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Genotypic and Phenotypic Correlation Study and Cluster Analysis between different Physiological Attributes of Cotton (*Gossypium hirsutum* L.) under different Regimes of Irrigation

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ABSTRACT

Cotton is a well-known agricultural and industrial crop that plays a significant role in Pakistan's economy. For this study, RCBD (Randomized Complete Block Design) using three replications was carried out to sow fifty different cotton genotypes. Results of the experiments showed that under normal and drought conditions, relative water content has highly significant and positive association with excise leaf water loss while at genotypic level, positively significant correlation with aforesaid traits has been found. Genotypes under study were assembled into five differing clusters by keeping a linkage space. Comparison of all five groups revealed that Cluster-1 is relevant to all the qualities being studied in both conditions as all these characters had the greatest value in the said group. The lowest ranked was observed for parameters under study in Cluster-5. These kinds of discoveries can be useful in planning the new hybridization programs to develop abiotic tolerance in the cotton.

INTRODUCTION

Cotton is used in a variety of products, including household items and medicinal ones. Among for cultivated species of cotton, two of the species are tetraploid and two are diploid. It has been estimated that cotton has been grown for 7,000 years. It is a very valuable and common agricultural commodity with industrial applications all over the world. Around 2.5% of the world's arable soil is planted with cotton in about hundred different countries. On a global scale of 29.271 million hectares, 105.340 million bales were produced in 2017, with the United States, China, India, Pakistan and Brazil being the top producers (USDA, 2017). In Pakistan's tropical and subtropical regions, cotton is grown and requires temperatures between (21°C and 30°C), rainfall between (50-100 cm), and temperature

ranges between 50-100 cm. (Bakhsh *et al.*, 2009; Azam *et al.*, 2017)

The main problem in dry and semi-arid locations for crop production is a lack of water for irrigation. Lack of sufficient water is a severe environmental stressor that effect photosynthetic process which lowers the crop yield (Lafitte *et al.*, 2007). While looking for various growth parameters, such as physiological and morphological modifications, performance observation of a crop may disclose the process of drought resistance, which is not entirely explicit (Hasegawa *et al.*, 2000). Correlations between genotype and phenotype are crucial for figuring out how closely physiologically relevant features are related to one another. In the beginning, some physiological processes are understated, while others are brought on by the

projection of moisture stress, which results in a reduction in yield in the end. Maintaining water supply through defensive measures and the creation of drought tolerant types can help to resolve this issue (Alishah and Ahmadikhah, 2009).

The appropriate and effective strategy that uses genetic alteration through breeding and careful variety selection to address the problem of drought in dry circumstances. Such genetic strategies might help cultivars recover their ability to thrive in these challenging circumstances. The first goal of breeding desired traits is to improve genotype performance under adverse situations. The system for recognizing the top strains for moisture deficit areas varies in terms of drought tolerance within both genotypic and phenotypic differences (Bray, 1997). Genetic data on relevant physiological and agronomic markers under drought stress conditions is needed when breeding to create cultivars that are drought tolerant. Relative water content (RWC) (Tahara *et al.*, 1990; Kumar and Singh, 1998), excised leaf water loss (Basal and Ünay, 2006), cell membrane thermo-stability (Kakani *et al.*, 2005; Azhar *et al.*, 2009), and cell membrane thermo-stability (Kakani *et al.*, 2005) are all significant considerations when evaluating cotton varieties for drought tolerance.

Therefore, a comparative research of 50 cotton genotypes was conducted to determine the physiological parameters that are playing key roles under drought stress in order to enhance our knowledge and understanding of the qualities that have contributed to plant persistence under irrigation stress. Acquire genetic data about physiological features in upland cotton under drought stress was a major purpose of said research work.

