

Cluster analysis, genotypic and phenotypic correlation among yield and fibre contributing traits in cotton (*Gossypium hirsutum* L.) germplasm under normal and drought conditions

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Abstract

Cotton is known as the most important agricultural as well as industrial crop all around the world. Fifty different cotton genotypes were used in this study using RCB Design repeated thrice. Results showed the existence of highly significant positive correlation between seed cotton yield with various parameters viz., Plant height (PH), number of bolls (NB), boll weight (BW) at phenotypic level and positive significant with these traits at genotypic level under normal condition. Non significant association of SCY with SL and SS. Under drought condition, SCY has highly significant positive correlation with the NB, and BW at phenotypic level and positive significant with these traits at genotypic level under drought condition. The 50 genotypes were placed into five distinct clusters Reference to comparison, Cluster-I is important for all the traits under study under both the conditions because these characters showed the highest value in this cluster. Cluster-V has the lowest values of these parameters. Such type of finding can be helpful in breeding programs for cotton improvement.

Keywords: Cluster analysis, correlation, germplasm, *Gossypium hirsutum*, yield traits

Introduction

Cotton is known as incredible fiber that has a wide range of uses, from fashion to home stuff to medical products. There are four kinds of cultivated cotton species including two tetraploid (New world) and two diploid (Old world) species. Cultivation of Cotton crop is at least 7000 years old. Cotton is known as the most precious and plentiful produced agricultural as well as industrial crop all over the World. More than 100 countries cover about 2.5% arable land of the world. In 2017, the cotton crop occupies an area of 29.27 million hectare that produced 105.34 million bales all over the World while United States of America, China, India, Pakistan and Brazil were the major contributor (USDA, 2017) [27]. Cotton is grown in tropical and subtropical areas; the cotton crop requires (21 °C to 30 °C), (50-100 cm) temperature and rainfall respectively in Pakistan. (Bakhsh *et al.*, 2009; Sial *et al.*, 2014; Azam *et al.*, 2017) [7, 25, 6]. Scarcity of irrigation water is key reason for crop failure under arid environments. It is the subsequent vital issue in the yield decrease followed by diseases (Khatri *et al.*, 2004) [17]. Yield is a complex inherited traits, it fluctuates on wide scale due to its interaction with environment. Yield can be increased by developing the better performing varieties. Genotypic and phenotypic correlations play important role for determining the degree where yield contributing traits are associated (Abu-Ameer *et al.*, 2011; in mullah *et al* 2006) [1, 11]. A number of physiological processes are exaggerated in the beginning, whereas others undergo by the protrusion of water stress, thus, the ultimate result is the reduction of yield. This loss in yield by drought can be minimized by keeping soil moisture availability through defense techniques and sowing promising cultivars for drought (Alishah and Ahmadikhah, 2009) [4]. An efficient which induced by genetic modification through

breeding and suitable selection for adaptation to the strategy which is clearly practical and cost-effective to reduce drought problem is that cultivars drought conditions. Genetic approaches may help breeding of cultivars to survive healthier in unfavorable conditions. The performance of genotypes in adverse conditions is of primary importance for breeding for desirable traits. The mechanism in expression for drought tolerance differ among genotypes and phenotypic variations are key apparatus to recognize the elite genotypes for water stressed areas (Bray, 1997) [9]. Therefore, the planned study was conducted to screen out potential drought tolerance varieties through various yield and fibre attributes. This information may support cotton breeder's for upcoming breeding programme.

Material and Methods

Fifty different cotton genotypes were collected from gene pool of Central Cotton Research Institute, Multan (CCRIM) wherein the field study was carried out at two moisture levels during crop season, 2013. The first treatment was stress free and irrigation was applied at planting and five post planting irrigations (750 mm). While drought was imposed in second treatment, by applying irrigation at planting and three supplemental irrigations (300 mm). The treatments were arranged according to RCB Design in split plot arrangements repeated thrice. The irrigation was kept in main plots and genotypes in sub-plots. The crop was sown on 27th May 2013 by dibbling the seeds on moist beds with 30 cm space in 75 cm apart beds. The plant population was maintained by uprooting weak and disease seedlings at 28 days after planting. The intra-row spaces were covered with polythene sheet in peak rainy season (July-August) to protect soil from expected rains as proposed by Pettigrew (2004) [21]. Data of different parameters viz., PH (cm), NB,

BW (g), yield of seed cotton (g/plant), SI (g), SL (mm), FS (g/tex) and SF ($\mu\text{g}/\text{inch}$).

Statistical Analysis

The lint samples were submitted to fiber testing lab to determine the fiber traits by High Volume Instruments (HVI-900-A) following procedures prescribed by ASTM Committee (1997) [5]. The data recorded were subjected genotypic and phenotypic correlations among the parameters through ANOVA and ANCOVA. Cluster analysis was performed by using Wrad's method (1963) [29]. Correlation amongst various traits were calculated using Kwon and Torrie (1964) [18].

