

Combining Ability Analysis of Agronomic and Fibre Traits under Irrigation and Drought in Cotton (*Gossypium* *hirsutum* L.)

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Abstract

This study was carried out for developing high yielding cotton genotypes having fiber superiority under drought stress conditions. Five upland cotton accessions were screened out as drought tolerant and three as drought susceptible on the basis of root shoot parameters. The results of root shoot screening experiment were verified in field screening on the basis of agronomical and physiological parameters. These eight genotypes were grown in glass house conditions and crossed in line \times tester mating design. During the next cotton season, these fifteen cotton hybrids and parents were sown in field conditions. Traits related to yield and fiber quality under the study showed significant variations among the accessions and their half sibs. Furthermore, the line MS-64 and tester BH-176 had better yield performance under water stress. The cross combinations viz., GS-444 \times MPS-11, and COOKER-315 \times Cyto-62 were the best for yield contributing traits. These combinations may be helpful for germplasm enhancement on large scale under water scarcity.

Keywords: Drought, Genetic analysis, Line \times Tester, Regimes

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Introduction

Cotton (*Gossypium hirsutum* L.) is one of the most important fiber as well as cash crops in the world. This crop is grown in tropical and sub-tropical areas of the more than 80 countries including USA, China, Brazil India and Pakistan (Singh, 2004). Cotton crop covered the area of 2.489 million hectares with production of 9.917 million bales, which is 14.2% less in area and 7.6% increase in production as per previous year. It contributes 1% and 5.2% in gross domestic product (GDP) and in value addition respectively in Pakistani agriculture (Anonymous, 2016-2017).

Cotton yield and production were affected by the water stress and species was considered more sensitive when compared with sorghum (Allen Jr et al., 2011). However, it showed relatively good survival due to deep and extensive root system under semi-arid regions (Bruner, 2015). The effects of water stress on various cotton growth stages and staple quality have been investigated (Zhang et al., 2016). Growth stages such as germination, emergence of seedling, and flowering were more sensitive than vegetative stages to water stress (Loka & Oosterhuis, 2012). Traits such as seed cotton yield, boll number were more sensitive to water stress than boll weight (Papastylianou & Argyrokastritis, 2014).

Yield and quality enhancement is the focus of cotton breeding. Moreover, developed elite germplasm may able to show stable performance across range of environments and agronomic practices. In order to cope with current scenario of climate change, breeding against water stress is fundamental to maintain plant growth and sustainable yield under stress condition (Rauf et al., 2016).

Inheritance of complex traits was known to be affected by the environment including supply of water. Water stress had squeezed the genetic variability and inheritance pattern associated with traits of interest. Traits showing additive type of genetic variability may be exploited as selection criteria to constitute pure lines under water stress (Ali et al., 2008; Khan et al., 2009). Recurrent selection has been recommended for the improvement of traits showing complex gene actions such as dominance, partial dominance and epistatic effects (Mukhtar et al., 2000a; Prasad et al., 2005; Esmail, 2007). Fiber length was studied by many scientists and different mechanisms of inheritance were determined for this trait. Nimbalkar et al. (2004) observed additive mode of gene action, Ahmed et al. (2006) observed over dominant mode of gene inheritance while Azhar et al. (2004) revealed additive and non-additive gene action for fiber length. Zhang et al. (2014) studied epistatic gene action for staple length. Kumar et al. (2014) calculated the gene action for bundle strength and showed non-additive type of gene action. Bertini et al. (2001), Singh and Chahal (2005), and Minhas et al. (2008) showed the additive, dominant and epistatic effects for fiber strength. Several findings have been given for the existence of additive and partial dominance for fiber fineness

(Mukhtar et al., 2000b; Singh and Chahal 2005; Minhas et al., 2008; Akhtar et al., 2008), that is much more important parameter for the textile industry.

For hybridization program, there is a need of the information about gene action and combining ability for selection of suitable parents. Therefore, this work was carried out for understanding the inheritance pattern of gene action and combining ability in the existing cotton germplasm yield and fiber quality parameters under drought.

Materials and methods

The present study was carried out in the field at Central Cotton Research Institute, Multan. Germplasm used herein was collected from Central Cotton Research Institute, Multan. Parental material comprise of five drought tolerant (MPS-11, BH-176, DPL-45, CYTO-62 and Tree Cotton) and three drought susceptible (MS-64, GS-444 and COOKER-315) accessions which were planted in glasshouse during offseason 2014-2015. The plants were self pollinated by covering the unopened flowers to maintain genetic purity of the studied cultivars. Selected accessions were mated in the line \times tester mating design. All accessions including parents and their half sibs were planted in drought as well as irrigated (control) regimes in triplicate arrangement under split plot in a randomized complete block design during the cotton cropping season 2015–2016. Irrigations were assign to the main plots while plant materials was in the sub plot. Irrigations in the stressed regimes was withheld at the reproductive stage to have lower soil moisture contents through out reproductive phase. Seeds were manually dibbled to 30 cm plant to plant distance and row to row spacing was 75 cm. Each genotype was sown in single row of 10 plants. All crop husbandry practices were applied as per requirement. Insecticides were sprayed to keep the insect pressure below the threshold level. Data on morphological traits in the field as well as in laboratory conditions were collected on five plants from each family. The traits were: number of bolls plant⁻¹, plant height (cm), average boll weight (g), seed index, seed cotton yield plant⁻¹, ginning out turn (%) and other fiber characteristics.