MATERIAL AND METHODS

From the Multan-based Central Cotton Research Institute's gene pool, fifty distinct cotton genotypes were gathered. 2013's crop season saw the completion of the field tests at the Central Cotton Research Institute's Multan experimental farm. There were preserved two moisture levels. While the first treatment did not include any stress, the second did. The treatments were set up in a split plot with three replications using a Randomized Complete Block design. On May 27, 2013, the seeds were scattered on damp beds, retaining a 30 cm plant-to-plant distance and 75 cm between rows. At 28 days following planting, weak and diseased seedlings were removed in

order to preserve the plant population. According to Pettigrew's suggestion, the intra-row spaces were shielded with the help of polythene sheets during the heaviest rainy season (Monsoon). The trial was designed in such a way that the sub-plots were allotted to the genotypes whereas irrigations levels (Normal and Deficit) were kept in main plots. In drought-stressed plots, total four irrigations were applied, including first irrigation at time of sowing. In non-stress plots, total six irrigations were applied at appropriate intervals. The data regarding relative water content, excised leaf water loss, stomatal conductance, photosynthesis rate, transpiration rate and cell membrane damage were measured.

Statistical Analysis

Through ANOVA and ANCOVA, the data on physiological characteristics were analyzed to calculate correlations between the traits genotype and phenotype. Using Ward's approach, cluster analysis was carried out (1963).

Correlation

According to Kwon and Torrie, the genotypic (rg) and phenotypic (rp) correlations between two traits were computed (1964).

Phenotypic Correlation

The observable connection between two qualities is called phenotypic correlation (rp).

The following is the phenotypic correlation between two traits.

$$\text{Phenotypic correlation}(rp) = \frac{P. Covxy}{\sqrt{P. Vx \times P. Vy}}$$

Where;

P.Covxy= Phenotypic-co-variance of x and y character.

P.Vx=Phenotypic-variance (x trait).

P.Vy=Phenotypic-variance (y Trait).

Genotypic Correlation

The heritable connection between two qualities is known as genotypic correlation. The following is the genotypic correlation (rg) among two characters:

$$\text{Genotypic Correlation}(rg) = \frac{G. Covx. y}{\sqrt{G. Vx \times G. Vy}}$$

Where;

G.Covx.y= Genetic covariance between x and y trait.

G.Vx= Genotypic variance of x trait.

G.Vy= Genotypic variance of y trait.

RESULTS AND DISCUSSION

Relative water content is the most intriguing physiological parameter among many other traits. At the genotypic level, relative water content is strongly positively correlated with excised leaf water loss (ELWL), rate of photosynthesis, transpiration rate and stomatal conductance while negatively correlated with cell membrane injury. It revealed that higher rate of cell injury will produce lower relative water content. Same pattern of correlation was also revealed from the data of phenotypic correlation. ELWL has a strong significant positive correlation with the rates of photosynthesis, transpiration and stomatal conductance and a significant negative correlation with cell membrane injury at the genotypic level, whereas it has a strong significant

positive correlation with the rates of photosynthesis, transpiration, and stomatal conductance and a significant negative correlation with cell injury at the phenotypic level. At the genotypic level, cell membrane damage has a negative and substantial link with rates of photosynthesis, transpiration, and stomatal conductance; however, at the phenotypic level, the correlation is negative and very significant. At the genotypic level, there is a negative significant link between transpiration rate and stomatal conductance, however at the phenotypic level, there is a highly significant correlation. Under both normal and drought conditions, there is a strong positive association between transpiration rate and stomata at the genotypic and phenotypic levels.

Table 1. Genotypic and Phenotypic correlation for physiological attributes under optimum irrigation condition.

Traits	Relative water content	ELWL	Cell injury	Rate of photosynthesis	transpiration rate	Stomatal conductance
Relative water content	-	0.45*	-0.44*	0.39*	0.41*	0.38*
Excised leaf water loss	0.43**	-	-0.43*	0.41*	0.55*	0.48*
Cell injury	-0.43**	-0.42**	-	-0.42*	-0.34*	-0.20*
Rate of photosynthesis	0.38**	0.40**	-0.41**	-	0.50*	0.50*
transpiration rate	0.40**	0.54**	-0.34**	0.50**	-	0.55*
Stomatal conductance	0.37**	0.47**	-0.20**	0.50**	0.54**	-

Table 2. Genotypic and Phenotypic correlation for physiological attributes under water deficit condition.