Results and Discussion

Correlation Analysis

Table-1 and 2 shows correlation among various traits. Plant height remained an important contributing factor towards yield. PH revealed significantly positive correlation with NB, SCY, SL and SS whereas significantly negative correlation with mic. It has been observed as non-significant correlation with BW and SI at genotypic level under normal condition. PH has highly positive significant correlation with SCY and highly negative significant correlation with mic SL and SS whereas, negative significant correlation with mic. Non-significant correlation with BW and SI at genotypic level under normal condition whereas positive non significant correlation with NB, BW SI and SL at phenotypic level under normal condition. While in case of drought condition, PH has psignificantly positive correlation with NB, BW, SCY and SL whereas negative significant correlation with mic. Non-significant correlation with SI and SL at genotypic level under drought condition. PH has highly significant positive correlation with BW and highly negative significant correlation with mic. It has positive significant with NB, SCY whereas negative non significant correlation with SL, however, positive non-significant correlation with SI and SS at phenotypic level under drought condition. Khan *et al.* (2009) [16], Murthy (1999) [20] and Camlho *et al.* (1994) [10] revealed PH remained positively correlated with SI and NB proved to have significantly positive association with BW, SCY and SI whereas negative significant with mic, positive non-significant with FS, negative with SL at genotypic level under normal condition. While at phenotypic level under normal condition, NB has highly significant positive association with BW, SCY whereas highly significant negative with mic, positive significant with SI, NB has positive significant association with BW, whereas positive non- significant negative with SI, SL, FS and mic at genotypic level under drought condition. While at phenotypic level under drought condition, NB has positive highly significant association with BW, SCY, positive non-significant with SI, SL, SS and mic. Similar results were reported by Karademir *et al.* (2009) [30, 15], Wanga *et al.* (2016) [28] and Bentol-Hoda *et al.* (2015) [8]. BW has significantly positive association with SCY whereas positive non-significant correlation with SI, negative non-significant with SL, FS and mic at genotypic level under normal condition. While at phenotypic level under normal condition, BW has highly significant positive association with SCY whereas negative highly non-significant with mic, bigger boll sizes are projected to turn out maximum yield production, but it is practiced that in cotton, medium with a greater number of bolls plant-1 give

highest production. It is generally well-known that drought conditions adversely affect the BW. In drought conditions, boll size minimized significantly which showed that cotton plant is highly susceptible to water stress, however varieties which recorded minimum decrease in BW are better preference to build up water stress breeding material. Plaut *et al.* (1992) [23] and Soomro *et al.* (2011) [26] revealed that inadequate supply of water at boll formation phase resulted in extensively lower production. SCY showed positive significant correlation with SI, negative non-significant with SL, FS and positive non-significant with mic at genotypic level under normal condition. While at phenotypic level under normal condition, SCY associated negatively highly significant with mic, positive non-significant with SI, negative non-significant with SL and SS. In case of drought condition SCY positively significant with FS, positively non-significant with SI, SL and mic at genotypic level. While at phenotypic level under drought condition, SCY has positive non-significant association with SI, SL, SS and mic. Iqbal *et al.* (2006) [12] showed the same findings. The observations of Karademir *et al.* (2011) [12] were opposite to this study Joshi *et al.* (2006) [13] showed positive interaction of seed cotton yield with plant height. SI correlated positively non-significant with fibre strength and mic, negatively non-significant with FL genotypic level under normal condition. While at phenotypic level under normal condition, SI associated negatively significant with staple length, positively non-significant with SS and mic. In case of drought condition SI negatively significant with FL, positively non-significant with mic and negatively non-significant with FS at genotypic level. While at phenotypic level under drought condition, SI has positive significant association with mic, negative significant with SL, negative non-significant with SL. Karademir *et al.* (2009) [30] showed no any effect of seed index on yield and fibre traits. SL correlated positively significant with FS, negatively non-significant with mic at genotypic level under normal condition. While at phenotypic level under normal condition, SL associated positively highly significant with SS, negatively non-significant with mic. In case of drought condition, SL correlated positively significant with FS, negatively non-significant with mic at genotypic level under normal condition. While at phenotypic level under normal condition, SL associated positively highly significant with SS, negatively non-significant with mic it is clear that for enhancing fibre traits than we must have to be very vigilant in breeding program. FS showed positive association with PH and SL, positive non-significant with NB and SI, negative non-significant with BW and SCY at genotypic and phenotypic level under normal conditions. Whereas, FS showed highly positive association with SL, positive non-significant with NB and SI. Under drought condition, FS showed positive significant association with PH and SCY, SL, positive non significant with NB and BW, negative non significant with seed index at genotypic under drought conditions. Whereas, fiber strength showed highly significant with SL, positive non-significant with other traits under study except SI that is negative non-significant under drought condition. Ahuja *et al.* (2006) [3] observed negative association between seed cotton yield and fibre strength in his study. FF is the promising trait which is much concerned by textile industry. FF showed negative significant association with PH, NB, SCY negative non-significant correlation with BW, SL, and SS at genotypic and

