

GENETIC VARIABILITY STUDIES OF SEED COTTON YIELD AND FIBRE QUALITY IN UPLAND COTTON (*GOSSYPIUM HIRSUTUM* L.) GROWN UNDER SALINITY STRESS

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Abstract

Cotton is a dynamic fibre crop in the world. It is susceptible to salinity stress, a major abiotic factor affecting crop growth, yield and fibre quality. In present study, six cotton genotypes were crossed in half diallel fashion to obtain 15 F₁ hybrids. Parents and their F₁ were sown under three salinity levels i.e. normal (S1 = 3.7 dSm⁻¹) moderate (S2 = 10 dSm⁻¹) and high (S3 = 15 dSm⁻¹) following split-plot arrangement under completely randomized design. Three salinity levels were maintained in main plot while 21 genotypes (15 F₁ and 6 parents) were sown in the subplot. Three replications were maintained for all parents and their F₁ crosses. At maturity, data were recorded for seed cotton yield, fibre length, fibre strength and fibre fineness for parents as well as for crosses. The data were analyzed using the Griffing approach to determine the combining ability effects and genetic components. Parent CIM-602 followed by FH-142 showed good GCA performance for all the observed traits at different levels of salt stress. MNH-886 × CIM-616 and CIM-616 × CIM-602 were best specific combiners for most of the traits under normal and salinity stress. While FH-142 × CIM-602 was the best specific combiner for fibre quality traits under all treatments. Further utilization of these genotypes might be helpful for the development of salt-tolerant cultivars.

Key words: Salinity stress, Cotton, Combining ability studies, Diallel analysis, Genetics.

Introduction

Salinity is one of the major abiotic stresses, which not only reduces plant growth but also in severe condition leads to plant death (Wang *et al.*, 2017). Saline condition occurs due to weathering of primary rocks or saline water irrigation or accumulation of un-leached salts in the root zone due to drought conditions (Basal & Turget, 2010). Excessive salts causes soil degradation, ion toxicity, nutrition imbalance and disorder of metabolic activities ultimately reducing plant growth and production (Zhang *et al.*, 2014; Dong, 2012). Salt stress limits agricultural production (up to 40%) all over the world (Wang *et al.*, 2017). It is also reported that 50% of arable land will be affected by salt stress up to 2050 (Butcher *et al.*, 2016). In Pakistan, about 6.2 × 10⁶ hectare of arable land is under saline condition (Bhatti & Azhar, 2002). Conventional methods for improving the salinity tolerance of crop varieties utilizes existing variation revealed by the screening of germplasm and enhancing the variation by combining desirable salinity tolerance traits from diverse parents into single variety (Ashraf, 2002). Plants can survive under saline conditions and evolve to better tolerate saline conditions through special strategies utilizing physiological, biochemical, and molecular mechanisms (Munns & Tester, 2008).

Cotton is a major fibre crop all over the world and in Pakistan. It is a mildly salinity tolerant crop having a threshold EC_e level of 7.7 dSm⁻¹ (Ashraf & Ahmad, 2000). Salinity is an important limiting factor for cotton production and quality worldwide. Salinity stress may be overcome for cotton adaptation by specific stress-related gene expression concluded by Ma *et al.*, (2011). However, variations among different cotton genotypes have been

observed under saline conditions (Hussain *et al.*, 2010). For bringing a change in any plant character against salt stress there are two main components. Firstly, there must be significant genetic variation (Rizwan *et al.*, 2021) and secondly this variability should be heritable (Deho *et al.*, 2021; Abro *et al.*, 2020). Thus, it is important to understand phenotypic traits inheritance under saline stress.

Therefore, keeping in view the above facts, present study was planned to investigate the genetic inheritance of seed cotton yield and fibre quality parameters at the adult stage under salinity stress. This study was conducted to understand the inheritance of yield and fibre quality traits for cotton salinity tolerance breeding programs.

Materials and Methods

The research work was conducted at experimental farm of the Department of Plant Breeding and Genetics, University of Agriculture Faisalabad, Pakistan during the year 2017-2018.