Traits	Relative water content	Excised leaf water loss	Cell injury	Rate of photosynthesis	transpiration rate	Stomatal conductance
Relative water content	-	0.56*	-0.36 *	0.44*	0.48*	0.42*
Excised leaf water loss	0.54**	-	-0.44*	0.59*	0.51*	0.47*
Cell injury	-0.35**	-0.43**	-	-0.60*	-0.54*	-0.41*
Rate of photosynthesis	0.43**	0.57**	-0.59**	-	0.51*	58*0.
transpiration rate	0.50**	0.54**	-0.53**	0.49**	-	0.55*
Stomatal conductance	0.41**	0.44**	-0.39**	0.55**	0.53**	-

In order to create new cultivars, genetic variation is essential. It also provides crucial information about the valuable material. The key technique in the selection of exact material is cluster analysis. Here, fifty genotypes were divided into five distinct clusters using Ward's

(1963) approach to analyze genetic diversity by cluster analysis utilizing Euclidian dissimilarity distance while maintaining 10 as the linkage distance for both normal condition (Figure.1) and for drought conditions (Figure.2).

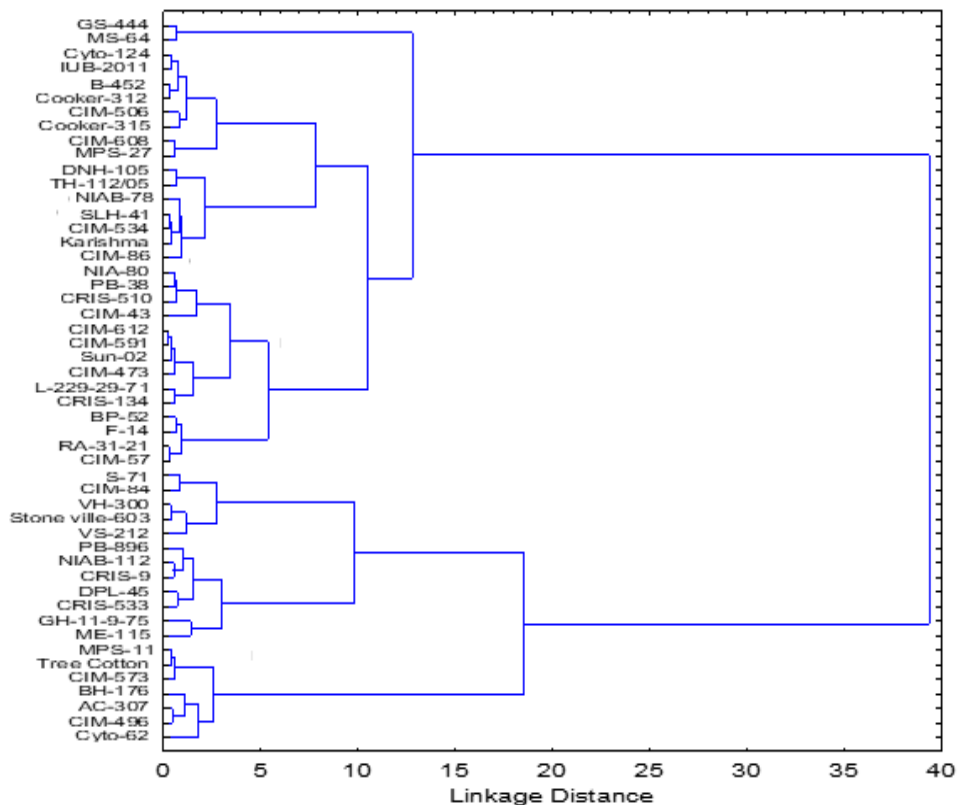


Figure 1. Dendrogram generated by Ward's method of cluster analysis under normal condition.

