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Assessment of genetic variability and traits association in upland cotton (*gossypium hirsutum l.*)

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Abstract
The present study was performed to explore genetic mechanism of yield related traits in upland cotton using thirty diverse regional cotton varieties at Cotton Research Sub-Station Raiwind, during kharif season 2015 using complete randomize block design in three replications. Analysis of variance depicted highly significant differences for all the selected traits *viz*, plant height, Days to first flower, Number of Monopodial branches, Number of Sympodial branches, Number of bolls/plant, Nodes/plant and seed cotton yield. All the traits revealed the phenotypic variance was slightly higher than genotypic variance; similarly, phenotypic coefficient of variance was greater than genotypic coefficient of variance which also predicts presence of additive genes for these traits. The Broad sense heritability (h_{BS}) estimates were observed high for all the traits under study, but in only four characters i.e. No. of Monopodial branches, Number of Sympodial branches, seed cotton yield and number of bolls/plants it coupled with high genetic gain also, which promised the further effective selection on phenotypic basis, while for other attributes indirect selection will be suitable. Seed cotton yield exhibited highly significant and positive relation with sympodial branches/plant and bolls/plant whereas it displayed negative association with other studied attributes.

Keywords: upland cotton, genetic analysis, yield traits, variance, heritability, genetic advance

1. Introduction
Upland cotton (*Gossypium hirsutum*) is an important cash crop due to the essential source of fiber production for the survival of textile industry. It is the most popular lint producing crop which domesticated by human in early years of permanent settlement, at the dawn of civilization. Archeological studies revealed that cotton was grown in our part of the world (Indus civilization) as early as 3500 BC, and have sustained its importance (Stein & Burton 1998, Moulheart *et al*. 2002). In our country, it covers an area of more than 2.9 million hectares with production of 10.07 million bales and accounts for 1.0 % to GDP and 5.1 percent to value addition (Anonymous, 2015-16) [3]. Thus, sustenance of millions of producers and of those associated along with the entire cotton value chain is dependent on this crop, but this very dependence on cotton can cause major financial setback, if production declined significantly. So, keeping in view the economic architecture of the country, it is necessary to develop new promising varieties which can fulfill the demand of high yield for producer and good quality for processer at the same time. Plant scientists have worked extensively to study the morphological, physiological and genetic causes of the yield, and related attributes to identify the different features which can effectively contribute to the ultimate goal i.e. yield.

Seed cotton yield is dependent upon the various morphological features and can interact affirmatively or contradictory in their trait association (Iqbal *et al.*, 2011; Magadum *et al.*, 2012; Rao *et al* 2013 and Baloch *et al* 2014) [7, 13, 15, 4], hence the Phenotypic outlook of plant is the consequence of environmental interaction with genotype. So, it becomes necessary to decipher the environmental and genetic causes of variation and thus investigation of allelic behavior, its potential and extent of transmit-ability and usefulness is preliminary to any breeding model (Ready *et al* 2016; Raza *et al* 2016 and Khan *et al* 2017) [16, 7]. Several researchers reported significant variability along with high heritability estimates and genetic gain in cotton genotypes for yield and yield contributing traits exists (Sundus *et al.*, (2010), Ahsan *et al.*, (2015) [2] & Abbas *et al*., (2015) [1] The assessment of heritability and genetic gain along with phenotypic and genotypic variance will provide us an insight about the usefulness of the trait (Khan *et al.*, 2010) [17]. The purpose of present study was to explore the variation for yield related morphological attributes and their interaction with one another among the available genotypes and ultimately identification of desirable genotypes for further breeding program.

2. Materials and methods
The experiment was conducted at Cotton Research Sub Station, Raiwind during the Kharif season 2015. Thirty genotypes (Table 1) of upland cotton were planted using Randomized Complete Block Design (RCBD) in three replications. The spacing between PXP and RxR was maintained as 30 cm and 75 cm respectively. All

recommended agronomic practices and inputs were applied uniformly.

In each replication 10 representative plants were selected and data was recorded for the following yield related attributes viz., days to first flower, Number of sympodial branches/plants, Number of monopodial branches/plants, Number of bolls/plants, Nodes/plant, Pant Height (cm), and Seed Cotton yield (Kg/ha).

All the data were subjected to analysis of variance technique according to Steel *et al*. (1997) [20] to calculate the significance level among genotypes through Statistix 8.1. Heritability (broad sense) was calculated according to method suggested by Singh & Chaudhary (1985) [19]. The simple correlation coefficient (r) of seed cotton yield with other yield components were also worked out according to Kwon & Terrie (1964).

