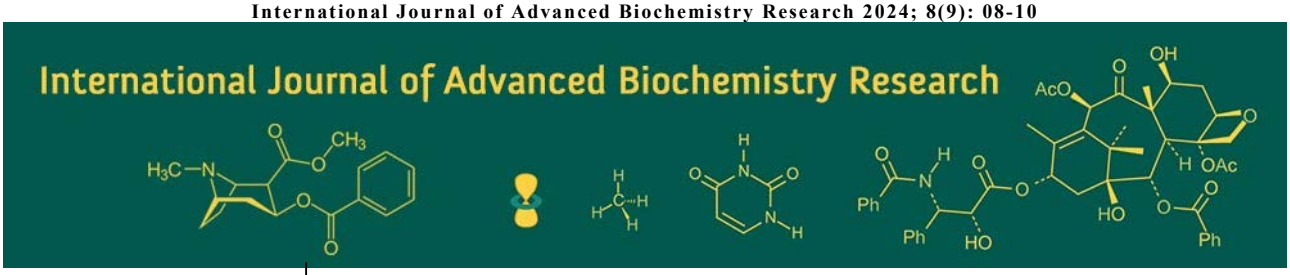

ISSN Print: 2617-4693
ISSN Online: 2617-4707
IJABR 2024; 8(9): 08-10
www.biochemjournal.com
Received: 07-06-2024
Accepted: 09-07-2024

SR Gamit
Department of Soil Science and Agricultural Chemistry, Biochemistry, NM College of Agriculture, Navsari Agricultural University, Navsari, Gujarat, India

HR Ramani
Main Cotton Research Station, Navsari Agricultural University, Athwa Farm, Surat, Gujarat, India

MD Khunt
Department of Agricultural Microbiology, Navsari Agricultural University, Navsari, Gujarat, India

Corresponding Author:
SR Gamit
Department of Soil Science and Agricultural Chemistry, Biochemistry, NM College of Agriculture, Navsari Agricultural University, Navsari, Gujarat, India

Biochemical appraisal of different plant parts of BT and non-BT cotton genotypes

SR Gamit, HR Ramani and MD Khunt

DOI: https://doi.org/10.33545/26174693.2024.v8.i9a.2040

Abstract
Cotton, also known as "white gold" and "king of fiber," is a crucial industrial crop in India. It belongs to the genus *Gossypiyum* and is grown on a commercial scale in India. Bt cotton, a type of cotton, is effective against the Bollworm pest complex and plays a dominant role in the country's industrial and agricultural economy. The study conducted at the Main Cotton Research Station, Athwa farm, Navsari Agricultural University, Surat, during the Kharif season of 2023-2024, analyzed biochemical parameters of Bt and Non-Bt cotton genotypes. The results showed that Bt cotton had the highest reducing sugar, proline, and flavanol, while Non-Bt cotton had the highest total soluble sugar, protein, total chlorophyll, and total phenol.

Keywords: Cotton, reducing sugar, TSS, protein, proline, total chlorophyll, phenol, and flavanol

Introduction
Cotton, a major fiber crop in India and the world belong to the genus *Gossypium* in the mallow family *Malvaceae* (Prajapat *et al*. 2018) [9]. It is the world's most important fiber crop and the second most important oil seed crop (Hutchinson *et al*. 1947) [5]. The primary product of the cotton plant is the lint that covers the seeds within the seed pod, or boll. India is an exception to most countries, with only 30% of its cotton production area planted to *G. hirsutum*, 17% to *G. arboretum*, 8% to *G. herbaceum*, and the remaining area planted to interspecific and intraspecific hybrids (Hutchinson *et al*. 1947) [5]. Bt cotton is a genetically modified (GM) cotton derived from *Bacillus thuringiensis* (Bt), a common soil bacterium. The gene, Cry-1AC, produces a protein toxic to lepidopteran (Bollworm) insects when ingested. Bt cotton has the added property of producing its biopesticide to protect itself from insect pests. It was introduced to reduce pesticide costs and improve cotton yield, quality, and net return. However, Bt cotton is less effective in controlling other pests like soil, sucking, and leaf roller pests. Bt cotton is environmentally safe and economically beneficial, leading to significant yield increases, reduced chemical sprays, and increased net profit for farmers (Abbas, 2018) [1].