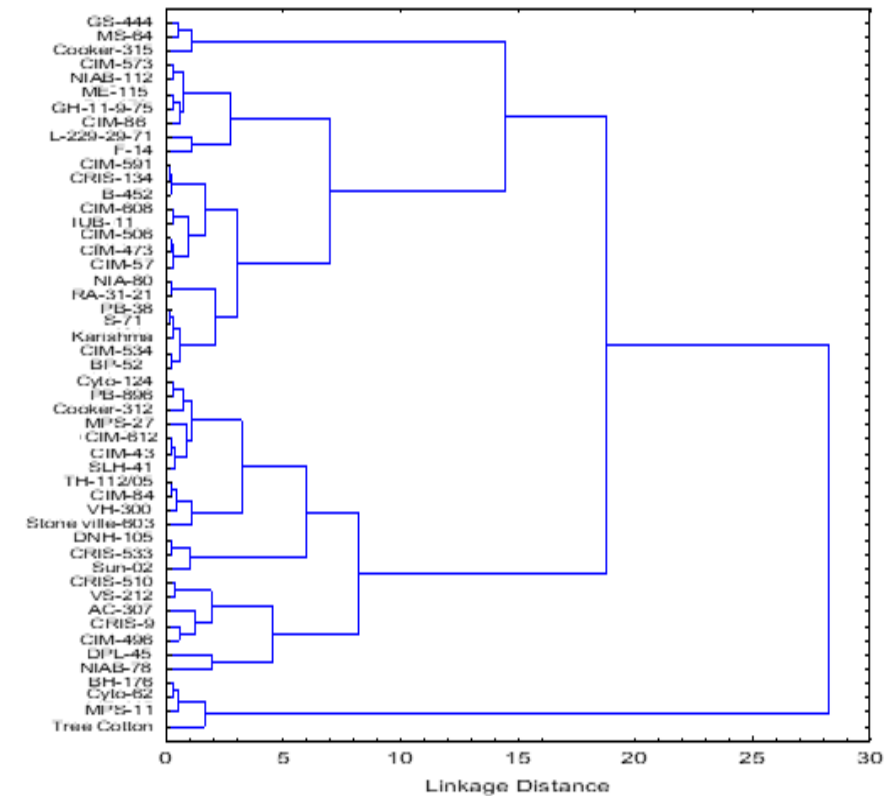


Figure 2 Dendrogram generated by Ward's method of cluster analysis s under drought condition.

These fifty genotypes were divided into five different clusters using cluster analysis. Each cluster's description of these accessions is prepared in Tables 4 and 5, respectively, under normal and drought conditions.

Table 3. Cluster members under normal condition.

Cluster Name	Cluster-1	Cluster-2	Cluster-3	Cluster-4	Cluster-5
Number of genotypes	5	11	13	18	3
Genotype Name	Cyto-62	SLH-41	CIM-496	CIM-506	Cooker-315
	DPL-45	GH-11-9-75	Tree cotton	MPS-27	MS-64
	MPS-11	CIM-86	CRIS-134	RA-31-21	GS-444
	BH-176	CIM-84	CIM-437	CRIS-533	
	CIM-573	NIA-80	CIM-608	Stoneville-603	
		CIM-591	IUB-2011	B-452	
		NIAB-78	CIM-57	CIM-534	
		Cooker-312	ME-115	PB-896	
		Karishma	CIM-612	NIAB-112	
		CRIS-510	VH-300	CIM-43	
		SUN-02	CRIS-9	TH-112/05	
			F-14	S-71	
			DNH-105	L-229-29-71	
				BP-52	
				VS-212	
				PB-38	
				AC-307	
				Cyto-124	

In both normal and drought conditions, Cluster-1 contained 5 accessions. Cluster-2 had thirteen accessions under drought conditions and eleven genotypes in normal conditions (Figure 1). Thirteen accessions and twelve genotypes were present in Cluster-3 under normal and drought circumstances, respectively. Additionally, Cluster-4 included a maximum of 18 sites in normal conditions and 17 sites in drought. In both cases, Cluster-5 had three accessions. The means of several characteristics for each cluster are displayed in Tables 4 and 5, respectively, for normal and drought conditions. In both settings, relative water content was measured, with cluster-1 recording the highest value and cluster-2 closely following. In both settings, Cluster-I was discovered to have the highest

values for ELWL, cell membrane Injury, photosynthetic rate, transpiration rate, and stomatal conductance. For all the features under consideration, Cluster-V displayed the lowest value (Tables 4 and 5) for normal and drought, respectively.

