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Research Note

Study of genotype x environment interactions and stability among diverse *Gossypium arboreum* L. genotypes for yield and related traits under North Western Plains

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Abstract

The present investigation was undertaken with an objective to determine the effect of genotype × environment (GE) interactions and stability on *Gossypium arboreum* genotypes belonging to different part of country for seed cotton yield and related traits. Seventeen Asiatic cotton genotypes were evaluated in randomized block design at Ludhiana, for two years (2010 and 2011) and at Faridkot for one year (2010). The significant genotypes, environments, genotype × environment interactions were observed for all traits. Stability parameters revealed LD694 and LD902 were most stable and significantly outperforming for most of the traits except halo length where DLsa1001 was ahead. Genotypes developed at Punjab were found to be more stable for most of the traits whereas genotypes from other centers can be used as germplasm for pre-breeding programmes.

Keywords

Gossypium arboreum, cotton, genotype x environment interactions, stability, Punjab

The excellent fibre and edible oil properties have made cotton the 'White Gold'. *Gossypium arboreum* originated and cultivated in India occupies third position after cotton hybrids (40%) and *G. hirsutum* (36%) but with introduction of Bt cotton the area under *G. arboreum* has further decreased yet *G. arboreum* is an excellent gene source for various agronomic traits *viz*., coarse fibre, early maturing and high fibre strength which are lacking in tetraploid cotton. (Kumar *et al.,* 2008). In Punjab wheat and rice are being extensively cultivated and this crop cycle has taken a tall on soil and water resources. For the diversification of agriculture cotton can prove to better alternative. Consistency in yield has always been a problem in cotton due to the strong influence of environment. The differential response of a genotype for a given trait across environments is result of genotype environment interaction (G × E). Its presence reduces the correlation between phenotype and genotype, and makes it difficult to judge the genetic potential of a genotype which ultimately reduces the progress of selection (Killi and Harem, 2006). The possible way to reduce genotype-environment interaction would be either selecting stable genotypes that interact least with the environments or to use stable environments for cultivating genotypes. As environment is a dynamic factor its stability is not possible. Hence genotype x environment interactions are always a matter of concern for the plant breeders in the development of improved cultivars. A commercially successful cultivar must perform consistently across diverse environments.

Stability studies in cotton are a vital part of breeding program prior to the release of new variety (Campbell *et al*., 2012). In the presence of significant genotype x environment, stability parameters are estimated to determine the potentiality of a genotype. Mean yield can't be the sole satisfactory basis because of G X E interaction hence emphasis should therefore be given on the evaluation of genotype over multi environment conditions to work out its effect. Genotype x environment interaction can be partitioned into components using regression analysis. Finlay and Wilkinson (1963) suggested that the mean yield and regression coefficient (b) of genotypes over environments provides information for selecting cultivars with broad adaptability that was further developed by Eberhart and Russell (1966) who added mean squared of deviation from regression (S^2d) in prediction of genotypes on the basis of their performance across environments. Using this model of various workers studied stability, adaptability, and interaction with environment (Naveed *et al.*, 2006; Meredith *et al.*, 2012; Kamrul *et al.*, 2013; Dewdar, 2013). Keeping this in view the present investigation was designed to analyze the genotype environmental interaction and stability of the genotypes from diverse locations across the country, under different geographical areas and years in Punjab.

The experimental material comprised of 17 genotypes consisting of seven genotypes from punjab LD327, LD866, LD902, LD210, LD575, LD733 and LD694; HD457 from Haryana; RG395 and RG8 from Rajasthan; KWA147 from Madhya Pradesh; MDL2643 from Andhra Pradesh and PA255, PA606, AH11, AH38 and DLSa1001from Maharashtra which were evaluated during years 2010-2011 in three environments (Fig.1). The performance trials of 17 cultivars selected from diverse origin were conducted at two testing sites one at Cotton Research Area, Punjab Agricultural University for two years 2010-2011 and other at Regional Station, Faridkot for one year 2010. The material was sown in randomized complete block design with three replications. Each entry was grown in a two-row plot 6.7m long with 96.5 cm spacing between rows. Recommended package practices were followed in raising the crop. Data for nine yield related traits *viz*., seed cotton yield per plant (g), number of bolls, boll weight (g), seed index (g), number of sympods and fibre quality traits *i.e*. halo length (mm), ginning out turn (%) was recorded on 10 competitive plants at each location. Single plant data for seed cotton yield was recorded after all pickings. Boll weight was determined on average weight of 20 well opened bolls. Ginning out turn percentage was determined by dividing the weight of the lint sample after ginning by the weight of the lint sample before ginning. Halo length was recorded with halo disc scale. Seed index was 100 seed weight.