Plant height (PH) in centimeter was determined at the time physiological maturity with measuring tape from the cotyledonary node to the apical meristem. Measurements were determined on ten guarded plants per line. The number of bolls plant⁻¹ (NBP) were counted manually in each tagged plant. Number of the bolls plant⁻¹ was mean of 5 plants. The average boll weight (g) (BW) was determined by dividing the total number of bolls plant⁻¹ to the total seed cotton yield obtained from single plant. Seed cotton yield (SCY) was sum of yield (g) obtained from each picking being done in three week time at regular interval. Each picking was done manually and put in Kraft paper bag. Lint was removed from the seed cotton samples on small lab scale ginning machine. The seed index (SI) refers to the mass of 100-seeds which were randomly drawn from the seed

lots. 100 seeds were counted and mass was determined on weighing balance. Ginning out-turn (lint %) (GOT) was defined as the mass of the lint obtained from each plants after ginning to the total mass of the seed cotton and is expressed as percentage. Each sample of seed cotton collected from single plant was ginned separately and weighed. Lint weighed values were used for determination of GOT percentage by using below formula:

$$GOT\% = \frac{\text{Weight of lint in a sample}}{\text{Weight of seed cotton in a sample}} \times 100$$

Table 1. Analyses of variance for traits such as plant height (PH), number of bolls plant⁻¹ (NB), boll weight (BW), seed cotton yield (SCY), and seed index (SI) of 15 crosses and 8 parents under irrigation

| Source of variation | DF | Mean sun of square | | | | |
|---------------------|----|--------------------|-----------|---------|-----------|---------|
| | | PH † | NB | BW | SCY | SI |
| Replications | 2 | 76.188ns | 3.145ns | 0.005ns | 5.84ns | 0.039ns |
| Treatments | 22 | 254.149** | 72.179** | 0.049** | 655.15** | 1.152** |
| Parent (P) | 7 | 305.185** | 137.786** | 0.037** | 1337.63** | 1.592ns |
| P × C | 1 | 37.739ns | 70.864** | 0.066** | 1038.10** | 0.001** |
| Crosses (C) | 14 | 244.089** | 39.470** | 0.054** | 286.55** | 1.015** |
| Lines (L) | 2 | 467.756** | 11.022* | 0.015ns | 45.44* | 0.602** |
| Testers (T) | 4 | 356.922** | 111.033** | 0.070** | 691.29** | 2.143** |
| L × T | 8 | 131.756 | 10.800 | 0.055 | 144.46 | 0.555 |
| Error | 44 | 63.052 | 2.493 | 0.001 | 9.50 | 0.084 |

Table 2. Analyses of variance for traits such as ginning out turn (GOT), Fiber length (FL), fiber strength (FS), Fiber fineness (FF) of 15 crosses and 8 parents under irrigation

| Source of variation | DF | Mean sun of square | | | |
|---------------------|----|--------------------|---------|----------|---------|
| | | GOT | FL | FS | FF |
| Replications | 2 | 0.446ns | 0.033ns | 0.503ns | 0.051ns |
| Treatments | 22 | 5.241** | 1.304** | 18.144** | 0.115** |
| Parent (P) | 7 | 4.750** | 1.021** | 26.239** | 0.059ns |
| P × C | 1 | 3.436** | 1.020* | 0.725ns | 0.151* |
| Crosses (C) | 14 | 5.616** | 1.466** | 15.342** | 0.140** |
| Lines (L) | 2 | 4.157** | 3.449** | 22.174** | 0.040ns |
| Testers (T) | 4 | 9.301** | 2.368** | 28.979** | 0.294** |
| L × T | 8 | 4.138 | 0.519 | 6.815 | 0.089 |
| Error | 44 | 0.433 | 0.186 | 0.301 | 0.037 |

Table 3. Analyses of variance for traits such as plant height (PH), number of bolls plant⁻¹ (NB), boll weight (BW), seed cotton yield (SCY), and seed index (SI) of 15 crosses and 8 parents under water stress

| Source of variation | DF | Mean sum of square | | | | |
|---------------------|----|--------------------|-----------|------------|-----------|-----------|
| | | PH † | NB | BW | SCY | SI |
| Replications | 2 | 66.623ns | 3.522ns | 0.004ns | 5.366ns | 0.221ns |
| Treatments | 22 | 202.899** | 51.524** | 0.076** | 360.637** | 0.815** |
| Parent (P) | 7 | 203.756** | 111.214** | 0.107** | 721.385** | 0.954** |
| P × C | 1 | 75.565ns | 3.170ns | 0.007ns | 918.800** | 4.569** |
| Crosses (C) | 14 | 211.565** | 25.133** | 0.065** | 140.394** | 0.477** |
| Lines (L) | 2 | 408.289** | 8.467ns | 0.019ns | 59.714** | 0.360** |
| Testers (T) | 4 | 254.089** | 30.744** | 0.107328** | 132.489** | 0.01778ns |
| L × T | 8 | 141.122 | 26.494 | 0.054434 | 164.517 | 0.73578 |
| Error | 44 | 63.052 | 2.493 | 0.001 | 9.50 | 0.084 |