3. Results & Discussion

Results of analysis of variance describes that all traits are highly significant ($p \leq 0.01$) which indicates the presence of variability among genotypes (Table 2), which can further be exploited in breeding program and promised the improvement in desired attributes. Sundas *et al*., (2010) studied variation in yield and yield related attributes and observed significant differences among genotypes.

3.1 Days to first flower: is an important character to determine earliness in cotton hence an important aspect for cotton breeders to incorporate this trait to develop early fruit setters. In present study its range varied from 61 days to 70 days (Table 3), however the lowest and statistically at par value was expressed by the cultivar FH-142 followed by MNH-886. The broad sense heritability and genetic advance was (98.1%) and (16.30) respectively. It also showed positive highly significant correlation with monopodia per plant; Nodes per plant and Plant height, but expressed negative inter relation for Sympodia^{-1} plant. Iqbal *et al* (2006) [7] also studied the morphological traits of cotton plant and reported the days to first flower as an important attribute to determine the earliness in cotton cultivars (Table 4)

3.2 Monopodial branches per plant: Numerical value varied from 1.0 to 3.7 for monopodia per plant among the genotypes and the cultivar FH-142 revealed minimum number of Monopodial branches while KZ-389 unveiled maximum number for this attribute. Heritability (85.6 %) with high genetic gain (56.52) was estimated (Table 3). Nodes per plant and plant height expressed highly positive association with this trait but sympodia and seed cotton yield have negative relationship for Monopodial branches per plant. Abbas *et al.*, (2015) [1] also describes the positive association of monopodial branches with plant height but reported negative association with first bud day.

3.3 Sympodial branches per plant: Number of bolls per plant and seed cotton yield demonstrated the affirmative significant connection with sympodia per plant r=0.8807 and r=0.6897 respectively (Table 4). The scale of variation for this feature among genotypes varied from 8.0 to 20.1 and cultivar FH-142 showed the peak value followed by IUB-222 and MNH-886, whereas the cultivar RH-627 displayed minimum value for this trait. Heritability and genetic gain were computed 86.7 and 34.5 respectively for this attribute. Desalegn *et al* (2009) [6] described the positive association of seed cotton yield with no of sympodial branches along with other traits.

3.4 Bolls per Plant: Among other yield related attributes Bolls per plant is very important feature associated with high yielding cultivars and discussed by many workers. Kumar *et al*. (2017) [5] studied the positive interaction of bolls number with monopodial branches, sympodial branches and plant height. Seed cotton yield expressed significant positive relation with no of bolls per plant and also displayed highly positive interaction with sympodial per plant (Table 4). Heritability value 63.7% coupled with genetic advance of 26.85 was gained through statistical analysis. On the basis of variation among genotypes the range varied from 13 bolls to 31 bolls per plant, where cultivar FH-142 followed by IUB-222 and AA-904 displayed maximum value while KZ-389 and SLH-4 revealed lowest number for this trait (Table 3). Khan *et al*., (2010) [8] also found significant variability for bolls per plant and other yield related traits.

3.5 Plant height (cm): The variation among genotypes regarding the plant height ranged 98 to 150 cm, while cotton cultivar NS-161 along with BH-180 presented the maximum value (150cm) for this feature, whereas cultivar MM-58 displayed lowest height (98 cm) (Table 3). Correlation study describes the very significant association of this trait with days to first flower, number of nodes and monopodial branches while revealed negative interaction with sympodia and seed cotton yield (Table 4). The Value of heritability recorded 98.7% with moderate genetic gain of 24.41. In present study plant height did not contributed positively to the seed cotton yield, however some researchers have claimed positive association of plant height with yield, (shahid *et al*., 2015).

3.6 Nodes per plant: On average nodes per plant varied from 18 to 42 among genotypes (Table 3). The cultivar Sitara-10 showed the maximum number for this trait while VH-178 displayed minimum nodes on per plant bases. Correlation statistics revealed that, plant height, monopodial branches and days to first flower have significant positive interaction with nodes per plant, whereas it contributed negatively to seed cotton yield and Sympodial branches per plant (Table 4). Approximation of heritability (*H*) and genetic advance valued as 79% and 30.76 respectively for this trait.

3.7 Seed Cotton Yield: As yield of cotton crop is illustration of many allied components, present statistics exhibited the highly significant and positive relation of yield with sympodial branches/plant, bolls/plant and displayed negative association with other studied attributes (Table 4). Baloch (2004) and Desalegen *et al* (2009) delineated the positive relationship of sympodial branches along with bolls number with that of seed cotton yield. Statistically attained value of heritability counted reasonably high 92.6% with genetic gain of 32.31 which indicates the possibility of improvement through direct selection for this attribute. Studied genotypes unfold a range of variation for yield in kg/ha, and minimum to maximum count was 1022 to 2750 kg respectively (Table 3), which indicates that this attribute have reasonable diversity among the studied sample, where

the cultivar FH-142 expressed the highest yield followed by iub-222 and MNH-886 while the cotton cultivar KZ-389 revealed the minimum yield.