Data from three environments (locations and years) was analyzed. Test of homogeneity Bartlett's test was made according to Gomez and Gomez (1984). The data was statistically analyzed following the method described by Eberhart and Russell model (1966) to determine the stability parameters regression coefficient (b) and mean squares of deviation from regression (S^2d).

The analysis of variance revealed significant differences among 17 Asiatic cotton (*G. arboreum*) genotypes for yield and related traits over three environments (Table.1). The genetic makeup and diverse nature of origin of genotypes could be possible reasons of that variation (Tuteja, 2006). The genotype x environment interaction was observed to be significant for all traits. The significant interaction was either due to non cross over interaction in which ranking of genotypes remains constant across environments and significant interaction is due to change in magnitude of response or cross over interaction in which significant change in rank from one environment to another (Baker, 1988; Blum, 1983; Matus, *et al.*, 1997). In present investigation LD694 had shown non crossover G x E interaction for most of the traits under consideration while other genotypes had crossover type of GxE interaction. Similar results were observed by Ali *et al.,* 2005 and Naveed *et al.,* 2006.

To determine the degree of stability of genotypes, (Eberhart and Rusell, 1966) environment x genotype x environment was partitioned into linear components i) environment (linear) and ii) genotype x environment (linear) which were found to be significant for all the traits under observation (Table.1). The first effect indicated that differences in environments (locations and years) generated disparities in genotypic response while latter effect revealed response of genetic divergence were taken into account along with environmental variations (Naveed *et al.*, 2006).

The pooled deviation have been considered as non linear component, its significance was observed for seed cotton yield and boll number which indicated that the major component for difference in stability was due to deviation from linear function. The unpredictable components (weather fluctuations, insect infestations and disease infections *etc*) of interaction have major role than the predictable components (soil type, fertilizer application etc) in the stability of aforesaid traits (Mehetre *et al.,* 2002; Dewdar, 2013).

High yielding genotypes are always a prime consideration along with their stability. In present investigation mean seed cotton yield per plant over all environments was observed to be 49.05g. Highest seed cotton yield per plant was revealed in LD575 (63.86g) followed by LD902 (62.52g) and LD694 (60.23g) (Table.2). The conclusions on stability solely based on mean performance are not reliable because due to presence of genotype x environment interaction genotypes responded differently to the changes in the environment (Tuteja, 2006). Hence for stability, high yield must be complemented with unity regression coefficient (b). The regression coefficient (b) approached to unity, along with high mean was observed in LD902 (0.94), LD694 (1.08) and LD575 (1.12). Another parameter, mean squares of deviation from regression (S^2d) helps in prediction of performance over the environments should approach to zero (Dewdar, 2013). In present study most genotypes deviated significantly for S^2d which lead to conclusion that prediction for SCY is not possible except LD694 (-1.36) and LD902 (-3.02).

The major reason of deviation from regression for yield was due to quantitative nature and environmental influence on it (Kamrul *et al.*, 2013). Low deviation from regression or more stability has been observed for the genotypes developed at Punjab centre. Singh & Bejiga (1990) concluded that origin of genotype has significant role in stability hence cultivars must be bred separately according to the environments.

Number of bolls is a contributing trait of yield. Highest boll number was found in LD694 (24.78), LD575 (23.82), AH38 (23.78) and PA255 (23.06) with an average of 21.14 (Table.2). The regression coefficient revealed non-significant deviation from unity in all genotypes except PA255 (2.03). High regression value depicts higher sensitivity to environmental change (below average stability) hence PA255 has greater specificity of adaptability to high yielding environments (Naveed *et al.*, 2006). The high mean genotypes coupled with unit regression coefficient and least deviation from zero for S^2d were LD694 (0.96 & -0.46), LD210 (1.11 & -0.96) and LD575 (1.18 & 0.89), respectively. These three genotypes fulfilled the criteria of a stable genotype over environments for boll number.