To develop the F₁, seeds of six selected cotton genotypes, AGC-501, MNH-886, FH-142, CIM-616, CIM-602 and KZ-191 (Table 1) were grown in earthen pots in the glasshouse during October-December 2017. Fifteen plants were maintained for each genotype. At the flowering stage, these six genotypes were crossed following half diallel fashion using three lines and three testers. All the plant protection and agronomic measures were observed to maintain healthy crop stand. At maturity, seed cotton was picked and ginned separately for each cross and obtained seed was prepared for the sowing of the next generation. F₁ seed of fifteen crosses and six parents were grown in earthen pots (soil used for pots filling had EC_e of 3.7 dSm⁻¹) in completely

randomized design with split-plot arrangement. Three salinity levels were maintained in main plot while 21 genotypes (15 F₁ and 6 parents) were sown in subplot during May 2018. Thirty days after the germination of seedlings, saline solution was applied to maintain the three salinity stress levels i.e. normal (S₁ = 3.7 dSm⁻¹), moderate (S₂ = 10 dSm⁻¹) and high (S₃ = 15 dSm⁻¹) salinity levels. Saline solution was applied in two splits with 48 hours intervals until final salinity levels were reached at 10 dSm⁻¹ and 15 dSm⁻¹. The salinity levels were maintained weekly, using the EC meter by adding proper quantity of salt solution. All other agronomic practices i.e., fertilizer, irrigation, weeding and pesticide were applied to maintain a healthy crop. At maturity, data for seed cotton yield were recorded. High Volume Instrument (HVI-900A) was used to analyze fibre quality character like fibre length, strength and fineness. The collected data were subjected to analysis using Griffing approach (Griffing, 1956) to find the general and specific combining ability and genetic components for each character.

Results

Mean squares values of genotypes showed highly significant variations (< 0.01) among 6 parents and 15 hybrids for seed cotton yield per plant, fibre length, strength and fineness (Table 2). Mean square values of GCA and SCA effects were also highly significant for seed cotton yield, fibre length, strength and fineness (Table 3).

In case of seed cotton yield, positive general combining ability effects are important, the main emphasis of any plant breeding program. Under normal condition positive and significant general combining effects were observed for FH-142 (2.696*), CIM-616 (8.869*) and CIM-602 (11.080*), under moderate salinity stress for CIM-616 (4.673*) and CIM-602 (9.381*) while under high salinity conditions for CIM-602 (4.066*) (Table 4). While studying the combinations for seed cotton yield under normal condition the crosses like AGC-501 × MNH-886 (17.678*), MNH-886

× CIM-616 (5.171*), FH-142 × CIM-616 (5.153*), FH-142 × KZ-191 (7.497*), CIM-616 × CIM-602 (15.112*) were positive and significant. Under moderate salinity stress the crosses like AGC-501 × MNH-886 (16.772*), AGC-501 × KZ-191 (8.628*), MNH-886 × CIM-616 (14.218*) while under high salinity level significant but positive specific combining ability effects were found in crosses MNH-886 × CIM-616 (8.41**) and FH-142 × KZ-191 (9.96**) (Table 5).

For fibre strength, positive but significant values are important. Higher positive and significant general combining ability effects were found in CIM-602 (0.796*, 1.444* and 1.404*) under normal, moderate and high salinity level. Under normal condition, positive but significant specific combining ability effects were found in crosses like AGC-501 × KZ-191 (0.900*) MNH-886 × CIM-616 (1.515*), FH-142 × CIM-602 (1.604*) while under high salinity level the crosses like MNH-886 × CIM-616 (1.51**) FH-142 × CIM-602 (1.249*) were significant (Table 5).

Table 1. Breeding material of cotton used in present study.

Parents	AGC-501, MNH-886, FH-142, CIM-616, CIM-602 and KZ-191
Hybrids (Half Diallel mating fashion)	AGC-501 × MNH-886
	AGC-501 × FH-142
	AGC-501 × CIM616
	AGC-501 × CIM-602
	AGC-501 × KZ-919
	MNH-886 × FH-142
	MNH-886 × CIM-616
	MNH-886 × CIM-602
	MNH-886 × KZ-919
	FH-142 × CIM-616
	FH-142 × CIM-602
	FH-142 × KZ-191
	CIM-616 × CIM-602
	CIM-616 × KZ-191
	CIM-602 × KZ-191

Table 2. Mean square values for 15 hybrids and their six parents treated with different salinity levels.