phenotypic level under normal conditions. Under drought condition, FF showed negative significant association with PH, non-significant with other traits at genotypic under drought conditions. Whereas, FF showed negative highly

significant with PH, positive significant with SI, on significant with other traits at phenotypic level under study under drought condition.

Table 1: Genotypic and phenotypic correlation for agronomic and fiber traits of fifty cotton genotypes under normal condition

Traits	PH	NB	BW	SCY	SI	SL	SS	MIC
Plant height	1.00	0.22*	0.10 NS	0.28*	0.04 NS	0.13*	0.17*	-0.33*
Number of bolls	0.22 NS	1.00	0.85*	0.94*	0.19	-0.04 NS	0.04 NS	-0.25*
Boll weight	0.09 NS	0.78**	1.00	0.81*	0.10 NS	-0.15 NS	-0.03 NS	-0.25 NS
Seed cotton yield	0.27**	0.92**	0.74**	1.00	0.15*	-0.04 NS	-0.01 NS	-0.28*
Seed index	0.04 NS	0.18*	0.09 NS	0.14 NS	1.00	-0.18 NS	0.02 NS	0.10 NS
Staple length	0.10 NS	-0.04 NS	-0.08 NS	-0.03 NS	-0.17*	1.00	0.33*	-0.16 NS
Staple strength	0.16*	0.03 NS	-0.03 NS	-0.01 NS	0.01 NS	0.29**	1.00	-0.13 NS
Micron ire	-0.31**	-0.21**	-0.22**	-0.23**	0.10 NS	-0.14 NS	-0.12 NS	1.00

Table 2: Genotypic and phenotypic correlation for agronomic and fiber traits of fifty cotton genotypes under drought condition

Traits	PH	NB	BW	SCY	SI	SL	SS	MIC
Plant height	1.00	0.20*	0.34*	0.22*	-0.05 NS	-0.12 NS	0.06*	-0.34*
Number of bolls	0.19*	1.00	0.94*	0.98*	0.06NS	0.06 NS	0.06 NS	0.01NS
Boll weight	0.31**	0.84**	1.00	0.92*	-0.05 NS	-0.09 NS	0.03 NS	-0.12NS
Seed Cotton Yield	0.21*	0.96**	0.83**	1.00	0.09NS	0.03 NS	0.11 *	0.07NS
Seed Index	0.06 NS	0.06NS	-0.05 NS	0.01NS	1.00	-0.22 *	-0.07 NS	0.20 NS
Staple Length	-0.12 NS	0.06 NS	-0.08 NS	0.02 NS	-0.20*	1.00	0.40*	-0.05 NS
Staple Strength	0.06 NS	0.04 NS	0.04 NS	0.10 NS	-0.07 NS	0.38**	1.00	-0.13 NS
Micron ire	-0.29**	0.01NS	-0.10NS	0.01NS	0.18*	-0.04 NS	-0.11 NS	1.00

Cluster analysis

Genetic variation is the key tool for developing new varieties and give correct information about importance of the material. Cluster analyses is the important weapon for the selection of right material. In this study, fifty accessions were placed into five distinct clusters by doing analysis of genetic diversity through cluster analysis on the basis of Euclidian dissimilarity distance by keeping 10 as linkage distance using Ward’s (1963) [29] method. (Figure.1) for normal and (Figure.2) for drought condition. For successful breeding program, the proficient genetic information plays very important role in the evaluation and selection of accessions especially for improving yield. some earlier researchers revealed that adequate quantity of genetic variation for water deficit exists in cotton due to this fact cotton is derivative from those environments which habitually familiarity for water shortages (Pettigrew and Meredith, 1994,2004; Lacape *et al.*, 1998) [21, 22, 19]. Thus, selection for drought resistance remained huge alarm for cotton breeders. Based on cluster means, the cluster have been recognized for the selection of parents for further hybridization programme. The accessions superior in the cluster may be engage in a multiple crossing programme to improve transgressive segregates with genetically high yield potential. Exploitation of genetic diversity by different agronomic and morphological characters have been done for victorious hybridization program which requires ideal selection as environment deeply manipulate on these characters and selection process (Ahmad *et al.* 2012) [2]. Thus, significant emphasis should be set to develop extremely fruitful cotton varieties. The production of cotton either in seed cotton yield or lint rely on traits like plant height, boll weight, number of bolls per plant, seed index, lint percentage (Salahuddin *et al.* 2010) [24]. Complete knowledge about the crop natural history, performance level and correlation of numerous agronomic traits with yield is essential for plant breeder to deal with cotton yield

restrictive constraints. Thus, the hybridization between accession of divergent cluster will direct for accretion of constructive genes in a single variety. This also recommended for creation of variability for evolving the varieties involving a huge number of various lines instead of closely associated ones.