3.8 Genotypic and Phenotypic Variances: For all the traits studied in this work, phenotypic variance(δ^2p***)*** was slightly greater than genotypic variance (δ^2g) similarly phenotypic coefficient of variance (PCV%) was greater than genotypic coefficient of variance (GCV%), hence describes the environmental effect on the expression of traits. Values of broad sense heritability was high for most of the traits, but only in four traits i.e Sympodial branches per plant, Monopodial branches per plant, nodes per plant and plant height, it coupled with higher genetic advance.

4. Tables and Figures

Table 1: List of Cotton Genotypes under study

1- FH-142	11- IR. NIBGEE-5	21- A-011
2- IUB-222	12- MM-58	22- BH-178
3- MNH-886	13- VH-282	23- SITARA-12M
4- FH-172	14- CIM-599	24- NH-161
5- AA-904	15- NIAB BT1	25- BH-180
6- VH-303	16- SILKEE	26- SB-149
7- AA-905	17- MNH-456	27- SITARA-11M
8- CIM-602	18- BGC-09	28- SITARA-10M
9- FH-118	19- A555	29- RH-627
10- IR-NIBGEE-4	20- SUN-1	30- KZ-389

Table 2: Mean square for Analysis of variance for yield and yield related traits in different upland cotton cultivars

Source Of variation	DF	Days taken to first flower	Monopodia^{-1}	Sympodia^{-1}	Bolls per plant	Plant height (cm)	Nodes per plant	Seed cotton yield
Replication	2	0.0111	0.1470	2.2968	9.0778	2.211	30.100	4441
Genotypes	29	73.8042**	1.3170**	23.704**	45.1605**	644.06**	76.546**	3090907**
ERROR	58	0.4709	0.0660	1.1549	7.1927	2.717	6.214	7956

Table 3: Data range, Genotypic and Phenotypic variance, coefficient of variation, Broad Sense heritability & genetic advance for various traits in *Gossypium hirsutum* L.

Characters	MAX. value	MIN. value	GV (δ^2g)	PV (δ^2p)	GCV%	PCV%	Heritability h^2 (B.S) %	Genetic advance
Days taken to first flower	70.0	52.0	24.44	24.91	7.98	8.06	98.1	16.30
Monopodial branches/Plant	3.7	1.0	0.41	0.48	29.65	32.04	85.6	56.52
Sympodial branches/plant	20.4	8.0	7.51	8.66	17.90	19.23	86.7	34.35
Bolls per Plant	31.0	13.0	12.65	19.84	16.32	20.44	63.7	26.85
Plant Height (cm)	150.0	98.0	213.78	216.5	11.79	11.87	98.7	24.14
Nodes Per plant	42.0	18.0	23.40	29.65	16.79	18.88	79.0	30.76
Seed cotton yield (kg/ha)	2750	1022	100380	108336	16.29	16.93	92.6	32.31

Table 4: Correlation (Pearson) among Morphological Attributes of Cotton

	BPP	DFF	MBP	NP	PH	SBP
DFF	-0.6706**					
MBP	-0.7409**	0.8279**				
NP	-0.3714**	0.4264**	0.5416**			
PH	-0.5382**	0.6348**	0.6765**	0.6318**		
SBP	0.6897**	-0.8214**	-0.8126**	-0.4390**	-0.5779**	
SCY	0.7536**	-0.8521**	-0.8294**	-0.3263**	-0.5050**	0.8807**

*Significant at 5% level, ** Significant at 1% level

BPP= bolls per plant, DFF= Days taken to first flower, MBP= Monopodia$^{-1,}$ NP=Nodes per plant, SBP=Sympodia$^{-1,}$ PH= Plant height, SCY= Seed cotton Yield

5. Conclusion

It can be inferred from experimental results and analysis that traits which displayed the maximum value of heritability and genetic advance coupled with maximum values of phenotypic and genotypic variation can be used for further selection. It is also evident that bolls per plant and Sympodial branches per plant have exhibited the most significant association with cotton yield and hence selection on the basis of these attributes will promise better yielding varieties.