Table 4. Analyses of variance for traits such as ginning out turn (GOT), Fiber length (FL), fiber strength (FS), Fiber fineness (FF) of 15 crosses and 8 parents under water stress

| Source of variation | DF | Mean sum of square | | | |
|---------------------|----|--------------------|-----------|-----------|-----------|
| | | GOT | FL | FS | FF |
| Replications | 2 | 0.345ns | 0.293ns | 1.368ns | 0.062ns |
| Treatments | 22 | 2.506** | 1.093** | 6.959** | 0.308** |
| Parent (P) | 7 | 2.287** | 0.440* | 6.588** | 0.328** |
| P × C | 1 | 23.031** | 0.238ns | 0.269ns | 0.231** |
| Crosses (C) | 14 | 1.149** | 1.480** | 7.622** | 0.305** |
| Lines (L) | 2 | 3.308ns | 0.186ns | 6.106** | 1.542** |
| Testers (T) | 4 | 0.8081ns | 1.28089** | 14.6758** | 0.22689ns |
| L × T | 8 | 0.7803 | 1.90322 | 4.4744 | 0.03406 |
| Error | 44 | 0.433 | 0.186 | 0.301 | 0.037 |

** , * and ns indicate significant at either $P < 0.01$ or $P \leq 0.05$, and non-significant ($P > 0.05$)

Traits related to fiber quality traits such as staple length (SL), staple strength (SS) and staple fineness (SF) were estimated on (HVI-900 high volume instrument, Switzerland). HVI-900 is used for determination of various fiber quality traits such as length, fineness and strength as per International Standards.

The data taken on the above characteristics from each treatment (controlled and stressed) were subjected for analysis following Steel et al. (1997) Later on, data were subjected to line \times tester analysis (Kemphorne, 1957) to assess the genetic variances..

Results

Genetic analysis of agronomic and fiber traits under normal water conditions:

All traits revealed highly significant ($P \leq 0.01$) differences due to treatments (Table 1-2). However, differences among the parents and interaction L \times T was insignificant for seed index (Table 1). Moreover, differences among testers and interaction L \times T was insignificant for fiber fineness (Table 2). In crosses, regarding to parents all traits were highly significant ($P \leq 0.01$). The interaction of parents \times crosses which signifies the hybrid vigor or heterosis, was highly significant ($P \leq 0.01$) for all traits except PH and SS which was insignificant ($P \geq 0.05$) for these two traits. SL and SF were significant ($P \leq 0.05$) for parents \times crosses interactions. Analysis of variances for parental female accessions was also highly significant for all traits except BW and SF, which showed non-significance differences while SCY and NBP, which were significant ($P \leq 0.05$). Male lines i.e. tester was also highly significant for all traits. For interaction of lines \times tester which signifies non additive genes, was highly significant ($P \leq 0.01$) for all traits except PH which was non-significant ($P \geq 0.05$) while SL and SF were significant ($P \leq 0.05$).

Genetic analysis of agronomic and fiber traits under drought condition

Water stress condition (Table 3-4) showed that all factors were highly significant under water stress treatments. Parental accessions revealed highly significant ($P \leq 0.01$) differences except SL, which was significant ($P \leq 0.05$). Moreover, half sib progenies i.e. cross combinations were also highly significant for all traits. All traits were highly significant ($P \leq 0.01$) except PH, NBP, BW for parents \times crosses, while SL and SS exhibited insignificant differences ($P \geq 0.05$). Moreover, female lines also exhibited highly significant differences for all traits except NBP, BW, GOT and SL, which were exhibiting non-significant results. There was also highly significant differences for all traits in case of male lines except for SF which showed had in-significant differences

among the male lines. Interaction of lines \times tester was also highly significant except SF which was insignificant. The GOT had significant ($P \leq 0.05$) interaction for lines \times tester.

Estimation of genetic components under irrigation

Table 5 show the combining ability as well as gene actions for fiber traits along with agronomic traits under normal condition. Our results showed preponderance of non additive gene action or higher magnitude of specific combining ability for all the agronomic and fiber traits including PH, NBP, BW, SI, SCY and GOT%, SL, SS and SF under irrigated regime. The specific combining ability variance values for seed cotton yield (44.98) and plant height (22.90) were observed. Ratio for the GCA to SCA was lesser than unity while ratio SCA to GCA was more than 1 for all observed traits. These ratios show non additive gene action such as indicated more dominant types of gene action. The SCY and PH had the highest values for both additive and dominance type of gene action. SCY had (13.54) and (44.98), while PH (9.74) and (22.90) had values of variances for GCA and SCA respectively. The σ^2_D / σ^2_A was lesser than unity for all traits under study which showed that absence of of dominance type of gene action while the values for σ^2_A / σ^2_D variance was higher than unity which showed additive type of gene action under water stress

Table 5. Genetic variances for agronomic (Plant height (PH); Number of Bolls (NB), Boll weigh (BW), Seed Cotton Yield (SCY), Seed index (SI), Ginning out turn (GOT) and fiber traits Fiber length (FL), Fiber strength (FS), Fiber Fineness (FF) under normal irrigation

