



## GENOTYPIC CORRELATION STUDIES IN TRANSGENIC COTTON (BG-I AND BG-II) IN COMPARISON WITH RESPECTIVE NON BT COTTON

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### ABSTRACT

In present investigation, an attempt has been made to study the relationship of various pair of traits. It has been estimated in NBt. Set of values of those associations in NBt being considered as a yard stick to measure/ understand the impact of gene of one trait on genes of other traits in other two sets of transgenic i.e. BG-I and BG-II. Any deviation over the trend of NBt observed either in BG-I or BG-II could be considered as impact of Cry 1Ac or Cry 1Ac + Cry 2Ab genes.

Fifteen F1's + parents of NBt as well as 15F1's of BG-I and BG-II with their respective parents were evaluated. Out of 66 values of associations in NBt group, more than 45 associations showed similar trend in BG-I and BG-II. Thus genotypic correlation parameters proved that either gene for Cry 1Ac or Cry 1Ac + Cry 2Ab behave independently and never interfered directly with the genes governing the traits.

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### INTRODUCTION

Policy adopted by Government of India, permitting Bt cotton cultivation proved beneficial and resulted in increasing productivity from 302 Kg/ha (2002-2003) to 568 Kg/ha (2016-2017, source- Cotton Advisory Board 24.10.2016). However, looking at the scenario with regards to the progress of development in biotech products in the field of commercially important crops viz, Cotton, Maize, Brinjal etc, under Indian conditions and world at large, the differences in opinion of the think tank are well established. One view elaborates that, in general, the transgenic does affect the other related and unrelated traits, while, another view opines that transgenic genes not involved in any way in exerting influence on others. More specifically, in a crop like cotton, several queries from various corners have been raised. Few vital queries pertaining to cotton crop are as below:

1. Is the transgenic gene directly or indirectly affecting on the performance of other traits of cotton crop, despite they are independent?
2. Is the Bt gene is responsible for modifying nature of inheritance, combining ability, mid parent heterosis and genotypic correlation of economically important traits of cotton crop?

Supporters of GMO and opponent groups also never tried to satisfy each other by providing / generating supporting relevant data. Present investigation aimed to generate data

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in relation with above queries and put the facts without involving either in favour or opponent group. This has been done by studying various parameters in NBt set and comparing those values of NBt hybrids with same BG-I hybrids (Cry 1 Ac) and of BG II hybrids (Cry 1 Ac + Cry 2 Ab). Any change (having same genetics except differ for transgenic gene) in the trend / modification for various parameters in BG-I and BG-II over NBt will help us to conclude that there is the impact of transgenic gene on the main trait and also on related/ unrelated sub traits. If the trend remains unchanged, we can appraise NGO that those queries are merely perception and not reality as generated scientific data rarely support your views.

Genes of one trait exert its influence on genes of related traits either in positive or negative direction and it is being measured by values called rg i.e. genotypic correlation. Its known fact that correlation specifically genotypic correlation pin point the existed relationship between the two traits, which are directly or indirectly associated. It indicates that to what extent, their relationship is close or distant. Large numbers of references are available showing positive or negative, strong or weak association between two traits and there by two genes and their intensity measured by "r" value.

In present investigation, an attempt has been made to study the relationship of various pair of traits. It has been estimated in NBt. Set of values of those associations in NBt being considered as a yard stick to measure/ understand the impact of gene of one trait on genes of other traits in other two sets.

