keep cotton growers inclined towards genetically modified germplasm in near future. However, more studies are required to confirm and establish these findings by conducting multi location field studies over time and space.

Authors' contribution

Kulvir Singh: Conceptualization, Methodology, Formal analysis, Writing - Original Draft

Sudhir Kumar Mishra: Analysis of data and interpretation, Software and Formal analysis

Manpreet Singh: Analysis of data and interpretation

Harjeet Singh Brar: Preparation of manuscript and data curation

Amarpreet Singh: Preparation of final manuscript and data curation

REFERENCES

Ahamd, M., W. M. Abbasi, M. Jamil, M. Iqbal, A. Hussain, M. F. Akhtar and F. Nazli. 2017. Comparison of rhizosphere properties as affected by different *Bt*- and non-*Bt*-cotton (*Gossypium hirsutum* L.) genotypes and fertilization. Environ. Monit. Assess. 189: 278.

AICRP. 2021. All India Coordinated Research Project on Cotton (2020–21). AICRP, New Delhi.

Arshad, M., A. Suhail, M. D. Gogi, M. Yaseen, M. Asghar, M. Tayyib, H. Karar, F. Hafeez, and U. N. Ullah. 2009. Farmers perceptions of insect pests and pest management practices in Bt cotton in the Punjab, Pakistan. Int. J. Pest. Manage. 55: 1-10.

Dhillon, M. and H. C. Sharma. 2013. Comparative studies on the effects of Bt-transgenic and non-transgenic cotton on arthropod diversity, seed cotton yield and bollworms control. J. Environ. Biol. 34: 67-73.

Dunfield, K. E. and J. J. Germida. 2004. Impact of genetically modified crops on soil- and plant-associated microbial communities. J. Environ. Qual. 33: 806-815.

Gul, S., N. U. Khan, S. Batool, M. J. Baloch, M. Munir, M. Sajid, A. Khakwani, S. A. Ghaloo, Z. Soomro and S. F. Kazmi. 2014. Genotype by environment interaction and association of morphoyield variables in upland cotton. J. Plant. Sci. 24: 262-271.

Hebbar, K. B., N. K. Perumal and B. M. Khadi. 2007. Photosynthesis and plant growth response to transgenic *Bt* cotton (*G. hirsutum* L.) hybrid under field condition. Photosynthetica. 45: 254-258.

Hlophe, N. L. and C. S. Mavuso. 2018. A comparative field assessment of *Bt* and non-*Bt* cotton varieties in Swaziland. Int. J. Dev. Sustain. 7: 2694-2703.

Hofs, J. L., D. Marais and M. Fok. 2006. Boll distribution patterns in *Bt* and non-*Bt* cotton genotypes: II. Study on small-scale farming systems in South Africa. Field Crops. Res. 98: 210-215.

Hosmath, J., D. P. Biradar, V. C. Patil, Y. B. Palled, L. H. Malligawad, S. Patil, A. Alagawadi and A. S. Vastrad. 2012.Performance of *Bt* and non-*Bt* cotton genotypes under leaf reddening malady situation. Karnataka J. Agric. Sci. 25: 36-38.

Li, X., C. Ding, X. Wang and B. Liu. 2015. Comparison of the physiological characteristics of transgenic insect-resistant cotton and conventional lines. Sci. Rep. 5: 8739.

Luqman, M., M. A. Raza, N. Shahid and M. Hassan. 2015. Performance of *Bt* cotton varieties under Khanewal conditions. Bulgarian J. Agric. Sci. 21: 105-108.

Martins, C., G. Beyene, J. L. Hofs, K. Krüger, C. van der Vyver and U. Schlüter. 2008. Effect of water-deficit stress on cotton plants expressing the *Bacillus thuringiensis* toxin. Ann. Appl. Biol. 152: 255-262.

Masto, R. E., P. K. Chhonkar, D. Singh and A. K. Patra. 2006. Changes in soil biological and biochemical characteristics in a long-term field trial on a sub-tropical inceptisol. Soil Biol. Biochem. 38: 1577-1582.

O'Callaghan, M., T. R. Glare, E. P. J. Burgess and L. A. Malone. 2005. Effects of plants genetically modified for insect resistance on non-target organisms. Ann. Rev. Entomol. 50: 271-292.

Pindi, P. K. and T. Sultana. 2013. Bacterial and fungal diversity in rhizosphere soils of *Bt* and non-*Bt*cotton in natural system. Bulgarian J. Agric. Sci. 19: 1306-1310.

Pray, C., D. Ma, J. Huang and F. Qiao. 2001. Impact of *Bt* cotton in China. World Dev. 29: 813-825.

Rosolem, C. A., M. V. M. Sarto, K. F. Rocha, J. D. L. Martins and M. S. Alves. 2019. Does the introgression of *Bt* gene affect physiological cotton response to water deficit? Planta Daninha. 37: e019187935.

Sanaullah, Y., H. N. Asghar, F. Ahmad, Z. A. Zahir and E. A. Waraich. 2016. Impact of Bt-cotton on soil microbiological and biochemical attributes. Plant Prod. Sci. 19: 458-467.

Sarkar, B., A. K. Patra, T. J. Purakayastha and M. Megharaj. 2009. Assessment of biological and biochemical indicators in soil under transgenic *Bt* and non-*Bt* cotton crop in a sub-tropical environment. Environ. Monit. Assess. 156: 595-604.

Shen, R. F., H. Cai and W. H. Gong. 2006. Transgenic *Bt* cotton has no apparent effect on enzymatic activities or functional diversity of microbial communities in rhizosphere soil. Plant Soil. 285: 149-159.

Singh, K., O. P. Choudhary, H. P. Singh, A. Singh and S. K. Mishra. 2019. Sub-soiling improves productivity and economic returns of cotton-wheat cropping system. Soil Tillage Res. 189: 131-139.

Velmourougane, K. and A. Sahu. 2013.Impact of transgenic cottons expressing cry1Ac on soil biological attributes. Plant Soil Environ. 59: 108-114.

Zaman, M., M. S. Mirza, S. Irem and Y. Zafar. 2015. A temporal expression of Cry1Ac protein in cotton plant and its impact on soil health. Int. J. Agric. Biol. 17: 280-288.

Zhang, Y. J., M. Xie, C. Li, G. Wu and D. L. Peng. 2014. Impacts of the transgenic CrylAc and CpTI insect-resistant cotton SGK321 on selected soil enzyme activities in the rhizosphere. Plant Soil Environ. 60: 401-406.