In present investigation, among all genotypes S^2d values for the boll weight and seed index were found to be zero which lead to conclusion that these traits were stable over environments and their performance could be predicted. Boll weight always complement to the yield. LD694 (2.57g) followed by AH11 (2.41g), LD327 (2.35g) and RG395 (2.35g) were observed to be higher for boll weight (Table.2). The regression coefficient revealed that LD694 (0.98) is more adaptable whereas RG395 (2.35) and AH11 (1.63) can be recommended for high yielding environments only. Seed index is another indicator of yield which contributes to cotton oil and animal feed. Highest seed index was observed in LD902 (5.92g), LD694 (5.76g), LD733 (5.73g) LD575 (5.70g) and AH11 (5.64g) (Table.2). The stability parameters *i.e*. regression coefficient was close to unity for most of high boll weight genotypes emphasizing the significance of LD733 (-0.14) for poor yielding and AH11 (3.39) for high yielding environments.

Sympods are the fruit bearing branches which directly affects the yield of the plant. High number of sympods were observed in LD694 (34.59) followed by LD902 (31.63), LD866 (28.56) and LD210 (25.85) with an average of 23.22 (Table.3). Both parameters of stability, regression coefficient (b) and deviation from regression (S^2d) were not significantly deviating from unity and zero, respectively for most of the genotypes. The genotypes with high sympod number across environments were also observed to be stable.

Halo length and ginning out turn percentage are the yield traits which give an overview of cotton fibre. In present study, DLSa1001 (24.60mm), PA606 (24.11mm) and LD733 (23.12mm) were the genotypes which had long fibre (Table.3). Regression coefficient value more than one was observed for most of the high halo length genotypes except DLSa1001 (1.01). It leads to conclusion that DLSa1001 is stable for halo length over the environments. Ginning out turn percentage was observed to be highest in LD694 (41.54%), LD327 (37.45%), LD866 (37.30%) and HD457 (37.04%). The regression coefficient values for these genotypes revealed that only LD694 (1.05) was close to unity, whereas HD457 (2.32), LD866 (1.33) and LD327 (1.24) have higher than one regression coefficient. The prediction can be possible because deviation from regression among high ginning out turn genotypes was close to zero. These results were in harmony with the observations by Nanjudan *et al.*, 2004 and Dewdar, 2013.

Conclusively, genotypes developed at Punjab have overall better adaptability over the locations and years for most of the yield and related traits. This leads conclusion that varieties must be developed according to the location specific for better adaptability in that particular geographical region. Among all the tested genotypes, DLSa1001 was found to be superior as well as stable for halo length, LD902 was observed to be stable for seed cotton yield, seed index and number of sympods, LD575 and LD210 for boll number, whereas LD694 genotype was found to be stable for most of the traits under observation. DLsa1001, AH11, PA255, HD457 and AH38 can be utilized as a germplasm in pre-breeding programmes.

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Table 1. Analysis of variance for seed cotton yield and its related traits

S. No.	ANOVA	Df	SCY	BN	BW	SI	SY	GOT	HL
1	Genotype	16	292.09**	14.32**	0.045**	0.27**	85.48**	8.95**	12.35**
2	Environment	2	5400.38**	720.82**	0.82**	1.05**	86.58**	8.46**	3.88**
3	Genotype x Environment	32	102.62*	17.07*	0.03*	0.06*	0.96*	3.48*	1.37*
4	Env. + Genotype x Env.	34	414.25**	58.47**	0.07**	0.12**	5.6**	3.89*	1.57*
5	Env. (linear)	1	10800.75**	1441.64**	1.63**	2.09**	173.16**	16.92**	7.77**
6	Genotype x Env. (linear)	16	50.45**	14.97**	0.036**	0.11**	1.58*	3.74*	1.49*
7	Pooled Deviation	17	145.68**	18.05**	0.01	0.005	0.32	1.14	0.23
8	Pooled Error	96	5.54	1.86	0.012	0.23	0.49	1.11	0.41

*P ≥ 0.05;**P≥0.01; SCY-seed cotton yield; BN- number of bolls; BW-boll weight; SI-seed index; SY-Number of sympods; GOT-ginning out turn; HL-halo length

Table 2. Mean performance and stability parameters for seed cotton yield and its related traits