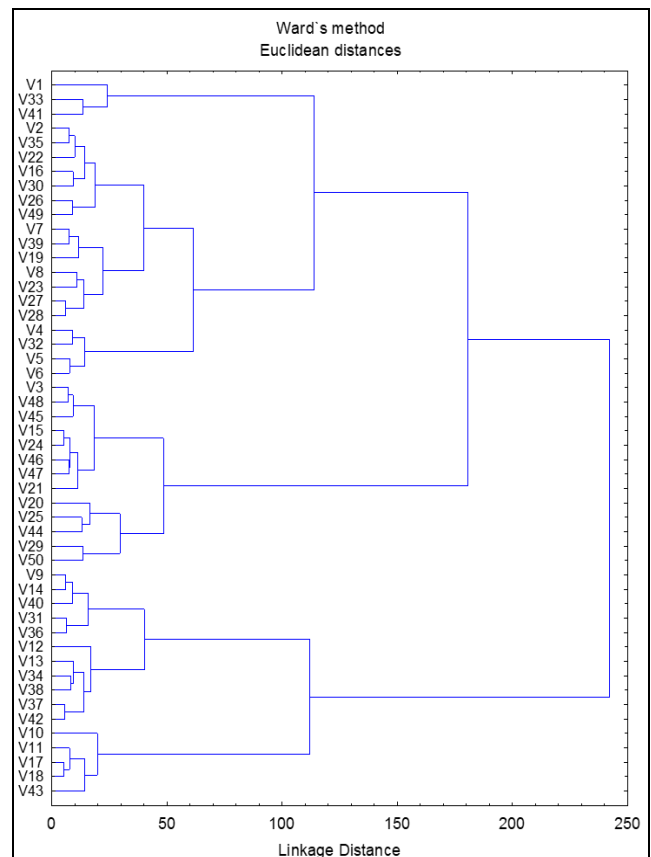


Fig: 1 Dendrogram generated by Ward’s method of cluster analysis among the 50 cotton genotypes under normal condition

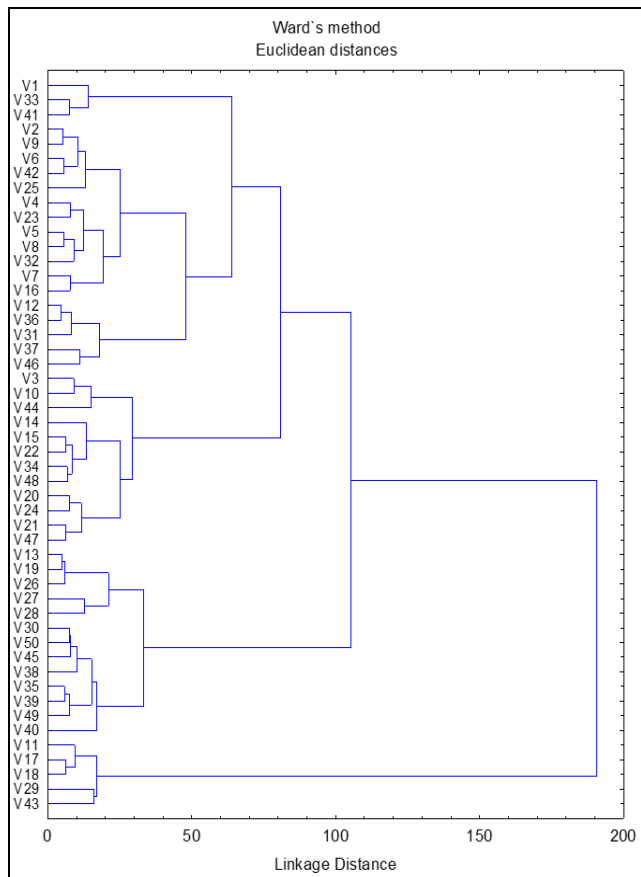


Fig. 2 Dendrogram generated by Ward's method of cluster analysis among the 50 cotton genotypes under Drought conditio.

Conclusion

It was concluded that information about characters that correlate with the yield is very important. Cluster analyses to select the best group of genotypes are also play important role. The genotypes in the group-I should be crossed with group-V for drought tolerance in cotton in future breeding programme.

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