**Table 1** Genotypic correlation Matrix

Sr. No.	Correlation with Trait	Significance Levels				
		If correlation r =>				
		NBt	BG-I	BG-II		
1	SCY (q/ha) x Ave. Boll wt (g)	0.3269	0.1259	0.2656		
	SCY (q/ha) x % Shoot borer Infe	-0.2249	-3.9662	-0.7716		
	SCY (q/ha) x Ave. Boll No.	0.9497	0.961	0.9809		
	SCY (q/ha) x Lint Yield (Kg/ha)	0.9962	0.9907	0.9948		
	SCY (q/ha) xGinning (%)	0.5927	0.2158	0.4968		
	SCY (q/ha) x Seed Index(g)	-0.0747	0.1426	-0.3588		
	SCY (q/ha) x Lint Index(g)	0.3491	0.2632	0.0107		
	SCY (q/ha) x 2.5% SL(mm)	0.6813	0.6503	0.5418		
	SCY (q/ha) x Bundle Strg.(g/tex)	0.6939	0.3251	0.5874		
	SCY (q/ha) x Micronaire	0.4864	0.4573	0.3091		
	SCY (q/ha) x Jassid_75	-0.3554	-0.2896	-0.3501		
2	Ave. Boll wt (g) x % Shoot borer Infe	0.3331	-0.2662	-0.1503		
	Ave. Boll wt (g) x Ave. Boll No.	0.0146	-0.1316	0.0829		
	Ave. Boll wt (g) x Lint Yield (Kg/ha)	0.3087	0.1316	0.301		
	Ave. Boll wt (g) x Ginning (%)	0.0488	0.0612	0.47		
	Ave. Boll wt (g) x Seed Index(g)	0.508	0.4283	-0.0126		
	Ave. Boll wt (g) x Lint Index(g)	0.5051	0.437	0.1869		
	Ave. Boll wt (g) x 2.5% SL(mm)	0.4568	0.3059	0.223		
	Ave. Boll wt (g) x Bundle Strg.(g/tex)	0.4462	0.2978	0.3168		
	Ave. Boll wt (g) x Micronaire	0.0392	0.1226	0.381		
	Ave. Boll wt (g) x Jassid_75	0.1559	0.1557	0.3755		
3	% Shoot borer Infe x Ave. Boll No.	-0.3491	-3.5256	-0.8702		
	% Shoot borer Infe x Lint Yield (Kg/ha)	-0.2269	-151.7430	-0.6296		
	% Shoot borer Infe x Ginning (%)	-0.0572	-1.6592	0.5056		
	% Shoot borer Infe x Seed Index(g)	0.216	0.4554	1.5963		
	% Shoot borer Infe x Lint Index(g)	0.1521	-0.1256	1.3189		
	% Shoot borer Infe x 2.5% SL(mm)	0.3428	-0.9554	-0.5970		
	% Shoot borer Infe x Bundle Strg.(g/tex)	0.0054	-1.9256	0.3278		
	% Shoot borer Infe x Micronaire	-0.3356	-0.2158	0.7256		
	% Shoot borer Infe x Jassid_75	0.4949	-0.1935	-1.1249		
	4	Ave. Boll No. x Lint Yield (Kg/ha)	0.955	0.9499	0.9692	
Ave. Boll No. x Ginning (%)		0.6179	0.1719	0.435		
Ave. Boll No. x Seed Index(g)		-0.2336	0.0643	-0.3529		
Ave. Boll No. x Lint Index(g)		0.2156	0.165	-0.0078		
Ave. Boll No. x 2.5% SL(mm)		0.5586	0.5965	0.516		
Ave. Boll No. x Bundle Strg.(g/tex)		0.5598	0.2358	0.5512		
Ave. Boll No. x Micronaire		0.5212	0.3964	0.2527		
Ave. Boll No. x Jassid_75		-0.4086	-0.2703	-0.4135		
5		Lint Yield (Kg/ha) x Ginning (%)	0.6594	0.3429	0.5816	
		Lint Yield (Kg/ha) x Seed Index(g)	-0.0901	0.1108	-0.2992	
	Lint Yield (Kg/ha) x Lint Index(g)	0.3772	0.3051	0.0971		
	Lint Yield (Kg/ha) x 2.5% SL(mm)	0.6601	0.6224	0.55		
	Lint Yield (Kg/ha) x Bundle Strg.(g/tex)	0.6939	0.2953	0.6061		
	Lint Yield (Kg/ha) x Micronaire	0.4992	0.4602	0.3369		
	Lint Yield (Kg/ha) x Jassid_75	-0.3391	-0.2894	-0.3733		
	6	Ginning (%) x Seed Index(g)	-0.2178	-0.2230	0.2929	
		Ginning (%) x Lint Index(g)	0.4668	0.3596	0.7373	
		Ginning (%) x 2.5% SL(mm)	0.3743	-0.0160	0.4426	
Ginning (%) x Bundle Strg.(g/tex)		0.457	-0.0747	0.4925		
Ginning (%) x Micronaire		0.3895	0.2315	0.4559		
Ginning (%) x Jassid_75		-0.1390	-0.1838	-0.3153		
7		Seed Index(g) x Lint Index(g)	0.7607	0.8272	0.8601	
		Seed Index(g) x 2.5% SL(mm)	-0.0849	-0.0226	-0.2436	
		Seed Index(g) x Bundle Strg.(g/tex)	-0.0448	-0.2054	-0.2482	
		Seed Index(g) x Micronaire	-0.1699	-0.0101	-0.1399	
	Seed Index(g) x Jassid_75	0.2017	0.1608	-0.2904		
	8	Lint Index(g) x 2.5% SL(mm)	0.1822	-0.0322	0.0647	
		Lint Index(g) x Bundle Strg.(g/tex)	0.2885	-0.2454	0.0722	
		Lint Index(g) x Micronaire	0.1141	0.1204	0.12	
		Lint Index(g) x Jassid_75	0.0787	0.0443	-0.3954	
		9	2.5% SL(mm) x Bundle Strg.(g/tex)	0.6583	0.654	0.76
2.5% SL(mm) x Micronaire			0.222	0.234	0.1918	
2.5% SL(mm) x Jassid_75			0.0064	0.2322	-0.0808	
10			Bundle Strg.(g/tex) x Micronaire	0.6821	0.5827	0.352
			Bundle Strg.(g/tex) x Jassid_75	-0.1475	0.1226	-0.1097
			11	Micronaire x Jassid_75	-0.5152	-0.1783