Genotypes	Seed Cotton Yield (g)			Number of Bolls			Boll weight (g)			Seed index (g)		
	Mean	b	S^2d	Mean	B	S^2d	Mean	B	S^2d	Mean	b	S^2d
LD327	45.59	1.00	32.45	21.99	0.96	74.89**	2.35	1.66*	0.00	5.34	1.04	0.02
LD694	60.63**	1.08	-1.36	24.78**	1.08	-0.46	2.57**	0.98	0.01	5.76**	0.99	0.04
LD866	51.85	1.03	14.63	22.13	0.93	-0.81	2.32	1.18	-0.04	5.05	1.17	0.01
LD902	62.56**	0.94	-3.02	21.52	0.95	15.45**	2.34	0.54*	-0.01	5.92**	0.81	0.02
LD210	56.96**	1.10	-4.33	23.01**	1.11	0.89	2.31	0.57	-0.01	5.38	1.12	0.05
LD575	63.86**	1.12	10.23	23.82**	1.18	-0.96	2.30	1.21	-0.06	5.70**	1.20	0.03
LD733	55.06	1.20	63.98*	18.48	0.92	4.33**	2.32	0.85	-0.01	5.73**	-0.14	0.01
HD457	58.83**	1.08	246.58**	20.07	0.48	-0.81	2.18	0.75	-0.01	5.58**	0.58	-0.02
RG395	53.03	1.54	442.16**	21.74	0.48	47.26**	2.35	2.35*	-0.05	4.98	1.68	-0.02
RG8	45.04	0.58	72.20**	20.08	0.66	74.69**	2.03	0.44	0.01	5.32	1.39	-0.02
KWA147	49.19	1.26	470.64**	19.77	0.90	-1.62	2.09	0.13*	-0.02	5.03	0.42	0.07
MDL2643	38.35	0.86	28.39**	19.10	1.36	4.71**	2.19	1.59*	0.04	5.20	2.12*	-0.02
PA255	38.22	0.82	449.59**	23.06**	2.03*	-1.71	2.29	0.39	-0.01	5.48	-0.09	-0.09
PA606	38.64	0.62	23.46**	20.50	0.53	-1.50	2.31	0.61	-0.07	5.51	-0.36	-0.02
AH11	35.51	0.78	79.66**	18.57	1.30	63.37**	2.41**	1.63*	-0.01	5.64**	3.39*	-0.08
AH38	47.18	1.45	99.51**	23.74**	1.60	-1.13	2.29	0.57	0.04	5.27	1.84	-0.01
DLSa1001	33.27	0.54	137.60**	16.97	0.54	-1.39	2.28	1.69*	0.01	4.94	-0.16	0.09
Mean	**49.05**			**21.14**			**2.29**			**5.40**		
SE±	**2.39**			**0.53**			**0.03**			**0.07**		

*P ≥ 0.05;**P≥0.01

Table 3. Mean performance and stability parameters for seed cotton yield and its related traits

Genotypes	Number of Sympods			Ginning outturn (%)			Halo length (mm)		
	Mean	b	S^2d	Mean	b	S^2d	Mean	B	S^2d
LD327	25.11	1.18	-0.47	37.45**	1.24	0.36	17.85	-0.21	-0.40
LD694	34.59**	0.96	0.10	41.54**	1.05	-0.11	18.85	0.95	-0.26
LD866	28.56**	0.97	-0.18	37.30**	1.33	0.22	19.96	0.83	-0.34
LD902	31.63**	1.12	0.17	35.95	-1.02	-0.60	19.46	-0.08	-0.24
LD210	26.85**	1.03	0.56	36.76	-0.91	-0.85	18.58	-0.26	-0.28
LD575	24.59	1.10	-0.27	36.03	1.30	-0.39	21.68	-0.80	-0.32
LD733	23.70	0.73	-0.08	36.09	1.22	0.00	23.12**	1.20	-0.24
HD457	22.70	1.41	0.14	37.04*	2.32	-0.74	22.01	-0.16	-0.35
RG395	24.33	0.82	-0.37	36.36	1.56	-0.79	18.37	2.65*	-0.39
RG8	21.85	0.74	-0.48	36.03	-0.99	1.86	19.97	0.46	-0.40
KWA147	25.04	0.76	-0.42	35.87	1.80	5.70	21.17	1.82	0.16
MDL2643	20.37	0.70	0.67	34.61	-1.65	-0.80	21.64	2.11*	-0.39
PA255	17.96	0.91	-0.49	35.30	2.20	-1.05	24.11**	1.53	-0.31
PA606	15.26	0.81	-0.49	35.41	2.56	-1.11	21.99	2.05	0.03
AH11	16.44	0.84	-0.28	34.37	1.69	1.09	21.78	2.14*	0.40
AH38	18.96	1.55	-0.48	34.41	1.95	-1.11	22.87**	1.76	0.61
DLSa1001	16.85	1.37	-0.47	34.03	1.35	-1.10	24.60**	1.01	-0.30
Mean	**23.22**			**36.15**			**21.06**		
SE±	**1.30**			**0.42**			**0.49**		