| Description | PH † | NB | BW | SCY | SI | GOT | FL | FS | FF |
|-----------------------------------|-------------|-----------|-----------|------------|-----------|------------|-----------|-----------|-----------|
| σ^2_{GCA} | 4.873 | 1.29 | 0.001 | 6.769 | 0.02 | 0.076 | 0.03 | 0.37 | 0.00 |
| | | 4 | | | 2 | | 9 | 5 | 3 |
| σ^2_{SCA} | 22.90 | 2.76 | 0.015 | 44.98 | 0.15 | 1.235 | 0.11 | 2.17 | 0.01 |
| | 1 | 9 | | 8 | 7 | | 1 | 1 | 7 |
| $\sigma^2_{GCA} / \sigma^2_{SCA}$ | 0.213 | 0.46 | 0.007 | 0.150 | 0.13 | 0.061 | 0.35 | 0.17 | 0.15 |
| | | 7 | | | 8 | | 5 | 3 | 1 |
| $\sigma^2_{SCA} / \sigma^2_{GCA}$ | 4.700 | 2.14 | 150.00 | 6.646 | 7.23 | 16.31 | 2.82 | 5.79 | 6.61 |
| | | 0 | 0 | | 0 | 4 | 0 | 6 | 5 |
| $\sigma^2_A (F=1)$ | 9.745 | 2.58 | 0.001 | 13.53 | 0.04 | 0.151 | 0.07 | 0.74 | 0.00 |
| | | 8 | | 8 | 3 | | 9 | 9 | 5 |
| $\sigma^2_D (F=1)$ | 22.90 | 2.76 | 0.015 | 44.98 | 0.15 | 1.235 | 0.11 | 2.17 | 0.01 |
| | 1 | 9 | | 8 | 7 | | 1 | 1 | 7 |
| $\sigma^2_D / \sigma^2_A (F=1)$ | 0.426 | 0.93 | 0.020 | 0.301 | 0.27 | 0.123 | 0.71 | 0.34 | 0.30 |
| | | 5 | | | 7 | | 0 | 5 | 2 |

| | | | | | | | | | |
|------------------------------------|-------|-----------|--------|-------|-----------|-------|-----------|-----------|-----------|
| σ^2_A / σ^2_D (F=1) | 2.350 | 1.07 0 | 50.000 | 3.323 | 3.61 5 | 8.152 | 1.40 8 | 2.89 8 | 3.30 8 |
|------------------------------------|-------|-----------|--------|-------|-----------|-------|-----------|-----------|-----------|

Estimation of genetic components under drought

Table 6 shows the combining ability as well as gene actions for fiber traits along with agronomic traits under normal condition. Results revealed higher magnitude of specific combining ability than general combining ability for all yield and quality traits, which indicated dominance variances associated with traits under irrigated regime for this particular set of plant material. The highest specific combining ability variance was shown by SCY and PH. The values of specific combining ability for SCY and PH was 51 and 36 respectively. Ratio of the GCA/SCA values was lesser than unity for all the traits while the SCA/GCA was greater than unity for traits such as NBP, BW, PH and GOT% which indicated that non additive gene action was more important than additive gene action. The PH had the highest values of additive (6.26) and dominant (35.96) type of gene action in non irrigated regime. The σ^2_D / σ^2_A was lesser than unity for all the traits related to yield and fiber quality, hence showing additive gene action under water stress regime. The values for σ^2_A / σ^2_D for the traits i.e. BW (10.46), NBP (128.59), SL (4.40) and PH (5.74) were higher than unity, hence depicting additive gene action under water stress regime.

Table 6. Genetic variances for agronomic traits i.e. Plant height (PH); Number of Bolls (NB), Boll weigh (BW), Seed Cotton Yield (SCY), Seed index (SI), Ginning out turn (GOT) and fiber traits Fiber length (FL), Fiber strength (FS), Fiber Fineness (FF) under water stress

| Description | PH † | NB | BW | SCY | SI | GOT | FL | FS | FF |
|------------------------------------|-------|--------|--------|------------|------------|------|------------|-------|-----------|
| σ^2_{GCA} | 3.13 | 0.03 | 0.001 | -0.52 | -0.01 | 0.02 | -0.01 | 0.148 | 0.01 |
| σ^2_{SCA} | 35.96 | 7.59 | 0.014 | 51.38 | 0.22 | 0.09 | 0.57 | 1.305 | - 0.01 |
| $\sigma^2_{GCA} / \sigma^2_{SCA}$ | 0.09 | 0.00 | 0.044 | -0.01 | -0.04 | 0.17 | -0.02 | 0.114 | - 1.80 |
| $\sigma^2_{SCA} / \sigma^2_{GCA}$ | 11.48 | 257.18 | 22.667 | - 99.18 | - 24.20 | 5.87 | - 48.44 | 8.802 | - 0.55 |
| σ^2_A (F=1) | 6.26 | 0.06 | 0.001 | -1.04 | -0.02 | 0.03 | - 0.023 | 0.296 | 0.02 |
| σ^2_D (F=1) | 35.96 | 7.59 | 0.014 | 51.38 | 0.22 | 0.09 | 0.57 | 1.305 | - 0.01 |
| σ^2_D / σ^2_A (F=1) | 0.17 | 0.01 | 0.096 | -0.02 | -0.08 | 0.34 | -0.04 | 0.227 | - 3.63 |

| | | | | | | | | | |
|------------------------------------|------|--------|-------|------------|------------|------|------------|-------|-----------|
| σ^2_A / σ^2_D (F=1) | 5.74 | 128.59 | 10.46 | - 49.54 | - 12.10 | 2.94 | - 24.22 | 4.400 | - 0.28 |
|------------------------------------|------|--------|-------|------------|------------|------|------------|-------|-----------|

General combining ability under irrigation

Table 6 shows the general combining ability for agronomic traits under normal condition. GS-444 a parental accessions, showed a positive General CA for traits such as SL, SS, FF, SI, SCY and BW under irrigated regime. However, the same accession showed negative GCA effects for plant height and GOT% under irrigated regime. The accession MS-64 was positive general combiner for traits i.e. SL and SI under irrigated regime. The same accession showed a positive GCA effect for GOT%, PH, SF and MBP under irrigated regime. The accession MS-64 has negative GCA for SS and SCY under irrigated regime. Accession COOKER-315 had positive general combining ability effects for the traits like GOT%, BW and PH under irrigated regime. The breeding line showed negative GCA effects for remaining traits under irrigated regime.