Materials and Methodology
The experiment was conducted during the *kharif* season of 2023-2024 at the Main Cotton Research Station, Navsari Agricultural University, Athwa-farm, Surat. Leaf, square, flower, boll, and seed samples were collected from open fields grown at the MCRS, Surat. Laboratory work was done at the Department of Soil Science and Agricultural Chemistry, NAU, Navsari. Four Bt and Non-Bt cotton genotypes were selected for study with 3 replication FCRD design. Biochemical parameters were performed after 45 DAS using standard methods.
Miller, (1972) [8] methods were used for Reducing sugar analysis from leaf samples and read at 510 nm using dextrose as standard. The content of TSS was determined by sadasivam and Manickam (1992) [10] with anthron method and read at 630 nm using glucose as standard. Protein analysis was done as per the standard method described by the method of Lowry *et al*. (1951) [6]. Protein content was observed at 660 nm using BSA as standard and the amount of protein presented as mg per gm. Proline analysis was estimated by the acid ninhydrin method described by the method of Bates *et al*. (1973) [11]. Proline content was observed at 520 nm using proline as standard.

The total chlorophyll content was determined by Arnon, (1949) [2] and read at 645 and 663 nm using 80% acetone as standard. Phenol was done by the method of Malick and Singh, 1980 [7]. Phenol was read at 650 nm using Catechol as standard and the amount of phenol was calculated as mg per gm. Flavanol content was estimated as per the method of Thimmaiah (1999) [12] standard curve of phloroglucinol was prepared and the amount of flavanol expressed as mg per g.

Results and Discussion

Biochemical parameters

The study analyzed four cotton genotypes Bt and Non-Bt and five different cotton plant parts. The highest total soluble sugar content (112.07 mg/g) was found in the G.Cot.Hy 10 genotype in the leaf, while the lowest (77.92 mg/g) was in the G.Cot.Hy 8 genotype in the flower. The highest reducing sugar content was (11.94 mg/g) found in the G.Cot.Hy 8 BG II genotype in the leaf, while the highest protein content (2.51 mg/g) was found in the G.Cot.Hy 8 genotype in the seed. The highest total chlorophyll content (2.24 mg/g) was found in the G.Cot.Hy 10 genotype in the leaf. The highest total phenol content (5.30 mg/g) was found in the G.Cot.Hy 8 in the seed, while the highest flavanol content (13.64 ml/g) was found in the G.Cot.Hy 8 BG II in the boll.

Table 1: Biochemical analysis of different plant parts *i.e.* leaf, square, flower, boll, and seed along with Bt and Non-Bt cotton genotypes has been presented in (G1: G.Cot.Hy 8 BG II, G2: G.Cot.Hy 10 BG II, G3: G.Cot.Hy 8, G4: G.Cot.Hy 10)

Genotypes	Reducing sugar (mg/g)	TSS (mg/g)	Protein (mg/g)	Proline (mg/g)	Total chlorophyll (mg/g)	Total phenol (mg/g)	Flavanol (ml/g)
G_1P_1	11.94	102.29	2.18	1.06	2.12	2.09	13.87
G_1P_2	9.84	80.39	1.31	1.30	1.21	3.16	12.73
G_1P_3	8.07	94.72	1.42	1.28	0.023	4.30	12.05
G_1P_4	9.96	90.26	1.58	0.93	1.04	3.67	13.64
G_1P_5	4.96	99.95	2.41	0.77	-	3.78	10.66
G_2P_1	11.30	95.58	1.93	1.27	1.93	2.20	11.20
G_2P_2	9.89	97.62	1.35	1.36	1.17	3.21	11.52
G_2P_3	9.91	88.20	1.64	1.65	0.037	3.37	11.26
G_2P_4	10.55	82.74	1.52	0.94	1.48	3.71	10.83
G_2P_5	5.61	99.34	2.13	1.25	-	4.18	11.17
G_3P_1	7.12	102.15	1.84	0.56	1.71	2.15	10.37
G_3P_2	9.95	88.917	1.33	0.95	1.05	3.70	11.68
G_3P_3	9.08	77.92	1.67	0.66	0.017	3.19	12.15
G_3P_4	9.97	89.38	1.42	1.24	1.11	3.44	13.22
G_3P_5	5.52	100.57	2.51	1.25	-	4.33	11.27
G_4P_1	11.34	112.07	1.67	1.09	2.24	2.22	11.60
G_4P_2	10.39	81.50	1.46	0.96	1.47	3.28	12.59
G_4P_3	7.61	84.38	1.35	0.93	0.017	3.47	12.46
G_4P_4	9.25	86.65	1.71	0.93	1.07	3.82	11.31
G_4P_5	4.86	95.40	2.13	1.47	-	5.30	11.35
CD at 5 %							
G	0.44	NS	NS	0.027	0.058	0.057	0.23
P	0.492	4.947	0.098	0.031	0.058	0.064	0.257
G × P	0.985	9.893	0.197	0.061	0.116	0.127	0.515
CV %	6.71	6.46	6.86	3.38	6.29	1.83	2.62