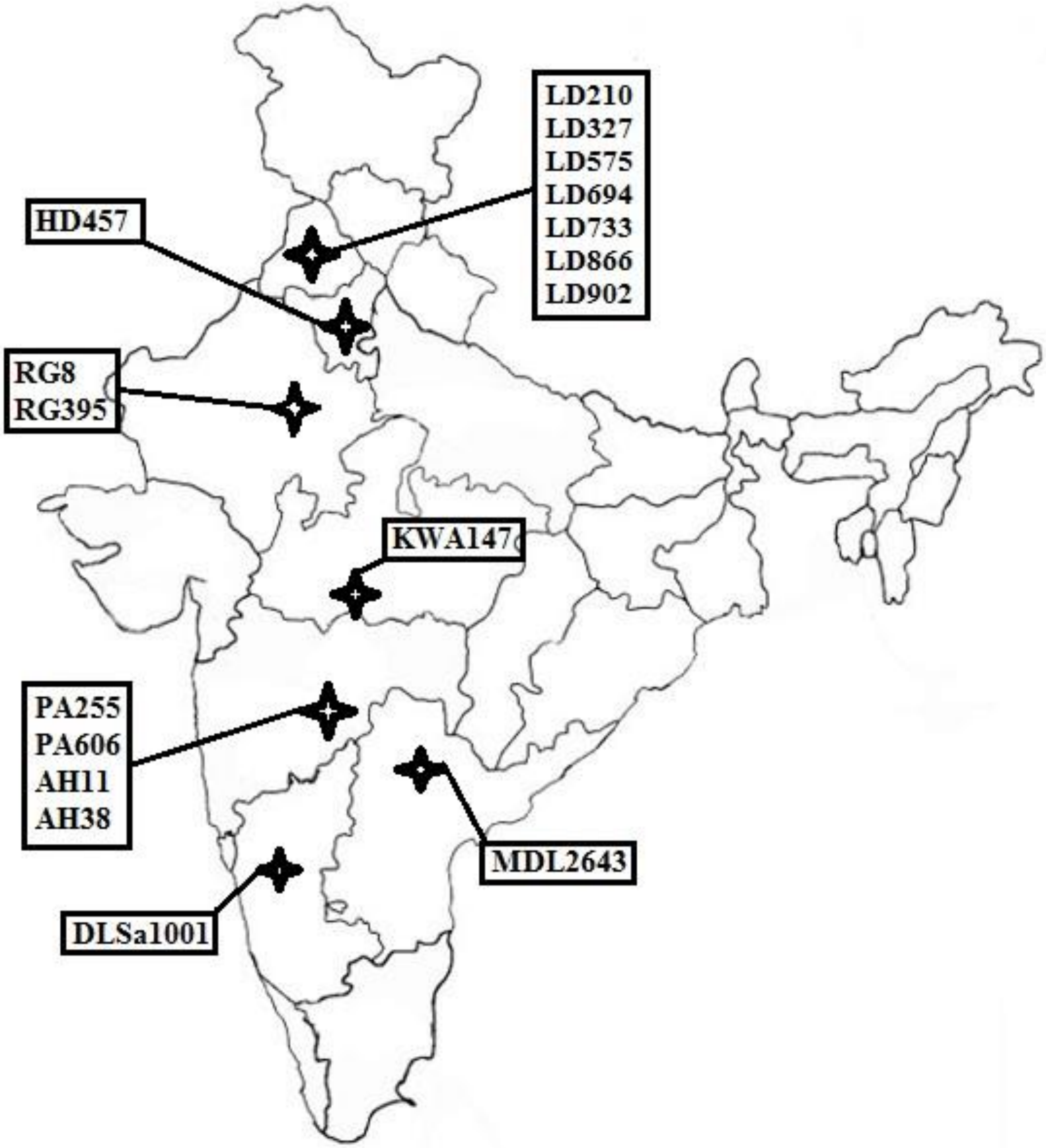

Fig.1 Geographic origin of 17 *Gossypium arboreum* genotypes collected from seven different states of India