Male line Cyto-62 was positive general combiner for SL, SS, SF and SI under irrigated regime while it was negative combiner for all other traits under study. Male tester "Tree cotton" showed positive general combining ability for SS under irrigated regime while it showed negative GCA effects for rest of traits. Positive General CA was shown by DPL-45 (tester) regarding traits such as GOT%, SS, PH, NBP, BW and SCY, while general CA for rest of the traits was negative. BH-176 (tester) showed positive general CA effects for SI while all other showed negative effects under irrigated regimes.

General combining ability under drought: The values of general combining ability for agronomical traits are shown in Table 8. Female accession, GS-444 had a positive general combining ability effects for staple strength, length, fineness, seed cotton yield, seed index and boll weight under water stress condition. However accession, GS-444 had negative GCA effects for PH and NBP under water stress condition. The female line MS-64 was positive general combiner for SL and SI under water stress condition. It showed a positive GCA effect for SF and NBP under water stress condition. Accession MS-64 was also positive general combiner for traits i.e. GOT%, BW and PH. The line MS-64 has negative general combining ability effects for SS and SCY under irrigated regime. Accession "COOKER-315" was positive general combiner for the traits like SCY and NBP under water stress conditions.

The male tester "Cyto-62" was positive general combiner for GOT%, NBP, BW, SCY, SL, SS, SF and SI under water stress conditions. The accession was negative general combiner for rest of the traits under study. The male tester "Tree cotton" was positive general combiner for SF, SI, BW and PH while the same accession had negative GCA for remaining traits under non-irrigated regime. "DPL-45" which was exploited as male

tester showed positive GCA for GOT%, SCY, BW and PH while it showed negative GCA effects for other traits under non irrigated regimes. The male line used as tester i.e. BH-176 had positive values for GOT% and SI while it was negative combiner for rest of traits. Male accessions “MPS-11” showed positive GCA effects for SF, PH, NBP and SCY.

Table 7. Estimation of GCA effects and their standard errors (SE) for agronomic i.e. Plant height (PH); Number of Bolls (NB), Boll weigh (BW), Seed Cotton Yield (SCY), Seed index (SI), Ginning out turn (GOT) and fiber traits Fiber length (FL), Fiber strength (FS), Fiber Fineness (FF) in lines and tester under irrigation

| Hybrids | Genotypes | PH [†] | NB | BW | SCY | SI | GOT | FL | FS | FF |
|-------------------------|-------------|-----------------|--------|-------|-------|-------|-------|-------|-------|-------|
| GCA for lines | GS-444 | -5.31 | 0.62 | 0.01 | 2.00 | 0.08 | -0.44 | 0.322 | 1.38 | 0.03 |
| | MS-64 | -0.51 | 0.356 | -0.04 | -0.81 | 0.14 | -0.15 | 0.23 | -0.47 | 0.03 |
| | COOKER-315 | 5.82 | -0.978 | 0.03 | -1.19 | -0.23 | 0.59 | -0.55 | -0.91 | -0.06 |
| SE _{GCA} lines | | 0.05 | 0.41 | 0.03 | 0.80 | 0.08 | 0.17 | 0.11 | 0.14 | 0.05 |
| SE _{gij} lines | | 3.74 | 0.74 | 0.05 | 1.45 | 0.14 | 0.31 | 0.20 | 0.26 | 0.09 |
| GCA for testers | Cyto-62 | -3.96 | -2.60 | -0.09 | -6.50 | 0.73 | -0.40 | 0.23 | 0.16 | 0.21 |
| | Tree Cotton | -7.96 | -2.71 | -0.03 | -7.02 | -0.59 | -0.87 | -0.63 | 0.81 | -0.15 |
| | DPL-45 | 7.71 | 3.96 | 0.14 | 12.03 | -0.19 | 0.31 | -0.05 | 0.78 | -0.15 |
| | BH-176 | -0.29 | -2.38 | -0.06 | -5.20 | 0.15 | -0.67 | -0.27 | -2.47 | -0.10 |
| | MPS-11 | 4.49 | 3.73 | 0.04 | 6.65 | -0.09 | 1.64 | 0.73 | 2.34 | 0.17 |

| | | | | | | | | | |
|-----------------------------------|----------|------|----------|------|----------|------|------|----------|----------|
| SE_{GCA} testers | 2.6 4 | 0.53 | 0.0 3 | 1.03 | 0.1 0 | 0.22 | 0.14 | 0.1 8 | 0.0 6 |
| SE_{gi ji} testers | 2.9 0 | 0.58 | 0.0 4 | 1.13 | 0.1 1 | 0.24 | 0.16 | 0.2 0 | 0.0 7 |