SOV/traits	Df	Seed cotton yield	GOT%	Fibre Length	Fibre Strength	Fibre Fineness
Salinity	2	5954.29**	30.67**	18.19**	11.04**	0.95**
Genotypes	20	1386.27**	6.33**	4.72	10.03**	0.48**
Salinity × Genotypes	60	64.65	0.24	0.16	0.38	0.04

*= Significant at p<0.05, **= Significant at p<0.01, n.s. = Non-significant.

Table 3. Mean square values for GCA and SCA effects for six parents and fifteen hybrids for seed cotton yield (g), fibre length (mm), fibre strength (g/tex) and fibre fineness (µg/inch) under normal (S₁ = 3.7 dSm⁻¹), moderate (S₂ = 10 dSm⁻¹) and high (S₃ = 15 dSm⁻¹) salinity levels.

Effects	Salinity level	Seed cotton yield	Fibre length	Fibre strength	Fibre fineness
GCA Effects	S1	665.51**	2.25**	7.33**	0.30**
	S2	456.38**	2.09**	5.71**	0.21**
	S3	119.1*	1.93**	4.88**	0.15**
SCA Effects	S1	104.09**	0.93*	3.94**	0.19**
	S2	110.91**	0.34**	2.79**	0.11**
	S3	97.30*	0.31*	2.69*	0.08**

n.s. = Non-significant, * = Significant at p<0.05, ** = Significant at p<0.01

Table 4. General combining ability effects of six parents for seed cotton yield SCY (g), fibre length FL (mm), fibre strength FS (g/tex) and fibre fineness FF (µg/inch) under normal (S₁ = 3.7 dSm⁻¹), moderate (S₂ = 10 dSm⁻¹) and high (S₃ = 15 dSm⁻¹) salinity levels.

Parents	GCA Effects for SCY			GCA Effects for fibre strength			GCA Effects for fibre fineness			GCA Effects for fibre length		
	S ₁	S ₂	S ₃	S ₁	S ₂	S ₃	S ₁	S ₂	S ₃	S ₁	S ₂	S ₃
AGC-501	-12.4*	-12.3*	-6.84*	-0.322	-0.76*	-0.512	-0.31*	-0.23*	-0.17*	-0.39*	-0.12	-0.133
MHN-886	-5.97*	-3.83*	-0.78	0.046	-0.530	-0.408	-0.07*	0.045	-0.009	-0.024	-0.27	-0.268
FH-142	2.69*	2.90	0.09	-0.192	-0.357	-0.288	0.013	0.066	0.039	-0.26	-0.25*	-0.228
CIM-616	8.86*	4.68*	3.22	-0.168	-0.386	-0.62*	0.288*	0.108*	0.161*	-0.23	0.006	0.015
CIM-602	11.08*	9.38*	4.07*	0.796*	1.44*	1.404*	0.089*	0.182*	0.125*	0.63**	1.01*	0.96*
KZ-191	-4.30*	-0.805	0.252	-0.160	0.59	0.423	-0.015	-0.18*	-0.153*	-0.23	-0.37*	-0.35*
SE (GCA)	0.90	1.72	1.82	0.19	0.32	0.29	0.008	0.05	0.06	0.064	0.11	0.13

*= Significant at p<0.05, **= Significant at p<0.01

Table 5. Specific combining ability effects of fifteen crosses for seed cotton yield (g) fibre strength FS(g/tex), fibre fineness FF(µg/inch) and fibre length FL (mm) under normal (S₁ = 3.7 dSm⁻¹), moderate (S₂ = 10 dSm⁻¹) and high (S₃ = 15 dSm⁻¹) salinity levels.