The development and selection of genotypes, particularly for enhancing for physiological qualities which ultimately boost yield, are crucial for an effective and suitable breeding programme. Cotton has enough genetic variety to be susceptible to drought, according to a number of former scientists. As a result, cotton is not native to environments where water shortages are a constant problem (Pettigrew and Meredith, 1994; Lacape *et al.*, 1998). So cotton breeders continued to be quite concerned about selection for drought resilience.

Table 4. Cluster members under drought condition

Cluster Name	Cluster-1	Cluster-2	Cluster-3	Cluster-4	Cluster-5
Number of genotypes	5	13	12	17	3
Genotype Name	Cyto-62	Karishma	CIM-57	ME-115	Cooker-315
	Tree cotton	S-71	IUB-2011	GH-11-9-75	MS-64
	DPL-45	CIM-43	CIM-612	Cooker-312	GS-444
	MPS-11	AC-307	CIM-608	NIAB-78	
	BH-176	CIM-86	F-14	CIM-591	
		CRIS-9	CIM-84	VS-212	
		CIM-496	PB-38	TH-112/05	
		BP-52	VH-300	RA-31-21	
		Stoneville-603	CRIS-510	PB-896	
		B-452	CRIS-134	MPS-27	
		L-229-29-71	CIM-573	CIM-534	
		NIAB-112	DNH-105	CRIS-533	
		NIA-80		CIM-437	
				SLH-341	
				CIM-506	
				SUN-02	
				Cyto-124	

Table 5. Alignment of genotypes in different clusters based on mean under normal condition.

Traits	Cluster-1	Cluster-2	Cluster-3	Cluster-4	Cluster-5
Relative water content	24.80	32.93	28.94	31.07	38.85
Excised leaf water loss	16.66	15.74	15.81	15.69	15.11
Cell injury	5.31	4.68	4.55	4.72	4.14
Photosynthesis rate	38.90	35.37	35.89	35.30	31.67
Transpiration rate	24.80	32.93	28.94	31.07	38.85
Stomatal conductance	16.66	15.74	15.81	15.69	15.11

Table 6. Alignment of genotypes in different clusters based on mean under drought condition.

Parameters	Cluster-1	Cluster-2	Cluster-3	Cluster-4	Cluster-5
Relative water content	54.51	46.72	43.28	47.56	37.78
Excised leaf water loss	1.23	0.64	0.67	0.66	0.35
Cell injury	36.50	46.24	53.12	58.87	66.30
Photosynthesis rate	12.96	11.65	11.56	11.64	11.20
Transpiration rate	3.41	2.80	2.84	2.78	2.19
Stomatal conductance	25.45	23.15	23.34	23.38	21.76

The cluster has been acknowledged for the best selection of genotypes as parents to initiate a subsequent hybridization programme based on the cluster means. To improve transgressive segregates with genetically sound physiological properties, the superior accessions

in the cluster might involve in a numerous crossing programme. Different physiological traits have been used to exploit genetic variety for successful hybridization programmes, which call for perfect selection because the environment has a profound

influence on these traits and the selection process (Ahmad *et al.* 2012). Therefore, it is important to take a really proactive and significant approach to developing incredibly profitable cotton types. The addition of beneficial genes to a single variety will be directed through hybridization between genotypes of diverse cluster. This also implied that there should be some degree of diversity for variations to evolve in relation to a large number of different lines rather than closely related ones.

CONCLUSION

It was determined that character information that corresponds to physiological features is crucial. The use of cluster analysis to choose the appropriate genotype group is crucial. In a future breeding programme, the genotypes in group I should be crossed with group V to improve cotton's ability to withstand drought.

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