Table 8. Estimation of GCA effects and their standard errors (SE) for agronomic i.e. Plant height (PH); Number of Bolls (NB), Boll weigh (BW), Seed Cotton Yield (SCY), Seed index (SI), Ginning out turn (GOT) and fiber traits Fiber length (FL), Fiber strength (FS), Fiber Fineness (FF) traits in lines and tester under water stress

| Hybrids | Genotypes | PH † | NB | BW | SCY | SI | GOT | FL | FS | FF |
|-----------------------------------|----------------|-----------|-----------|-----------|-----------|-----------|-------|-----------|-----------|-----------|
| GCA for lines | GS-444 | - 4.96 | - 0.40 | 0.03 | 1.61 | 0.06 | 0.02 | 0.10 | 0.68 | 0.33 |
| | MS-64 | 5.44 | - 0.47 | 0.01 | - 2.23 | 0.12 | 0.46 | 0.02 | - 0.09 | - 0.02 |
| | COOKER- 315 | - 0.49 | 0.87 | - 0.04 | 0.63 | - 0.18 | -0.48 | - 0.12 | - 0.59 | - 0.31 |
| SE_{GCA} lines | | 1.49 | 0.50 | 0.0 | 0.83 | 0.07 | 0.19 | 0.12 | 0.19 | 0.19 |
| SE_{gi ji} lines | | 2.72 | 0.91 | 0.06 | 1.52 | 0.13 | 0.34 | 0.21 | 0.35 | 0.35 |
| GCA for testers | Cyto-62 | - 3.93 | 0.36 | 0.09 | 1.41 | 0.06 | 0.31 | 0.47 | 0.55 | 0.05 |
| | Tree Cotton | 0.73 | - 0.76 | 0.01 | - 3.34 | 0.01 | -0.49 | - 0.13 | - 0.68 | 0.02 |
| | DPL-45 | 4.73 | - 0.87 | 0.11 | 0.48 | - 0.06 | 0.03 | - 0.27 | - 0.67 | - 0.22 |
| | BH-176 | - 6.82 | - 1.76 | - 0.06 | - 3.99 | 0.02 | 0.15 | - 0.39 | - 1.19 | - 0.06 |
| | MPS-11 | 5.29 | 3.02 | - 0.15 | 5.44 | - 0.03 | -0.01 | 0.32 | 1.98 | 0.21 |
| SE_{GCA} testers | | 1.92 | 0.64 | 0.04 | 1.07 | 0.10 | 0.24 | 0.15 | 0.25 | 0.08 |
| SE_{gi ji} testers | | 2.11 | 0.71 | 0.04 | 1.18 | 0.10 | 0.26 | 0.16 | 0.27 | 0.08 |

Estimation of SCA under irrigation

Positive SCA effects for plant height were shown by crosses GS-444 × DPL-45, GS-444 × BH-176, MS-64 × DPL-45, COOKER-315 × Cyto-62 and COOKER-315 × DPL-45 (Table 9). For number of bolls, significant and positive SCA effects were found for GS-444 × Cyto-62, GS-444 × DPL-45 and COOKER-315 × Cyto-62. For boll weight GS-444 × Tree Cotton, GS-444 × DPL-45 and COOKER-315 × DPL-45 expressed the best

SCA estimates. For seed cotton yield cross combinations; i.e., GS-444 × Tree Cotton and GS-444 × DPL-45 revealed significant positive SCA values. Positive SCA effects for seed index were shown by crosses GS-444 × DPL-45, GS-444 × BH-176, MS-64 × DPL-45 and MS-64 × BH-176. For GOT%, significant and positive SCA effects were found for GS-444 × Cyto-62, GS-444 × DPL-45, GS-444 × BH-176, MS-64 × Cyto-62 and COOKER-315 × Tree Cotton. For fiber length GS-444 × DPL-45, GS-444 × BH-176, MS-64 × Cyto-62 and MS-64 × BH-176 expressed the best SCA estimates. Crosses such as GS-444 × Tree Cotton, GS-444 × Cyto-62, COOKER-315 × Cyto-62, GS-444 × DPL-45 and COOKER-315 × Tree Cotton showed Positive SCA effects for fiber strength. Fiber fineness also showed significant positive SCA values in combinations such as GS-444 × Cyto-62, GS-444 × BH-176, MS-64 × Cyto-62, COOKER-315 × Cyto-62 and COOKER-315 × Tree Cotton. While negative SCA values were observed for the remaining traits in different combinations.

Specific combining ability under drought

Positive SCA effects for plant height were shown by crosses GS-444 × DPL-45, MS-64 × Cyto-62, GS-444 × MPS-11, MS-64 × MPS-11, MS-64 × Tree Cotton, COOKER-315 × Tree Cotton and COOKER-315 × DPL-45 (Table 10). For number of bolls, significant and positive SCA effects were found for GS-444 × MPS-11, MS-64 × Tree Cotton, COOKER-315 × Tree Cotton, COOKER-315 × Cyto-62, and MS-64 × MPS-11. For boll weight GS-444 × Cyto-62, MS-64 × Cyto-62 and COOKER-315 × Cyto-62 expressed the best SCA estimates. For seed cotton yield cross combinations; i.e., GS-444 × Tree Cotton, GS-444 × DPL-45, GS-444 × MPS-11, MS-64 × MPS-11 and COOKER-315 × Cyto-62 revealed significant positive SCA values. Positive SCA effects for seed index were shown by crosses GS-444 × Cyto-62, GS-444 × DPL-45, GS-444 × MPS-11, MS-64 × Cyto-62, MS-64 × BH-176 and COOKER-315 × Tree Cotton. For GOT%, significant and positive SCA effects were found for GS-444 × Cyto-62, GS-444 × BH-176, MS-64 × Cyto-62, MS-64 × DPL-45 and MS-64 × BH-176. For fiber length GS-444 × Cyto-62, MS-64 × Cyto-62, MS-64 × DPL-45, MS-64 × MPS-11, COOKER-315 × Cyto-62 and COOKER-315 expressed the best SCA estimates. Positive SCA effects for fiber strength were indicated by crosses; i.e., GS-444 × Cyto-62 GS-444 × MPS-11, MS-64 × MPS-11 COOKER-315 × Cyto-62 and COOKER-315 × Tree Cotton. Significant positive SCA values were observed for fiber fineness in the combinations GS-444 × Cyto-62, GS-444 × Tree Cotton, GS-444 × DPL-45, GS-444 × MPS-11, MS-64 × Cyto-62, MS-64 × DPL-45 and MS-64 × BH-176. While negative SCA values were observed for the remaining traits in different combinations.