6. References

1. Abbas HG, Mahmood A, Ali Q. Genetic variability and correlation analysis of cotton yield traits. Journal of Agricultural Research, 2015; 53(4).
2. Ahsan MZ, Majidino MS, Bhutto H, Soomroo AW, Panhwar PH, Channa AR, *et al*. Genetic variability, coefficient of variance, heritability and Genetic advance of some *Gossypium hirsutum* L. Accessions. Journal of Agricultural Research, 2015; 7(2).
3. Anonymous. Economic Survey of Pakistan, Ministry of Finance, Govt. of Pakistan, 2015.
4. Baloch MJ. Genetic variability and heritability estimates of some polygenic traits in upland cotton. Pakistan Journal of Scientific and Industrial Research. 2004; 42:451-454.
5. Baloch MJ, Kumar C, Jatoi WA, Rind IH. Phenotypic correlation and regression analysis of yield and fibre traits in upland cotton (*Gossypium hirsutum* L.). Pakistan Journal of Agriculture, Agricultural Engineering and Veterinary Sciences. 2014; 30(2):135-146.
6. Desalegn Z, Ratanadilok N, Kaveeta R. Correlation and heritability for yield and fiber quality parameters of Ethiopian cotton. Kasetsart Journal-Natural Science. 2009; 43(1):1-11.
7. Iqbal M, Hayat K, Khan RSA, Sadiq A, Noor-ul-Islam. Correlation and path coefficient analysis for earliness and yield traits in cotton (*G. hirsutum* L.). Asian Journal of Plant Sciences. 2006; 5:341-344.
8. Iqbal M, Ali CM, Zafar IM, Mahmood H, Abdul N, Noor I, *et al*. Correlation and path coefficient analysis of earliness and agronomic characters of upland cotton in Multan. Journal of Agronomy, 2003; 2:160-168.
9. Iqbal M, Chang MA, Jabbar A, Iqbal MZ, Hassan M, Islam N, *et al* Inheritance of earliness and other

characters in upland cotton. Journal of Biological Sciences. 2011; 3(6):585-590.
10. Khan NU, Marawat KB, Hassan G, Farhatullah, Batool S, Makhdoom K, Ahmad W, Khan HU. Genetic variation and heritability for cotton seed, fiber and oil traits in *Gossypium hirsutum L*. Pakistan Journal of Botany. 2010; 42(1):615-625.
11. Khan A, Fiaz S, Bashir I. Estimation of Genetic Effects Controlling Different Plant Traits in Cotton (Gossypium Hirsutum L.) Under Clcuv Epidemic Condition. Cercetari Agronomice in Moldova. 2017; 50(1):47-56.
12. Kumar KS, Nidagundi JM, Hosamani AC. Correlation Analysis for Agro-morphological Features in Upland Cotton under Rainfed Conditions. International Journal of Current Microbiology and Applied Sciences. 2017; 6(5):2593-2596.
13. Magadum S, Banerjee U, Ravikesavan R, Gangapur D, Boopathi NM. Variability and heritability analysis of yield and quality traits in interspecific population of cotton (*Gossypium* Spp.). Bioinfolet. 2012; 9(4A):484-487.
14. Moulherat C, Tengberg M, Haquet JRMF, Mille BT. "First Evidence of Cotton at Neolithic Mehrgarh, Pakistan: Analysis of Mineralized Fibres from a Copper Bead". Journal of Archaeological Science. 2002; 29(12):1393-1401.
15. Rao PJM, Gopinath M. Association analysis of yield and fibre quality characters in upland cotton (*Gossypium hirsutum* L.). Australian Journal of Basic and Applied Sciences. 2013; 7(8):787-790.
16. Raza H, Khan NU, Khan SA, Gul S, Latif A, Hussain I, *et al*. Genetic variability and correlation studies in F4 populations of upland cotton. Journal of Animal and Plant Science, 2016; 26(4).
17. Reddy BK, Reddy V. Genetic variability and heritability in upland cotton (*Gossypium hirsutum* L.). International Journal of Agricultural Sciences and Veterinary Medicine. 2016; 4(3):17-21.
18. Shahzad MT, Ijaz F, Khan O, Saleem B, Hassan U. Correlation, Path Analysis & Heritability Among Some Yield and Fibre Related Traits of *Gossypium hirsutum* L., Cotton Genomics and Genetics. 2015; 6(4):1-7.
19. Singh RK, Chaudhary BD. Biometrical Methods in Quantitative Genetic Analysis. Kalyani Publishers Ludhiana, New Delhi, 1985, pp. 102-164.
20. Steel RGD, Torrie JH, Dickey DA. Principles and Procedures of Statistics: A Biometrical Approach, 3rd edition. McGraw Hill Book Co. Inc. New York, 1997.