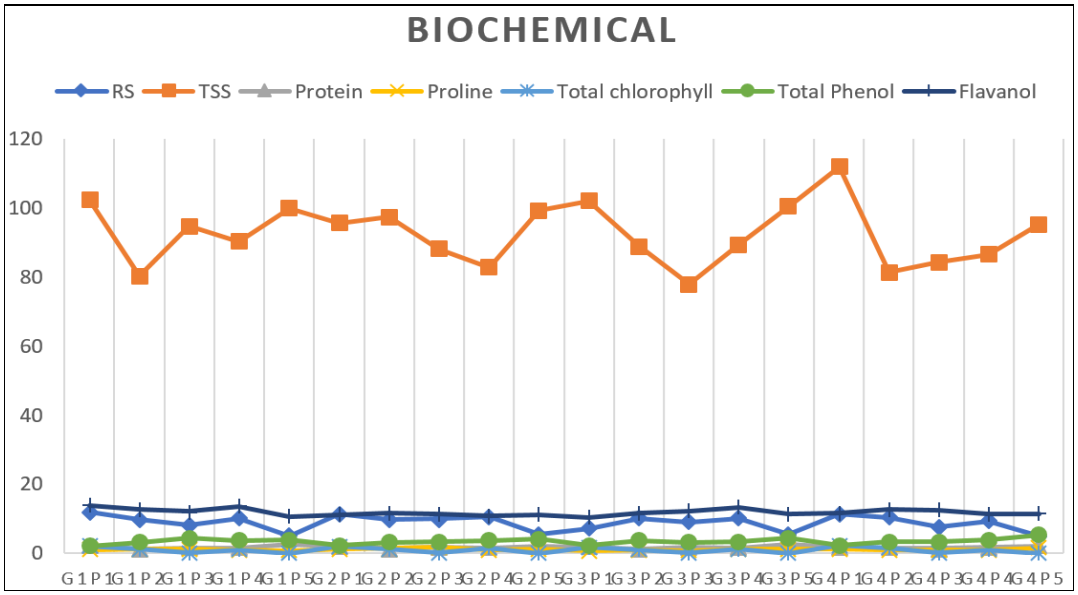

Fig 1: Biochemical analysis of different plant parts *i.e.* leaf, square, flower, boll, and seed along with Bt and Non-Bt cotton genotypes has been presented.

Conclusion

Bt cotton showed the highest reducing sugar, proline, and flavanol while Non-Bt cotton recorded the highest total soluble sugar, protein, total chlorophyll, and total phenol content. The highest reducing sugar and flavanol in the leaf and proline are found in the square of Bt cotton genotypes G.Cot.Hy 8 BG II. Non-Bt cotton showed the highest TSS and total chlorophyll in the leaf of cotton genotype G.Cot.Hy 8 BG II. The highest content of protein was found in the seed of cotton genotype G.Cot.Hy 8.

References

1. Abbas MST. Genetically engineered (modified) crops (*Bacillus thuringiensis* crops) and the world controversy on their safety. Egypt J Biol Pest Control. 2018;28(1):1-12.
2. Arnon DI. Copper enzymes in isolated chloroplasts. Polyphenoloxidase in Beta vulgaris. Plant Physiol. 1949;24(1):1.
3. Chinard F. Photometric estimation of proline and ornithine. J Biol Chem. 1952;199:91-95.
4. Heimler D, Vignolini P, Dini MG, Romani A. Rapid tests to assess the antioxidant activity of *Phaseolus vulgaris* L. dry beans. J Agric Food Chem. 2005;53(8):3053-3056.
5. Hutchinson JB, Silow RA, Stephens SG. The Evolution of Gossypium and the Differentiation of the Cultivated Cottons. Nature. 1947;162:716.
6. Lowry OH, Rosebrough NL, Farr AL, Randall RJ. Protein measurement with the Folin Phenol reagent. J Biol Chem. 1951;193:265-275.
7. Malick CP, Singh MB. In: Plant enzymology and histo enzymology. New Delhi: Kalyani Publications; c1980. p. 286.
8. Miller GL. Use of dinitrosalicylic acid reagent for determination of reducing sugars. Anal Chem. 1972;31:426-428.
9. Prajapat P, Singh D, Tripathi S, Patel K, Abbas H, Patel P. Effect of water stress on antioxidative enzymes and glycine betaine content in drought susceptible cotton (*Gossypium hirsutum* L.) genotypes. Indian J Biochem Biophys. 2018;55:198-204.
10. Sadasivam S, Manickam A. In: Biochemical methods for agricultural sciences. New Delhi: Wiley Eastern Limited; c1992. p. 189-191.
11. Bates LS, Waldren RP, Teare ID. Rapid determination of free proline for water-stress studies. Plant and soil. 1973 Aug;39:205-207.
12. Thimmaiah N. Structure and Performance of Indian Organised Manufacturing Industries during Pre and Post Reform Period. Asian Journal of Research in Business Economics and Management. 2015;5(4):72-87.