Table 9. Estimation of specific combining ability (SCA) effects and their standard errors (SE) for agronomic i.e. Plant height (PH); Number of Bolls (NB), Boll weigh (BW), Seed Cotton Yield (SCY), Seed index (SI), Ginning out turn (GOT) and fiber traits Fiber length (FL), Fiber strength (FS), Fiber Fineness (FF) in lines and tester under irrigation

| Cross combinations | PH † | NB | BW | SCY | SI | GOT | FL | FS | FF |
|---------------------------------|-------------|-----------|-----------|------------|-----------|------------|------------|-----------|-----------|
| GS-444 × Cyto-62 | -7.91 | 0.27 | - 0.01 | -3.10 | -0.26 | 0.05 | - 0.200 | 0.82 | 0.29 |
| GS-444 × Tree Cotton | -6.71 | -0.80 | 0.11 | 2.01 | -1.12 | -0.92 | - 0.907 | 0.24 | - 0.54 |
| GS-444 × DPL-45 | 7.62 | 10.87 | 0.34 | 34.02 | 1.12 | 0.10 | 1.01 | 3.48 | - 0.35 |
| GS-444 × BH-176 | 3.42 | -0.62 | - 0.04 | -1.04 | 0.99 | 0.50 | 0.59 | - 1.44 | 0.03 |
| GS-444 × MPS-11 | 10.62 | 5.64 | - 0.02 | 10.44 | 0.70 | 1.63 | 1.15 | 4.04 | 0.29 |
| MS-64 × Cyto-62 | -0.38 | -0.69 | - 0.07 | -2.02 | 2.31 | 0.73 | 1.60 | - 0.29 | 0.28 |
| MS-64 × Tree Cotton | - 14.58 | -6.29 | - 0.23 | - 20.93 | -0.77 | -2.68 | -0.56 | - 2.54 | - 0.01 |
| MS-64 × DPL-45 | 0.62 | -1.69 | - 0.24 | -5.29 | 0.27 | -0.02 | -0.56 | - 0.88 | - 0.01 |
| MS-64 × BH-176 | - 16.38 | -3.69 | - 0.21 | - 16.51 | 0.44 | -1.19 | 0.38 | - 3.71 | 0.22 |
| MS-64 × MPS-11 | 12.76 | 7.71 | 0.22 | 15.96 | -0.35 | 2.87 | 1.567 | 5.52 | 0.38 |
| COOKER-315 × Cyto-62 | 8.62 | 0.31 | - 0.01 | 4.29 | -0.14 | -0.05 | -0.04 | 3.07 | 0.11 |
| COOKER-315 × Tree Cotton | -6.04 | -0.02 | 0.05 | -2.52 | -0.57 | 1.76 | -0.33 | 1.39 | 0.14 |
| COOKER-315 × DPL-45- | 6.64 | -0.40 | 0.22 | -4.85 | -0.17 | -0.70 | -1.50 | - 3.53 | - 0.32 |
| COOKER-315 × BH-176 | 7.84 | -7.80 | - 0.07 | -9.58 | -0.10 | -2.39 | -1.84 | - 4.57 | - 0.42 |
| COOKER-315 × MPS-11 | -6.16 | -0.80 | - 0.04 | -0.93 | -0.09 | 0.31 | -0.36 | - 1.60 | - 0.08 |

| | | | | | | | | | |
|--------------------------|------|------|------|------|-------|-------|------|------|------|
| SE for SCA effect | 4.59 | 0.91 | 0.06 | 1.78 | 0.167 | 0.381 | 0.25 | 0.32 | 0.11 |
|--------------------------|------|------|------|------|-------|-------|------|------|------|

Table 10. Estimation of specific combining ability (SCA) effects and their standard errors (SE) for agronomic i.e. Plant height (PH); Number of Bolls (NB), Boll weigh (BW), Seed Cotton Yield (SCY), Seed index (SI), Ginning out turn (GOT) and fiber traits Fiber length (FL), Fiber strength (FS), Fiber Fineness (FF) in lines and tester under water stress