Crosses	SCA effects for seed cotton yield			SCA effects for FS			SCA effects for FF			SCA effects for FL		
	S ₁	S ₂	S ₃	S ₁	S ₂	S ₃	S ₁	S ₂	S ₃	S ₁	S ₂	S ₃
AGC-501 × MNH-886	17.678*	16.772*	4.69	-0.131	-0.101	-0.116	0.018	0.35	0.23**	0.21	-0.457	-0.1235
AGC-501 × FH-142	-2.011	-9.830*	-2.05	-1.669*	-1.649	-1.659**	-0.105*	-0.24	0.19**	0.17	-0.384	-0.107
AGC-501 × CIM-616	-13.760*	-2.672	-0.44	-1.217*	-1.177	-1.197*	-0.435*	-0.02	-0.33**	-0.35**	0.401	0.0255
AGC-501 × CIM-602	-15.976*	-14.138*	4.99	-0.466	-0.496	-0.481	0.064*	0.08	0.24**	-0.17	-0.797*	-0.1205
AGC-501 × KZ-191	-3.004	8.628*	-1	0.900*	0.88	0.89	0.633*	-0.09	0.34**	0.22*	-0.461	0.0545
MNH-886 × FH-142	-3.793	-4.336	-0.8	0.364	0.324	0.344	-0.100*	0.18**	-0.2	-0.02	0.129	0.2495*
MNH-886 × CIM-616	5.171*	14.218*	8.41**	1.515*	1.505	1.51**	0.255*	-0.05	0.09**	0.32**	0.179	-0.0595
MNH-886 × CIM-602	-5.590*	-13.98*	-5.41	-0.054	-0.104	-0.079	0.004	0.13	-0.05	-0.22	0.101	0.0735
MNH-886 × KZ-191	-4.615*	-9.669*	1.2	0.153	0.203	0.178	0.188*	0.01	0.04	-0.07	0.217	-0.156
FH-142 × CIM-616	5.153*	-7.665	-3.02	-0.317	-0.407	-0.362	0.187*	0.3**	0.03	0.07	-0.382	0.158
FH-142 × CIM-602	-0.227	6.826	-2.7	1.604*	0.894	1.249*	-0.274*	-0.05	-0.01	-0.07	0.554*	0.215*
FH-142 × KZ-191	7.497*	4.751	9.96**	-0.225	-0.255	-0.24	0.120*	-0.16**	0.07**	0.02	0.296	-0.221**
CIM-616 × CIM-602	15.112*	7.794	-0.61	0.600	0.8	0.7	0.156*	-0.15**	0.07**	-0.03	1.139*	0.115
CIM-616 × KZ-191	1.644	6.813	6.29	0.011	0.041	0.026	0.115*	-0.24**	0	0.05	0.380	0.215**
CIM-602 × KZ-191	-0.053	1.948	-5.38	-0.260	-0.23	-0.245	-0.164*	0.48**	0.02	0.05	-0.491	-0.22**
SE (SCA)	2.03	3.90	2.33	0.42	0.235	0.607	0.018	0.051	0.032	0.11	0.25	0.09

Table 6. Genetic components for seed cotton yield (g), fibre length (mm), fibre strength (g/tex) and fibre fineness (µg/inch) under normal (S₁ = 3.7 dSm⁻¹), moderate (S₂ = 10 dSm⁻¹) and high (S₃ = 15 dSm⁻¹) salinity levels.

Effects	Salinity level	Seed cotton yield	Fibre length	Fibre strength	Fibre fineness
δ ² gca	S ₁	70.18	1.53	0.05	0.03
	S ₂	43.18	0.22	0.03	0.013
	S ₃	37.459	0.09	0.01	0.009
δs ² sca	S ₁	96.39	0.54	0.61	0.09
	S ₂	82.5	0.23	0.42	0.03
	S ₃	33.65	0.110	0.23	0.025

For fibre fineness, negative combining ability effects are important. Under normal condition AGC-501 (-0.305*) and MNH-886 (-0.070*), while the genotypes like AGC-501 (-0.223* and -0.163*) and KZ-191 (-0.178* and -0.153*) showed significant negative value of general combining ability under moderate and high salinity stress conditions respectively (Table 5). For specific combining ability effects regarding fibre fineness under normal condition the crosses like AGC-501 × FH-142 (-0.105*), AGC-501 × CIM-616 (-0.435*), MNH-886 × FH-142 (-0.100*), FH-142 × CIM-602 (-0.274*) and CIM-602 × KZ-191 (-0.164*) showed negative significant value. The crosses like FH-142 × KZ-191 (-0.16**), CIM-616 × CIM-602 (-0.15**) and CIM-616 × KZ-191 (-0.24**) showed significant negative value under moderate salinity stress while the cross AGC-501 × CIM-616 (-0.33**) showed significant negative value under high salinity stress condition (Table 5).