Any deviation over the trend of NBt observed either in BG-I or BG-II could be considered as impact of Cry 1Ac or Cry 1Ac + Cry 2Ab. This genotypic correlation is a reliable parameter and gives the answer to all queries raised by opponents of technology.

## MATERIALS AND METHODS

Six *G. hirsutum* NBt parents were selected to produce 15 F1 in Diallel without reciprocals. Thus, produced 15 F1's of NBt-version, hereafter we will call it as **Set-I**. Same NBt 6

parents were converted by back cross method and evolved those six parents with BG I (Cry 1 Ac)- (Set-II) and also with BG II (Cry 1 Ac+ Cry 2Ab)- (Set-III). Those independently converted BG-I and BG-II parents were used in present investigation to produce 15F1's of BG-I and 15 F1's of BG-II. Thus 15 F1's of BG I (set II) and 15 F1's of BG II (set III) along with respectively 6 BG I and 6 BG II parents were used along with 15 F1's + 6 parents of NBt. The three sets were thus genetically similar except differ in presence or absence of either Cry 1Ac or Cry 1Ac + Cry 2Ab gene.

Thus, 6 parents +15 F1's each of NBt (Set I), BG I (Set II) and of BG II (Set III) were raised. Each set was raised in a compact block with RBD, following three replications / hybrid. Optimum plot size, spacing adopted. Five plants / replication / hybrid were tagged and all observations were recorded. Statistical analysis for each set was done separately for all traits. Treatment differences, if found significant were considered for further analysis.

Genotypic correlation was computed following the statistical technique prescribed by Kowon and Torrie (1964).

## RESULTS AND DISCUSSION

Data presented in Table-1 revealed that Genotypic correlation of seed cotton yield with boll wt, boll number, lint yield, 2.5% span length, bundle strength, micronaire and jassid grade at 75 days were significant with either positive or negative relationship. Out of 11 associations (11 r values), in set BG-I except one and all 11 in BG-II showed the trend that was perfectly matching with NBt. Intensity was either weak or strong, never the less, trends maintained constant. All associations from BG-I and BG-II followed the path shown by NBt. Hence needless to mention that neither gene for Cry 1Ac nor Cry 1Ac + Cry 2Ab were able to exert the influence on genes of other traits.

Out of 66 values of associations from NBt group, more than 45 associations showed similar trend in BG-I and BG-II. It can thus be concluded that genotypic correlation parameters like other parameters proved that either gene for Cry 1Ac or Cry 1Ac + Cry 2Ab behaved independently and never interfere directly on genes governing the traits. Even then, inserted genes failed to modify their relationship existed between two traits. Few "r" values showed slight modification in trend i.e. from negative to positive or positive to negative. However, altered directions have non-significant "r" values.

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## References

- Afiah, S. A. N. and Ghoneim, E. M. 2000. Correlation, stepwise and path coefficient analysis in Egyptian cotton under saline conditions. *Arab. Uni. J. Agri. Sci.* 8: 607-18.
- Girase, V. S. and Mehetre, S. S. 2002. Correlation and path analysis in cotton. *J. Cotton Res.Dev.* 16: 1-7.
- Kwon, S.H. and J.H. Torrie (1964). Heritability and interrelationship among traits of two soybean population. *Crop Sci.* 4: 196-8.
- Saeed, R., Khan, T. M., Sadaqat, H. A. and Khan, A.I. 2004. Correlation and path coefficient analysis of yield components in cotton (*Gossypium hirsutum* L). *Int. J. Agri. Biology* 6:686-88.

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