| Cross combinations | PH † | NB | BW | SCY | SI | GOT | FL | FS | FF |
|---------------------------------|-------------|-----------|-----------|------------|-----------|------------|-----------|-----------|-----------|
| GS-444 × Cyto-62 | -1.27 | - 0.16 | 0.01 | -7.13 | 0.30 | 0.12 | 0.533 | 0.733 | 0.11 |
| GS-444 × Tree Cotton | - 11.00 | - 1.76 | - 0.01 | 0.48 | - 0.20 | -0.23 | -0.25 | -0.30 | 0.23 |
| GS-444 × DPL-45 | 4.93 | - 1.76 | - 0.07 | 3.68 | 0.36 | -0.13 | -0.58 | -0.53 | 0.22 |
| GS-444 × BH-176 | - 11.93 | - 5.04 | - 0.05 | -5.05 | - 0.79 | 0.85 | -0.23 | -0.28 | 0.00 |
| GS-444 × MPS-11 | 4.33 | 8.02 | - 0.06 | 19.12 | 0.25 | 0.04 | -0.25 | 2.86 | 0.59 |
| MS-64 × Cyto-62 | 4.60 | - 1.31 | 0.05 | -0.60 | 0.61 | 2.44 | -0.25 | 0.29 | 0.28 |
| MS-64 × Tree Cotton | 4.73 | 0.40 | - 0.05 | -8.30 | - 0.06 | - 0.210 | -0.42 | -1.08 | - 0.05 |
| MS-64 × DPL-45 | -5.33 | - 1.87 | - 0.07 | -4.99 | - 0.32 | 0.31 | 0.32 | -0.14 | 0.10 |
| MS-64 × BH-176 | -1.07 | 2.13 | - 0.04 | -4.72 | 0.88 | 0.55 | -0.24 | -0.31 | 0.39 |
| MS-64 × MPS-11 | 21.62 | 2.96 | - 0.13 | 11.10 | - 0.27 | -0.08 | 2.03 | 4.58 | - 0.14 |
| COOKER-315 × Cyto-62 | -5.11 | 4.69 | 0.16 | 17.88 | - 0.83 | -1.60 | 1.18 | 1.94 | - 0.26 |
| COOKER-315 × Tree Cotton | 14.49 | 1.36 | - 0.04 | -0.28 | 0.26 | -0.51 | 0.49 | 0.67 | 0.13 |
| COOKER-315 × DPL-45- | 8.51 | - 1.49 | 0.43 | -4.60 | - 0.18 | -0.42 | -1.08 | -3.19 | - 1.02 |

Discussion

Natural or induced selection are the two main pre-requisites for cotton variety development against water stress. Firstly, the existence of genetic variations for certain characters and secondly, these variations must be controlled genetically. Now, hard work is being done to develop genetic population up to the maturity of the plants. Whole plant data against drought in the previous studies are not available in *G. hirsutum* (Khalid et al., 2010). Keeping in view, five upland cotton genotypes (MPS-11, BH-176, DPL-45, CYTO-62 and Tree Cotton) were screened as drought tolerant and In contrast, three genotypes (GS-444, MS-64 and COOKER-315) were identified as sensitive to drought. When the data were analyzed genetically for various traits showed the function of genetic components under irrigation and drought. All the agronomic and fiber traits including plan height(PH), boll weight(BW), number of bolls, seed index(SI), seed cotton yield, GOT%, staple strength(SS), staple length(SL), fiber fineness(FF) showed higher values of specific CA than general CA under normal condition. Plant height(PH) and seed cotton yield showed the highest specific CA under normal condition. Same was the result for all the traits except (FF)fiber fineness under drought condition which showed non-additive type of gene action. The finding of Javid et al. (2014) coincide with present results, whilst Karademir et al. (2009) showed additive type of gene action for fiber length and fiber fineness. So, this result agree with present findings in case of fiber finenes.

Moreover, plant breeders must have known how about genetic variations of parents and combinations in Varity development through introgression for drought tolerance in field crops as explained by Singh and Narayanam (2000). Previous reports indicated non-additive type of gene action in cotton for these parameters under drought tolerance (Shakoor et al., 2010 and Sarwar et al., 2012). Comparison of GCA for eight parents (three lines and five testers) showed that lines namely MS-64, GS-444, and COOKER-315 and testers (BH-176,MPS-11,DPL-45, CYTO-62 and Tree Cotton) were the best in general combiners for most of the parameters. This material must be used for the improvement in drought tolerance with high yield in upland cotton. Amongst the different combinations, MS-64 × MPS-11 showed best results for plant height, fiber length and fiber strength (Roy et al., 2002).by virtue of high GCA estimates. Cross of GS-444 × MPS-11 was best for number of bolls, seed cotton yield and fiber fineness due to the involvement of MPS-11 having good GCA but GS-444 had poor and negative GCA. For boll weight, seed index and ginning out turn %, crosses COOKER-315 × DPL-45, MS-64 × BH-176 and MS-64 × Cyto-62revealed good presentation due to good general combining ability of DPL-45and MS-64. Specific CA showed dominant gene action and it is limited for selection of best parents for some of characters (Franco et al., 2001). Therefore, both general CA and specific CA effects are important. The

involvement of one of parent with maximum GCA would enhance favorable alleles occurrence. Most of pairing having good SCA possessions is by virtue of good GCA of the parents, showed additive genetic effects prevalence (Kenga et al., 2004). Higher SCA property of parents under crossing with low GCA indicated non-additive genetic effects, and appeal to the researcher to delay early generation selection (Saidaiah et al., 2010). Reverse the situation with having significant SCA because it helps early generation selection (Roy et al., 2002). Variations in genetic pairing as well as environmental factors contributed towards fluctuating performance of parents and hybrids (Pettersen et al., 2006). The non-additive type of gene action was observed and this further indicates that this plant material may be considered for hybrids development (Vaghela et al., 2016).

Conclusion

The information obtained on the basis of data analyzing by the use of different biometrical approaches, from these observations it is the message for breeders for the selection of wanted parameters must not be executed up to later generations. These findings are restricted for plant material under trial and thus, may not be comprehensive most of the area under cotton cultivation undergo severe water shortage. Therefore, this knowledge should be substantiated by another trial which may comprise of reasonable cotton genotypes, conducted under various environmental conditions in order to boost adaptability of our presented commercial cotton varieties under stress and build up improved drought tolerance plant material.

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