The higher value is important for fibre length in cotton. The best general combiner was CIM-602 under normal (0.626**), moderate (1.009*) and high salinity (0.962*) stress condition for staple length (Table 4). The crosses like AGC-501 × KZ-191 (0.22*), MNH-886 × CIM-616 (0.32**) under normal condition, the crosses like FH-142 × CIM-602 (0.554*), CIM-616 × CIM-602 (1.139*) under moderate salinity and the crosses like MNH-886 × FH-142 (0.2495*), FH-142 × CIM-602 (0.215*) and CIM-616 × KZ-191 (0.215**) under high saline conditions showed positive significant values (Table 5).

The variance due to specific combining ability effect was greater for seed cotton yield, fibre length, fibre strength and fibre fineness under normal moderate and high salinity stress conditions (Table 6).

Discussion

Cotton is a major fibre crop all over the world and in Pakistan. It is a mildly salinity tolerant crop having a threshold EC_e level of 7.7 dSm^{-1} (Ashraf & Ahmad, 2000). The cotton plant is relatively tolerant to salinity stress and possesses a certain degree of variability in salinity tolerance at the specie level (Dai & Hezhong, 2014). Salinity is an important limiting factor for cotton production and quality worldwide. In the past, most of the researchers have screened the cotton germplasm on seedling stage (Peng *et al.*, 2016; Wang *et al.*, 2016) but in the present study, the evaluation of genetic material was done at maturity as the yield is an ultimate objective of any breeding program (Nabi *et al.*, 2010). Salinity stress may be overcome for cotton adaptation by specific stress-related gene expression concluded by Ma *et al.*, (2011). However, variations among different cotton genotypes have been observed under saline conditions (Hussain *et al.*, 2010). In this study, 6 Parents and their 15 F_1 were grown under three salinity levels i.e. normal ($S_1 = 3.7 \text{ dSm}^{-1}$), moderate ($S_2 = 10 \text{ dSm}^{-1}$) and high ($S_3 = 15 \text{ dSm}^{-1}$) salinity stress conditions. At maturity, data were collected for seed cotton yield, fibre length, strength and fineness for parents and for crosses. Parent CIM-602 showed good GCA performance for all the observed traits followed by FH-142 under normal, moderate and high salt stress conditions. While for the SCA, the best specific combiners were MNH-886 \times CIM-616 and CIM-616 \times CIM-602 for most of the traits under normal and salinity stress conditions. While FH-142 \times CIM-602 was the best specific combiner for all fibre quality traits under all salinity levels. Therefore, we can use these combinations in the development of hybrids for salt-affected areas of Pakistan. Variation in performance of parents and hybrids could be justified based on differences in genetic make-up and environmental conditions prevailing during the study (Bernier *et al.*, 1993; Abro *et al.*, 2020). In the present study, our main emphasis was seed cotton yield and fibre quality traits. It had been proven earlier that the assessments of genetic material for agronomic and quality traits are best selection criteria under abiotic stresses (Bhatti *et al.*, 2006; Alishah & Ahmadikhah, 2009).

The variance due to specific combining ability effect was greater for seed cotton yield, fibre length, fibre strength and fibre fineness under normal, moderate and high salinity stress conditions indicating the dominant role of non-additive genes. The studies of Neelima *et al.*, (2004) and Shakeel *et al.*, (2001) appeared to agree with the present investigation. The non-additive gene action for all the traits revealed the possibility of using such plant material for the development of hybrids (Singh & Singh, 1999). India and China has attained self-sufficiently in cotton production through the successful adoption of hybrid cotton (Nachimuthu and Webb 2017; Gao *et al.*, 2016). However, at present cotton hybrid development research is at early stage of development in Pakistan.

Conclusion

CIM-602 followed by FH-142 was found good general combiners for all studied traits. MNH-886 \times CIM-616 and CIM-616 \times CIM-602 were best specific combiners for most of the traits under normal and salinity stress. FH-142 \times CIM-602 was the best specific combiner for fibre quality traits under all treatments. These crosses may be considered in hybrid development programs to exploit heterobeltiosis in the mentioned traits. Furthermore, non-additive gene action for all the traits suggested the possibility of using plant material for cotton hybrid development for the salt-affected area of Pakistan.

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